Functional Characterisation of Small Signalling Peptides and a Receptor Kinase Involved in Root Architecture Development in *Arabidopsis* and Crop Species

Nathan Czyzewicz, MRes, BSc (Hons)

Thesis submitted to the University of Nottingham for the degree of Doctor of Philosophy

30 SEPTEMBER 2016

Acknowledgements:

I would like to acknowledge my supervisors Ive De Smet and Martin Broadley, as well as Malcolm Bennett, Darren Wells, and Ute Voβ for their guidance and support throughout my PhD.

Thanks to the BBSRC and Bayer CropScience for co-funding this project, with gratitude to Younousse Saidi for organising my visit and activities for my industrial placement.

Special thanks also to Steph Smith, Leanne Williams, Brigitte Van De Cotte, Elisabeth Stes, Lam Dai Vu, Natalia Nikonorova, Jonathan Atkinson, Susan Zappala, Evan Murphy and Priya Ramakrishna for their friendship and technical assistance.

Finally, I thank my wife Emma Czyzewicz, my father Steve Czyzewicz, and my friends Nick Adcock, Eva Patzewitz and Jason Irwin for their moral support, indulging my (other) obsessions with BBQ and bikes, and generally helping me to stay sane over the last 4 years.

Contents:

Chapter:	Title:	Page:
	Thesis Abstract	1
Chapter 1	An Introduction to Root Architecture and its Importance to Global Food Security	3
Chapter 2	Message in a bottle: small signalling peptide outputs during growth and development	40
Chapter 3	Modulation of Arabidopsis and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide	57
Chapter 4	The Arabidopsis thaliana CLAVATA3/EMBRYOSURROUNDING REGION 26 (CLE26) peptide is able to alter root architecture of Solanum lycopersicum and Brassica napus	73
Chapter 5	Antagonistic Peptide Technology for the Functional Dissection of CLE Peptides Revisited	79
Chapter 6	CLE26 (Phospho)proteomics Screening Reveals Putative Effectors of CLE26 Signalling	88
Chapter 7	The Growing Story of (ARABIDOPSIS)CRINKLY4	124
Chapter 8	Yeast 2-Hybrid and Co-Immunoprecipitation Reveal Novel Putative ACR4 Interacting Proteins	138
Chapter 9	Materials and Methods	195
Appendix 1	PP2A-3 interacts with ACR4 and regulates formative cell division in the Arabidopsis root	210
Appendix 2	277 Putative ACR4 Interacting Proteins Were Identified by ACR4 Co-immunoprecipitation	217
Appendix 3	List of Plant Lines and Primers Used	224
Appendix 4	Alignment of 9 UNK-like Family Members	226
Appendix 5	Sequences and Annotations of 691 UNK Orthologues	234
Appendix 6	Alignment of UNK and 5 Most Similar Orthologues	351
Appendix 7	Gel Images of Genotyping Analyses	359

Thesis Abstract

Post-embryonic root development is a plastic process by which plants are able to interface with the rhizosphere in order to provide anchorage, and increase surface area available for acquisition of nutrients and water. While root growth is governed primarily by auxin/cytokinin interactions, roots are able to sense the presence of surrounding nutrient deposits and changes to environmental conditions – directing growth accordingly – due to the action of signalling cascades.

This thesis presents data pertaining to the characterisation of two signalling elements involved in governing root architecture; the small signalling peptide CLAVATA/EMBRYO SURROUNDING REGION 26 (CLE26), and the receptor kinase ARABIDOPSIS CRINKLY 4 (ACR4).

Initially, the origins and evolutionary history of root architecture are explored, and an overview of signalling elements involved in root architectural development is provided, before discussing the potential benefits that manipulation of signalling events may allow in targeted crop improvement.

To provide background on peptide signalling, the physiological and biochemical effects of small signalling peptides are discussed in view of the current literature, demonstrating the diverse range of developmental processes which are known to be regulated by these ligands and their known receptors. Following this, functional characterisation analyses indicate CLE26 as a novel, potent inhibitor of primary root growth and protophloem development in *Arabidopsis,* and is also shown to induce a similar effect upon exogenous application to several crop species. Furthermore, data is presented demonstrating the clear requirement for functional analysis during the development phase of creating antagonistic peptides, as a previously described antagonistic peptide technology was not applicable in all cases. Concluding the exploration of CLE26 signalling, a phosphoproteomics screen was conducted to probe further into CLE26

function, determining 23 putative effectors of CLE26 signalling, which are discussed in view of their potential to mediate CLE26 signalling, according to current literature.

Next, the known roles of ACR4 and its orthologues are reviewed, demonstrating the importance of ACR4 signalling in many developmental processes, including regulation of asymmetric cell division during post-embryonic root development. Although ACR4 activity is known to regulate asymmetric cell division in both columella stem cells and lateral root primordia, little is known about the downstream mediators of ACR4 signalling. In an attempt to fill this gap in knowledge, yeast 2-hybrid and co-immunoprecipitation approaches were employed. These two parallel proteomics screens together resulted in identification of 19 putative interactors of ACR4 signalling (PAIPs), which are discussed as potential mediators of ACR4 signalling in view of current literature. Of the identified PAIPs, three were further characterised by loss of function analysis, demonstrating that loss of PHOSPHOLIPASE Iγ2 and a PROTEIN OF UNKNOWN FUNCTION (At1g49840/UNK) was able to affect root architecture. Further *in-silico* characterisation of UNK reveals its similarity to soluble phospholipase receptors, which, alongside PLA-Iγ2, may potentially implicate ACR4 as a key player in a novel mechanism involved in regulation of bioactive lipid production.

Chapter 1: An Introduction to Root Architecture and its Importance to Global Food Security

Author Contribution:

I wrote this chapter and compiled all diagrams except where otherwise noted.

Chapter 1: Introduction

Abstract

Roots are vital to plant development, simultaneously providing a secure anchor, and an interface through which the plant interacts with the rhizosphere. Root architectural development is an adaptable process, allowing the plant to alter nutrient uptake or respond to changing environmental conditions. This chapter reviews the evolutionary history of root architecture, compares root systems in monocot and dicot models, and provides an overview of several elements able to regulate root architectural development. Finally, the potential benefits of targeted improvement of root architecture are discussed.

1.1 Origin of Roots

Plants are sessile organisms, and as such, they are far more limited in resource availability compared to animals. It is therefore imperative that plants are able to efficiently utilise all resources available to them in order to live long enough to reproduce. Early plants consisted of single celled algae and filamentous colonies similar to the phytoplankton present in the oceans today. These early plants were carried by oceanic currents, and thrived in areas of high nutrient availability, but were unable to individually maintain a position in favourable conditions (Raven & Edwards, 2000). The evolution of multi-cellularity allowed for the specialisation of cells to perform specific tasks, and a requirement for this was a corresponding increase in cell-to-cell communication. When plants emerged onto land approximately 470 million years ago (Rubinstein, et al., 2010), one of the primary problems

facing them was the availability of water and nutrients. The earliest terrestrial plants were likely similar in morphology to extant bryophytes (Figure 1), with a root system consisting of rhizoids (Raven & Edwards, 2000). These primitive roots consist of cylindrical or branched extensions of the lower epidermis, which embed into the rhizosphere and allow water and nutrient uptake, but unlike true roots, they lack a root cap and differentiated vascular tissues (Raven & Edwards, 2000).

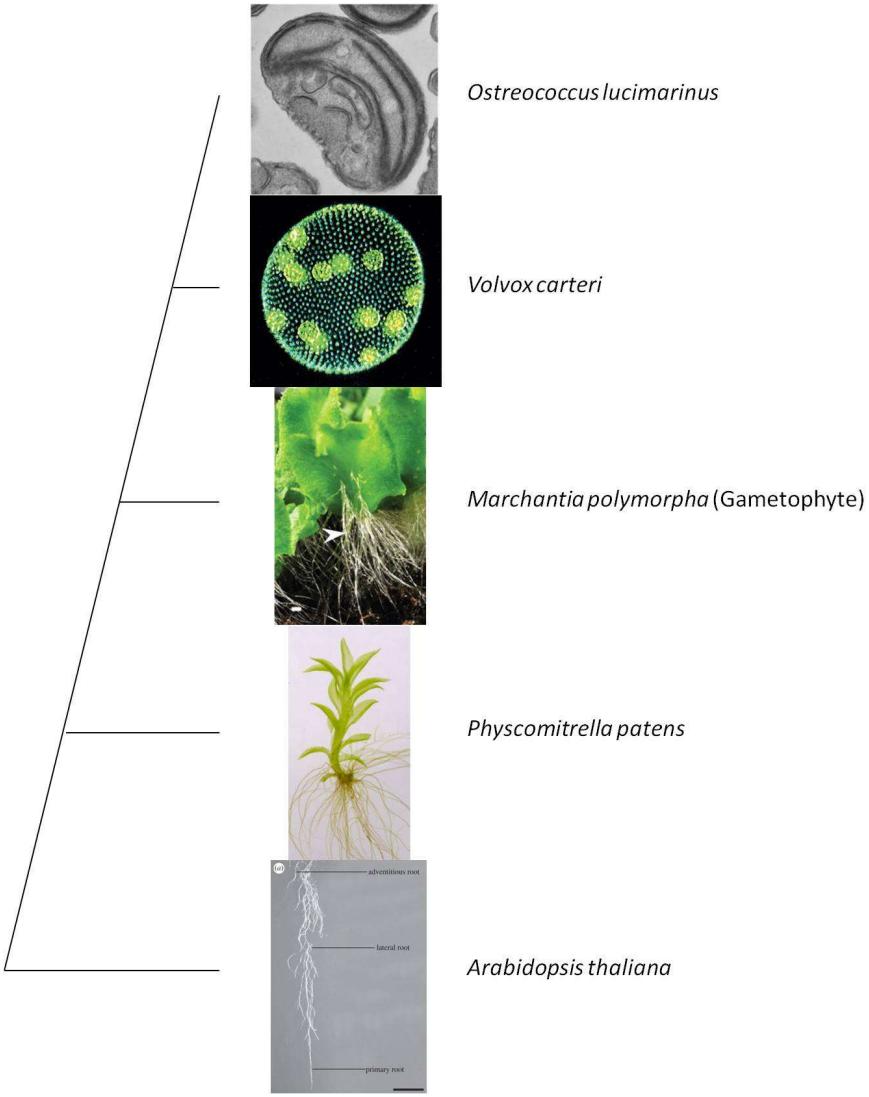


Figure 1: Evolution of multicellularity allowed for the development of specialised tissues - including roots, additionally requiring a corresponding increase in cell-to-cell communication. The picoeukaryote *Ostreococcus lucimarinus* is one of the closest extant relatives to the earliest plants; existing as a unicellular organism containing a single chloroplast and mitochondrion (Lanier, et al., 2008). *Volvox carteri* forms small colonies and reproduces by forming new colonies inside the parent, which then rupture to release the daughter colonies (Schmitt & Sumper, 2003). The *Marchantia polymorpha* gametophyte develops unicellular rhizoids - extrusions of the lower epidermis - which are used for anchorage, as well as mineral and water uptake (Jones & Dolan, 2012). The bryophyte *Physcomitrella patens* also relies on rhizoids for nutrient absorption, but has developed multicellular structures for this purpose (Sakakibara, et al., 2003). The tracheophyte *Arabidopsis thaliana* exhibits a "true" root system, incorporating several layers of specialised tissues to increase efficiency of absorption and transport of minerals and water (Smith & De Smet, 2012). Figure adapted from Lanier et al., (2008), Schmitt & Sumper, (2003), Jones & Dolan, (2012), Sakikabara, et al., (2003), and Smith and De Smet (2012).

Another major change to root architecture occurred in the Early Devonian period, where some species such as *Nothia aphylla* developed tracheids for internal water transport, while true xylem vessel elements were developed by others, such as *Asteroxylon mackiei* (Raven & Edwards, 2000). These adaptations are still found in plants today, with tracheids being the predominant cell type in gymnosperms, and vessel elements are present in angiosperms.

The development of mass flow for water and dissolved minerals is widely believed to have been key to the rise of terrestrial plants, though other adaptations have evolved to maximise efficiency of nutrient uptake.

1.2 Root Architecture – a monocot – dicot comparison

Root architecture can be exceedingly complex, and varies greatly between – and indeed within – species (Figure 2a-b) (Hodge, et al., 2009; Smith & De Smet, 2012). Although the primary and seminal roots in monocot species resemble the *Arabidopsis* primary and lateral roots respectively, and are similarly involved in the initial phase of postembryonic growth; monocot organisms become increasingly reliant upon the adventitious root growth (including crown roots) for anchorage and nutrient uptake as they mature (Atkinson, et al., 2014). Indeed, it has been reported that despite their importance to initial growth, in some cases, the primary and seminal roots do not persist in mature monocots (Hochholdinger, et al., 2004).

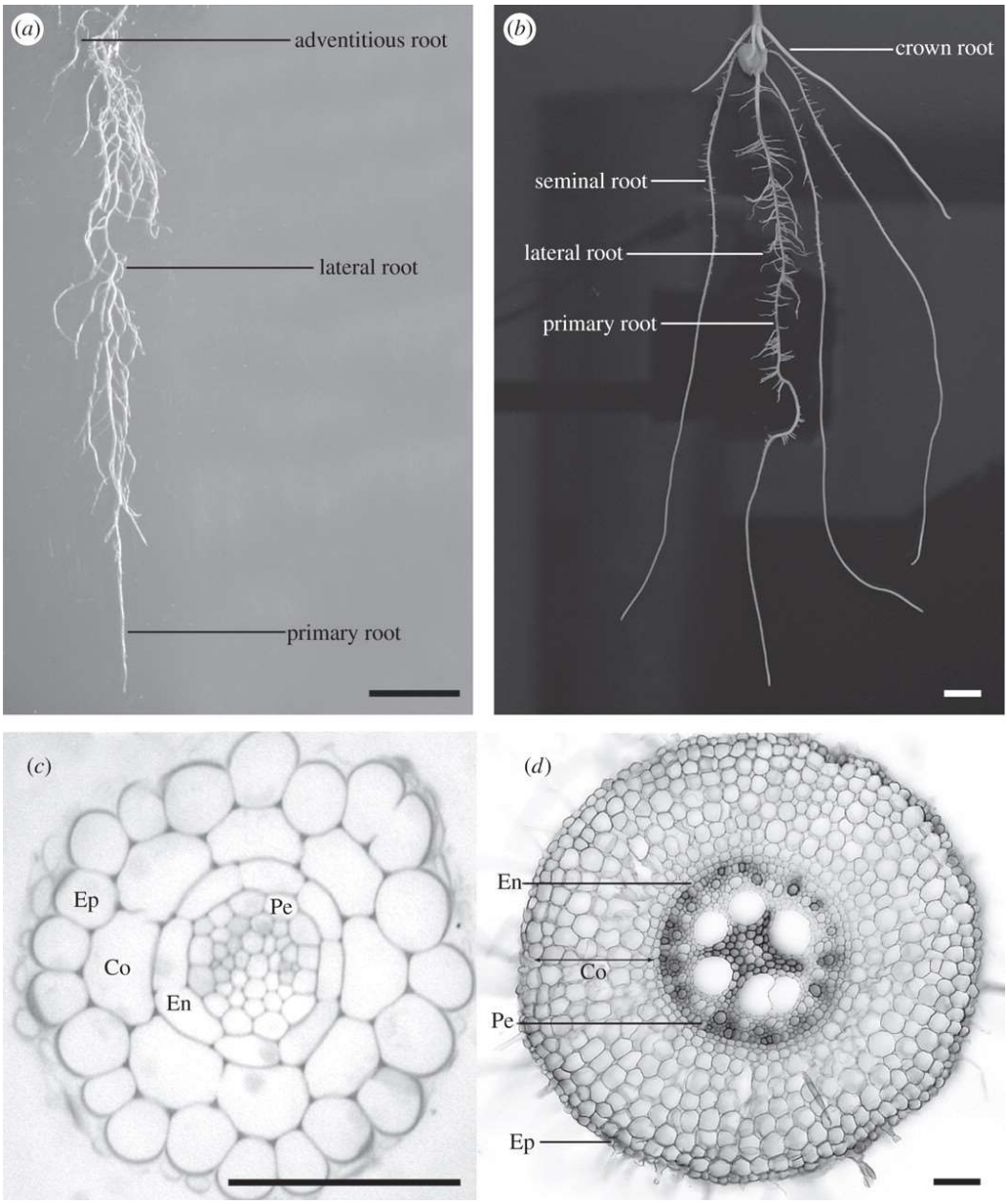


Figure 2: Root architecture varies between species, but all roots contain similar key tissues. A & B - Root architecture of Arabidopsis thaliana (A), and Zea mays (B). C & D - Transverse sections of Arabidopsis thaliana (C) and Zea mays (D) primary roots with tissue types annotated Ep - epidermis, Co - cortex, En - endodermis, Pe - pericycle. (Smith & De Smet, 2012).

In most vascular plants, the primary root consists of a cylindrical bundle of specialised tissues (Figure 2c-d) with a region of multipotent stem cells at the distal apex – the root apical meristem (RAM), which is defined during the earliest stages of embryo development (Benfey & Scheres, 2000; Péret, et al., 2009). It is from the RAM that all primary root tissue is derived,

with several distinct regions of initials present around the central quiescent centre (QC), which divide asymmetrically – sometimes multiple times – to give rise to specialised tissues – columella, lateral root cap, epidermis, cortex, endodermis and stele. Each cell type has a discrete set of functions; columella cells protect the stem cell niche, and contain gravisensing statoliths. Along with the lateral root cap cells, they produce mucilage, lubricating the root tip as it pushes through the rhizosphere. The epidermis provides protection to the tissues underneath, and differentiates further into trichoblasts and atrichoblasts, allowing for extension of root hairs in the former. Cortical cells provide support and structure for the other tissues, as well as starch storage. Mature endodermis contains the casparian strip, which reduces apoplastic loss of water and dissolved minerals from the relatively concentrated internal environment. The stele eventually gives rise to the vascular tissues, the xylem and phloem, allowing for bulk flow transport of minerals and water to the shoot, and transport of sugars and hormones generated by the shoot to the root respectively. In order to exploit new environments, the RAM is pushed through the rhizosphere by a combination of cell division and expansion of the cells laid down on the side proximal to the shoot. As these cells become more distal to the RAM, phytohormones - primarily auxin and cytokinin - initiate signalling cascades which drive the differentiation of tissues in the basal meristem region.

1.3 Control of Root Development

As the complexity of plant life increased from single celled phytoplankton, through algae, bryophytes, and finally to vascular plants, so too did the complexity of the signalling systems required to co-ordinate growth and development. Continued biotechnological analysis has so far revealed that *Arabidopsis* has evolved ~9 phytohormones, >600 putative receptor kinases and >1000 putative secreted peptides to facilitate communication between organelles, cells, and tissues. Many of these signalling molecules are involved in developmental processes, governing the correct deposition of cells and imbuing each cell with an identity, directing development of specialised tissues and organs. The classical phytohormones such as auxins, cytokinins, giberellins and abscisic acid are responsible for most systemic signalling. These phytohormonal signals, and cross talk between them, are able to differentially regulate genes, causing initiation and inhibition of signalling cascades. In addition to phytohormones, there are also other signals including mobile transcription factors, RNA, and peptides which can similarly affect cell identity and development in response to biotic and abiotic stress, though these are generally active over a shorter distance.

Phytohormones

Auxin

Auxin is a key signal in Arabidopsis root development, and is unique among phytohormones as its distribution is facilitated by polar transport. Indole-3-acetic acid (IAA), the major form of auxin, is synthesised in the shoot apical meristem and leaf primordia, and is transported from shoot to root in a carrier mediated fashion facilitated by auxin influx and efflux carriers.

AUXIN1/LIKE AUX1 (AUX1/LAX) family members are the main family of auxin influx carriers and function as auxin/H+ symporters, actively increasing the cellular uptake of IAA by utilising proton-motive force (van Berkel, et al., 2013; Swarup & Péret, 2012). Indeed, the accumulation of intracellular auxin by LAX3 facilitates formation of an auxin sink surrounding lateral root primordia, leading to expression of cell wall remodelling enzymes that contribute to lateral root emergence (Swarup & Péret, 2012).

Conversely, PIN-FORMED (PIN) family members form the major group of IAA efflux carriers. Polarity of auxin movement is mainly provided by the asymmetric localisation of PIN family auxin efflux carriers. At cytoplasmic pH (pH 7), IAA forms a weak acid, IAA^-, which is membrane impermeable and requires auxin efflux carriers for efflux out of the cell. Thus asymmetric localisation of auxin efflux carriers facilitate polar movement of IAA.

PIN proteins involved in PAT are commonly polarised to either the shootward or rootward surface of cells dependent on phosphorylation status of a central hydrophilic loop, which is governed by the activity of PINOID and PROTEIN PHOSPHATASE 2A, resulting in a directional flow of auxin. In the protophloem, AUX1 and PIN1 polarise to the shootward and rootward membrane surfaces respectively, causing auxin to be directed to the root apical meristem, thus maintaining an auxin maximum which defines the root apical meristem (Kleine-Vehn, et al., 2006). In the surrounding tissues, PIN2 directs auxin shootward, resulting in a fountain pattern which distributes auxin throughout the basal meristem, and minimises radial diffusion of IAA (Kleine-Vehn, et al., 2006). PIN proteins are also crucial for the root gravitropic response, as PIN3 and PIN7 relocalise to the lower face of the columella cells upon a gravistimulus, thus creating a differential auxin gradient between upper and lower sides of the root. This perturbation of auxin flux results in decreased auxin availability on the upper

root surface, and subsequent cell expansion, thus causing the roots to bend downwards. (Swarup & Bennett, 2014).

The root apical auxin maximum is required for the formation and maintenance of the quiescent centre and surrounding initials (Overvoorde, et al., 2010), which provide the founding cells for all root tissue. These initials divide asymmetrically to form specific tissues in response to spatiotemporal cues from peptides and mobile transcription factors, eg CLAVATA3/EMBRYO SURROUNDING REGION (CLE) peptides and SHORT-ROOT (Long, et al., 2015), and the daughter cells subsequently differentiate into columella, epidermis, cortex, endodermis, and stele (vascular) tissues. Analysis of auxin maxima formation in *DR5::GUS* reporter lines has also demonstrated that oscillations of auxin are responsible for priming xylem pole pericycle cells in the basal meristem to form lateral root primordia (De Smet, et al., 2007), although asymmetric division does not occur until the cells are several millimetres distal to the RAM (Péret, et al., 2009). In order to "found" a lateral root primordium, pairs of pericycle cells are primed by exposure to auxin on alternating xylem poles every 15 hours in the basal meristem (De Smet, et al., 2007). Auxin induced priming of pericycle cells induces expression of *GATA TRANSCRIPTION FACTOR 23 (GATA23)* – a gene responsible for establishing lateral root founder cell identity – in an IAA28 dependent manner (De Rybel, et al., 2010). As the primed cells become more distal to the meristem, they are exposed to a second auxin signal, which is attributed to transient expression of *PIN3* in vasculature and endodermal tissues surrounding founder cells (Marhavý, et al., 2013). This second auxin signal causes degradation of INDOLE ACETIC ACID 14 (IAA14) - a repressor of transcription factors AUXIN RESPONSE FACTOR 7 (ARF7) and ARF19 (Péret, et al., 2009). This allows ARF7 and ARF19 to upregulate genes involved in lateral root initiation, causing the primed pericycle cells to divide asymmetrically, giving rise to a new meristem - the lateral root primordium.

Interestingly, PIN3:GFP was no longer observed after the primordium reached 3 cell layers, suggesting that the PIN3-mediated polar auxin transport is required only until LRI is established (Marhavý, et al., 2013).

Cytokinin

Auxin is not the only hormone involved in root architectural development. Interplay between auxin and cytokinin gradients governs the identity of different root zones. In the root, the highest concentrations of auxin are found towards the RAM, where it acts to encourage growth and maintains the meristematic region (Su, et al., 2011). As cells become more distal to the RAM, auxin availability decreases and cytokinin concentration increases, causing differentiation of tissues in the basal meristem. At increasingly distal positions to the RAM, cytokinin becomes ever more dominant over auxin, and this change in the ratio of hormones causes cell differentiation and expansion, forming mature tissues. Furthermore, cytokinin is required for root thickening and secondary growth in the basal meristem, as cytokinin-deficient mutants *isopentenyl transferase (ipt) 1, ipt3, ipt5* and *ipt7* exhibit decreased secondary growth in the root cambium (Matsumoto-Kitano, et al., 2008).

In lateral root development, cytokinin acts to suppress lateral root initiation via downregulation of cyclins responsible for the G_2 to M transition (Chang, et al., 2013; Li, et al., 2006). In the lateral root founder cells, activity of ADENYLATE ISOPENTENYLTRANSFERASE 5 (IPT5) and LONELY GUY 4 (LOG4) generates isopentenyl adenine – a precursor to cytokinin – which diffuses to surrounding cells and is converted into trans-zeatin by CYTOKININ HYDROXYLASE CYP735A (Chang, et al., 2015). This process forms a gradient of cytokinin which is comparatively low in the lateral root founder cells, and higher in the surrounding tissues, and acts to restrict asymmetric cell divisions in flanking cells (Chang, et al., 2015). It has also

been demonstrated that cytokinin interferes with PIN1 trafficking in lateral root founder cells by retargeting PIN1 to the vacuole, where it is degraded (Laplaze, et al., 2007; Marhavý, et al., 2011), which may potentially compliment the formation of the localised auxin maximum resulting from accumulation of PIN3 (Marhavý, et al., 2013), by restricting polarised auxin transport.

Ethylene

Ethylene has a similarly antagonistic role to auxin during root development, encouraging differentiation and inhibiting cell proliferation (Wang, et al., 2002). There are several responses attributed to ethylene signalling across species. In Arabidopsis, the presence of ethylene inhibits cell division in the RAM (Street, et al., 2015), and interacts (alongside strigolactones) with auxin, to promote root hair elongation in root trichoblasts as part of the phosphorous stress response (Kapulnik, et al., 2010; Lei, et al., 2010). Interestingly, it has recently been indicated that *GATA23* is upregulated indirectly by ETHYLENE RESPONSE FACTOR 9, which acts to decrease expression of *RALF34*, a peptide hormone (Murphy, et al., 2016). Expression of *RAPID ALKALINIZATION FACTOR 34 (RALF34)* is observed in cells flanking lateral root founder cells, and may therefore serve to restrict *GATA23* expression to the founder cells, preventing further asymmetric cell division (Murphy, et al., 2016). This responsiveness to both ethylene and auxin signalling suggests that GATA23 represents a key player in establishing lateral root founder cell identity. Finally, in rice, ethylene is key to development of aerenchyma, and for induction of epidermal cell death, allowing for emergence of adventitious roots and tolerance of hypoxic flood conditions (Yukiyoshi & Karahara, 2014).

Gibberellin

Gibberellins are involved in a number of developmental processes during development, from seed germination to cell expansion (Davière & Achard, 2013). Some of the major advances to crop yield during the "green revolution" in the 1960s were resultant from semi-dwarfed varieties of wheat and rice with altered gibberellin signalling (Davière & Achard, 2013). Gibberellins act by triggering degradation of DELLA repressors of gene activation in a GIBBERELLIN INSENSITIVE DWARF1 (GID1)-dependent manner. In *Arabidopsis*, gibberellin acts to promote root growth by enabling cell expansion in the endodermis, which further allows growth in other root tissues (Ubeda-Tomás, et al., 2008). Furthermore, it has been suggested that gibberellin signalling may mediate the auxin/cytokinin antagonism in lateral root development, as auxin degrades DELLA proteins, and gibberellins mitigate cytokinin-induced root growth inhibition (Julkowska & Testerink, 2015). Interestingly, gibberellin mediated root growth is inhibited during salt stress, by ERF5/ERF6 mediated upregulation of *GIBBERELLIN 2 – OXIDASE 6 (GA2ox6)*, which acts to degrade gibberellin (Dubois, et al., 2013). Similarly, in iron-deficient conditions, DELLA proteins accumulate in the RAM, inhibiting primary root growth, but are excluded from the root differentiation zone, allowing for FER-like IRON-DEFICIENCY INDUCED TRANSCRIPTION FACTOR-induced iron uptake (Wild, et al., 2016). Thus, it appears that gibberellin is a key player in mediating developmental and stress responses during root development.

Strigolactone

Strigolactones are a relatively recently identified group of phytohormones involved in inhibition of lateral organ branching (Gomez-Roldan, et al., 2008; Jiang, et al., 2016). In *Arabidopsis* roots, strigolactones are upregulated in response to the absence of phosphate

and inhibit the lateral root priming and emergence in a DWARF14/MORE AXILLIARY GROWTH2 dependent manner, but do not affect initiation of lateral root primordia (Jiang, et al., 2016; Kumar, et al., 2015). On a cellular level, strigolactones reduce auxin transport by triggering the depolarisation of PIN-FORMED proteins, but increase auxin perception through upregulation of TIR1, thereby inhibiting primary root growth and increasing root hair development, reminiscent of a classic phosphate-stress response (Kapulnik & Koltai, 2014).

Jasmonic Acid

Jasmonic acid (JA) is involved in mediating tolerance to a variety of stress responses, from mechanical wounding from herbivorous pests to salt and drought stress, and is well known for its ability to inhibit root growth in a COI1/JAZ10/MYC2-dependent manner (Gasperini, et al., 2015; Wasternack & Hause, 2013). The root growth inhibition in JA-treated roots is twofold, affecting both cell division in the RAM and elongation in the differentiation zone, however these processes can be uncoupled by modulation of repression of JA signalling by NOVEL INTERACTOR OF JASMONATE ZIM-DOMAIN *(NINJA)*, as *ninja* only show decreased elongation of cells in the root elongation zone, suggesting that NINJA represses JA signalling in this region, but has no effect on JA/MYC2 induced repression of *PLETHORA (PLT)* in the RAM (Gasperini, et al., 2015). PLT is a transcription factor involved in maintenance of the RAM and is able to regulate polar auxin transport to maintain the quiescent centre and columella. Repression of PLT activity by JA signalling causes aberrant differentiation in the root apical meristem, and loss of the QC stem cell niche (Aida, et al., 2004; Chen, et al., 2011).

Abscisic Acid

Abscisic acid (ABA) is similarly involved in abiotic stress tolerance, primarily salt and drought tolerance, and ABA signalling requires the ABSCISIC ACID INSENSITIVE (ABI) group of response

elements, which include transcription factors (ABI3, ABI4 and ABI5) and protein phosphatases (ABI1 and ABI2) (Duan, et al., 2013). ABA signalling is able to cross-talk with multiple other phytohormone signalling pathways including auxin and jasmonic acid signalling to maintain growth of the primary root in water stress conditions (Cutler, et al., 2010). Interestingly, the presence of ABA enhances lateral root development in *M. truncatula* prior to emergence (Gonzalez, et al., 2015), and enhances lateral root emergence in *Arabidopsis* (De Smet, et al., 2006). Interestingly, in contrast to the effect on primary root, endodermal expression of ABA also inhibits lateral root growth post-emergence by promoting lateral root quiescence in response to saline conditions in *Arabidopsis* (Duan, et al., 2013).This potentially indicates that ABA signalling triggers adaptation of root architecture to find water deeper in the soil.

Brassinosteroids

Brassinosteroids are relatively short-distance signalling molecules, generally acting synergistically with auxin in the cells in which they are synthesised, and neighbouring tissues (Symons, et al., 2008; Symons & Reid, 2004; Nemhauser, et al., 2004). Brassinosteroids require the DWARF family of sterol reductases for synthesis from campesterol (Choe, et al., 1999), and the BRASSINOSTEROID INSENSITIVE (BRI)/BRI1-like (BRL) family of receptor kinases for activity (Caño-Delgado, et al., 2004). Brassinosteroid signalling has a similar effect to ABA insomuch as it is able to increase primary root growth in stress conditions. This effect is achieved by promotion of cell division in the epidermis, and differentiation in the stele (González-García, et al., 2011; Wei & Li, 2016). Interestingly, this difference in function between epidermis and stele also suggests that the various BRI/BRL receptor kinases are able to differentially interpret the brassinosteroid signal dependent on tissue type – presumably via different ratios of brassinosteroid receptors. Indeed, while BRI1 is expressed ubiquitously,

the BRL family members are restricted to the vascular bundles, suggesting that BRI1 regulates epidermal division, and the remaining BRL family members promote differentiation of vascular tissues (Caño-Delgado, et al., 2004).

Summary

This range of hormones is relatively small by comparison to the number of effects they are able to induce – even in combination with each other. Often, hormonal signalling is not a direct process of up/downregulation of genes, but instead acts as a governing signal activating various interlinked signalling cascades, which are able to interpret the hormonal signals, combined with spatiotemporal cues and cross-talk from other signalling networks to enable the optimal adaptation of plant organs to their surrounding environment.

Signalling Cascades

Phytohormones act as primary systemic signals, and are able to elicit multiple responses by activation and repression of downstream signals. Signalling resulting from the presence of one phytohormone is often subject to interference from the presence of other phytohormones. For example, auxin and cytokinin have seemingly opposite effects on some aspects of development, encouraging division or differentiation respectively, but at equal concentrations of both hormones, cells continue to divide, but remain undifferentiated (Su, et al., 2011). Interpretation of phytohormone signalling is enabled by distinct modules, which often include mutual targets for activation and repression (Su, et al., 2011).

Primary targets of hormone signalling are often named “response factors” (e.g. AUXIN RESPONSE FACTORs, CYTOKININ RESPONSE FACTORs, and ETHYLENE RESPONSE FACTORs),

and are transcription factors involved in up- and down-regulation of secondary signalling proteins involved in regulation of further downstream signalling machinery (Overvoorde, et al., 2010; Šimášková, et al., 2015). Signalling cascades initiated in response to phytohormone signalling are involved in all developmental processes, regulating a plethora of transcription factors, transport proteins, and enzymes involved in production and regulation of secondary signalling metabolites. Some notable examples are described in more detail below.

Mobile Transcription Factors

Transcription factors are up- or down-regulated in response to perception of phytohormones or environmental or biotic stress, and although the majority are active at an intracellular level, some notable examples have been observed to form juxtacrine or endocrine signals.

SHORT-ROOT (SHR) is a mobile transcription factor which is expressed in the stele and acts as a juxtacrine signal involved in maintenance and positioning of the stem cell niche via upregulation of SCARECROW (SCR) (Sabatini, et al., 2003). Additionally, both SHR and SCR are required for the correct formation of the cortex and endodermal cell layers, with loss of function mutants resulting in a short root phenotype (Helariutta, et al., 2000).

Another example of a mobile transcription factor is ELONGATED HYPOCOTYL 5 (HY5), which promotes light dependent carbon assimilation in the aerial tissues (Chen, et al., 2016). HY5 is additionally reported to act as an autocrine signal between shoot and root, triggering root-derived auto-expression of *HY5* and upregulating the expression of nitrate transporter *NRT2.1* (Chen, et al., 2016). In this manner, it is suggested that HY5 may be responsible for coordinating light mediated root growth and nitrate uptake (Chen, et al., 2016).

RNAs

In addition to regulation by transcription factors, gene expression can also be altered locally and systemically by the action of several types of non-coding RNA (Benkovics & Timmermans, 2014).

APOLO is a long non-coding RNA (lncRNA) located 5148 bp upstream of the kinase *PINOID (PID)*, and expression of *APOLO* is co-induced with *PID* in response to auxin application (Ariel, et al., 2014). *APOLO* is reported to mediate closure of a chromatin loop in the promoter region of *PID,* forming a negative feedback mechanism to *APOLO/PID* expression (Ariel, et al., 2014). Since PID-mediated phosphorylation regulates polarity of the auxin transporter PIN-FORMED 2 (PIN2), which is involved in polar auxin transport during gravotropism, it is suggested that *APOLO* expression may be involved with "fine tuning" the gravotropic response (Ariel, et al., 2014).

Interestingly, it has been demonstrated that in addition to its role in meristem maintenance and endodermis/cortex cell file differentiation, SHORTROOT (SHR) upregulates microRNAs miR165/166 in the endodermis (Carlsbecker, et al., 2010). These microRNAs are required for the correct differentiation of the vascular elements and regulation of meristem size (Carlsbecker, et al., 2010). Following upregulation by SHR, miR165/166 diffuse into the stele, where they repress expression of five *HD-ZIP III* transcription factors, including *PHABULOSA (PHB)*, which is responsible for determining vascular pattern. *shr* has decreased expression of *pMIR165/166,* and correspondingly expression of *PHB* increases throughout the stele (Carlsbecker, et al., 2010). Additionally, the *phb shr* double mutant results in restored primary root length and vascular development, suggesting that SHR, miR165/166, and PHB

interactions form a signalling loop responsible for the regulation of vascular patterning (Carlsbecker, et al., 2010).

Signalling Peptides

Signalling peptides are short (5-75 aa) chains of protein, which commonly act as ligands for receptor-like protein kinases. In turn, receptor-like protein kinases are able to elicit an array of physiological and biochemical changes in response to hormonal and environmental stimuli by causing phosphorylation of effector proteins.

Several examples of small peptide signals and known associated receptors are reviewed in detail in the next section about small signalling peptides and their effects on development (Chapter 2).

Receptor Kinases

In addition to the aforementioned signalling elements, another class of signalling effectors – receptor kinases – function as mediators of signalling cascades, and are able to alter substrate conformation by attaching a negatively charged phosphate group to their substrates. This process is reversible by the action of phosphatase enzymes, resulting in dynamic regulation of substrate activity. One class of receptor kinase involved in growth and development are the membrane-associated receptor kinases. These kinases are identifiable by the presence of an extracellular ligand-binding domain, transmembrane sequence, and an intracellular kinase domain. Membrane-associated receptor kinases are responsible for the perception of ligand molecules in the extracellular environment, and enable the plant to adapt growth in response to biotic and/or abiotic changes in the environment, for example HISTIDINE KINASE1 acts as an osmosensor, and its activity results in the upregulation of abscisic acid in response to drought and salt stress (Tran, et al., 2007). Similarly, a receptor complex formed of the

receptor kinases FLAGELLIN SENSING 2 and BRI1-ASSOCIATED KINASE 1 is able to recognise pathogen-associated molecular patterns and initiate innate immune responses, including stomatal closure and programmed cell death in response to pathogen invasion (Li, et al., 2014). This response is further enabled by the receptor-like cytoplasmic kinase (RLCK) BOTRYTIS INDUCIBLE KINASE 1 (BIK1). Lacking an extracellular domain, RLCKs are able to move between subcellular compartments, and commonly act as intermediary effectors of membrane-associated receptor kinase signalling. In this example, FLS2/BAK1 dependent phosphorylation of BIK1 in response to pathogen-associated molecular pattern recognition activates BIK1, enabling the downstream phosphorylation of the NADPH oxidase RbohD, which results in stomatal closure (Li, et al., 2014).

Interestingly, RLCKs are not restricted to transducing signals from membrane associated receptor kinases. AvrPphB SUSCEPTIBLE PROTEIN 1 (PBS1) is an RLCK which regulates RESISTANCE TO PSEUDOMONAS SYRINGAE PROTEIN 5 (RPS5) dependent effector triggered immunity (ETI). RPS5 interacts with PBS1 by means of an N-terminal coiled-coil domain, and this interaction is disrupted by the *Pseudomonas syringae* avirulence effector AvrPphB, a cysteine protease, which cleaves PBS1 (Shao, et al., 2003). The resulting dissociation of PBS1 removes the inhibition of RPS5 activity, resulting in induction of the ETI response, indicating PBS1 as a critical ETI sensor for response to *P. syringae* infection (Zhang, et al., 2010).

In addition to the perception of environmental stimuli, membrane associated receptor kinases are involved in perception of endocrine and paracrine signals involved in regulating plant development. An example of this is the receptor kinase CLAVATA1 (CLV1), and co-receptor CLV2, which form a receptor complex, able to perceive the secreted CLV3 peptide,

and transduction of this signal results in regulation of asymmetric cell division in the shoot apical meristem via suppression of the transcription factor *WUSCHEL*.

Several further examples of small peptide signals and known associated receptors are reviewed in detail in the next section about small signalling peptides and their effects on development (Chapter 2).

1.4 Global Food Security

Climate change and population increase are among the major challenges of modern society. Global temperatures are rising, causing the retreat of polar ice caps, and a corresponding increase in sea level; and simultaneously, more arid regions are experiencing further reduction in volume and frequency of rainfall (Schmidhuber & Tubellio, 2007). If greenhouse gas emissions continue, the likely result will be a drastic reduction of viable land area for crop growth. Simultaneously, the global population is increasing, and is predicted to reach 9-10 billion by 2050 (Bavel, 2013; Ehrlich & Harte, 2015). With this increase in population comes the increasingly demanding requirement for universal access to nutritious and affordable food (Garnett, et al., 2013). Currently, approximately 800 million people in a global populace of 7.3 billion (11%) are unable to access enough, or sufficiently nourishing food, with up to 50% of the global populace having diets that are deficient in at least one essential nutrient (Ehrlich & Harte, 2015).

To approach the deficit in food availability, there are two main options, utilise more land for crop growth, or increase yield from the current global farming infrastructure (Garnett, et al., 2013; Edgerton, 2009). Both options have drawbacks, inasmuch that increasing land use for

crop growth correspondingly decreases biodiversity in the area, and increases greenhouse gas emissions through expanded use of agricultural equipment (Garnett, et al., 2013). Additionally, global availability of viable land for expansion of crop growth is decreasing due to expansion of desert regions (Gornall, et al., 2010).

Furthermore, it is also difficult to intensify crop growth on currently available land, since developing countries have little or no access to industrial fertiliser, and even in more developed countries, much of the applied fertiliser becomes inaccessible to crops due to loss via water drainage and exploitation by opportunistic organisms (Garnett, et al., 2013; Gornall, et al., 2010). Additionally, affecting both scenarios are increasingly erratic meteorological conditions, resulting in periods of drought or flood depending on the latitude; and increasing prevalence of crop diseases and pest species (Wheeler & von Braun, 2013; Ehrlich & Harte, 2015). From this perspective, there are multiple issues facing farmers and agricultural workers globally, with pressure to maximise yield and, concurrently, to preserve biodiversity and promote beneficial species (eg. pollinating bees) (Buri, et al., 2014). Current practise in developed countries is addition of fertilisers and installation of irrigation systems to maximise yield by providing near-optimal growth conditions for crop species, and use of herbicides and pesticides to prevent growth of opportunistic pest plants and herbivorous species respectively, is commonplace (Tilman, et al., 2002). However, this approach is not sustainable due to diminishing returns of fertiliser (Tilman, et al., 2002), and use of chemical pesticides often results in resistance in pest species eg. bacterial pathogens or insects, and broad-spectrum insecticides often contribute to decreased populations of beneficial species in areas where they are applied (Fairbrother, et al., 2014). Although traditional crop breeding programmes endeavour to breed more efficient plants with increased yield and stress/disease tolerances by selecting for desirable traits, and have in some cases been

successful (Reynolds, et al., 1999), it is becoming increasingly apparent that this is an inefficient process, and for a sustainable increase in yield, assistance from (bio)technological innovations and improvement of farming practises is required (Tilman, et al., 2002; Ehrlich & Harte, 2015). One technological innovation that has been developed to control herbivorous insect pests without impacting on bee populations is the "dropleg" spray application system, utilising a length of metal tubing to redirect the application of pesticide underneath the canopy of crops (Jones, 2014; Rüegg & Total, 2013). This limits application of the pesticide to the non-flowering tissues, and also prevents excessive drift of insecticide, both of which decrease the impact on pollinating bee populations. However, this technology is currently limited to crop species planted in rows (eg. maize), as densely growing plants such as barley or wheat would limit the distribution of herbicide. Additionally, this technology only addresses a single aspect of yield maximisation. Other processes, including application of fertiliser and herbicides, are still required, and are comparatively inefficient (Tilman, et al., 2002). From this perspective, biotechnological innovation directed at improving the efficiency of nutrient absorption and disease resistance are as necessary as the direct increase of yield via breeding in order to make any increase in yield sustainable for future farming and food availability.

1.5 Potential Benefits of Targeted Improvement of Root Architecture

The "green revolution" of the 1930-1960s formed the foundation for the modern farming system, advocating the use of irrigation, pesticides, and nitrogen-based fertilisers to increase yield on novel high-yield wheat and rice cultivars (Hedden, 2003; Pingali, 2012). Advances in

technology have also increased the efficiency of agricultural techniques such as sowing, allowing increased and more homogenously distributed quantities of seed to be planted in the same area, effectively increasing yield per unit area, and contributing to decreasing global food shortages, tripling food production with only a 30% increase in land utilised for agricultural purposes (Wik, et al., 2008). These practises have however, created an increased reliance upon the use of fertilisers and pesticides to maximise yield and reduce loss to herbivorous pests and disease, respectively (Hawkesford, 2014). It is becoming increasingly apparent that due to diminishing returns on fertiliser investments, increased pesticide resistance in insect and bacterial species, decreased water availability and increased temperatures, coupled with the need to feed an ever-expanding global populace while maintaining biodiversity, there is need for crop improvement beyond what is available from conventional breeding schemes (Mba, et al., 2012).

Historically, breeding schemes focused solely on increasing yield in ideal or near-ideal conditions, whereas the requirement for crop species that grow in increasingly adverse conditions was largely ignored (Mba, et al., 2012). In recent years, breeding techniques have given rise to several "tolerant" varieties of crops (Lopes, et al., 2011), however, further work must be done to increase the potential variety of available food, since the Food and Agriculture Organisation defines food security as "all people, at all times, having physical, social and economic access to sufficient, safe, and nutritious food that meets their dietary needs and food preferences for an active and healthy life" (Schmidhuber & Tubellio, 2007). From this perspective, it is paramount that all avenues of potential crop improvement are explored.

The deficit in resilient crop cultivars may potentially be alleviated by targeted crop improvement, selecting for genetic traits that may improve survivability in adverse conditions, and/or decrease the need for fertiliser application, with the eventual aim of producing improved yield using decreased inputs (Mba, et al., 2012; Hawkesford, 2014). Determining how plants control root growth will allow us to make informed and targeted approaches to modify and improve the interface between plant and rhizosphere, and thus improve crop yield. To this end, advances in deciphering signalling events leading to abiotic stress tolerance has led to the identification and characterisation of multiple transcription factors and kinases, as well as factors involved in phytohormone synthesis, degradation and distribution, which are responsible for abotic stress adaptations (Todaka, et al., 2015). This hypothesis-driven approach has enabled the engineering of drought, salt, cold, and osmotic stress tolerance in rice (as one example), using genes from a number of donor species, including rice, arabidopsis, tomato, maize, barley and pea (Todaka, et al., 2015). However, such transgenic crops often have unwanted traits such as hypersensitivity to phytohormone signalling or decreased yield under control conditions, in addition to those engineered into the genome. From this perspective an understanding of how, where and why each gene is regulated, both transcriptionally and post transcriptionally, and manipulation of the inherent plasticity of the root system may be key to improving traits involved in water uptake and nutrient availability, and may further assist in preventing loss of inputs via soil erosion.

References

Aida, M. et al., 2004. The PLETHORA Genes Mediate Patterning of the Arabidopsis Root Stem Cell Niche. *Cell,* 119(1), pp. 109-120.

Ariel, F. et al., 2014. Noncoding transcription by alternative RNA polymerases dynamically regulates an auxin-driven chromatin loop. *Molecular Cell,* 55(3), pp. 383-396.

Atkinson, J. et al., 2014. Branching Out in Roots: Uncovering Form, Function and Regulation. *Plant Physiology,* 166(2), pp. 538-550.

Bavel, J., 2013. The world population explosion: causes, backgrounds and projections for the future. *Facts, Views and Vision Issues in Obsetrics, Gynaecology and Reproductive Health,* 5(4), pp. 281-291.

Benfey, P. & Scheres, B., 2000. Root Development. *Current Biology,* 10(22), pp. R813-815.

Benkovics, A. & Timmermans, M., 2014. Developmental patterning by gradients of mobile small RNAs. *Current Opinion in Genetic Development,* Volume 27, pp. 83-91.

Buri, P., Humbert, J. & Arlettaz, R., 2014. Promoting Pollinating Insects in Intensive Agricultural Matrices: Field-Scale Experimental Manipulation of Hay-Meadow Mowing Regimes and Its Effects on Bees. *Public Library of Science One,* 9(1), p. doi: 10.1371/journal.pone.0085635.

Caño-Delgado, A. et al., 2004. BRL1 and BRL3 are novel brassinosteroid receptors that function in vascular differentiation in Arabidopsis. *Development,* 131(21), pp. 5341-5351.

Carlsbecker, A. et al., 2010. Cell signalling by microRNA165/6 directs gene dose-dependent root cell fate. *Nature,* 465(7296), pp. 316-321.

Chang, L., Ramireddy, E. & Schmülling, T., 2013. Lateral root formation and growth of Arabidopsis is redundantly regulated by cytokinin metabolism and signalling genes. *Journal of Experimental Botany,* 64(16), pp. 5021-5032.

Chang, L., Ramireddy, E. & Schmülling, T., 2015. Cytokinin as a positional cue regulating lateral root spacing in Arabidopsis. *Journal of Experimental Botany,* 66(15), pp. 4759-4768.

Chen, Q. et al., 2011. The Basic Helix-Loop-Helix Transcription Factor MYC2 Directly Represses PLETHORA Expression during Jasmonate-Mediated Modulation of the Root Stem Cell Niche in Arabidopsis. *Plant Cell,* 23(9), pp. 3335-3352.

Chen, X. et al., 2016. Shoot-to-Root Mobile Transcription Factor HY5 Coordinates Plant Carbon and Nitrogen Acquisition. *Current Biology,* 26(5), pp. 640-646.

Choe, S. et al., 1999. The Arabidopsis dwarf1 mutant is defective in the conversion of 24-methylenecholesterol to campesterol in brassinosteroid biosynthesis. *Plant Physiology,* 119(3), pp. 897-907.

Cutler, S., Rodrguez, P., Finkelstein, R. & Abrams, S., 2010. Abscisic Acid: Emergence of a Core Signalling Network. *Plant Biology,* Volume 61, pp. 651-679.

Davière, J. & Achard, P., 2013. Gibberellin signaling in plants. *Development,* 140(6), pp. 1147-1151.

De Rybel, B. et al., 2010. A Novel Aux/IAA28 Signaling Cascade Activates GATA23-Dependent Specification of Lateral Root Founder Cell Identity. *Current Biology,* 20(19), pp. 1697-1706.

De Smet, I. et al., 2007. Auxin-dependent regulation of lateral root positioning in the basal meristem of Arabidopsis. *Development,* Volume 134, pp. 681-690.

De Smet, I., Zhang, H., Inzé, D. & Beeckman, T., 2006. A novel role for abscisic acid emerges from underground. *Trends in Plant Science,* 11(9), pp. 434-439.

Duan, L. et al., 2013. Endodermal ABA Signaling Promotes Lateral Root Quiescence during Salt Stress in Arabidopsis Seedlings. *Plant Cell,* 25(1), pp. 324-341.

Dubois, M. et al., 2013. ETHYLENE RESPONSE FACTOR6 Acts as a Central Regulator of Leaf Growth under Water-Limiting Conditions in Arabidopsis. *Plant Physiology,* 162(1), pp. 319-332.

Edgerton, M., 2009. Increasing Crop Productivity to Meet Global Needs for Feed, Food, and Fuel. *Plant Physiology,* 149(1), pp. 7-13.

Ehrlich, P. & Harte, J., 2015. Opinion: To feed the world in 2050 will require a global revolution. *Proceedings of the National Academy of Sciences of the United States of America,* 112(48), pp. 14743-14744.

Fairbrother, A., Purdy, J., Anderson, T. & Fell, R., 2014. Risks of neonicotinoid insecticides to honeybees. *Environmental Toxicology and Chemistry,* 33(4), pp. 719-731.

Garnett, T. et al., 2013. Sustainable Intensification in Agriculture: Premises and Policies. *Science,* 341(6141), pp. 33-34.

Gasperini, D. et al., 2015. Multilayered Organization of Jasmonate Signalling in the Regulation of Root Growth. *PLOS Genetics,* 11(6), p. doi:10.1371/journal.pgen.1005300.

Gomez-Roldan, V. et al., 2008. Strigolactone inhibition of shoot branching. *Nature,* 455(7210), pp. 189-194.

Gonzalez, A. et al., 2015. Abscisic acid promotes pre-emergence stages of lateral root development in Medicago truncatula. *Plant Signaling and Behavior,* 10(1), p. DOI: 10.4161/15592324.2014.977741.

González-García, M. et al., 2011. Brassinosteroids control meristem size by promoting cell cycle progression in Arabidopsis roots. *Development,* Volume 138, pp. 849-859.

Gornall, J. et al., 2010. Implications of climate change for agricultural productivity in the early twenty-first century. *Philosophical Transactions of the Royal Society of London Category B: Biological Sciences,* 365(1554), pp. 2973-2989.

Hawkesford, M., 2014. Reducing the reliance on nitrogen fertilizer for wheat production. *Journal of Cereal Science,* 59(3), pp. 276-283.

Hedden, P., 2003. The genes of the Green Revolution. *Trends in Genetics,* 19(1), pp. 5-9.

Helariutta, Y. et al., 2000. The SHORT-ROOT Gene Controls Radial Patterning of the Arabidopsis Root through Radial Signaling. *Cell,* 101(5), pp. 555-567.

Hochholdinger, F., Park, W., Sauer, M. & Woll, K., 2004. From weeds to crops: genetic analysis of root development in cereals. *Trends in Plant Science,* 9(1), pp. 42-48.

Hodge, A. et al., 2009. Plant root growth, architecture and function. *Plant and Soil,* 321(1), pp. 153-187.

Jiang, L. et al., 2016. Strigolactones spatially influence lateral root development through the cytokinin signaling network. *Journal of Experimental Botany,* 67(1), pp. 379-389.

Jones, D., 2014. *Farmers Weekly.* [Online] Available at: http://www.fwi.co.uk/arable/drop-leg-sprayer-can-improve-pest-control.htm [Accessed 03 MAR 2016].

Jones, V. & Dolan, L., 2012. The evolution of root hairs and rhizoids. *Annals of Botany,* 110(2), pp. 205-212.

Julkowska, M. & Testerink, C., 2015. Tuning plant signaling and growth to survive salt. *Trends in Plant Science,* 20(9), pp. 586-594.

Kapulnik, Y. & Koltai, H., 2014. Strigolactone Involvement in Root Development, Response to Abiotic Stress, and Interactions with the Biotic Soil Environment. *Plant Physiology,* Volume 166, pp. 560-569.

Kapulnik, Y. et al., 2010. Strigolactones interact with ethylene and auxin in regulating root-hair elongation in Arabidopsis. *Journal of Experimental Botany,* 62(8), pp. 2915-2924.

Kleine-Vehn, J. et al., 2006. Subcellular Trafficking of the Arabidopsis Auxin Influx Carrier AUX1 Uses a Novel Pathway Distinct from PIN1. *Plant Cell,* 18(11), pp. 3171-3181.

Kumar, M., Pandya-Kumar, N., Kapulnik, Y. & Koltai, H., 2015. Strigolactone signaling in root development and phosphate starvation. *Plant Signaling and Behavior,* 10(7), p. doi: 10.1080/15592324.2015.1045174.

Lanier, W., Moustafa, A., Bhattacharya, D. & Comeron, J., 2008. EST analysis of Ostreococcus lucimarinus, the most compact eukaryotic genome, shows an excess of introns in highly expressed genes.. *PLOS ONE,* 3(5), p. e2171.

Laplaze, L. et al., 2007. Cytokinins Act Directly on Lateral Root Founder Cells to Inhibit Root Initiation. *Plant Cell,* 19(12), pp. 3889-3900.

Lei, M. et al., 2010. Ethylene signalling is involved in regulation of phosphate starvation-induced gene expression and production of acid phosphatases and anthocyanin in Arabidopsis. *New Phytologist,* 2011(189), pp. 1084-1095.

Li, L. et al., 2014. The FLS2-Associated Kinase BIK1 Directly Phosphorylates the NADPH Oxidase RbohD to Control Plant Immunity. *Cell Host & Microbe,* 15(3), pp. 329-338.

Li, X., Mo, X., Shou, H. & Wu, P., 2006. Cytokinin-Mediated Cell Cycling Arrest of Pericycle Founder Cells in Lateral Root Initiation of Arabidopsis. *Plant & Cell Physiology,* 47(8), pp. 1112-1123.

Long, Y., Scheres, B. & Blilou, I., 2015. The logic of communication: roles for mobile transcription factors in plants. *Journal of Experimental Botany,* 66(4), pp. 1133-1144.

Lopes, M., Araus, J., van Heerden, P. & Foyer, C., 2011. Enhancing drought tolerance in C4 crops. *Journal of Experimental Botany,* 62(9), pp. 3135-3153.

Marhavý, P. et al., 2011. Cytokinin Modulates Endocytic Trafficking of PIN1 Auxin Efflux Carrier to Control Plant Organogenesis. *Developmental Cell,* 21(4), pp. 796-804.

Marhavý, P. et al., 2013. Auxin reflux between the endodermis and pericycle promotes lateral root initiation. *The European Molecular Biology Organisation Journal,* 32(1), pp. 149-158.

Matsumoto-Kitano, M. et al., 2008. Cytokinins are central regulators of cambial activity. *Proceedings of the National Academy of Science of the United States of America,* 105(50), pp. 20027-20031.

Mba, C., Guimaraes, E. & Ghosh, K., 2012. Re-orientating crop improvement for the changing climatic conditions of the 21st century. *Agriculture and Food Security,* 1(7), pp. DOI: 10.1186/2048-7010-1-7.

Murphy, E. et al., 2016. RALFL34 regulates formative cell divisions in Arabidopsis pericycle during lateral root initiation. *Journal of Experimental Botany,* 67(16), pp. 4863-4875.

Nemhauser, J., Mockler, T. & Chory, J., 2004. Brassinosteroids Regulate Root Growth, Development, and Symbiosis. *PLOS Biology,* 2(9), p. DOI: 10.1371/journal.pbio.0020258.

Overvoorde, P., Fukaki, H. & Beeckman, T., 2010. Auxin Control of Root Development. *Cold Spring Harbour Perspectives in Biology,* 2(a001537).

Overvoorde, P., Fukaki, H. & Beeckman, T., 2010. Auxin Control of Root Development. *Cold Spring Harbour Perspectives in Biology,* 2(6), p. 10.1101/cshperspect.a001537.

Péret, B. et al., 2009. Arabidopsis lateral root development: an emerging story. *Trends in Plant Science,* 14(7), pp. 399-408.

Pingali, P., 2012. Green Revolution: Impacts, limits, and the path ahead. *Proceedings of the National Academy of Sciences of the United States of America,* 109(31), pp. 12302-12308.

Raven, J., 1975. Transport of Indoleacetic acid in plant cells in relation to pH and electrical potential gradients, and it's significance for polar IAA transport. *New Phytologist,* 74(2), pp. 163-172.

Raven, J. & Edwards, D., 2000. Roots: evolutionary origins and biogeochemical significance. *Journal of Experimental Botany,* 52(Suppl 1), pp. 381-401.

Reynolds, M., Rajaram, S. & Sayre, K., 1999. Physiological and Genetic Changes of Irrigated Wheat in the Post–Green Revolution Period and Approaches for Meeting Projected Global Demand. *Crop Science,* 39(6), pp. 1611-1621.

Rubery, P. & Sheldrake, A., 1974. Carrier-mediated auxin transport. *Planta,* 118(2), pp. 101-121.

Rubinstein, C. et al., 2010. Early Middle Ordovician evidence for land plants in Argentina (eastern Gondwana). *New Phytologist,* 188(2), pp. 365-369.

Rüegg, J. & Total, R., 2013. *Dropleg – Application Technique for better targeted sprays in row crops,* Waedenswil: Agroscope.

Sabatini, S., Heidstra, R., Wildwater, M. & Scheres, B., 2003. SCARECROW is involved in positioning the stem cell niche in the Arabidopsis root meristem. *Genes & Development,* 17(3), pp. 354-358.

Sakakibara, K. et al., 2003. Involvement of auxin and a homeodomain-leucine zipper I gene in rhizoid development of the moss Physcomitrella patens. *Development,* Volume 130, pp. 4835-4846.

Schmidhuber, J. & Tubellio, F., 2007. Global food security under climate change. *Proceedings of the National Academy of Sciences of the United States of America,* 104(50), pp. 19703-19708.

Schmitt, R. & Sumper, M., 2003. Developmental biology: How to turn inside out. *Nature,* Volume 424, pp. 499-500.

Shao, F. et al., 2003. Cleavage of Arabidopsis PBS1 by a bacterial type III effector. *Science,* Volume 301, pp. 1230-1233.

Šimášková, M. et al., 2015. Cytokinin response factors regulate PIN-FORMED auxin transporters. *Nature Communications,* Volume 6, p. doi:10.1038/ncomms9717.

Smith, S. & De Smet, I., 2012. Root system architecture: insights from Arabidopsis and cereal crops. *Philosophical Transactions of the Royal Society Biology,* Volume 367, pp. 1441-1452.

Street, I. et al., 2015. Ethylene Inhibits Cell Proliferation of the Arabidopsis. *Plant Physiology,* 169(1), pp. 338-350.

Su, Y., Liu, Y. & Zhang, X., 2011. Auxin–Cytokinin Interaction Regulates Meristem Development. *Molecular Plant,* 4(4), pp. 616-625.

Swarup, R. & Bennett, M., 2014. Auxin Transport: Providing a Sense of Direction During Plant Development. *Biochemical Society Transactions,* 28(4), pp. 481-485.

Swarup, R. & Péret, B., 2012. AUX/LAX family of auxin influx carriers—an overview. *Frontiers in Plant Science,* p. https://doi.org/10.3389/fpls.2012.00225.

Symons, G. & Reid, J., 2004. Brassinosteroids Do Not Undergo Long-Distance Transport in Pea. Implications for the Regulation of Endogenous Brassinosteroid Levels. *Plant Physiology,* 135(4), p. 2196–2206.

Symons, G., Ross, J., Jager, C. & Reid, J., 2008. Brassinosteroid Transport. *Journal of Experimantal Botany,* 59(1), pp. 17-24.

Tilman, D. et al., 2002. Agricultural sustainability and intensive production practices. *Nature,* Volume 418, pp. 671-677.

Todaka, D., Shinozaki, K. & Yamaguchi-Shinozaki, K., 2015. Recent advances in the dissection of drought-stress regulatory networks and strategies for development of drought-tolerant transgenic rice plants. *Frontiers in Plant Science,* 6(84), p. doi: 10.3389/fpls.2015.00084.

Tran, L. et al., 2007. Functional analysis of AHK1/ATHK1 and cytokinin receptor histidine kinases in response to abscisic acid, drought, and salt stress in Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America,* 104(51), pp. 20623-20628.

Ubeda-Tomás, S. et al., 2008. Root growth in Arabidopsis requires gibberellin/DELLA signalling in the endodermis. *Nature Cell Biology,* 10(5), pp. 625-628.

van Berkel, K., de Boer, R., Scheres, B. & ten Tusscher, K., 2013. Polar auxin transport: models and mechanisms. *Development,* Volume 140, pp. 2253-2268.

Wang, K., Li, H. & Ecker, J., 2002. Ethylene Biosynthesis and Signaling Networks. *The Plant Cell,* 14(Supplement 1), pp. S131-S151.

Wasternack, C. & Hause, B., 2013. Jasmonates: biosynthesis, perception, signal transduction and action in plant stress response, growth and development. An update to the 2007 review in Annals of Botany. *Annals of Botany,* 111(6), pp. 1021-1058.

Wei, Z. & Li, J., 2016. Brassinosteroids Regulate Root Growth, Development, and Symbiosis. *Molecular Plant,* 9(1), pp. 86-100.

Wheeler, T. & von Braun, J., 2013. Climate Change Impacts on Global Food Security. *Science,* 341(6145), pp. 508-513.

Wik, M., Pingali, P. & Brocai, S., 2008. *Global Agricultural Performance : Past Trends and Future Prospects,* Washington, DC: World Bank.

Wild, M. et al., 2016. Tissue-Specific Regulation of Gibberellin Signaling Fine-Tunes Arabidopsis Iron-Deficiency Responses. *Developmental Cell,* 37(2), pp. 190-200.

Yukiyoshi, K. & Karahara, I., 2014. Role of ethylene signalling in the formation of constitutive. *Annals of Botany PLANTS,* Volume 6, p. doi: 10.1093/aobpla/plu043.

Zhang, J. et al., 2010. Receptor-like cytoplasmic kinases integrate signaling from multiple plant immune receptors and are targeted by a Pseudomonas syringae effector. *Cell Host Microbe,* Volume 7, pp. 290-301.

Chapter 2: Message in a bottle: small signalling peptide outputs during growth and development

Published as Czyzewicz N, Yue K, Beeckman T, De Smet I. (2013) *Journal of Experimental Botany* 64(17):5281-5296

Author Contribution:

I wrote parts of the paper (Abstract, Introduction, Growth and development, Regulation of vascular development, Regulation of stomatal development, Regulation of lateral root initiation and development, Regulation of root waving and gravitropism, Regulation of gametophyte development and fertilization, Regulation of nodulation, Control of transcription factor expression, Effect on auxin transport, Alkalinisation of the extracellular environment, Evolutionary aspects of small signalling peptides and conclusion), contributed to figures (Table 1, Figures 1 and 2), and was involved in development of the manuscript.

Journal of Experimental Botany, Vol. 64, No. 17, pp. 5281–5296, 2013
doi:10.1093/jxb/ert283 Advance Access publication 7 September, 2013

Journal of Experimental Botany
www.jxb.oxfordjournals.org

REVIEW PAPER

Message in a bottle: small signalling peptide outputs during growth and development

Nathan Czyzewicz[1,*], Kun Yue[2,3,*], Tom Beeckman[2,3,†] and Ive De Smet[1,2,3,4,†,‡]

[1] Division of Plant and Crop Sciences, School of Biosciences, University of Nottingham, Sutton Bonington Campus, Loughborough, Leicestershire LE12 5RD, UK
[2] Department of Plant Systems Biology, VIB, Technologiepark 927, B-9052 Ghent, Belgium
[3] Department of Plant Biotechnology and Genetics, Ghent University, Technologiepark 927, B-9052 Ghent, Belgium
[4] Centre for Plant Integrative Biology, University of Nottingham, Sutton Bonington LE12 5RD, UK

* These authors contributed equally to this work.
† These authors contributed equally to this work.
‡ To whom correspondence should be addressed. E-mail: ive.desmet@psb.vib-ugent.be

Received 13 June 2013; Revised 22 July 2013; Accepted 25 July 2013

Abstract

Classical and recently found phytohormones play an important role in plant growth and development, but plants additionally control these processes through small signalling peptides. Over 1000 potential small signalling peptide sequences are present in the *Arabidopsis* genome. However, to date, a mere handful of small signalling peptides have been functionally characterized and few have been linked to a receptor. Here, we assess the potential small signalling peptide outputs, namely the molecular, biochemical, and morphological changes they trigger in *Arabidopsis*. However, we also include some notable studies in other plant species, in order to illustrate the varied effects that can be induced by small signalling peptides. In addition, we touch on some evolutionary aspects of small signalling peptides, as studying their signalling outputs in single-cell green algae and early land plants will assist in our understanding of more complex land plants. Our overview illustrates the growing interest in the small signalling peptide research area and its importance in deepening our understanding of plant growth and development.

Key words: *Arabidopsis*, development, evolution, growth, small signalling peptides, transcription factors.

Introduction

A small number of classical and newly found phytohormones are heavily involved in plant growth and development (Vanstraelen and Benkova, 2012). For a long time, it was a challenge to explain how a handful of chemicals could produce the large number of physiological and biochemical responses required during development. Lately, however, it has become apparent that, like mammalian systems, plants also make use of small signalling peptides to steer growth and development. These small signalling peptides are mainly associated with receptors (including receptor kinases) situated in specific cells and tissues, and are able to elicit a vast array of biological and physiological responses, allowing the plant to develop and adapt to changes in the surrounding environment.

Several genetic, biochemical, and *in silico* studies have been undertaken to unravel the identity of these small signalling peptides (Lease and Walker, 2006; Butenko *et al.*, 2009; Murphy *et al.*, 2012). Small signalling peptides mainly range in size between 5 and 75 aa, but there are a few exceptions (see below). Most—but by no means all—small signalling peptides are cleavage products from precursor peptides. Several of these precursors are modified post-translationally prior to cleavage of the mature peptide sequence, and this post-translational modification can be critical to function.

Abbreviations: NCR, nodule-specific cysteine-rich; QC, quiescent centre; RAM, root apical meristem; RNAi, RNA interference; SAM, shoot apical meristem.

© The Author 2013. Published by Oxford University Press on behalf of the Society for Experimental Biology. All rights reserved. For permissions, please email: journals.permissions@oup.com

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

The mature, functional, secreted small signalling peptide is often perceived by a membrane-associated receptor and regulates a signal transduction pathway, but some are not secreted (Butenko *et al.*, 2009; Matsuzaki *et al.*, 2010; Matsubayashi, 2011; Murphy *et al.*, 2012). To date, however, a mere handful of small signalling peptides have been functionally characterized and few have been linked to a receptor (Butenko *et al.*, 2009; Murphy *et al.*, 2012).

In the *Arabidopsis* genome, over 600 putative receptor-like kinase proteins have been detected (Shiu and Bleecker, 2001), while over 1000 putative small signalling peptide sequences can be recognized (Lease and Walker, 2006). There are several ways to explain this seeming overabundance of putative small signalling peptides. First, as receptors commonly form complexes, it may be that interacting proteins are able to alter the conformation of the receptor, allowing a single receptor protein to perceive multiple ligands and to activate multiple, distinct signalling cascades based on alternative protein associations (for example type I interferons, which are important cytokines for innate immunity against viruses and cancer; Thomas *et al.*, 2011). Secondly, possibly not all putative small signalling peptides are secreted and/or perceived by a receptor, and they might have receptor-independent roles, although this does not exclude a signalling function. Thirdly, it is possible that some small signalling peptides are secreted to regulate the interaction between plant and symbiotic organisms (e.g. *Rhizobia*) or as a deterrent to pathogenic bacteria (Van de Velde *et al.*, 2010). Fourthly, there is also potential for functional redundancy in a number of peptides; for example, the active 12 aa CLE consensus sequence of CLE1 and CLE4 is perfectly conserved, and both peptides are expressed in the same tissue (Strabala *et al.*, 2006). Finally, it remains to be seen whether all putative small signalling peptides are produced by the plant and if they are perceived or functional at all. It is also noteworthy that small signalling peptides are distinct from microproteins, which appear mainly to target transcriptional regulators that bind to DNA as active homodimers (Staudt and Wenkel, 2011).

While several recent reviews describe the role of a limited number of small signalling peptides and their genetic and biochemical interaction with (potential) receptors (Butenko *et al.*, 2009; De Smet *et al.*, 2009; Murphy *et al.*, 2012), a comprehensive summary of downstream effects is lacking. This review therefore focuses on the molecular, biochemical, and morphological changes triggered by small signalling peptides in *Arabidopsis*. However, we also include some notable studies in other plant species in order to illustrate the varied effects that can be induced by small signalling peptides.

Phenotypical effects of peptides: growth and development

Peptides are involved in a wide range of growth and developmental processes. Before we elaborate on their signalling outputs, we will first provide an overview of the growth and developmental processes for which peptides have been proposed to play a role (Fig. 1, Table 1).

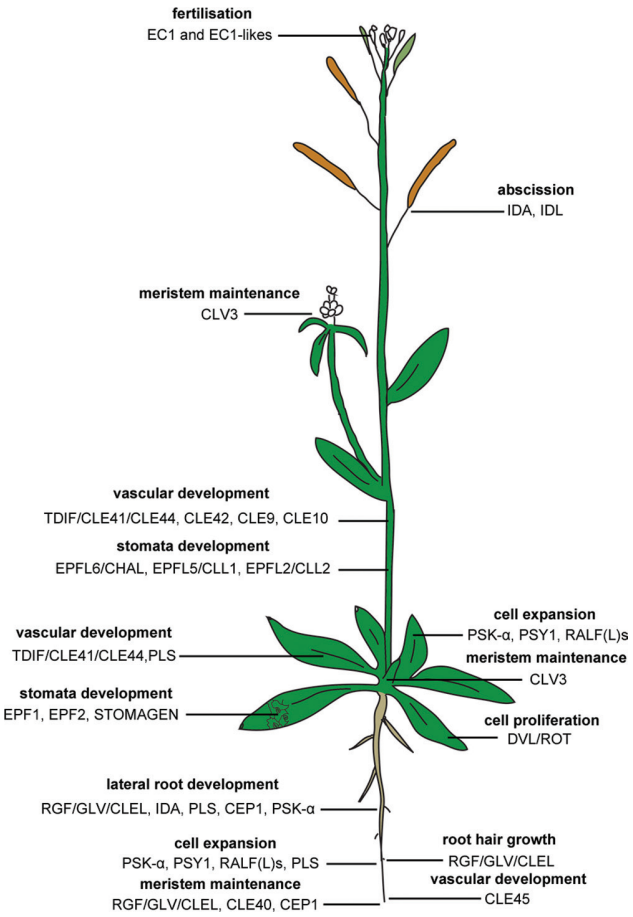


Fig. 1. Small signalling peptides in *Arabidopsis* growth and development. A simplified illustration of an *Arabidopsis* plant indicating some major developmental processes and the involved small signalling peptides.

Regulation of cell division and differentiation in primary meristems

Control of meristem size and activity, through regulating cell division and differentiation, is critical for the correct development of the primary plant body (Scheres, 2007). There are many molecular mechanisms—such as phytohormone-mediated signalling, cell cycle regulation, and protein movement—involved in regulating cell division and differentiation (De Veylder *et al.*, 2007; Barton, 2010; De Smet and Beeckman, 2011; Van Norman *et al.*, 2011), and small signalling peptides also play a role (Fig. 1).

The CLAVATA (CLV)/EMBRYO SURROUNDING REGION (ESR)-RELATED PROTEIN (CLE) family has been shown to affect root, shoot, and flower meristem maintenance and stem-cell divisions. The *Arabidopsis* CLE family comprises 32 peptides, each consisting of 12–13 aa, and containing a CLV3/ESR consensus sequence (Strabala *et al.*, 2006; Betsuyaku *et al.*, 2011*a*). CLV3 is perhaps the best-characterized small signalling peptide, and is demonstrated as a mobile signal controlling the size of the *Arabidopsis* shoot apical meristem (SAM) (Clark *et al.*, 1995) (Fig. 2A). *clv3* mutant plants have enlarged SAM regions,

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Table 1. *Peptide families and biological function*

CEP, C-TERMINALLY ENCODED PEPTIDE; CLE, CLAVATA (CLV)/EMBRYO SURROUNDING REGION-RELATED; DVL/ROT, DEVIL/ROTUNDIFOLIA; EC1, EGG CELL-SECRETED PROTEIN 1; EPF–EPFL, EPIDERMAL PATTERNING FACTOR–EPF-LIKE; IDA–IDL, INFLORESCENCE DEFICIENT IN ABSCISSION– IDA-LIKE; PLS, POLARIS; PSK-α, PHYTOSULFOKINE-α; PSY1, PLANT PEPTIDE CONTAINING SULFATED TYROSINE 1; RALF–RALFL, RAPID ALKALINIZATION FACTOR–RALF-LIKE; RGF/GLV/CLEL, ROOT GROWTH FACTOR/GOLVEN/CLE-LIKE; TPD1, TAPETUM DETERMINANT 1.

Peptide family	Number in family (at present)	Mature peptide sequence length (aa)[a]	Biological function(s)
CEP	5	15 (CEP1)	(Lateral) root development
CLE	32	12–13 (CLV3)	Meristem maintenance, stem-cell division, vascular development
DVL/ROT	24	41–145	Cell proliferation (leaves, trichomes)
EC1	5	?	Sperm activation
EPF–EPFL	11	44 (STOMAGEN) –76	Stomata development
IDA–IDL	6	20	Organ abscission, lateral root emergence
PLS	1	36	Cell expansion, root development, vascular development, leaf patterning
PSK-α	6	5	Cell proliferation and differentiation, cell expansion
PSY1	3	16–18	Cell proliferation and differentiation, cell expansion
RALF–RALFL	34	49	Cell expansion
RGF/GLV/CLEL	11	13 (RGF1) –14 (GLV1) –18	Maintenance of root apical meristem stem-cell niche, gravitropism, lateral root development
TPD1	1	?	Anther development

? Unknown or not investigated
[a] Information in parentheses gives examples of available MS and/or NMR data.

as well as increased floral meristem size (Clark *et al.*, 1995). Overexpression of *CLV3* and application of CLV3 peptide result in an early termination of the SAM (Fiers *et al.*, 2005; Kondo *et al.*, 2006). These observations indicate that CLV3 has a key role in the maintenance of the SAM stem-cell niche in *Arabidopsis* by downregulating stem-cell proliferation in meristematic tissue (Suzaki *et al.*, 2008).

CLE40 is the functional analogue of CLV3 in the root apical meristem (RAM) (Fiers *et al.*, 2005) (Fig. 2B). Overexpression of *CLE40* and application of CLE40 peptide result in consumption of the meristematic tissue and termination of root growth (Hobe *et al.*, 2003). Conversely, the *cle40* mutant displays delayed differentiation of columella stem cells (Hobe *et al.*, 2003).

Likewise, although no aberrant phenotype was observed in *cle19* knockout mutants, 35S promoter-mediated overexpression of *CLE19* results in a short root phenotype that is caused by complete differentiation of root meristem cells (Casamitjana-Martinez *et al.*, 2003; Fiers *et al.*, 2004). In addition, growth of seedlings on medium containing CLE19 similarly causes termination of the RAM, and close observation of the roots revealed that CLE19 peptide treatment results in delayed separation of the endodermis and cortex (Fiers *et al.*, 2005; Stahl *et al.*, 2009).

ROOT GROWTH FACTOR (RGF)/GOLVEN (GLV)/CLE-LIKE (CLEL) peptides belong to a family of 11 peptides, which are 13–18 aa and seven of which are expressed in the RAM (Matsuzaki *et al.*, 2010; Whitford *et al.*, 2012; Fernandez *et al.*, 2013*a*, *b*). Overexpression of *RGF1* and application of RGF1 peptide results in an enlarged meristematic region. Single *rgf1* knockout mutants do not show an aberrant root phenotype, but triple *rgf1 rgf2 rgf3* mutants display a shortened root phenotype, indicating their role as positive regulators of meristem maintenance and root growth (Matsuzaki *et al.*, 2010).

C-TERMINALLY ENCODED PEPTIDE (CEP) peptides belong to a family of, so far, five peptides, which are about 15 aa (Ohyama *et al.*, 2008). Overexpression of *C-TERMINALLY ENCODED PEPTIDE 1* (*CEP1*) results in a shortened root phenotype, which stems from a reduced number of cells in the meristematic zone and reduced cell size in the mature region (Ohyama *et al.*, 2008). Similarly, treatment with CEP1 peptide results in root growth arrest (Ohyama *et al.*, 2008).

Regulation of cell expansion

During development, growth rate depends on two parameters: cell production rate and cell size, and these parameters are controlled by several plant hormones (Beemster and Baskin, 1998; Breuninger and Lenhard, 2010; Gonzalez *et al.*, 2012). However, an increasing number of small signalling peptides appear to also play a role in cell expansion (Fig. 1).

Two sulfated peptides, the pentapeptide PHYTOSULFOKINE-α (PSK-α) and the 18 aa glycopeptide PLANT PEPTIDE CONTAINING SULFATED TYROSINE 1 (PSY1), promote proliferation of cells in culture (Matsubayashi *et al.*, 1996; Matsubayashi and

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

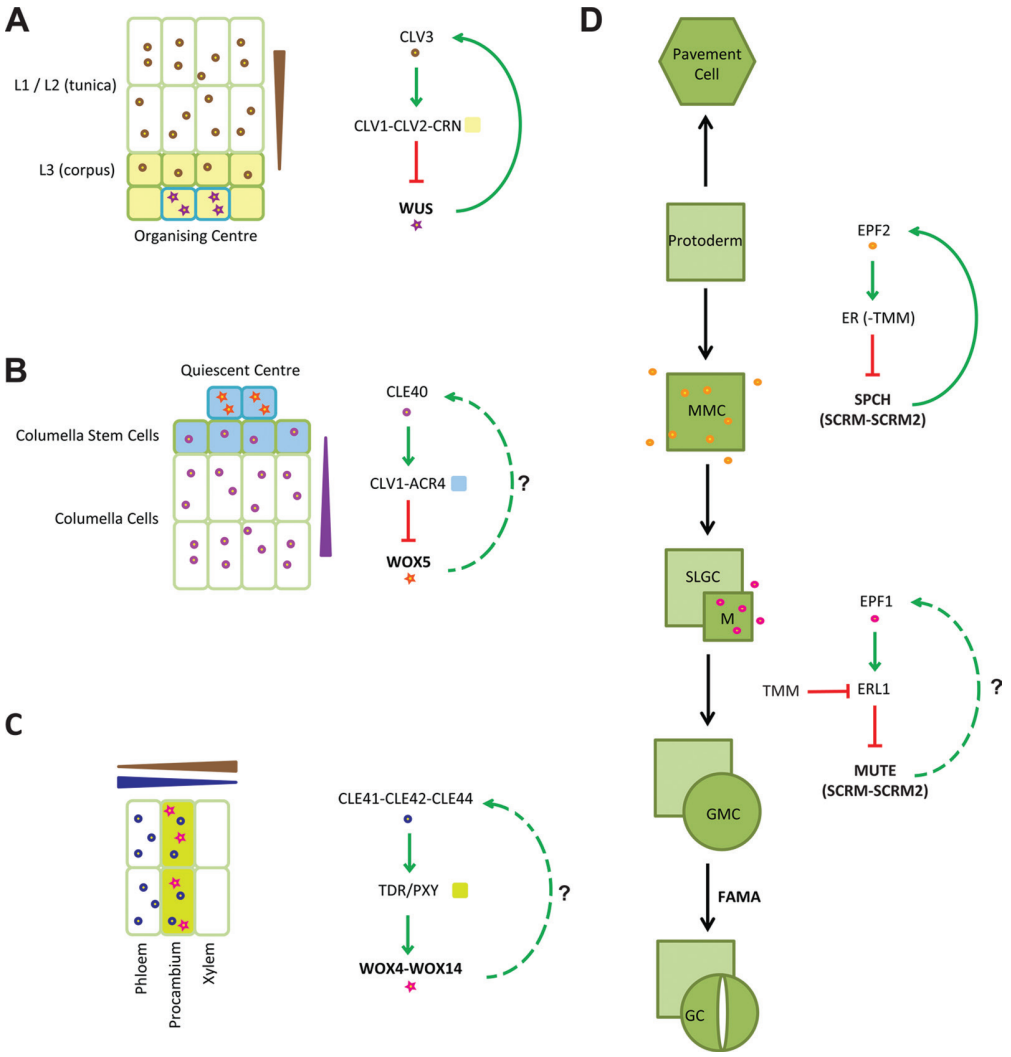


Fig. 2. Small signalling peptide–transcription factor feedback loops. Schematic representation of (A) shoot apical meristem, (B) root apical meristem, (C) vascular development, and (D) stomatal development, highlighting the major components of the signalling cascade, namely the small signalling peptide, the receptor kinase complex members, and the downstream transcription factor.

Sakagami, 1996; Yang *et al.*, 1999, 2000, 2001; Amano *et al.*, 2007; Komori *et al.*, 2009). However, *in planta*, PSK-α and PSY1 appear to be associated mainly with cell expansion. Overexpression of *PSK4*, the most prominently expressed *PSK*-α precursor gene, leads to a faster growth of *Arabidopsis* roots (Matsubayashi *et al.*, 2006*a*). Similarly, treatment with PSK-α results in a significant increase in primary root length of wild-type seedlings. The promoting effect on root elongation is essentially the consequence of a positive effect on cell elongation, namely meristematic cells became larger in PSK-α-treated plants resulting in an overall larger meristem (Kutschmar *et al.*, 2009). Similarly, hypocotyl protoplasts expand in the presence of PSK-α in a dose-dependent manner (Stuhrwohldt *et al.*, 2011). Likewise, overexpression of *PSY1* and application of natural PSY1 peptide results in increased root growth and/or larger cotyledons, again mainly due to increased cell size (Amano *et al.*, 2007).

RAPID ALKALINIZATION FACTORs (RALFs) and RALF-LIKE (RALFL) peptides are a family of 34 genes in *Arabidopsis* that give rise to an approximately 49 aa mature peptide (Pearce *et al.*, 2001; Olsen *et al.*, 2002; Bedinger *et al.*, 2010; Cao and Shi, 2012). Plants grown on medium to which RALF peptide has been added display an immediate cessation of primary root growth (Pearce *et al.*, 2001). Overexpression of *AtRALF1* and *AtRALF23* results in a dwarf phenotype, while downregulation of *NaRALF* in *Nicotiana attenuata* promotes root elongation (Wu *et al.*, 2007; Matos *et al.*, 2008; Srivastava *et al.*, 2009). While there is clearly a RALF- and RALFL-mediated effect on growth, this is probably through controlling cell expansion. Similarly, the tomato (*Solanum lycopersicum*) *SlPRALF* is specifically expressed in pollen, and synthetic SlPRALF peptide acts as a negative regulator of pollen-tube elongation (Covey *et al.*, 2010).

Finally, the reduction in root length in *polaris* (*pls*), mutant for a gene encoding a 36 aa peptide, is mainly because root meristem and cortex cells are shorter and more radially expanded than in the wild type (Casson *et al.*, 2002).

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Regulation of cell proliferation

As mentioned above, cell proliferation plays an important role during plant growth. The DEVIL/ROTUNDIFOLIA (DVL/ROT) peptides, which are 41–145 aa and for which no evidence for post-translational processing or secretion exists, have been shown to play a role in cell proliferation (Fig. 1). Overexpression of *DVL*/*ROT* family members results in pleiotropic phenotypes, including a decrease in cell proliferation in the leaf blade, clustered inflorescences, shortened pedicels, short siliques with horned tips, and protrusions on the base of trichomes (Narita *et al.*, 2004; Wen *et al.*, 2004; Ikeuchi *et al.*, 2011; Valdivia *et al.*, 2012).

Regulation of vascular development

Vascular tissues, composed of xylem, phloem, and procambium/cambium, are important for plants to transport water and nutrients throughout their structures and to provide mechanical support (Scarpella and Helariutta, 2010). The (pro)cambium cells are vascular stem cells between xylem and phloem and are able to differentiate into both tissues (Fukuda, 2004).

TRACHEARY ELEMENT DIFFERENTIATION INHIBITOR FACTOR (TDIF) is a CLE peptide that was first identified from a *Zinnia* cell culture and that controls the tracheary element differentiation (Fukuda and Komamine, 1980; Kondo *et al.*, 2006). In *Arabidopsis*, *TDIF* is encoded by *CLE41* and *CLE44* (Fukuda *et al.*, 2007). *TDIF*/*CLE41*/*CLE44* acts as a phloem-derived, non-cell-autonomous signal to promote the proliferation of cambial cells while suppressing xylem differentiation in leaf, root, hypocotyl, and stem vasculature (Hirakawa *et al.*, 2008; Etchells and Turner, 2010; Hirakawa *et al.*, 2010) (Fig. 2C). In wild-type cambium, cell divisions are mostly periclinal, but *CLE41* overexpression lines display cambial cell division in a range of different orientations. In addition, these lines exhibit phloem expanding towards the centre of the hypocotyl and inflorescence stem and developing in regions where xylem is normally localized (Etchells and Turner, 2010). Cambium and protoxylem cell-identity markers indicate that application of CLE41 peptide promotes proliferation of vascular cells, although delaying downstream differentiation into phloem and xylem cell lineages (Whitford *et al.*, 2008). Additionally, TDIF treatment activates both periclinal and anticlinal division of cambial cells in hypocotyls, enlarging the hypocotyl stele (Hirakawa *et al.*, 2008). In contrast, the hypocotyl stele of *cle41* mutants is thinner than in the wild type but can be enlarged by TDIF treatment (Hirakawa *et al.*, 2010).

The amino acid sequence of CLE42 is highly similar to that of TDIF (Kondo *et al.*, 2006), and *CLE42* overexpression lines also display more cells in vascular bundles and an increased diameter of the hypocotyl cylinder (Etchells and Turner, 2010). However, in contrast to *CLE41* and *CLE44*, *CLE42* seems to be expressed in the SAM and axillary meristems, and not in the vasculature, and appears mostly to regulate branching (Yaginuma *et al.*, 2011). Furthermore, two other *Arabidopsis* genes, *CLE9* and *CLE10*, encode the same dodecapeptide and are specifically expressed in the stele. Both overexpression of *CLE10* and CLE10 peptide treatment inhibit protoxylem vessel formation (Kondo *et al.*, 2011).

Overexpression of *CLE45* results in a lack of germination and, although one plant was recovered, the overexpression of *CLE45* results in extreme dwarfism and death (Depuydt *et al.*, 2013). However, application of synthetic CLE45 peptide produced a weaker phenotype that was not lethal to the plant and impeded the transition from proliferation to differentiation in root phloem cells, suggesting a role for CLE45 during phloem development (Depuydt *et al.*, 2013).

Finally, *pls* mutants are defective in leaf vascular development, displaying a reduced leaf vascularization compared with wild type (Casson *et al.*, 2002; Liu *et al.*, 2010).

Regulation of stomatal development

Stomata are an adaptation of land plants that allow controlled gas and water exchange (Hara *et al.*, 2007). Stomata consist of two guard cells, which are able to mechanically alter their shape to create a pore in the epidermis. These guard cells are products of a succession of symmetric and asymmetric cell divisions in which several small signalling peptides are involved (Shimada *et al.*, 2011; Torii, 2012*b*) (Fig. 1).

EPIDERMAL PATTERNING FACTOR 1 (EPF1, 52 aa) and EPF2 (52 aa) belong to a family of 11 EPF and EPF-LIKE peptides, which are thought to be involved in regulation of epidermal cell development (Hara *et al.*, 2009). Typically, these secreted cysteine-rich peptides contain six or eight conserved cysteines in the C-terminal mature peptide region (Torii, 2012*a*). Overexpression of *EPF1* results in reduced numbers of stomata, leading to decreased overall growth and sterility (Hara *et al.*, 2007). In the most severe overexpression lines, no stomata were formed at all, suggesting that EPF1 functions in a dose-dependent manner (Hara *et al.*, 2007). The *epf1* knockout mutants displayed an increase in stomatal density and, additionally, had clusters of stomata (Hara *et al.*, 2007). This suggests that the mature EPF1 peptide (Ohki *et al.*, 2011) is able to control both the number and the spacing of stomata (Fig. 2D). EPF2 restricts asymmetric cell division during stomatal development (Hunt and Gray, 2009). *epf2* knockout mutants display large numbers of small epidermal cells and few mature pavement cells (Hunt and Gray, 2009). Overexpression of *EPF2* results in a reduction of stomata development, and increased numbers of cells enter into the pavement cell lineage (Hunt and Gray, 2009). It is thought that the EPF2 peptide regulates the number of cells entering the stomatal cell lineage, preventing the production of mature pavement cells but also inhibiting the formation of stomata (Hunt and Gray, 2009; Ohki *et al.*, 2011) (Fig. 2D).

In addition to the EPFs, there are 9 EPF-LIKE (EFPL) peptides, ranging from 45 to 76 aa (Hara *et al.*, 2009; Torii, 2012*a*), but, for example, EPFL6/CHALLAH (CHAL) and CHALLAH-LIKE (CLL) peptides are expressed in the vasculature (*CHAL*) and cotyledon bases (*EPFL5*/*CLL1* and *EPFL2*/*CLL2*) (Ohki *et al.*, 2011). In agreement with their expression pattern, the *chal*, *cll1*, and *cll2* single and the

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

triple *chal cll1 cll2* mutants display no differences in stomatal development (Abrash *et al.*, 2011). In contrast, exogenous application of EPFL4 and EPFL5 synthetic peptides does result in decreased numbers of stomata (Hara *et al.*, 2009). Overexpression lines of *CHAL*, *CLL1*, and *CLL2* displayed a significantly decreased number of stomata (Abrash *et al.*, 2011). Taken together, it appears that EPFL6/CHAL, EPFL5/CLL1, and EPFL2/CLL2 inhibit stomatal development in *Arabidopsis* stems and hypocotyls (Abrash *et al.*, 2011).

STOMAGEN/EPFL9, a 45 aa peptide, acts as a mesophyll-derived positive regulator of guard cell development (Sugano *et al.*, 2009). Overexpression of *STOMAGEN* results in an increased stomata count, as well as decreased incidence of the one-cell spacing of stomata. RNA interference (RNAi)-mediated knockdown of *STOMAGEN* results in decreased numbers of stomata (Sugano *et al.*, 2009). STOMAGEN has an antagonistic relationship with EPF1 and EPF2, as RNAi-mediated knockdown of STOMAGEN in the *epf1 epf2* mutant displayed no significant difference in stomatal density compared with the wild type, whereas the *efp1 epf2* mutant displayed increased numbers of stomata (Sugano *et al.*, 2009). Similarly, simultaneous application of synthetic EPF2 and STOMAGEN also revealed this antagonistic relationship between the two peptides, indicating that they may share a common receptor, or that the signalling pathways in which the two peptides are involved have antagonistic functions (Ohki *et al.*, 2011; Shimada *et al.*, 2011).

Regulation of lateral root initiation and development

Lateral root formation is a major determinant of root system architecture to aid water uptake, acquisition of nutrients, and anchorage of plants (Smith and De Smet, 2012). During lateral root initiation, a subset of xylem pole pericycle cells undergo a limited number of anticlinal asymmetric cell divisions, followed by periclinal division of the small daughter cells and additional rounds of cell divisions, which eventually lead to a lateral root primordium that breaks through the overlying tissues (Péret *et al.*, 2009). Significant progress has been achieved in understanding the role of phytohormones such as auxin and cytokinin during lateral root development (Benkova and Bielach, 2010; De Smet and Beeckman, 2011; De Smet, 2012; Lavenus *et al.*, 2013), but a few peptides have also been reported to affect this process (Fig. 1).

All the *RGF*/*GLV*/*CLEL* gene family members, except *GLV1*, are expressed during lateral root development (Fernandez *et al.*, 2013*a*). Overexpression of *GLVs* results in inhibition of lateral root development and root branching (Fernandez *et al.*, 2013*a*). Similarly, overexpression of *CLEL6* or *CLEL7* dramatically delays lateral root development in *Arabidopsis*, and this cannot be rescued by exogenous application of the lateral root-inducing phytohormone auxin (Meng *et al.*, 2012). Additionally, the pericycle cells in the *CLEL6* and *CLEL17* overexpression lines appear to divide asymmetrically as well as symmetrically, preventing the formation of a central core of small pericycle cells and progression to the next developmental stage (Meng *et al.*, 2012).

Recently, INFLORESCENCE DEFICIENT IN ABSCISSION (IDA), which is known mainly for its role in abscission (see below) (Butenko *et al.*, 2003), was shown to control lateral root architecture (Kumpf *et al.*, 2013). Interestingly, lateral root initiation is not affected in *ida* mutants, but the percentage of late stages of lateral root primordia is much higher, suggesting that IDA represses lateral root emergence (Kumpf *et al.*, 2013).

In addition, a few other peptide families have been associated with lateral root development. For example, *PLS* is expressed in lateral root tips and the *pls* mutant displays a reduced number of lateral roots (Casson *et al.*, 2002; Chilley *et al.*, 2006). Also, *CEP1* is expressed in lateral root primordia and, when overexpressed, reduces lateral root growth (Ohyama *et al.*, 2008). Finally, similar to its effect on the primary root, externally applied PSK-α promotes lateral root elongation (Kutschmar *et al.*, 2009).

Regulation of root waving and gravitropism

Gravitropism is the process by which a plant governs the directional growth of both root and shoot in response to gravity. This process requires cells that can sense gravity, followed by differential growth (Morita, 2010).

Exogenous peptide application and overexpression of *GLV1*/*RGF6*, *GLV2*/*RGF9*, and *GLV3*/*RGF4* results in loss of a gravitropic response in roots and leads to a curled root phenotype (Whitford *et al.*, 2012). However, only *GLV3* is expressed in the root, while *GLV1* and *GLV2* are expressed in the leaves, hypocotyl, and flowers (Whitford *et al.*, 2012). Interestingly, both RNAi targeted against *GLV1* and *GLV2* and overexpression of *GLV1* and *GLV2* result in altered hypocotyl gravicurvature. Overexpression of *GLV3* also reduces hypocotyl gravicurvature, while RNAi lines had no effect on this process, suggesting that strict control of expression prevents overlapping functions between homologues (Whitford *et al.*, 2012). The latter is supported by the distinct expression patterns of the *GLVs* during growth and development (Fernandez *et al.*, 2013*a*)

cle40 knockout mutants also display a subtle root waving phenotype (Fiers *et al.*, 2005). This may, however, be related to the loss of control over cell division or, alternatively, the minor agravitropism might be induced by the delayed differentiation of columella stem cells (see above), resulting in a deficient starch accumulation (Stahl and Simon, 2009).

Regulation of root-hair patterning and development

Root hairs are important as they increase the surface area for uptake of water and minerals. Root hairs consist of single cells that have differentiated from epidermal precursors in response to a positional cue from the cortex (Grebe, 2012). This positional cue regulating development and spacing of root hairs is also thought to involve small signalling peptides (Fig. 1).

Two members of the *RGF*/*GLV*/*CLEL* family, *GLV4* and *GLV8*, are expressed in the rhizodermis, and regulate root-hair size and shape (Fernandez *et al.*, 2013*a*). *GLV4* is

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

expressed in all epidermal cells, whereas *GLV8* expression is only observed in non-hair cells. The *glv8* loss-of-function and *amiRglv4* roots displayed shorter root hairs compared with wild type. In contrast, overexpression of *GLV4*, *GLV5*, and *GLV8* resulted in an increased frequency of branched root hairs (Fernandez *et al.*, 2013*a*).

Finally, downregulation of *NaRALF* in *Nicotiana attenuata* prevents tip growth of root-hair trichoblasts, resulting in localized bulges, which eventually burst (Wu *et al.*, 2007).

Regulation of gametophyte development and fertilization

In angiosperms, female gametophyte development is essential for the production of seeds. Seed development is initiated when pollen adheres to the stigma, resulting in the formation of a pollen tube through the carpel tissue, which connects to the egg cell through the mycropylar space. Two sperm nuclei are then delivered to the female gametophyte, the first fertilizes the egg, while the second fuses with the central cell in order to form the endosperm (Drews and Koltunow, 2011). With respect to the male gametophyte, mature tapetal cells are important for nourishment of developing pollen in *Arabidopsis* (Yang *et al.*, 2003).

EGG CELL 1 (EC1) is a cysteine-rich peptide present in wheat egg cells (Sprunck *et al.*, 2012). In *Arabidopsis*, five EC1-like genes are expressed in female reproductive tissues and activate sperm during fertilization. A combination of knockout and RNAi-mediated knockdown of this highly functionally redundant peptide family results in reduced fertilization of ovules and a decreased seed count upon maturation of the silique (Sprunck *et al.*, 2012).

EGG APPARATUS 1 (ZmEA1) in *Zea mays*, CYSTEINE-RICH PEPTIDE 1 (TfCRP1)/LURE1 and TfCRP3/LURE2 in *Torenia fournieri*, and TcCRP1 in *Tillandsia concolour* function as chemoattractants secreted from the ovule to attract pollen tubules to the micropyle (Kanaoka *et al.*, 2011; Márton *et al.*, 2012; Okuda *et al.*, 2013). For example, knockdown of ZmEA1 decreased the ability of the pollen tube to locate the micropyle, and application of synthetic ZmEA1 caused maize pollen tubes to grow towards the source on agar plates (Márton *et al.*, 2005; Márton *et al.*, 2012). In addition, *ZmEA1* expressed in *Arabidopsis* ovules similarly attracts maize pollen tubes (Márton *et al.*, 2012).

Finally, RNAi-mediated knockdown of *Zea mays* EGG APPARATUS-LIKE1 (ZmEAL1), a 49 aa cysteine-rich peptide secreted from the egg cell, results in differentiation of antipodal cells to secondary central cells (Krohn *et al.*, 2012).

TAPETUM DETERMINANT1 (TPD1) is involved in development of tapetal cells in *Arabidopsis* anthers (Yang *et al.*, 2003). The *tpd1* mutant is unable to form pollen, and contained decreased numbers of tapetal cells and increased numbers of microsporocytes, suggesting that *TPD1* is responsible for differentiation of tapetal precursors into mature tapetal cells (Yang *et al.*, 2003). Overexpression of *TPD1* results in enlarged tapetal cells and delayed degeneration of the tapetum, suggesting that *TPD1* is also involved in maintenance of tapetum (Yang *et al.*, 2005). Overexpression of *TPD1* additionally causes carpel cells to continue dividing until maturation of the silique, resulting in wider siliques than wild-type *Arabidopsis* (Yang *et al.*, 2005).

Regulation of abscission

Abscission is an important process through which plants get rid of unwanted organs such as flowers, leaves, and fruit when they are damaged or have served their purpose (Sexton and Roberts, 1982; Patterson, 2001).

IDA, which is expressed in the abscission zone, plays an important role in abscission. The *ida* loss-of-function mutants can form an abscission zone but cannot complete floral abscission, which leads to dry floral organs still attached to the plant after dehiscence of seeds (Butenko *et al.*, 2003). In contrast, overexpression of *IDA* leads to an increased number of abscission zone cells and results in ectopic abscission of sepals and silique valves (Stenvik *et al.*, 2006). Similarly, IDA-LIKE (IDL) peptides appear to play a similar role, and *IDL* coding regions can partially rescue the phenotype of *ida* mutants (Stenvik *et al.*, 2008).

Regulation of nodulation

Legumes form root nodules in order to establish a symbiotic relationship with *Rhizobia*. This mutually beneficial relationship allows the *Rhizobia* to proliferate in an optimal environment to convert atmospheric nitrogen to ammonium, which is then used by legumes to allow growth on nitrate-deficient soils (Osipova *et al.*, 2012).

RHIZOBIA INDUCED CLE1 (RIC1), RIC2 and NITRATE INDUCED CLE1 (NIC1) belong to a family of CLE consensus peptides present in legume roots, which are involved in autoregulation of root nodulation, a mechanism of inhibition of nodule formation by already induced or existing root nodules (Reid *et al.*, 2013). Overexpression of *GmRIC1* resulted in complete suppression of nodulation in *Glycine max* (Reid *et al.*, 2011), while knockdown of *RIC1* and *RIC2* in *Medicago truncatula* resulted in increased nodulation (Mortier *et al.*, 2010). Interestingly, structurally similar CLE peptides also reduce nodulation, when exogenously applied (Osipova *et al.*, 2012).

Another class of cysteine-rich 3–5 kDa peptides has been observed in nodules of inverted repeat-lacking clade legumes, such as *Medicago*, *Pisum*, and *Trifolium*, but are not present in non-inverted repeat-lacking clade legumes, such as *Lotus.* These peptides have been named nodule-specific cysteine-rich (NCR) peptides, and are structurally similar to cysteine-rich antimicrobial proteins (Van de Velde *et al.*, 2010). Application of NCR035 alters the membrane structure of *Rhizobia*, inhibiting bacterial cell division and differentiation and causing the accumulation of larger terminally differentiated bacteroids in *Lotus* (Van de Velde *et al.*, 2010). Application of NCR035, NCR055, and NCR247 to *Rhizobia in vitro* similarly inhibits cell division, and at higher concentrations leads to cell death (Van de Velde *et al.*, 2010). It is likely that the plant expresses the *NCR* peptides in a strictly controlled fashion, causing terminal bacteroid differentiation but not cell death.

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Molecular and biochemical effects of peptides

The morphological phenotypes described above are the consequence of molecular and biochemical changes triggered by small signalling peptides. In this section, we will illustrate the most prominent effects (Figs 2 and 3).

Control of transcription factor expression

Although the precise mechanism of signalling is generally not known, it has been demonstrated for several small signalling peptides that their respective mode of action ultimately leads to altered transcription factor expression patterns (Fig. 2).

CLV3 is expressed primarily in the stem cells of the L1 and L2 layers of the SAM (Fletcher *et al.*, 1999; Meng and Feldman, 2011), and CLV3 has been shown to interact directly with the CLV1 ectodomain (Ogawa *et al.*, 2008). The CLV3 peptide migrates to the L3 layer of the SAM, where it interacts with CLV1 and CLV2 in the SAM stem cells. The CLV1−CLV2−CORYNE (CRN)/SUPPRESSOR OF OVEREXPRESSION OF LIGAND LIKE PROTEIN 1–2 (SOL2) receptor complex acts to transduce the CLV3 signal (Fiers *et al.*, 2005; Müller *et al.*, 2008). The outcome of this signalling cascade will be the suppression of *WUSCHEL* (*WUS*) expression in the organizing centre (Fletcher *et al.*, 1999) (Fig. 2A). WUS, a homeobox transcription factor implicated in both up- and downregulation of genes involved in stem-cell maintenance in the L3 layer of the SAM (Brand *et al.*, 2000; Leibfried *et al.*, 2005; Yadav *et al.*, 2010), is thought to migrate from the organizing centre to the nucleus of adjacent stem cells, where it interacts directly with DNA and triggers *CLV3* expression, thus initiating a negative feedback loop (Kieffer *et al.*, 2006; Yadav *et al.*, 2011). As would be predicted from these interactions, *clv1* and *clv2* knockout mutants display a similar phenotype to *clv3* knockout mutants, inasmuch as they accumulate large numbers of stem cells containing *WUS* at the SAM (Clark *et al.*, 1995; Diévart *et al.*, 2003). WUS also activates expression of *AGAMOUS* (*AG*) in the floral meristem (Lohmann *et al.*, 2001). The presence of AG causes the suppression of *WUS*, suggesting that there may be a CLV–CLE-like signalling loop that also controls the development of floral meristems (Lenhard *et al.*, 2001; Lohmann *et al.*, 2001).

CLE40 is expressed by differentiated columella cells in the RAM, and in *cle40* expression of *WUSCHEL-RELATED HOMEOBOX 5* (*WOX5*)—a quiescent centre (QC) marker and columella stem-cell fate regulator—expands laterally to stem cells (Stahl *et al.*, 2009). Exogenous application of a synthetic CLE40 peptide to the *cle40* mutant restores expression of *WOX5* by restricting it to the QC (Stahl *et al.*, 2009; Stahl and Simon, 2012). Genetic evidence suggests that CLE40 may bind to ARABIDOPSIS CRINKLY4 (ACR4), a receptor-like kinase present in columella stem cells and to a lesser extent in the QC and developing epidermis in the root tip region. The CLE40 peptide is thought to migrate to the columella stem cells, where it interacts with ACR4, and this interaction inhibits the expression of *WOX5* in the QC (Stahl *et al.*, 2009) (Fig. 2B). As ACR4 is able to form heterodimers with CLV1 in the RAM, this supports a CLE40–CLV1–ACR4 complex regulating a homeobox transcription factor in the RAM, similar to the CLV3–CLV1–CLV2 mechanism in the SAM (Stahl *et al.*, 2009, 2013; Stahl and Simon, 2012; Williams and De Smet, 2013). While CLE40 signalling in the columella does not require CLV2 (Stahl *et al.*, 2013), *clv2* mutants were demonstrated to suppress the short root phenotype induced by *CLE19* overexpression (Casamitjana-Martinez *et al.*, 2003), which indicates that RAM development may be controlled by multiple overlapping signalling pathways.

In addition to CLEs, *RGF1* is expressed in the QC and columella stem cells and RGF1 peptide diffuses into the surrounding cells, where it is involved in the spatial regulation of *PLETHORA* (*PLT*) expression in areas of auxin maxima (Matsuzaki *et al.*, 2010). The transcription factor *PLT* is expressed in response to auxin and is required (along with SHORTROOT and SCARECROW) for the correct patterning and maintenance of the root stem-cell niche (Aida *et al.*, 2004). The *plt1 plt2* mutant shows little or no response to RGF1 peptide, and RGF1 peptide treatment causes expansion of PLT2 to the basal zone of the meristem but not the accumulation of *PLT2* transcripts, indicating that RGF1 regulation of PLT2 is largely at the post-transcriptional level (Matsuzaki *et al.*, 2010). In addition, PIN-FORMED (PIN) auxin efflux facilitators and PLTs form a network controlling auxin-mediated root patterning: *PLT* genes maintain *PIN* transcription and PIN proteins restrict *PLT* expression, which stabilizes the position of the stem-cell niche (Grieneisen *et al.*, 2007). In this context, RGF/GLV/CLEL peptides affect the polarized auxin transport required for root stem-cell specification by acting on the membrane localization of PIN2 (Whitford *et al.*, 2012) (see below). Interestingly, the *PLT* genes are required for maintaining *PIN2* and the response to auxin in the RAM (Galinha *et al.*, 2007). This may indicate a chain of events where some RGF/GLV/CLEL family members initiate localized auxin maxima through regulating localization of PIN proteins, while other RGF/GLV/CLELs respond to this increase in auxin and regulate the patterning of the RAM stem-cell niche via PLTs, or a combination of these events. This is, in part, supported by the transcriptional upregulation of some *RGF/GLV/CLELs* following auxin treatment, while other *RGF/GLV/CLELs* are not affected by auxin (Zhou *et al.*, 2010; Whitford *et al.*, 2012).

Application of CLE45 excluded *ALTERED PHLOEM DEVELOPMENT* (*APL*)—a transcription factor required for phloem identity—from the meristematic region (Depuydt

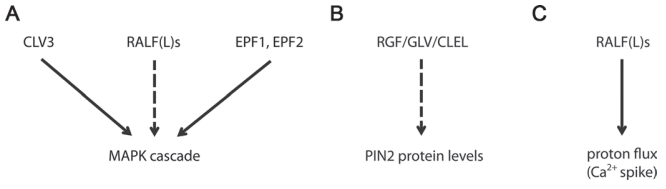


Fig. 3. Other direct and/or indirect outputs of small signalling peptides. Illustration of small signalling peptides affecting (A) MAPK cascades, (B) PIN2 protein levels, and (C) proton flux.

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

et al., 2013). Given that *barely any meristem 3* (*bam3*) mutants are insensitive to CLE45 peptide treatment, this suggests that the interaction between CLE45 and BAM3, a receptor kinase required for the development of vascular strands in the leaf (DeYoung *et al.*, 2006), may be key to controlling the development of phloem tissue. Also implicated in the control of protophloem identity is the transcriptional co-regulator BREVIS RADIX (BRX). As *brx* null mutants display inhibited protophloem development, it is suggested that BRX may play a role in inducing protophloem development, thus creating a feedback loop with BAM3 signalling (Depuydt *et al.*, 2013).

CLE41 (and CLE42) and PHLOEM INTERCALATED WITH XYLEM (PXY)/TDIF RECEPTOR (TDR) were identified as a ligand–receptor pair that regulates vascular cell division and differentiation, and vascular bundle organization (Fisher and Turner, 2007; Hirakawa *et al.*, 2008). The *pxy* knockout mutant exhibits a small reduction in vascular cell number (Fisher and Turner, 2007). In the *pxy* mutant, *WUSCHEL-RELATED HOMEOBOX4* (*WOX4*) expression is downregulated (Agusti *et al.*, 2011). *WOX4* is expressed mainly in the tissues closely associated with the vasculature in the whole plant, which is similar to the *PXY* expression pattern, and WOX4 promotes vascular cell division (Ji *et al.*, 2010). Specifically, *WOX4* expression can be rapidly upregulated by application of TDIF, and analysis of *wox4-1*, *tdr-1*, and *tdr-1 wox4-1* mutants indicated that WOX4 is necessary for the enhancement of procambial cell proliferation by TDIF signalling (Hirakawa *et al.*, 2010; Suer *et al.*, 2011) (Fig. 2C). Recently, WOX14 has also been shown to be a downstream component of PXY signalling, as *WOX14* is downregulated in *pxy* mutants and upregulated in *CLE41* overexpressing lines. *WOX14* is expressed predominantly in vascular tissue, and acts redundantly with WOX4 in regulation of vascular cell division (Etchells *et al.*, 2013). Also, it appears that the ethylene–ETHYLENE RESPONSE FACTOR (ERF) pathway is parallel to the CLE41–PXY pathway in controlling the maintenance of plant vascular systems, and that the ethylene–ERF pathway is repressed by PXY-mediated signalling (Etchells *et al.*, 2012). In addition, a (genetic) interaction between *PXY* and the receptor kinase *ERECTA* (*ER*) may represent a novel signalling pathway that co-ordinates differential growth over several cell layers in *Arabidopsis* via non-cell autonomous factors acting downstream of *ER* (Etchells *et al.*, 2013). Finally, along with CLE41 and CLE42, microarray and mutant analyses indicate that CLE10 inhibits the vascular development via inhibiting cytokine negative regulators in a CLV2-dependent manner (Kondo *et al.*, 2011).

STOMAGEN is a mesophyll-derived small signalling peptide, which positively regulates stomatal development, causing upregulation of several transcription factors—depending on the stage of protoderm differentiation—into the guard cell lineage (Shimada *et al.*, 2011). EPF1 and EPF2 restrict stomatal development in an antagonistic process to STOMAGEN. EPF1 and EPF2 act separately on different cell lineages to restrict stomatal development. Interestingly, STOMAGEN, EPF1, and EPF2 are all indicated to bind competitively to the TOO MANY MOUTHS (TMM)–ERECTA family (ERf) receptor complex (Shimada *et al.*, 2011). It is thought that EPF stimulation of TMM–ERf complexes triggers a mitogen-activated protein kinase (MAPK) cascade (see below), culminating in repression of SPEECHLESS (SPCH), MUTE, and FAMA transcription factor function, while STOMAGEN binds these complexes but does not cause repression (Shimada *et al.*, 2011) (Fig. 2D). SPCH, MUTE, and FAMA are thought to act in complexes with SCREAM1 (SCRM1) and SCRM2 to determine cell fate at different stages of development (Kanaoka *et al.*, 2008). Additionally, SCRM1–SCRM2–SPCH complexes result in the upregulation of EPF2, initiating a negative feedback loop to suppress further expression of *SPCH* in the presence of STOMAGEN (Torii, 2012*a*). It has also been suggested that, instead of several distinct ERf/TMM complexes detecting EPF1 or EPF2 competitively with STOMAGEN, these proteins are all part of one large complex, which is able to bind EPF1, EPF2, and STOMAGEN, but each peptide interacts with different regions of the complex, which regulates *SPCH* expression accordingly (Jewaria *et al.*, 2013).

During abscission, IDA—interacting with HAESA (HAE) and HAE-LIKE 2 (HSL2) (Stenvik *et al.*, 2008)—affects the transcription factor BREVIPEDICELLUS (BP)/KNOTTED-LIKE FROM ARABIDOPSIS THALIANA1 (KNAT1), which in turn regulates expression of *KNAT2* and *KNAT6* (Shi *et al.*, 2011).

ZmEAL1 is secreted by the egg cell in the ovule, and functions to define antipodal cell fate by positive regulation of the transcription factor INDETERMINATE GAMETOPHYTE 1 (IG1) (Krohn *et al.*, 2012). As IG1 has been indicated to limit proliferation in the embryo sac, promoting the correct differentiation of embryo cells (Evans, 2007), it was suggested that this may be due to aberrant proliferation, causing incorrect placement of pluripotent cells, which differentiate into incorrect cell types due to lack of correct signalling pathways present at their location (Krohn *et al.*, 2012). If this is the case, it may indicate that the egg cell forms an organizing centre in order to maintain cell niches once cell fate has been determined (Krohn *et al.*, 2012).

While it is clear from these examples that small signalling peptides affect transcription factors, in most cases the intermediate steps from small signalling peptide to transcriptional effect have not been identified.

Phosphorylation

Protein phosphorylation by kinases and dephosphorylation by phosphates represent a major mechanism regulating cell signalling (Terol *et al.*, 2002; Choudhary and Mann, 2010). Some small signalling peptides have been proposed to signal through a MITOGEN-ACTIVATED PROTEIN KINASE (MAPK) cascade, as such controlling transcription factor activity (see above) and/or other downstream events (Fig. 3A). However, while this is clearly an important aspect of small signalling peptide outputs, this has only been explored in a limited way.

For example, application of RALF results in activation of MAPKs (Bedinger *et al.*, 2010). However, as the most rapid response to RALF application is a transient Ca^{2+} spike in the

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

cytoplasm, it is possible that the primary function of RALF peptides is to induce a Ca^{2+} signalling cascade, and that MAPK activation and proton flux are downstream targets of this cascade (Bedinger *et al.*, 2010)

Signalling from CLV receptors upon CLV3-mediated activation co-ordinates the activity of MAPKs, specifically MPK6, during SAM homeostasis (Betsuyaku *et al.*, 2011*b*).

EPF1 and EPF2 activate MPK6, which is part of an MAPK module, resulting in the phosphorylation and destabilization of the transcription factor SPEECHLESS (SPCH) and subsequent decrease of the number of stomatal lineage cells (Lee *et al.*, 2012; Jewaria *et al.*, 2013).

Effect on auxin transport

PIN proteins are key auxin efflux carriers and are essential for the establishment of a proper auxin maximum and therefore regulate root patterning (Grunewald and Friml, 2010). Interestingly, *pin2* mutants are resistant to GLV peptide treatment. In addition, following GLV treatment, PIN2 protein levels increase at the membrane, but the polarity of PIN2 does not change and other auxin transporters, such as AUX1, PIN1, and PIN3, are not affected (Fig. 3B). This indicates that PIN2 is a target of the *GLV* signalling pathway (Whitford *et al.*, 2012), affecting auxin transport and consequently gravitropic response. Some *GLV* genes are expressed during lateral root and root-hair development (Fernandez *et al.*, 2013*a*) and, possibly, GLVs also act here—at least partly—via changing auxin gradients, which is crucial for lateral root development (Péret *et al.*, 2009) and root-hair formation (Jones *et al.*, 2009), by regulating intracellular vesicle trafficking and plasma membrane localization of PIN2. However, in this context, auxin treatment cannot recover the lateral root defect caused by overexpressing *CLEL6* or *CLEL7* (Meng *et al.*, 2012).

PLS plays an important role in auxin homeostasis, as free indole-3-acetic acid concentrations in *pls* knockout mutants are much lower than in the wild type (Chilley *et al.*, 2006). The *pls* mutant is defective in ethylene signalling and can be complemented by knocking down the function of the ETHYLENE RECEPTOR 1 (ETR1), indicating that *pls* mutants are hypersensitive to ethylene. Ethylene can inhibit auxin transport (Suttle, 1988), and enhanced ethylene signalling in *pls* represses auxin transport and disturbs auxin homeostasis. Presumably PLS regulates root growth and lateral root development via ethylene-mediated control of auxin signalling (Chilley *et al.*, 2006).

Effect on brassinosteroid signalling

Two PSK receptors, PHYTOSULFOKINE RECEPTOR 1 (PSKR1) and PSKR2, have been identified (Matsubayashi *et al.*, 2006*a*,*b*; Kutschmar *et al.*, 2009; Stuhrwohldt *et al.*, 2011). Genetic and pharmacological data indicate that PSK perception in atrichoblasts generates a brassinosteroid-dependent signal that travels to neighbouring trichoblast cells. However, PSK signalling does not appear to significantly alter the expression of key brassinosteroid synthesis genes, indicating that the regulation may occur at the protein level, possibly in the brassinosteroid signalling cascade (Hartmann *et al.*, 2013).

Alkalinization of the extracellular environment

The receptor for RALF is currently unknown, although 25 and 120 kDa proteins have been detected by photoaffinity cross-linking in *Lycopersicon peruvanium* (Scheer *et al.*, 2005). Exogenous application of AtRALF1 induces a Ca^{2+} spike in the cytoplasm, suggesting that the RALF receptor may be involved in control of proton flux, thus influencing uptake of ions, metabolites, water, and hormones (Fig. 3C) (Bedinger *et al.*, 2010). Application of RALFs and RALFLs cause alkalinization of the surrounding medium more rapidly than SYSTEMIN, a wound-inducible defence-related peptide that causes alkalinization of medium when added to cultures of *Lycopersicon peruvanium* (Pearce *et al.*, 2001; Ryan *et al.*, 2002; Bedinger *et al.*, 2010; Covey *et al.*, 2010). Similarly, the effect of *Nicotiana attenuata NaRALF* on root hairs is also associated with disrupted apoplastic pH regulation (Wu *et al.*, 2007).

Cell-wall remodelling

Cell separation during lateral root emergence requires modifications to the cell wall, and breaking down of cell walls is done by several cell-wall-modifying enzymes such as EXPANSINs (EXPs), PECTINASEs, and POLYGALACTURONASEs (PGs) (Petersen *et al.*, 1996; Roberts *et al.*, 2002; Rose, 2004). In roots, the expression of *XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6* (*XTR6*) and *EXP17* is reduced and delayed in *ida* roots, suggesting that IDA controls cell-wall remodelling during lateral root formation (Kumpf *et al.*, 2013). Similarly, in stage 15 *ida* mutant receptacles, several glycosyl hydrolases are differentially expressed (Niederhuth *et al.*, 2013), supporting the suggestion that IDA-mediated cell-wall remodelling is also important during abscission.

Chemo-attractant for pollen tube growth

The pollen tube grows by membrane extension (Campanoni and Blatt, 2007). ZmEA1 acts as a chemo-attractant to the growing pollen tube and is internalized into the pollen tubule by vesicular action and rapidly degraded (Márton *et al.*, 2012). Although the receptor for ZmEA1 is unknown, it has recently been demonstrated that simultaneous inactivation of receptor-like cytoplasmic kinases LOST IN POLLEN TUBE GUIDANCE 1 (LIP1) and LIP2 in *Arabidopsis* results in decreased sensitivity to AtLURE1, which is homologous to ZmEA1 (Liu *et al.*, 2013). This suggests that these ligand–receptor interactions are critical for the correct directional growth of the pollen tube during fertilization (Liu *et al.*, 2013).

Activation of sperm during fertilization

EC1-like peptides activate sperm during fertilization (Sprunck *et al.*, 2012). Application of the synthetic forms of EC1.1

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

peptides to isolated sperm induced migration of HAPLESS2 (HAP2)—the only known plant gamete fusogen—from the sperm cytoplasm to the membrane, indicating that the EC1 family of peptides are involved in *Arabidopsis* gamete fusion (Sprunck *et al.*, 2012).

Evolutionary aspects of small signalling peptides

Common themes—such as regulation of transcription factor expression (Fig. 2), protein stability, phosphorylation, and alkalinization—regarding the downstream effects of small signalling peptides are emerging, but due to off-target effects, redundancy, and lack of knockout mutants, it is often complicated to study this aspect of their signalling. To reduce the number of variables, it would therefore be helpful if small peptide signalling could be studied in simpler, evolutionary older model systems. For example, several of the small signalling peptide families are conserved in the moss *Physcomitrella patens* (Rychel *et al.*, 2010; Cao and Shi, 2012).

CLE peptides have been detected in many species of varying complexity, from 89 detected peptides in rice (*Oryza sativa*) to a single non-redundant peptide in the green alga *Chlamydomonas reinhardtii* (Oelkers *et al.*, 2008). This indicates that CLE peptides are a relatively old group of peptides in terms of evolution, as they are present in single-celled organisms. This may indicate that different members of the CLE family have evolved over time to fill niche roles in signalling in a multicellular context and for different processes of development. Different residues critical for function within different CLE peptides indicate that mutations in peptide and receptor protein sequences may have contributed to the plethora of CLE peptides and their respective receptor proteins since the unicellular life form (Reid *et al.*, 2013; Strabala *et al.*, 2006). As the majority of CLE peptides share a CLE consensus region (SKRLVPSGPNPLHN), which is adequate to induce a short root phenotype when applied ectopically, it is possible that the remainder of the pro-precursor protein may be involved in subcellular cell or tissue localization, providing additional specificity to CLE peptide localization in addition to tissue-specific expression under control of promoter regions (Strabala *et al.*, 2006). RALF(L)s can similarly be phylogenetically traced back to early land plant species such as *Selaginella moellendorffii* (two family members) and *Physcomitrella patens* (three family members), and RALF(L) peptides from a wide range of higher plant species contain a conserved YISY sequence, which is required for alkalinization (Pearce *et al.*, 2010; Cao and Shi, 2012).

A single EPF-like peptide was found in *P. patens*, while a gene containing the TYNE motif, otherwise unique to STOMAGEN, was found in *S. moellendorffii* (Rychel *et al.*, 2010). Together with homologues for TMM and YODA in *P. patens*, this suggests that the signalling pathway controlling spacing of stomata is a fundamental and ancient pathway (Rychel *et al.*, 2010).

As small signalling peptides, and the downstream receptors and transcription factors, have homologues in early land plant species, studying how signalling pathways have evolved by determining interactions and downstream components in, for example, *P. patens*, will yield significant insight into the evolution of more complex signalling systems in higher plants.

Conclusion

In conclusion, extensive progress has been made with respect to unravelling the downstream effects of small signalling peptides. However, much work remains to be done to identify receptors, to describe phosphorylation cascades, and to reveal targets. The increased interest from the research community, the availability of novel tools, technical improvements, and evolutionary angles will help to advance the field in the coming years. It is, however, important to note that, while the overexpression of small signalling peptide genes or the application of synthetic peptides belonging to the same family often leads to similar phenotypes, these effects might not always be physiologically relevant. In future, more effort will have to go into the characterization of expression patterns and the identification of knockout and/or knockdown lines for small signalling peptides.

Acknowledgements

This work was supported by a BBSRC David Phillips Fellowship (BB_BB/H022457/1) and a Marie Curie European Reintegration Grant (PERG06-GA-2009–256354) to IDS, and a BBSRC CASE Studentship to N.C. Work in the laboratory of TB was in part financed by the Interuniversity Attraction Poles Programme (IAP VI/33 and IUAP P7/29 'MARS') from the Belgian Federal Science Policy Office. KY has been awarded a scholarship under the State Scholarship Fund by the China Scholarship Council.

References

Abrash EB, Davies KA, Bergmann DC. 2011. Generation of signaling specificity in Arabidopsis by spatially restricted buffering of ligand–receptor interactions. *The Plant Cell* **23,** 2864–2879.

Agusti J, Lichtenberger R, Schwarz M, Nehlin L, Greb T. 2011. Characterization of transcriptome remodeling during cambium formation identifies MOL1 and RUL1 as opposing regulators of secondary growth. *PLoS Genetics* **7,** e1001312.

Aida M, Beis D, Heidstra R, Willemsen V, Blilou I, Galinha C, Nussaume L, Noh Y-S, Amasino R, Scheres B. 2004. The *PLETHORA* genes mediate patterning of the arabidopsis root stem cell niche. *Cell* **119,** 109–120.

Amano Y, Tsubouchi H, Shinohara H, Ogawa M, Matsubayashi Y. 2007. Tyrosine-sulfated glycopeptide involved in cellular proliferation and expansion in Arabidopsis. *Proceedings of the National Academy of Sciences, USA* **104,** 18333–18338.

Barton MK. 2010. Twenty years on: the inner workings of the shoot apical meristem, a developmental dynamo. *Developmental Biology* **341,** 95–113.

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Bedinger PA, Pearce G, Covey PA. 2010. RALFs: peptide regulators of plant growth. *Plant Signaling and Behavior* **5,** 1342–1346.

Beemster GTS, Baskin TI. 1998. Analysis of cell division and elongation underlying the developmental acceleration of root growth in *Arabidopsis thaliana*. *Plant Physiology* **116,** 1515–1526.

Benkova E, Bielach A. 2010. Lateral root organogenesis—from cell to organ. *Current Opinion in Plant Biology* **13,** 677–683.

Betsuyaku S, Sawa S, Yamada M. 2011a. The function of the CLE peptides in plant development and plant–microbe interactions. *Arabidopsis Book* **9,** e0149.

Betsuyaku S, Takahashi F, Kinoshita A, Miwa H, Shinozaki K, Fukuda H, Sawa S. 2011b. Mitogen-activated protein kinase regulated by the CLAVATA receptors contributes to shoot apical meristem homeostasis. *Plant and Cell Physiology* **52,** 14–29.

Brand U, Fletcher JC, Hobe M, Meyerowitz EM, Simon R. 2000. Dependence of stem cell fate in Arabidopsis on a feedback loop regulated by CLV3 activity. *Science* **289,** 617–619.

Breuninger H, Lenhard M. 2010. Control of tissue and organ growth in plants. *Plant Development* **91,** 185–220.

Butenko MA, Patterson SE, Grini PE, Stenvik GE, Amundsen SS, Mandal A, Aalen RB. 2003. INFLORESCENCE DEFICIENT IN ABSCISSION controls floral organ abscission in Arabidopsis and identifies a novel family of putative ligands in plants. *Plant Cell* **15,** 2296–2307.

Butenko MA, Vie AK, Brembu T, Aalen RB, Bones AM. 2009. Plant peptides in signalling: looking for new partners. *Trends in Plant Science* **14,** 255–263.

Campanoni P, Blatt MR. 2007. Membrane trafficking and polar growth in root hairs and pollen tubes. *Journal of Expimental Botany* **58,** 65–74.

Cao J, Shi F. 2012. Evolution of the RALF gene family in plants: gene duplication and selection patterns. *Evolutionary Bioinformatics* **8,** 271–292.

Casamitjana-Martinez E, Hofhuis HF, Xu J, Liu CM, Heidstra R, Scheres B. 2003. Root-specific CLE19 overexpression and the sol1/2 suppressors implicate a CLV-like pathway in the control of Arabidopsis root meristem maintenance. *Current Biology* **13,** 1435–1441.

Casson SA, Chilley PM, Topping JF, Evans IM, Souter MA, Lindsey K. 2002. The POLARIS gene of Arabidopsis encodes a predicted peptide required for correct root growth and leaf vascular patterning. *The Plant Cell* **14,** 1705–1721.

Chilley PM, Casson SA, Tarkowski P, Hawkins N, Wang KLC, Hussey PJ, Beale M, Ecker JR, Sandberg GK, Lindsey K. 2006. The POLARIS peptide of Arabidopsis regulates auxin transport and root growth via effects on ethylene signaling. *Plant Cell* **18,** 3058–3072.

Choudhary C, Mann M. 2010. Decoding signalling networks by mass spectrometry-based proteomics. *Nature Reviews Molecular Cell Biology* **11,** 427–439.

Clark SE, Running MP, Meyerowitz EM. 1995. CLAVATA3 is a specific regulator of shoot and floral meristem development affecting the same processes as CLAVATA1. *Development* **121,** 2057–2067.

Covey PA, Subbaiah CC, Parsons RL, Pearce G, Lay FT, Anderson MA, Ryan CA, Bedinger PA. 2010. A pollen-specific RALF from tomato that regulates pollen tube elongation. *Plant Physiology* **153,** 703–715.

De Smet I. 2012. Lateral root initiation: one step at a time. *New Phytologist* **193,** 867–873.

De Smet I, Beeckman T. 2011. Asymmetric cell division in land plants and algae: the driving force for differentiation. *Nature Reviews Molecular Cell Biology* **12,** 177–188.

De Smet I, Voβ U, Jurgens G, Beeckman T. 2009. Receptor-like kinases shape the plant. *Nature Cell Biology* **11,** 1166–1173.

De Veylder L, Beeckman T, Inzé D. 2007. The ins and outs of the plant cell cycle. *Nature Reviews Molecular Cell Biology* **8,** 655–665.

Depuydt S, Rodriguez-Villalon A, Santuari L, Wyser-Rmili C, Ragni L, Hardtke CS. 2013. Suppression of Arabidopsis protophloem differentiation and root meristem growth by CLE45 requires the receptor-like kinase BAM3. *Proceedings of the National Academy of Sciences, USA* **110,** 7074–7079.

DeYoung BJ, Bickle KL, Schrage KJ, Muskett P, Patel K, Clark SE. 2006. The CLAVATA1-related BAM1, BAM2 and BAM3 receptor kinase-like proteins are required for meristem function in Arabidopsis. *The Plant Journal* **45,** 1–16.

Diévart A, Dalal M, Tax FE, Lacey AD, Huttly A, Li J, Clark SE. 2003. CLAVATA1 dominant-negative alleles reveal functional overlap between multiple receptor kinases that regulate meristem and organ development. *Plant Cell* **15,** 1198–1211.

Drews GN, Koltunow AM. 2011. The female gametophyte. *The Arabidopsis Book* **9,** e0155.

Etchells JP, Provost CM, Mishra L, Turner SR. 2013. WOX4 and WOX14 act downstream of the PXY receptor kinase to regulate plant vascular proliferation independently of any role in vascular organisation. *Development* **140,** 2224–2234.

Etchells JP, Provost CM, Turner SR. 2012. Plant vascular cell division is maintained by an interaction between PXY and ethylene signalling. *PLoS Genetics* **8,** e1002997.

Etchells JP, Turner SR. 2010. The PXY-CLE41 receptor ligand pair defines a multifunctional pathway that controls the rate and orientation of vascular cell division. *Development* **137,** 767–774.

Evans MM. 2007. The indeterminate gametophyte1 gene of maize encodes a LOB domain protein required for embryo sac and leaf development. *The Plant Cell* **19,** 46–62.

Fernandez A, Drozdzecki A, Hoogewijs K, Nguyen A, Beeckman T, Madder A, Hilson P. 2013a. Transcriptional and functional classification of the GOLVEN/ROOT GROWTH FACTOR/CLE-like signaling peptides reveals their role in lateral root and hair formation. *Plant Physiology* **161,** 954–970.

Fernandez A, Hilson P, Beeckman T. 2013b. GOLVEN peptides as important regulatory signaling molecules of plant development. *Journal of Experimental Botany* **64,** 5263–5268.

Fiers M, Golemiec E, Xu J, van der Geest L, Heidstra R, Stiekema W, Liu C-M. 2005. The 14-amino acid CLV3, CLE19, and CLE40 peptides trigger consumption of the root meristem in Arabidopsis through a CLAVATA2-dependent pathway. *The Plant Cell* **17,** 2542–2553.

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Fiers M, Hause G, Boutilier K, Casamitjana-Martinez E, Weijers D, Offringa R, van der Geest L, van Lookeren Campagne M, Liu C-M. 2004. Mis-expression of the CLV3/ESR-like gene CLE19 in Arabidopsis leads to a consumption of root meristem. *Gene* **327,** 37–49.

Fisher K, Turner S. 2007. PXY, a receptor-like kinase essential for maintaining polarity during plant vascular-tissue development. *Current Biology* **17,** 1061–1066.

Fletcher JC, Brand U, Running MP, Simon R, Meyerowitz EM. 1999. Signaling of cell fate decisions by CLAVATA3 in Arabidopsis shoot meristems. *Science* **283,** 1911–1914.

Fukuda H. 2004. Signals that control plant vascular cell differentiation. *Nature Reviews Molecular Cell Biology* **5,** 379–391.

Fukuda H, Hirakawa Y, Sawa S. 2007. Peptide signaling in vascular development. *Current Opinion in Plant Biology* **10,** 477–482.

Fukuda H, Komamine A. 1980. Establishment of an experimental system for the study of tracheary element differentiation from single cells isolated from the mesophyll of *Zinnia elegans*. *Plant Physiology* **65,** 57–60.

Galinha C, Hofhuis H, Luijten M, Willemsen V, Blilou I, Heidstra R, Scheres B. 2007. PLETHORA proteins as dose-dependent master regulators of Arabidopsis root development. *Nature* **449,** 1053–1057.

Gonzalez N, Vanhaeren H, Inzé D. 2012. Leaf size control: complex coordination of cell division and expansion. *Trends in Plant Science* **17,** 332–340.

Grebe M. 2012. The patterning of epidermal hairs in Arabidopsis—updated. *Current Opinion in Plant Biology* **15,** 31–37.

Grieneisen VA, Xu J, Maree AFM, Hogeweg P, Scheres B. 2007. Auxin transport is sufficient to generate a maximum and gradient guiding root growth. *Nature* **449,** 1008–1013.

Grunewald W, Friml J. 2010. The march of the PINs: developmental plasticity by dynamic polar targeting in plant cells. *EMBO Journal* **29,** 2700–2714.

Hara K, Kajita R, Torii KU, Bergmann DC, Kakimoto T. 2007. The secretory peptide gene EPF1 enforces the stomatal one-cell-spacing rule. *Genes and Development* **21,** 1720–1725.

Hara K, Yokoo T, Kajita R, Onishi T, Yahata S, Peterson KM, Torii KU, Kakimoto T. 2009. Epidermal Cell density is autoregulated via a secretory peptide, EPIDERMAL PATTERNING FACTOR 2 in Arabidopsis leaves. *Plant and Cell Physiology* **50,** 1019–1031.

Hartmann J, Stuhrwohldt N, Dahlke RI, Sauter M. 2013. Phytosulfokine control of growth occurs in the epidermis, is likely to be non-cell autonomous and is dependent on brassinosteroids. *The Plant Journal* **73,** 579–590.

Hirakawa Y, Kondo Y, Fukuda H. 2010. TDIF peptide signaling regulates vascular stem cell proliferation via the WOX4 homeobox gene in Arabidopsis. *Plant Cell* **22,** 2618–2629.

Hirakawa Y, Shinohara H, Kondo Y, Inoue A, Nakanomyo I, Ogawa M, Sawa S, Ohashi-Ito K, Matsubayashi Y, Fukuda H. 2008. Non-cell-autonomous control of vascular stem cell fate by a CLE peptide/receptor system. *Proceedings of the National Academy of Sciences, USA* **105,** 15208–15213.

Hobe M, Muller R, Grunewald M, Brand U, Simon R. 2003. Loss of CLE40, a protein functionally equivalent to the stem cell restricting signal CLV3, enhances root waving in Arabidopsis. *Development Genes and Evolution* **213,** 371–381.

Hunt L, Gray JE. 2009. The signaling peptide EPF2 controls asymmetric cell divisions during stomatal development. *Current Biology* **19,** 864–869.

Ikeuchi M, Yamaguchi T, Kazama T, Ito T, Horiguchi G, Tsukaya H. 2011. ROTUNDIFOLIA4 regulates cell proliferation along the body axis in Arabidopsis shoot. *Plant and Cell Physiology* **52,** 59–69.

Jewaria PK, Hara T, Tanaka H, Kondo T, Betsuyaku S, Sawa S, Sakagami Y, Aimoto S, Kakimoto T. 2013. Differential effects of peptides stomagen, EPF1, and EPF2 on activation of the MAP kinase MPK6 and the SPCH protein level. *Plant and Cell Physiology* (Epub ahead of print].

Ji J, Shimizu R, Sinha N, Scanlon MJ. 2010. Analyses of WOX4 transgenics provide further evidence for the evolution of the WOX gene family during the regulation of diverse stem cell functions. *Plant Signaling and Behavior* **5,** 916–920.

Jones AR, Kramer EM, Knox K, Swarup R, Bennett MJ, Lazarus CM, Leyser HMO, Grierson CS. 2009. Auxin transport through non-hair cells sustains root-hair development. *Nature Cell Biology* **11,** 78–84.

Kanaoka MM, Kawano N, Matsubara Y, Susaki D, Okuda S, Sasaki N, Higashiyama T. 2011. Identification and characterization of TcCRP1, a pollen tube attractant from *Torenia concolor*. *Annals of Botany* **108,** 739–747.

Kanaoka MM, Pillitteri LJ, Fujii H, Yoshida Y, Bogenschutz NL, Takabayashi J, Zhu J-K, Torii KU. 2008. SCREAM/ICE1 and SCREAM2 specify three cell-state transitional steps leading to Arabidopsis stomatal differentiation. *Plant Cell* **20,** 1775–1785.

Kieffer M, Stern Y, Cook H, Clerici E, Maulbetsch C, Laux T, Davies B. 2006. Analysis of the transcription factor WUSCHEL and its functional homologue in Antirrhinum reveals a potential mechanism for their roles in meristem maintenance. *Plant Cell* **18,** 560–573.

Komori R, Amano Y, Ogawa-Ohnishi M, Matsubayashi Y. 2009. Identification of tyrosylprotein sulfotransferase in Arabidopsis. *Proceedings of the National Academy of Sciences, USA* **106,** 15067–15072.

Kondo T, Sawa S, Kinoshita A, Mizuno S, Kakimoto T, Fukuda H, Sakagami Y. 2006. A plant peptide encoded by CLV3 identified by in situ MALDI-TOF MS analysis. *Science* **313,** 845–848.

Kondo Y, Hirakawa Y, Kieber JJ, Fukuda H. 2011. CLE peptides can negatively regulate protoxylem vessel formation via cytokinin signaling. *Plant and Cell Physiology* **52,** 37–48.

Krohn NG, Lausser A, Juranić M, Dresselhaus T. 2012. Egg cell signaling by the secreted peptide ZmEAL1 controls antipodal cell fate. *Developmental Cell* **23,** 219–225.

Kumpf RP, Shi CL, Larrieu A, Sto IM, Butenko MA, Péret B, Riiser ES, Bennett MJ, Aalen RB. 2013. Floral organ abscission peptide IDA and its HAE/HSL2 receptors control cell separation during lateral root emergence. *Proceedings of the National Academy of Sciences, USA* **110,** 5235–5240.

Kutschmar A, Rzewuski G, Stuhrwohldt N, Beemster GTS, Inzé D, Sauter M. 2009. PSK-α promotes root growth in Arabidopsis. *New Phytologist* **181,** 820–831.

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Lavenus J, Goh T, Roberts I, Guyomarc'h S, Lucas M, De Smet I, Fukaki H, Beeckman T, Bennett M, Laplaze L. 2013. Lateral root development in Arabidopsis: fifty shades of auxin. *Trends in Plant Science* **8,** 450–458.

Lease KA, Walker JC. 2006. The Arabidopsis unannotated secreted peptide database, a resource for plant peptidomics. *Plant Physiology* **142,** 831–838.

Lee JS, Kuroha T, Hnilova M, Khatayevich D, Kanaoka MM, McAbee JM, Sarikaya M, Tamerler C, Torii KU. 2012. Direct interaction of ligand-receptor pairs specifying stomatal patterning. *Genes and Development* **26,** 126–136.

Leibfried A, To JP, Busch W, Stehling S, Kehle A, Demar M, Kieber JJ, Lohmann JU. 2005. WUSCHEL controls meristem function by direct regulation of cytokinin-inducible response regulators. *Nature* **438,** 1172–1175.

Lenhard M, Bohnert A, Jurgens G, Laux T. 2001. Termination of stem cell maintenance in Arabidopsis floral meristems by interactions between WUSCHEL and AGAMOUS. *Cell* **105,** 805–814.

Liu J, Mehdi S, Topping J, Tarkowski P, Lindsey K. 2010. Modelling and experimental analysis of hormonal crosstalk in Arabidopsis. *Molecular Systems Biology* **6,** 373.

Liu J, Zhong S, Guo X, Hao L, Wei X, Huang Q, Hou Y, Shi J, Wang C, Gu H. 2013. Membrane-bound RLCKs LIP1 and LIP2 are essential male factors controlling male-female attraction in Arabidopsis. *Current Biology* **23,** 993–998.

Lohmann JU, Hong RL, Hobe M, Busch MA, Parcy F, Simon R, Weigel D. 2001. A molecular link between stem cell regulation and floral patterning in Arabidopsis. *Cell* **105,** 793–803.

Márton ML, Cordts S, Broadhvest J, Dresselhaus T. 2005. Micropylar pollen tube guidance by Egg Apparatus 1 of maize. *Science* **307,** 573–576.

Márton ML, Fastner A, Uebler S, Dresselhaus T. 2012. Overcoming hybridization barriers by the secretion of the maize pollen tube attractant ZmEA1 from Arabidopsis ovules. *Current Biology* **22,** 1194–1198.

Matos JL, Fiori CS, Silva-Filho MC, Moura DS. 2008. A conserved dibasic site is essential for correct processing of the peptide hormone AtRALF1 in *Arabidopsis thaliana*. *FEBS Letters* **582,** 3343–3347.

Matsubayashi Y. 2011. Post-translational modifications in secreted peptide hormones in plants. *Plant and Cell Physiology* **52,** 5–13.

Matsubayashi Y, Hanai H, Hara O, Sakagami Y. 1996. Active fragments and analogs of the plant growth factor, phytosulfokine: structure–activity relationships. *Biochemical and Biophysical Research Communications* **225,** 209–214.

Matsubayashi Y, Ogawa M, Kihara H, Niwa M, Sakagami Y. 2006a. Disruption and overexpression of Arabidopsis phytosulfokine receptor gene affects cellular longevity and potential for growth. *Plant Physiology* **142,** 45–53.

Matsubayashi Y, Sakagami Y. 1996. Phytosulfokine, sulfated peptides that induce the proliferation of single mesophyll cells of *Asparagus officinalis* L. *Proceedings of the National Academy of Sciences, USA* **93,** 7623–7627.

Matsubayashi Y, Shinohara H, Ogawa M. 2006b. Identification and functional characterization of phytosulfokine receptor using a ligand-based approach. *Chemical Record* **6,** 356–364.

Matsuzaki Y, Ogawa-Ohnishi M, Mori A, Matsubayashi Y. 2010. Secreted peptide signals required for maintenance of root stem cell niche in Arabidopsis. *Science* **329,** 1065–1067.

Meng L, Buchanan BB, Feldman LJ, Luan S. 2012. CLE-like (CLEL) peptides control the pattern of root growth and lateral root development in Arabidopsis. *Proceedings of the National Academy of Sciences, USA* **109,** 1760–1765.

Meng L, Feldman LJ. 2011. CLE genes may act in a variety of tissues/cells and involve other signaling cascades in addition to CLV3-WUS-like pathways. *Plant Signaling and Behavior* **6,** 105–108.

Morita MT. 2010. Directional gravity sensing in gravitropism. *Annual Review of Plant Biology* **61,** 705–720.

Mortier V, Den Herder G, Whitford R, Van de Velde W, Rombauts S, D'haeseleer K, Holsters M, Goormachtig S. 2010. CLE peptides control *Medicago truncatula* nodulation locally and systemically. *Plant Physiology* **153,** 222–237.

Müller R, Bleckmann A, Simon R. 2008. The receptor kinase CORYNE of Arabidopsis transmits the stem cell-limiting signal CLAVATA3 independently of CLAVATA1. *Plant Cell* **20,** 934–946.

Murphy E, Smith S, De Smet I. 2012. Small signaling peptides in Arabidopsis development: how cells communicate over a short distance. *Plant Cell* **24,** 3198–3217.

Narita NN, Moore S, Horiguchi G, Kubo M, Demura T, Fukuda H, Goodrich J, Tsukaya H. 2004. Overexpression of a novel small peptide ROTUNDIFOLIA4 decreases cell proliferation and alters leaf shape in *Arabidopsis thaliana*. *The Plant Journal* **38,** 699–713.

Niederhuth CE, Patharkar OR, Walker JC. 2013. Transcriptional profiling of the Arabidopsis abscission mutant *hae hsl2* by RNA-Seq. *BMC Genomics* **14,** 37.

Oelkers K, Goffard N, Weiller GF, Gresshoff PM, Mathesius U, Frickey T. 2008. Bioinformatic analysis of the CLE signaling peptide family. *BMC Plant Biology* **8,** 1.

Ogawa M, Shinohara H, Sakagami Y, Matsubayashi Y. 2008. Arabidopsis CLV3 peptide directly binds CLV1 ectodomain. *Science* **319,** 1150083.

Ohki S, Takeuchi M, Mori M. 2011. The NMR structure of stomagen reveals the basis of stomatal density regulation by plant peptide hormones. *Nature Communications* **2,** 512.

Ohyama K, Ogawa M, Matsubayashi Y. 2008. Identification of a biologically active, small, secreted peptide in Arabidopsis by in silico gene screening, followed by LC-MS-based structure analysis. *The Plant Journal* **55,** 152–160.

Okuda S, Suzuki T, Kanaoka MM, Mori H, Sasaki N, Higashiyama T. 2013. Acquisition of LURE-binding activity at the pollen tube tip of *Torenia fournieri*. *Molecular Plant* **6,** 1074–1090.

Olsen AN, Mundy J, Skriver K. 2002. Peptomics, identification of novel cationic Arabidopsis peptides with conserved sequence motifs. *In Silico Biology* **2,** 441–451.

Osipova MA, Mortier V, Demchenko KN, Tsyganov VE, Tikhonovich IA, Lutova LA, Dolgikh EA, Goormachtig S. 2012. WUSCHEL-RELATED HOMEOBOX5 gene expression and interaction of CLE peptides with components of the systemic control add two pieces to the puzzle of autoregulation of nodulation. *Plant Physiology* **158,** 1329–1341.

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Patterson SE. 2001. Cutting loose. abscission and dehiscence in Arabidopsis. *Plant Physiology* **126,** 494–500.

Pearce G, Moura DS, Stratmann J, Ryan CA. 2001. RALF, a 5-kDa ubiquitous polypeptide in plants, arrests root growth and development. *Proceedings of the National Academy of Sciences, USA* **98,** 12843–12847.

Pearce G, Yamaguchi Y, Munske G, Ryan CA. 2010. Structure–activity studies of RALF, rapid alkalinization factor, reveal an essential—YISY—motif. *Peptides* **31,** 1973–1977.

Péret B, De Rybel B, Casimiro I, Benkova E, Swarup R, Laplaze L, Beeckman T, Bennett MJ. 2009. Arabidopsis lateral root development: an emerging story. *Trends in Plant Science* **14,** 399–408.

Petersen M, Sander L, Child R, van Onckelen H, Ulvskov P, Borkhardt B. 1996. Isolation and characterisation of a pod dehiscence zone-specific polygalacturonase from *Brassica napus*. *Plant Molecular Biology* **31,** 517–527.

Reid DE, Ferguson BJ, Gresshoff PM. 2011. Inoculation- and nitrate-induced CLE peptides of soybean control NARK-dependent nodule formation. *Molecular Plant-Microbe Interactions* **24,** 606–618.

Reid DE, Li D, Ferguson BJ, Gresshoff PM. 2013. Structure–function analysis of the GmRIC1 signal peptide and CLE domain required for nodulation control in soybean. *Journal of Experimental Botany* **64,** 1575–1585.

Roberts JA, Elliott KA, Gonzalez-Carranza ZH. 2002. Abscission, dehiscence, and other cell separation processes. *Annual Review of Plant Biology* **53,** 131–158.

Rose JKC. 2004. Identification and characterization of glucanase inhibitor proteins: uncovering the molecular arms race in the plant cell wall. *Phytopathology* **94,** S136-S136.

Ryan CA, Pearce G, Scheer J, Moura DS. 2002. Polypeptide hormones. *Plant Cell* **14,** S251-S264.

Rychel A, Peterson K, Torii K. 2010. Plant twitter: ligands under 140 amino acids enforcing stomatal patterning. *Journal of Plant Research* **123,** 275–280.

Scarpella E, Helariutta Y. 2010. Vascular pattern formation in plants. *Current Topics in Developmental Biology* **91,** 221–265.

Scheer JM, Pearce G, Ryan CA. 2005. LeRALF, a plant peptide that regulates root growth and development, specifically binds to 25 and 120 kDa cell surface membrane proteins of *Lycopersicon peruvianum*. *Planta* **221,** 667–674.

Scheres B. 2007. Stem-cell niches: nursery rhymes across kingdoms. *Nature Reviews Molecular Cell Biology* **8,** 345–354.

Sexton R, Roberts JA. 1982. Cell biology of abscission. *Annual Review of Plant Physiology and Plant Molecular Biology* **33,** 133–162.

Shi CL, Stenvik GE, Vie AK, Bones AM, Pautot V, Proveniers M, Aalen RB, Butenko MA. 2011. Arabidopsis class I KNOTTED-like homeobox proteins act downstream in the IDA-HAE/HSL2 floral abscission signaling pathway. *Plant Cell* **23,** 2553–2567.

Shimada T, Sugano S, Hara-Nishimura I. 2011. Positive and negative peptide signals control stomatal density. *Cellular and Molecular Life Sciences* **68,** 2081–2088.

Shiu S-H, Bleecker AB. 2001. Plant receptor-like kinase gene family: diversity, function, and signaling. *Science STKE* **2001,** re22.

Smith S, De Smet I. 2012. Root system architecture: insights from Arabidopsis and cereal crops. *Philosophical Transactions of the Royal Society B: Biological Sciences* **367,** 1441–1452.

Sprunck S, Rademacher S, Vogler F, Gheyselinck J, Grossniklaus U, Dresselhaus T. 2012. Egg cell-secreted EC1 triggers sperm cell activation during double fertilization. *Science* **338,** 1093–1097.

Srivastava R, Liu JX, Guo HQ, Yin YH, Howell SH. 2009. Regulation and processing of a plant peptide hormone, AtRALF23, in Arabidopsis. *The Plant Journal* **59,** 930–939.

Stahl Y, Grabowski S, Bleckmann A, *et al.* 2013. Moderation of Arabidopsis root stemness by CLAVATA1 and ARABIDOPSIS CRINKLY4 receptor kinase complexes. *Current Biology* **23,** 362–371.

Stahl Y, Simon R. 2009. Is the Arabidopsis root niche protected by sequestration of the CLE40 signal by its putative receptor ACR4? *Plant Signal Behaviour* **4,** 634–635.

Stahl Y, Simon R. 2012. Peptides and receptors controlling root development. *Philosophical Transactions of the Royal Society B: Biological Sciences* **367,** 1453–1460.

Stahl Y, Wink RH, Ingram GC, Simon R. 2009. A signaling module controlling the stem cell niche in Arabidopsis root meristems. *Current Biology* **19,** 909–914.

Staudt AC, Wenkel S. 2011. Regulation of protein function by 'microProteins'. *EMBO Reports* **12,** 35–42.

Stenvik GE, Butenko MA, Urbanowicz BR, Rose JKC, Aalen RB. 2006. Overexpression of INFLORESCENCE DEFICIENT IN ABSCISSION activates cell separation in vestigial abscission zones in Arabidopsis. *Plant Cell* **18,** 1467–1476.

Stenvik GE, Tandstad NM, Guo Y, Shi CL, Kristiansen W, Holmgren A, Clark SE, Aalen RB, Butenko MA. 2008. The EPIP peptide of INFLORESCENCE DEFICIENT IN ABSCISSION is sufficient to induce abscission in Arabidopsis through the receptor-like kinases HAESA and HAESA-LIKE2. *Plant Cell* **20,** 1805–1817.

Strabala TJ, O'Donnell PJ, Smit A-M, Ampomah-Dwamena C, Martin EJ, Netzler N, Nieuwenhuizen NJ, Quinn BD, Foote HCC, Hudson KR. 2006. Gain-of-function phenotypes of many CLAVATA3/esr genes, including four new family members, correlate with tandem variations in the conserved CLAVATA3/ESR domain. *Plant Physiology* **140,** 1331–1344.

Stuhrwohldt N, Dahlke RI, Steffens B, Johnson A, Sauter M. 2011. Phytosulfokine-α controls hypocotyl length and cell expansion in *Arabidopsis thaliana* through phytosulfokine receptor 1. *PLoS One* **6,** e21054.

Suer S, Agusti J, Sanchez P, Schwarz M, Greb T. 2011. WOX4 imparts auxin responsiveness to cambium cells in Arabidopsis. *Plant Cell* **23,** 3247–3259.

Sugano SS, Shimada T, Imai Y, Okawa K, Tamai A, Mori M, Hara-Nishimura I. 2009. Stomagen positively regulates stomatal density in Arabidopsis. *Nature* **463,** 241–244.

Suttle JC. 1988. Effect of ethylene treatment on polar IAA transport, net IAA uptake and specific binding of *N*-1-naphthylphthalamic acid in tissues and microsomes Isolated from etiolated pea epicotyls. *Plant Physiology* **88,** 795–799.

Suzaki T, Yoshida A, Hirano H-Y. 2008. Functional diversification of CLAVATA3-related CLE proteins in meristem maintenance in rice. *Plant Cell* **20,** 2049–2058.

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Terol J, Bargues M, Carrasco P, Perez-Alonso M, Paricio N. 2002. Molecular characterization and evolution of the protein phosphatase 2A B′ regulatory subunit family in plants. *Plant Physiology* **129,** 808–822.

Thomas C, Moraga I, Levin D, *et al.* 2011. Structural linkage between ligand discrimination and receptor activation by type I interferons. *Cell* **146,** 621–632.

Torii KU. 2012a. Mix-and-match: ligand-receptor pairs in stomatal development and beyond. *Trends in Plant Science* **17,** 711–719.

Torii KU. 2012b. Two-dimensional spatial patterning in developmental systems. *Trends in Cell Biology* **22,** 438–446.

Valdivia ER, Chevalier D, Sampedro J, Taylor I, Niederhuth CE, Walker JC. 2012. DVL genes play a role in the coordination of socket cell recruitment and differentiation. *Journal of Experimental Botany* **63,** 1405–1412.

Van de Velde W, Zehirov G, *et al.* 2010. plant peptides govern terminal differentiation of bacteria in symbiosis. *Science* **327,** 1122–1126.

Van Norman JM, Breakfield NW, Benfey PN. 2011. Intercellular communication during plant development. *Plant Cell* **23,** 855–864.

Vanstraelen M, Benkova E. 2012. Hormonal interactions in the regulation of plant development. *Annual Review of Cell and Developmental Biology* **28,** 463–487.

Wen J, Lease KA, Walker JC. 2004. DVL, a novel class of small polypeptides: overexpression alters Arabidopsis development. *The Plant Journal* **37,** 668–677.

Whitford R, Fernandez A, De Groodt R, Ortega E, Hilson P. 2008. Plant CLE peptides from two distinct functional classes synergistically induce division of vascular cells. *Proceedings of the National Academy of Sciences, USA* **105,** 18625–18630.

Whitford R, Fernandez A, Tejos R, *et al.* 2012. GOLVEN secretory peptides regulate auxin carrier turnover during plant gravitropic responses. *Developmental Cell* **22,** 678–685.

Williams EL, De Smet I. 2013. Development: CLAVATA1 joins the club of root stem cell regulators. *Current Biology* **23,** R245–R247.

Wu J, Kurten EL, Monshausen G, Hummel GM, Gilroy S, Baldwin IT. 2007. NaRALF, a peptide signal essential for the regulation of root hair tip apoplastic pH in *Nicotiana attenuata*, is required for root hair development and plant growth in native soils. *The Plant Journal* **52,** 877–890.

Yadav RK, Perales M, Gruel J, Girke T, Jönsson H, Reddy GV. 2011. WUSCHEL protein movement mediates stem cell homeostasis in the Arabidopsis shoot apex. *Genes and Development* **25,** 2025–2030.

Yadav RK, Tavakkoli M, Reddy GV. 2010. WUSCHEL mediates stem cell homeostasis by regulating stem cell number and patterns of cell division and differentiation of stem cell progenitors. *Development* **137,** 3581–3589.

Yaginuma H, Hirakawa Y, Kondo Y, Ohashi-Ito K, Fukuda H. 2011. A novel function of TDIF-related peptides: promotion of axillary bud formation. *Plant and Cell Physiology* **52,** 1354–1364.

Yang HP, Matsubayashi Y, Hanai H, Sakagami Y. 2000. Phytosulfokine-α, a peptide growth factor found in higher plants: its structure, functions, precursor and receptors. *Plant and Cell Physiology* **41,** 825–830.

Yang HP, Matsubayashi Y, Nakamura K, Sakagami Y. 1999. *Oryza sativa* PSK gene encodes a precursor of phytosulfokine-α, a sulfated peptide growth factor found in plants. *Proceedings of the National Academy of Sciences, USA* **9,** 13560–13565.

Yang HP, Matsubayashi Y, Nakamura K, Sakagami Y. 2001. Diversity of Arabidopsis genes encoding precursors for phytosulfokine, a peptide growth factor. *Plant Physiology* **127,** 842–851.

Yang SL, Jiang L, Puah CS, Xie LF, Zhang XQ, Chen LQ, Yang WC, Ye D. 2005. Overexpression of TAPETUM DETERMINANT1 alters the cell fates in the Arabidopsis carpel and tapetum via genetic interaction with excess microsporocytes1/extra sporogenous cells. *Plant Physiology* **139,** 186–191.

Yang SL, Xie LF, Mao HZ, Puah CS, Yang WC, Jiang L, Sundaresan V, Ye D. 2003. Tapetum determinant1 is required for cell specialization in the Arabidopsis anther. *Plant Cell* **15,** 2792–2804.

Zhou W, Wei L, Xu J, *et al.* 2010. Arabidopsis tyrosylprotein sulfotransferase acts in the auxin/PLETHORA pathway in regulating postembryonic maintenance of the root stem cell niche. *Plant Cell* **22,** 3692–3709.

Downloaded from http://jxb.oxfordjournals.org/ at Bayer CropScience on April 7, 2016

Chapter 3: Modulation of Arabidopsis and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide

Published as Czyzewicz N, Shi CL, Vu LD, Van De Cotte B, Hodgman C, Butenko MA, De Smet I. (2015) Journal of Experimental Botany 66(17):5229-5243

Author Contribution:

I was involved with the planning of, and conducted the CLE(X)::GUS expression screening, CLE1/4, 7, 26 and 27 peptide treatment root trait analyses, CLE26 dose/response analysis, CLE26 alanine scan, crop peptide treatments, peptide modification analysis, phylogenetic screens, CLE26 treatment reporter line screening, and *cle26* characterisation experiments.

I wrote the paper (excluding CLE peptide expression is regulated by hormones and environmental triggers and genevestigator analyses) contributed to figures (excluding Table 1, Figures 9 and 10, Supplemental Figures 7, 9 and 10), and was involved in development of the manuscript.

Journal of Experimental Botany, Vol. 66, No. 17 pp. 5229–5243, 2015
doi:10.1093/jxb/erv360 Advance Access publication 17 July 2015
This paper is available online free of all access charges (see http://jxb.oxfordjournals.org/open_access.html for further details)

RESEARCH PAPER

Modulation of *Arabidopsis* and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide

Nathan Czyzewicz[1], Chun-Lin Shi[2], Lam Dai Vu[3,4,5,6], Brigitte Van De Cotte[3,4], Charlie Hodgman[7], Melinka A. Butenko[2] and Ive De Smet[1,3,4,7,*]

[1] Division of Plant and Crop Sciences, School of Biosciences, University of Nottingham, Leicestershire LE12 5RD, UK
[2] Department of Biosciences, Section for Genetics and Evolutionary Biology, University of Oslo, N-0316 Oslo, Norway
[3] Department of Plant Systems Biology, VIB, B-9052 Ghent, Belgium
[4] Department of Plant Biotechnology and Genetics, Ghent University, B-9052 Ghent, Belgium
[5] Department of Medical Protein Research, VIB, B-9000 Ghent, Belgium
[6] Department of Biochemistry, Ghent University, B-9000 Ghent, Belgium
[7] Centre for Plant Integrative Biology, School of Biosciences, University of Nottingham, Leicestershire LE12 5RD, UK

*To whom the correspondence should be addressed. E-mail: ive.desmet@psb.vib-ugent.be

Received 1 April 2015; Revised 1 June 2015; Accepted 26 June 2015

Editor: Ruediger Simon

Abstract

Plant roots are important for a wide range of processes, including nutrient and water uptake, anchoring and mechanical support, storage functions, and as the major interface with the soil environment. Several small signalling peptides and receptor kinases have been shown to affect primary root growth, but very little is known about their role in lateral root development. In this context, the CLE family, a group of small signalling peptides that has been shown to affect a wide range of developmental processes, were the focus of this study. Here, the expression pattern during lateral root initiation for several CLE family members is explored and to what extent CLE1, CLE4, CLE7, CLE26, and CLE27, which show specific expression patterns in the root, are involved in regulating root architecture in *Arabidopsis thaliana* is assessed. Using chemically synthesized peptide variants, it was found that CLE26 plays an important role in regulating *A. thaliana* root architecture and interacts with auxin signalling. In addition, through alanine scanning and *in silico* structural modelling, key residues in the CLE26 peptide sequence that affect its activity are pinpointed. Finally, some interesting similarities and differences regarding the role of CLE26 in regulating monocot root architecture are presented.

Key words: *Arabidopsis thaliana*, auxin, *Brachypodium distachyon*, CLE26, root, wheat.

Introduction

A small number of phytohormones have an impact on plant growth and development (Vanstraelen and Benkova, 2012;Davière and Achard, 2013; El-Showk *et al.*, 2013; Yoon and Kieber, 2013), but how this small number of chemical mediators can modulate the large number of physiological and biochemical responses required during growth and development remains an open question. Lately, however, it has become apparent that small signalling peptides provide an additional layer of control to steer growth and development (Murphy *et al.*, 2012; Czyzewicz *et al.*, 2013; Murphy and De Smet,

© The Author 2015. Published by Oxford University Press on behalf of the Society for Experimental Biology.
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0/), which permits unrestricted reuse, distribution, and reproduction in any medium, provided the original work is properly cited.

2014). Small signalling peptides generally range in size between four and 75 amino acid residues and most—but not all—are cleavage products from precursor peptides (Murphy *et al.*, 2012; Czyzewicz *et al.*, 2013). Several of these precursors are post-translationally modified prior to cleavage, and this post-translational modification can be critical for peptide activity and binding affinity for their receptor partners (Butenko *et al.*, 2009, 2014; Matsuzaki *et al.*, 2010; Matsubayashi, 2011; Murphy *et al.*, 2012; Shinohara and Matsubayashi, 2013).

The CLV3/EMBRYO SURROUNDING REGION (ESR)-related (CLE) peptide family is an ancient group of signalling peptides that has been shown to affect a wide range of developmental processes (Strabala *et al.*, 2006; Miyawaki *et al.*, 2013). The *Arabidopsis thaliana* CLE family is comprised of 32 peptides, each consisting of 12–13 amino acids, and containing a CLV3/ESR consensus sequence (Strabala *et al.*, 2006; Betsuyaku *et al.*, 2011). These CLE peptides are products of a larger precursor protein, which is translated and post-translationally modified prior to cleavage. However, only a few of the CLE peptides have been functionally characterized, and for most it is unknown which receptor(s) mediate(s) their signal (Strabala *et al.*, 2006; Shinohara and Matsubayashi, 2013). CLV3, the founding member of the CLE family, is perhaps the best characterized of the CLE peptides and exerts a crucial function as a mobile signal controlling the size of the *A. thaliana* shoot apical meristem (Clark *et al.*, 1995; Fletcher *et al.*, 1999; Ogawa *et al.*, 2008; Ohyama *et al.*, 2009; Shinohara and Matsubayashi, 2013). Since mature CLE peptides display a high degree of redundancy with known receptors (Strabala *et al.*, 2006; Wang and Fiers, 2010), it is likely that strict tissue-specific control of expression and/or the formation of co-receptor complexes provides signalling specificity. An example of this redundancy is seen for CLV3, CLE19, and CLE40, which all trigger consumption of the root apical meristem in *A. thaliana*, resulting in a short root phenotype, but only *CLE40* is actually expressed in the root apical meristem (Hobe *et al.*, 2003). The CLV3, CLE19, and CLE40 peptides all show an effect on the root meristem through a CLAVATA2 (CLV2)-dependent pathway (Fiers *et al.*, 2005), while CLV3 and CLE40 require CLV1 as part of a receptor complex to initiate the downstream signalling cascade (Ohyama *et al.*, 2009; Stahl *et al.*, 2013).

In land plants, the correct development of root architecture is vital for maximum uptake of water and minerals for growth. Root architecture differs greatly between species and can also be highly dynamic within a species if subjected to biotic or abiotic stress (Smith and De Smet, 2012). In addition to controlling primary root growth, developing lateral roots is another strategy which allows the plant to maximize the area over which nutrients are absorbed, and further allows the plant to anchor itself more firmly in the soil (Smith and De Smet, 2012). Lateral root primordia are formed from ~3 pairs of xylem pole pericycle cells from distinct cell files, which are primed by exposure to auxin in the basal meristem (Kurup *et al.*, 2005; De Smet *et al.*, 2007). Upon further exposure to auxin in the differentiation zone, the nuclei of these primed cells move toward a central point, and the cells divide asymmetrically to form two central small daughter cells, and two distal large daughter cells—the stage 1 primordium (De Smet *et al.*, 2007). These cells divide asymmetrically in a strictly regulated manner through seven further stages, during which the primordium pushes through the endodermis, epidermis, and cortex, and becomes the emerged lateral root (Péret *et al.*, 2009; Lavenus *et al.*, 2013).

Here, CLE peptides, which—based on their expression profile—are likely candidates for regulating root architecture, were identified. To explore further their *in vivo* involvement in root development, their root growth response to synthetic peptide treatment was assessed. Based on the results, one member of the CLE family, namely CLE26, subsequently became the focus of the study, and its function and relationship to auxin signalling and response in *A. thaliana* were explored. By employing CLE26 peptide treatment on roots of *Brachypodium distachyon* and wheat, to what level there is functional conservation between *A. thaliana* and monocots was also investigated.

Materials and methods

Plant lines

A. thaliana lines expressing the β-glucuronidase gene (*GUS*) under the control of *CLE* peptide promoters were obtained from the Nottingham Arabidopsis Stock Centre (NASC) and/or provided by Jennifer Fletcher (Jun *et al.*, 2010) (Supplementary Table S1 available at *JXB* online). The following previously published lines were used: *arf7 arf19* (Okushima *et al.*, 2007), *pDR5::GUS* (De Smet *et al.*, 2007), *35S:DII:VENUS* (Brunoud *et al.*, 2012; Vernoux *et al.*, 2011), and *pPIN1::PIN1*:GFP (Benková *et al.*, 2003). The *cle26-1* (N689781) SALK T-DNA line was genotyped by PCR using primers designed by the T-DNA Primer Design Tool (signal.salk.edu) (*cle26-1* Forward, ACCCATTTTGTGTTTTTGCAC; *cle26-1* Reverse, ATTATACGCGTGGACCACTTG; and SALK LBb, ATTTTGCCGATTTCGGAAC) and using the following PCR conditions: 94 °C 5 min, 40× (94 °C 30 s, 60 °C 30 s, 72 °C 1 min), 72 °C 5 min.

Growth conditions

A. thaliana and *B. distachyon* seeds were surface sterilized by immersion in 70% ethanol for 30 s, followed by immersion in 25% bleach for 20 min, and were then vernalized at 4 °C. The *A. thaliana* seedlings were grown at 20–22 °C, with 24 h daylight under fluorescent lamps [150 µM $(m^2)^{-1}$ min^{-1}] on 12 × 12 cm square Petri dishes containing 50 ml of half-strength Murashige and Skoog (1/2 MS) agar [2.154 g of MS medium (Duchefa), 0.1 g of myo-inositol (Sigma-Aldrich), 0.5 g of MES (Sigma-Aldrich) 1% (w/v) agar (Sigma) per litre of distilled water] containing the appropriate concentration of peptide diluted in water until 12 days after germination (DAG). Wheat seeds were surface sterilized by immersion in 5% hypochlorite for 15 min, before washing three times in water. Wheat and *B. distachyon* seedlings were grown at 20–22 °C, with 24 h daylight in 100 ml boiling tubes containing 20 ml of 1/2 MS agar with the appropriate concentration of peptide until 10–12 DAG. For GUS analyses, seedlings were grown at 20–22 °C, with 24 h daylight on 8 cm radius round Petri dishes containing 20 ml of 1/2 MS agar until 6 DAG. For quantitative PCR (qPCR) analyses, *A. thaliana* seedlings were grown at constant light conditions on 1/2 MS agar for 7 DAG and then transferred to 1 µM CLE26p for 24 h, or at 5 DAG to 1 µM 1-naphthaleneacetic acid (NAA). For green fluorescent protein (GFP) studies, seeds were surface sterilized by immersion in 70% ethanol for 30 s, followed by 20 min immersion in 20% bleach (final concentration

1% hypochlorite). Sterilized seeds were washed three times in sterile distilled water, before vernalizing for 24 h at 4 °C. Sterile, vernalized seeds were germinated and grown on 1/2 MS medium [0.01% myo-inositol (Sigma-Aldrich), 0.05% MES (Sigma-Aldrich), and 1% (w/v) agar] until 5 DAG.

Synthetic peptides

Synthetic peptides were ordered from GenScript (www.genscript.com/) and were used at the following purities: CLE1/4p (98.8% or 98.2%), CLE7p (94.8% or 88.9%), CLE27p (71.2% or 73.6%), CLE26p (94,2, 89.6, 84.6, or 99.7%), mCLE26p 1A (92.1%), mCLE26p 2A (91.6%), mCLE26p 3A (99.4%), mCLE26p 4A (98.2%), mCLE26p 5A (98.6%), mCLE26p 6A (84.9%), mCLE26p 7A (94.3%), mCLE26p 8A (99.1%), mCLE26p 10A (97.5%), mCLE26p 11A (94.3%), and mCLE26p 12A (94.7%). All peptides used were diluted to a 10 mM stock solution, correcting for purity [volume required for 10 mM×(purity/100)], and sequentially diluted to working concentrations prior to use. Stock and working solutions were stored at –20 °C.

Root architecture measurements

Emerged *A. thaliana* or *B. distachyon* lateral roots were counted using a dissection microscope. *B. distachyon* was removed from agar tubes by heating in a 95 °C water bath until the agar was melted, and mounted in 12×12 cm plates in sterile, distilled water prior to analysis. Photos of the plates were taken using a digital camera mounted on a fixed stand before and after counting lateral roots. Primary root length and lateral root numbers were measured by use of FIJI (Schindelin *et al.*, 2012) and analysed in Excel. Lateral root density was calculated as the total number of emerged lateral roots/total primary root length.

GUS screening

Seedlings at 10–12 DAG were stained in GUS staining solution (0.05 M sodium phosphate buffer, 5 mM potassium ferrocyanide, 5 mM potassium ferricyanide, 1 mM 5-bromo-4-chloro-3-indolyl-β-D-glucuronide) until the stain was visible under a dissection microscope, before stopping the reaction by immersion in 70% ethanol for 5 min. The seedlings were then cleared by incubation in acidified methanol [20% (v/v) methanol, 4% (v/v) HCl] for 15 min, followed by incubation in alkalinized ethanol [60% (v/v) ethanol, 7% (w/v) NaOH]. The ethanol concentration was then gradually decreased by 15–20 min incubations in each of 40, 20, and 10% ethanol, before storage and analysis of the expression pattern in distilled water (Malamy and Benfey, 1997). Stained seedlings were imaged using a Leica DMRB binocular microscope and Leica Application Suite (Leica). When necessary to improve figure quality, brightness and contrast of the images were modified using Photoshop and, in such cases, all related figures were treated the same.

GFP analysis

Seedlings grown in the presence of CLE26p or 5-day-old seedlings transferred to fresh plates containing CLE26p were analysed by confocal microscopy (Leica TCS SP5) at 5 DAG or at different time points (0, 6, and 24 h), respectively.

RNA extraction, cDNA synthesis, and (q)RT–PCR analysis

Total RNA was isolated with Trizol reagent (Invitrogen) or by using the RNeasy Mini Plant Kit (Qiagen) according to the manufacturer's instructions. Poly(dT) cDNA was prepared from 2 mg of total RNA with Superscript II/III reverse transcriptase (Invitrogen) and quantified on an LightCycler 480 apparatus (Roche Diagnostics) with the SYBR Green I Master kit (Roche Diagnostics) according to the manufacturer's instructions using gene-specific primers (CLE26 FW 5′-ACCATTCCCTTCGTCTCCA-3′ and CLE26 REV 5′-CGTCGTTCCTTGAACCATCT-3′). Three biological repeats were performed on a pool of seedlings and all individual reactions were done in triplicate. Graphs show one representative analysis. Data were analysed with qBase (Hellemans *et al.*, 2007) and normalized to *EEF1a4* (EEF1α4_FW 5′-CTGGAGGTTTTGAGGCTGGTAT-3′ and EEF1α4_REV 5′-CCAAGGGTGAAAGCAAGAAGA-3′) and/or *ARP7* (ARP7_FW 5′-ACTCTTCCTGATGGACAGGTG-3′ and ARP7_REV 5′-CTCAACGATTCCATGCTCCT-3′). To detect CLE26.1 and CLE26.2 splice variants, RNA was extracted with RNeasy (Qiagen), cDNA was prepared with an iScript cDNA Synthesis Kit (Bio-Rad), and specific primers (CLE26_F ATGCGAAATAACCATTCCCTTC and CLE26.2_AS TTATGCTCTTCCTGGTGGTCG or CLE26.1_AS TCATACAGAAACATCCAAGACACAT) were used for PCR [94 °C 3 min, 40× (94 °C 30 s, 55 °C 30 s, 72 °C 1 min), 72 °C 7 min].

Genevestigator analyses

Genevestigator (www.genevestigator.com) was used to assess transcriptional regulation of *CLE* genes for which microarray probes are available, using settings with a fold change of 2 and a *P*-value of 0.05.

Phylogenetic analyses

Full-length *A. thaliana* CLE peptide precursor sequences were obtained from Uniprot for all known *A. thaliana* CLE peptides. These sequences were used to BLAST for similar sequences in *Zea mays*, *Oryza sativa, B. distachyon*, *Brassica rapa*, *Selaginella moellendorffii*, and *Physcomitrella patens* using Phytozome v9.1 (Goodstein *et al.*, 2011). The indicated sequences were aligned with *A. thaliana* CLE peptide precursors to identify the conserved CLE region, and phylogenetic trees were built in CLC Workbench using the 12–13 amino acid conserved domains. The mature 12 amino acid sequences from *A. thaliana* and *B. distachyon* were further used to create a Weblogo alignment using WebLogo3 (Crooks *et al.*, 2004).

Structure prediction

The precursor protein was submitted to PHYRE for standard tertiary structure prediction and analysis (www.sbg.bio.ic.ac.uk/phyre2) (Kelley and Sternberg, 2009). The predicted secondary structure, model ranking, and relevant extra figures are shown in the Supplementary data at *JXB* online. Rotamers of Arg5 and Asp8 (Dunbrack, 2002) were explored and structural figures produced using Chimera v.1.5.3 (Pettersen *et al.*, 2004).

Results and discussion

CLE peptide expression is regulated by hormones and environmental triggers

Root architecture is controlled by hormonal and environmental cues (Smith and De Smet, 2012; Tian *et al.*, 2014). For example, auxin positively regulates several aspects of lateral root initiation, primordium development, and emergence (De Smet, 2012; Lavenus *et al.*, 2013), and abscisic acid (ABA) is crucial for salt-regulated root growth dynamics and acts—for instance—on meristem activation (De Smet *et al.*, 2003; Ding and De Smet, 2013; Duan *et al.*, 2013). Also, in response to various nutrient deficiencies, the root system displays high plasticity (Gruber *et al.*, 2013; Tian *et al.*, 2014). It is therefore not unexpected that gene expression of factors regulating root architecture is under hormonal and environmental

control, and a number of reports suggest this to be the case for *CLE* expression. Specifically nitrate and phosphate appear to affect *CLE* expression strongly in various species during the regulation of root architecture and/or nodulation, as do cytokinin and gibberellin (Okamoto *et al.*, 2009; Funayama-Noguchi *et al.*, 2011; Reid *et al.*, 2011; Mortier *et al.*, 2012; Araya *et al.*, 2014; Bidadi *et al.*, 2014; Lim *et al.*, 2014). To assess comprehensively the influence of hormones, nutrients, and abiotic stresses on the regulation of *CLE* expression in *A. thaliana*, available microarray data sets were probed. The combined analysis for those *CLE* genes—for which data were available and focusing on hormones and environmental triggers that had a significant effect—is shown in Table 1. Strikingly, *CLE2* and *CLE6* were mainly down-regulated by hormones, nutrients, and stress, while *CLE12* was mainly up-regulated. *CLE3*, *CLE26*, *CLE27*, *CLE41*, *CLE44*, and *CLE46* showed variable responses to the selected stimuli. For example, *CLE26*, *CLE41*, and *CLE44* are down-regulated by salicylic acid, while ABA and auxin up-regulated *CLE27*, *CLE41*, and/or *CLE44*. In conclusion, it indeed appears that environmental cues and hormone levels effect *CLE* expression, possibly during primary and lateral root growth and development. However, these global transcript data do not provide any information on where and when *CLE* genes relevant for root architecture are expressed.

Primary and lateral root CLE *expression patterns in* A. thaliana

The expression pattern for several *CLE* genes has been described previously (Sharma *et al.*, 2003; Geier *et al.*, 2008; Hirakawa *et al.*, 2008; Jun *et al.*, 2010; Depuydt *et al.*, 2013). However, to evaluate which CLE peptides might play a role in mediating *A. thaliana* root architecture comprehensively and comparably, the expression patterns of 20 *CLE* genes in the primary root tip and during lateral root development were profiled using previously published *pCLE::GUS* fusions (Jun *et al.*, 2010) under the growth conditions used here. This analysis revealed distinct expression patterns, both in the root tip and during early stages of lateral root development (Supplementary Figs S1–S4

Table 1. *Hormonal and environmental control of CLE expression*

	Hormones					
	Brassinosteroids	**ABA**	**Auxin**	**Jasmonic acid**	**Salicyclic acid**	
CLE2	–	–	–			
CLE3						
CLE6	–					
CLE12		+	–	+		
CLE26					–	
CLE27			+			
CLE41		+			–	
CLE44		+	+		–	
CLE46						
	Nutrients					
	Glucose	**Iron deficiency**	**Nitrate**	**Phosphate deficiency**	**Sulphur deficiency**	
CLE2	–	–	+		–	
CLE3				+		
CLE6	–	–		–		
CLE12	+			+	+	
CLE26						
CLE27						
CLE41	+					
CLE44		+				
CLE46						
	Stresses					
	Anoxia	**Cold**	**Drought**	**Heat**	**Hypoxia**	**Salt**
CLE2				–	–	
CLE3						
CLE6	–	+	–	–	–	
CLE12		+	+			+
CLE26						
CLE27						
CLE41				–		
CLE44		+	–			
CLE46			+			

+, significant up-regulation; –, significant down-regulation.

at *JXB* online). The majority of the observations are in agreement with an earlier report (Jun *et al.*, 2010); however, expression of *pCLE3::GUS*, *pCLE16::GUS*, and *pCLE17::GUS* was not observed in the vasculature. Given that the expression of *CLE* genes can be subject to environmental control (Table 1), the differences in expression observed could potentially be due to variations in growth conditions.

Based on the observed *CLE* expression patterns, a subset of CLEs was used for further analyses. Expression of *pCLE6::GUS*, *pCLE22::GUS*, *pCLE25::GUS*, *pCLE26::GUS*, and *pCLE27::GUS* was observed in the basal meristem, with *CLE6*, *CLE22*, *CLE25*, and *CLE26* expression seemingly restricted to the stele and with *CLE26* being the most strongly expressed (Fig. 1A; Supplementary Fig. S1 at *JXB* online). The latter expression patterns may indicate a role in lateral root patterning via establishment of the vascular pattern and/or priming of pericycle cells (De Smet *et al.*, 2007; Parizot *et al.*, 2008, 2012). During the early stages of lateral root development, *pCLE27::GUS* was specifically expressed in the asymmetrically dividing pericycle cells (Fig. 1C). Based on this expression pattern (in the core of the lateral root initiation site), it was hypothesized that CLE27 could be a positive regulator of early stages of lateral root development. In contrast, during lateral root initiation and development, *pCLE1::GUS*, *pCLE4::GUS*, and *pCLE7::GUS* were expressed in the vasculature and pericycle, but excluded from the developing primordium (Fig. 1D–F). Based on these expression patterns (excluded from the lateral root initiation site), it is hypothesized that these CLEs may be negative regulators of early stages of lateral root development.

Synthetic CLE peptides affect A. thaliana *primary and lateral root growth and development*

To characterize further the involvement of *CLE* genes with an interesting lateral root-associated expression pattern and/or a regulation by hormonal or environmental triggers, chemically synthesized CLE peptides (CLEps) corresponding to the predicted products of the respective *A. thaliana CLE* genes (AtCLEp, referred to as CLEp) were used. CLE1p, CLE4p, CLE7p, CLE26p, and CLE27p were selected but, since CLE1 and CLE4 have the same mature peptide sequence, they were represented by one synthetic peptide (CLE1/CLE4p) (Fig. 2A). Based on their expression patterns, a repressive (CLE1, CLE4, and CLE7) or inductive effect on lateral root development (CLE26 and CLE27) was hypothesized for the selected peptides. To test the biological activity of the chemically synthesized peptides, initially a high concentration (compared with likely normal physiological conditions) of 10 μM CLEp was applied to wild-type *A. thaliana* seedlings. This revealed a significant effect of all assayed CLE peptides, namely decreased primary root length (between a 76% and 94% decrease), decreased lateral root number (between a 57% and 88% decrease), and increased lateral root density (between a 98% and 179% increase) (Fig. 2B–D; Supplementary Fig. S5 at *JXB* online). The decrease in primary root length was predictable, since overexpression of *CLE* genes or application of chemically synthesized CLE peptides often results in consumption of the root apical meristem and/or a short primary root, and is possibly a non-specific response to high concentrations of exogenously applied peptide (Casamitjana-Martinez *et al.*, 2003; Fiers *et al.*, 2005; Kinoshita *et al.*, 2007; Jun *et al.*, 2010; Depuydt *et al.*, 2013). In addition, the increased lateral root density by CLE1, CLE4, and CLE7 is in contrast to the hypothesized effect, namely a decrease in lateral root development. It is, however, possible that the increased lateral root density is a consequence of the dramatically reduced primary root growth.

Subsequently, it was assessed whether these chemically synthesized CLE peptides also affected root architecture at a lower, more physiologically relevant concentration (10 nM). Analyses of *A. thaliana* seedlings grown on 10 nM CLEp revealed that only those seedlings grown on CLE26p displayed a significant 83% decrease in primary root length, a 72% decrease in lateral root number, and a 94% increase in lateral root density compared with the control (Fig. 2E–G; Supplementary Fig. S5 at *JXB* online). However, there was no obvious effect of CLE1p, CLE4p, and CLE7p on primary root length and neither did these seedlings display a reduced lateral root density. A dose–response analysis further indicated that CLE26p is able to restrict primary root growth and increase lateral root density in *A. thaliana* at a minimum concentration of 1 nM (Fig. 3A–C). This is a similar activity threshold to other peptides, such as, for example,

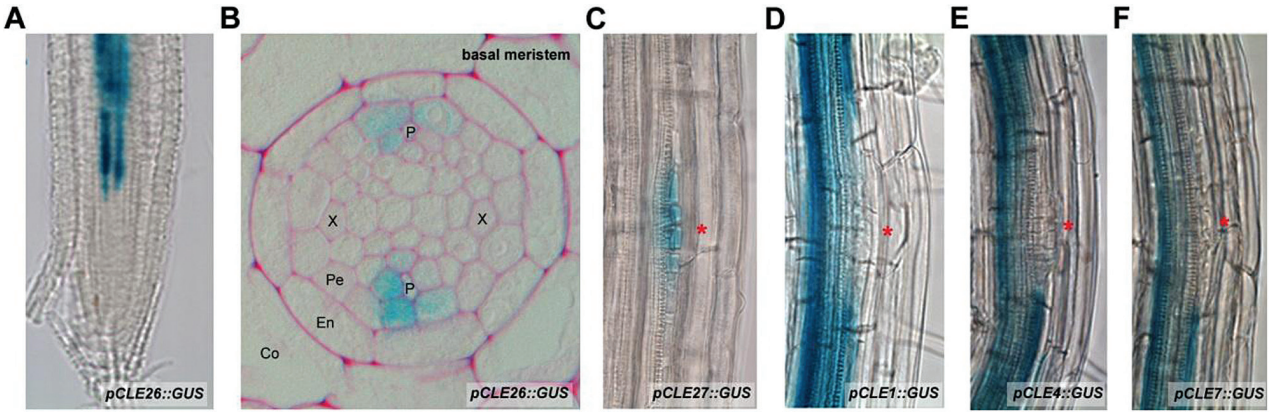


Fig. 1. *CLE* expression visualized through *pCLE::GUS* lines. (A, B) *pCLE26::GUS* in the primary root tip: (A) whole mount; (B) transverse section in the basal meristem. (C–F) *pCLE::GUS* during early stages of *A. thaliana* lateral root development: (C) *pCLE27::GUS*; (D) *pCLE1::GUS*; (E) *pCLE4::GUS*; (F) *pCLE7::GUS*. A red asterisk indicates the position of the lateral root primordium. Seedling age, 5–7 d after germination.

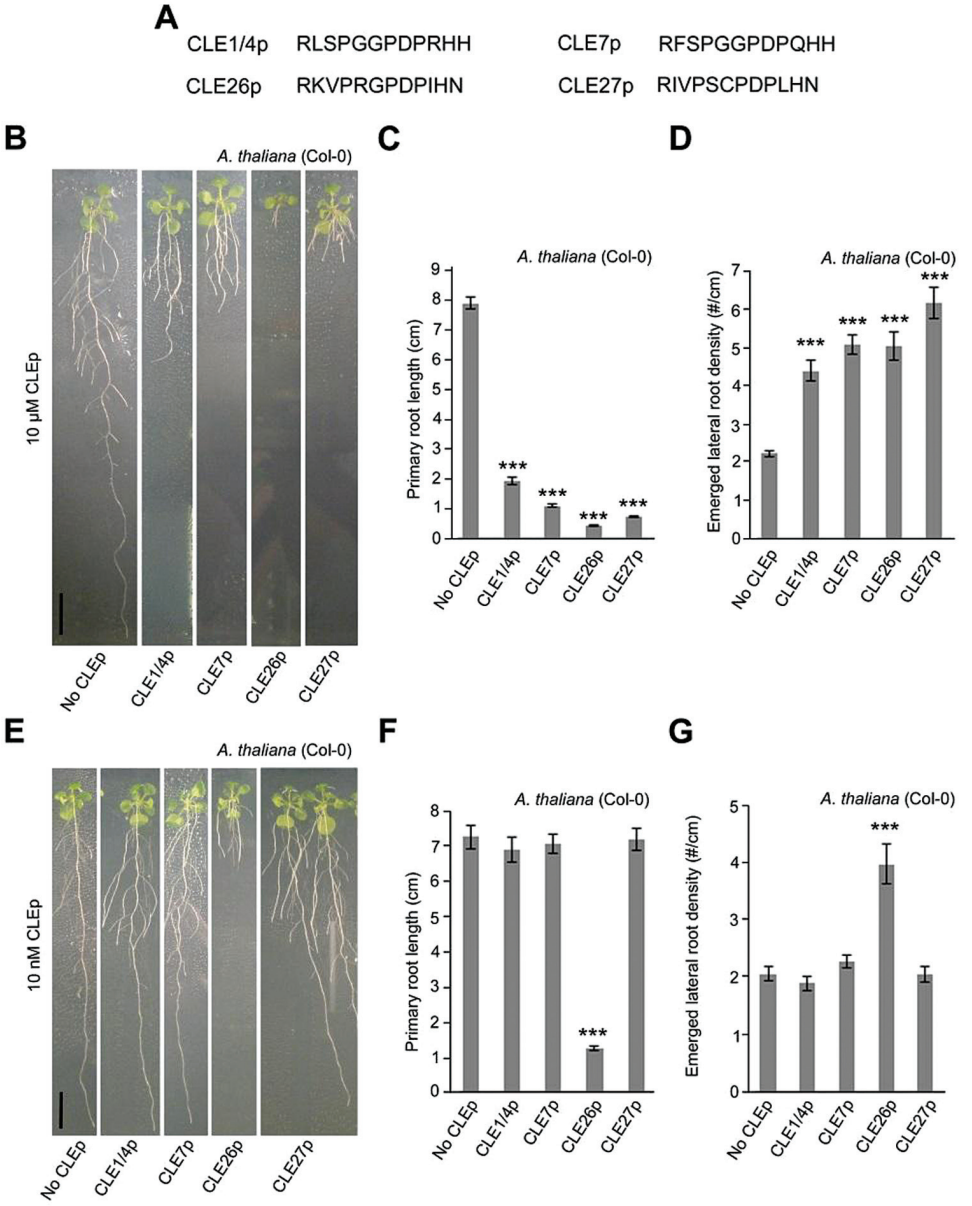


Fig. 2. CLE peptide treatment of *A. thaliana*. (A) Sequence of synthetic CLE peptides used. (B–G) Treatment of wild-type seedlings with 10 µM (B, C) or 10 nM CLE peptide (E–G). Representative pictures of CLE26p-treated wild-type seedlings at 12 d after germination (B and E). Quantification of primary root length (C and F) and emerged lateral root density (D and G) for CLE26p-treated wild-type seedlings. The bar graphs indicate the mean ±SE. Statistical significance (Student's *t*-test) compared with the no peptide treatment is indicated: ***P<0.01. Scale bar=1 cm. (This figure is available in colour at *JXB* online.)

RALF, which is also active in the nanomolar range (Pearce *et al.*, 2001), and TDIF (CLE41/CLE44), which is active in the picomolar range (Sawa *et al.*, 2006). Surprisingly, the present CLE26p application data (at higher concentrations) are not in agreement with earlier observations based on overexpression of *CLE26* (Strabala *et al.*, 2006), but correspond to another report that showed that 19 CLE peptides are able to induce a short root phenotype (Kinoshita *et al.*, 2007). In agreement with the present results, the latter study also showed that among all CLE peptides tested, CLE26p is the most effective one in inducing the short-root phenotype in *A. thaliana*. Intriguingly, CLE26p resulted in a subtle, but significant, increase in primary root length at a concentration of 0.1 nM and 0.01 nM (Fig. 3B), and it is possible that the previously reported *CLE26* overexpression lines (which could be mild overexpressors) (Strabala *et al.*, 2006) capture this. Taken together, the results suggest that CLE26 plays a role in *A. thaliana* primary and lateral root growth and development.

CLE26 *is expressed at the phloem pole*

To gain insight into the effect of CLE26p in relation to its expression pattern at cellular resolution, transverse root sections of *pCLE26::GUS* seedlings were analysed. This revealed that *CLE26* is expressed in the stele at the phloem pole (Fig. 1B), which is in agreement with a genome-wide expression profiling of xylem and phloem–cambium isolated from the root hypocotyl of *A. thaliana* where a phloem–cambium bias was reported (Zhao *et al.*, 2005). It was recently proposed that CLE45, BAM3, and BRX might interact to guide the proper

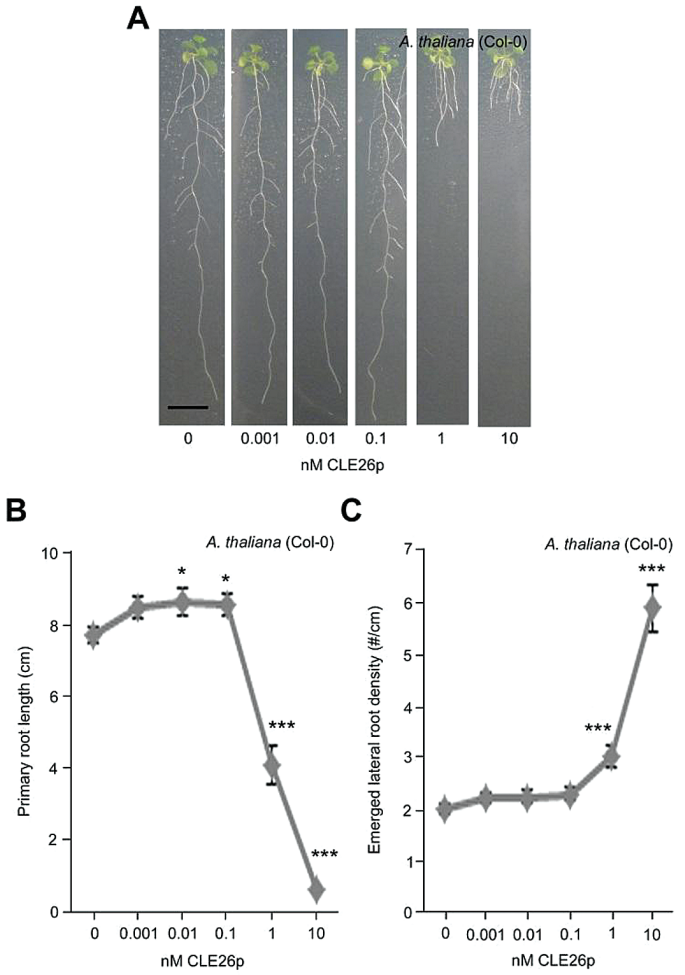


Fig. 3. CLE26p concentration gradient on *A. thaliana*. (A) Representative pictures of CLE26p-treated wild-type seedlings at 12 d after germination. (B, C) Quantification of primary root length (C) and emerged lateral root density (D) for CLE26p-treated wild-type seedlings. The graphs indicate the mean ±SE. Statistical significance (Student's *t*-test) compared with no peptide treatment is indicated: ***$P<0.01$; *$P<0.05$. Scale bar=1 cm. (This figure is available in colour at *JXB* online.)

transition of protophloem cells from proliferation to differentiation, which could determine the growth capacity of the root meristem (Depuydt *et al.*, 2013; Rodriguez-Villalon *et al.*, 2014), and it is possible that CLE26 has a similar function. To support this, fewer cells expressing the protophloem marker *pAT2G18380::GFP* (S32; Lee *et al.*, 2006) were observed in CLE26p-treated root tips (Supplementary Fig. S6 at *JXB* online). It is, however, unlikely that CLE26 signals through the same pathway as CLE45 as a *bam3* mutant is equally sensitive to CLE26 as the wild type (Depuydt *et al.*, 2013), ruling out BAM3 as a putative CLE26 receptor. However, CLE26 displayed similar strong binding affinity for BAM1 and BAM2, and moderate affinity for CLV1 and CLV2 (Guo *et al.*, 2010), making these receptors good candidates for mediating the CLE26 phenotype.

CLE26 peptide sequence–activity analyses identify key amino acids

Given that application of low—possibly physiologically more relevant—concentrations of CLE26p gave a reduction in primary root length and an increase in lateral root density, it was decided to focus on CLE26p for a more in-depth analysis of the sequence–activity relationship. To identify amino acids critical for CLE26p function, an alanine scan was performed using primary root length and lateral root density as biological assays (Fig. 4A–D; Supplementary Fig. S5 at *JXB* online). Seedlings grown on media containing 10 µM mCLE26p^{R1A}, mCLE26p^{P4A}, mCLE26p^{R5A}, mCLE26p^{G6A}, mCLE26p^{D8A}, mCLE26p^{P9A}, mCLE26p^{I10A}, mCLE26p^{H11A}, and mCLE26p^{N12A} showed no significant decrease in primary root length compared with untreated *A. thaliana*, and were significantly different from non-mutated CLE26p treatment (Fig. 4C). The total number of emerged lateral roots was similarly not decreased for these mCLE26p variants compared with the CLE26p control treatment (Supplementary Fig. S5). This suggested that these amino acid residues are critical for CLE26 function. In contrast, amino acid residues 2 and 3 do not appear to be critical for CLE function, since mCLE26p^{K2A} and mCLE26p^{V3A} displayed the same, but a less strong effect on primary root length as the non-mutated CLE26p variant (a decrease of between 52% and 63%) (Fig. 4C). Interestingly, mCLE26p^{P7A} displayed increased activity, with respect to both primary root length (a further decrease of 11%) and lateral root density (a further increase of 32%), compared with wild-type CLE26p (Fig. 4C, D). Finally, mCLE26p^{D8A} resulted in a slightly longer root than untreated seedling roots, but did not have an effect on lateral root density (Fig. 4C, D). Taken together, the series of alanine-substituted CLE26 peptides revealed several amino acids which are critical for bioactivity of CLE26, and pinpointed mCLE26p^{P7A} and mCLE26p^{D8A} as a hyperactive and a possible antagonistic peptide, respectively. Previous analyses of critical amino acid residues in, for example, CLE41/CLE44 [also referred to as TRACHEARY ELEMENT DIFFERENTIATION INHIBITORY FACTOR (TDIF)] (Ito *et al.*, 2006) and CLV3 (Kondo et al, 2008) identified similar amino acids that are important for the peptide to have the required bioactivity.

Structural modelling of CLE26p explains the mCLE26p^{P7A} effect

CLE26 has similar residues at the N- and C-termini as CLV3 that are critical for correct function in *A. thaliana*, and mutation of more central amino acids causes a similar reduction in bioactivity to that reported for CLV3 (Kondo *et al.*, 2008) (Fig. 5A). That these amino acids are critical for function indicates that they contribute to the correct conformation for ligand−receptor interaction. Structural analysis of CLE26 indicates that Gly6 and Pro7 form the sharp bend of a hairpin, potentially putting the proteolytic cleavage sites close together. This resembles earlier CLE structure predictions (Meng and Feldman, 2010). Rotamer analysis also showed that this conformation brings Arg5 and Asp8 into close proximity to form a salt bridge, potentially increasing the stability of the mature peptide (Fig. 5B). Surface hydrophobicity analysis suggested that one surface of this structure bulges and is predominantly basic, owing to Arg5, while the opposite surface is uncharged and has a cavity (Fig. 5C). These two surfaces could be involved in binding to receptors. The flanking

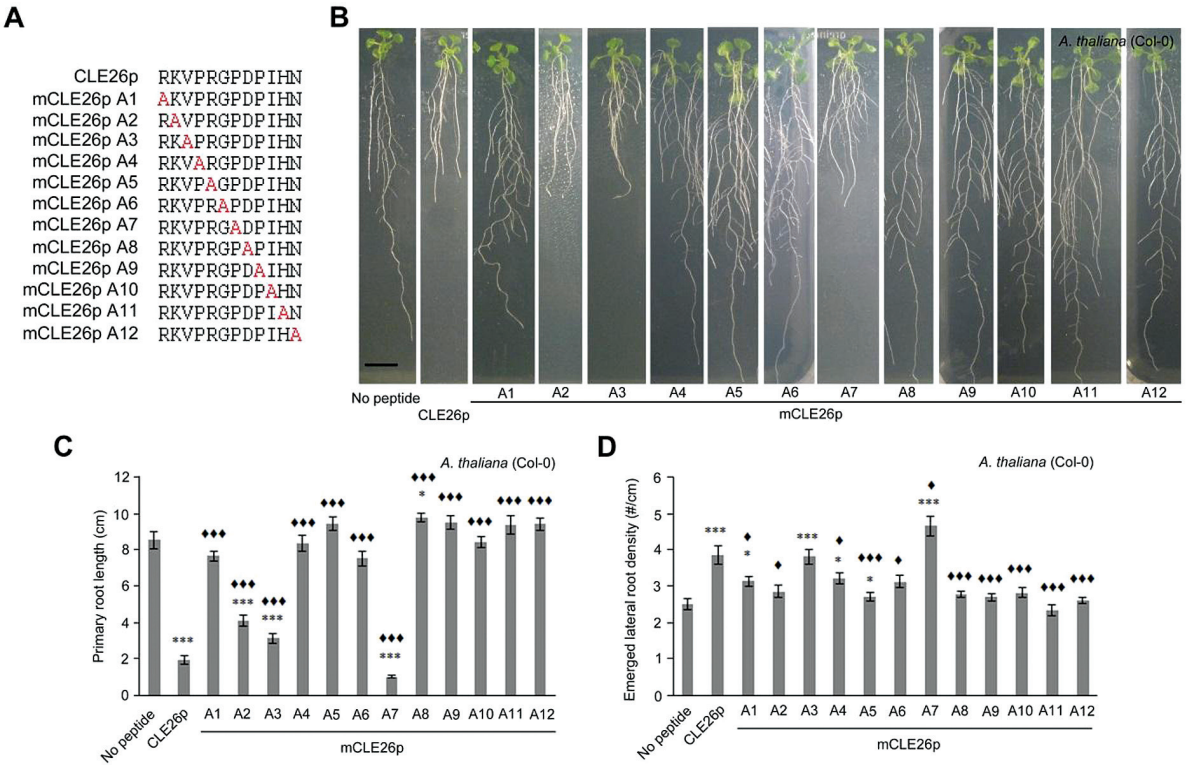


Fig. 4. CLE26p alanine scanning on *A. thaliana*. (A) Sequence of synthetic CLE peptides used. (B) Representative pictures of mCLE26p-treated wild-type seedlings at 12 d after germination. (C, D) Quantification of primary root length (C) and emerged lateral root density (D) for mCLE26p-treated wild-type seedlings. The bar graphs indicate the mean ±SE. Statistical significance (Student's *t*-test) compared with no peptide (*) and to CLEp treatment (♦) is indicated: ***/♦♦♦P<0.001, */♦P<0.05. Scale bar=1 cm. (This figure is available in colour at *JXB* online.)

precursor sequences are predicted to be α-helices, which may interact prior to mature peptide cleavage, facilitating the formation of a hairpin, and one of these could be membrane associated (Supplementary Fig. S7 at *JXB* online). It has been shown that CLV3p is hydroxylated on each of its proline residues and that the proline at position 7 in the CLV3 peptide is also arabinosylated, enhancing binding to CLV1 and CLV2 (Kondo *et al.*, 2006; Ohyama *et al.*, 2009; Shinohara and Matsubayashi, 2013). CLE26p also contains a proline residue at position 7, and it is worth noting that hydroxyl and arabinose side chains would point towards the arginine–aspartate surface noted above, perturbing their positions slightly (Fig. 5B). Similar modifications in CLE26p might be mimicked by mCLE26p^{P7A}, potentially increasing binding affinity for its orphan receptor and explaining the enhanced biological activity. Indeed, the mCLE26p^{P7A} effect could be mimicked by using a CLE26p variant that is hydroxylated at position 7 (CLE26p^{P7Hyp}) (Fig. 5D,E). The alanine at position 7 allows more flexibility in the arms of the hairpin, potentially enabling the arginine–aspartate surface to adopt a more favourable conformation for binding. Molecular dynamics studies of β-1,2-linked tri-arabinosylated CLV3p^{P7} suggest that the effect of the trisaccharide is to bring the N- and C-terminal ends of the peptide closer together (Shinohara and Matsubayashi, 2013), making it more like the hairpin model of CLE26.

The PXGPXP motif is conserved in most CLE peptides (Ito *et al.*, 2006), further indicating that formation of a bent hairpin structure is probably important for ligand–receptor interactions. Interestingly the highly conserved proline at position 7 is not critical for bioactivity of TDIF, CLV3, or CLE26. It is possible that the proline to alanine amino acid exchange at position 7 does not affect the peptide structure and thus does not affect activity, or that this conserved proline at position 7 is a target for post-translational modifications to 'fine-tune' the bioactivity of CLE peptides.

AtCLE26p affects Brachypodium *and wheat root architecture*

To investigate whether the effect of CLE26p observed in *A. thaliana* also extends to monocots, the primary root length of CLE26p-treated *B. distachyon* (Bd21) and wheat was analysed. CLE26p treatment of *B. distachyon* and wheat resulted in a short primary root compared with the untreated control (Fig. 6A–C). These results were similar to those in *A. thaliana* and suggested that an orthologue of AtCLE26 may also be involved in regulating primary root growth in monocots. However, in contrast to *A. thaliana*, CLE26p application failed to induce any obvious change to lateral root density in *B. distachyon* (Fig. 6D).

To explore CLE26 orthologues in monocots, CLE proteins were searched for in *Z. mays*, *O. sativa* and *B. distachyon*. A WebLogo alignment of mature peptide sequences from *A. thaliana* and *B. distachyon* indicated that mature CLE sequences are highly conserved, both within and between species (Fig. 7A, B). Phylogenetic analyses and sequence alignments indicated that *A. thaliana* mature CLE25 and CLE26 peptides are very similar and only differed at position 5 (asparagine and arginine, respectively) (Fig. 7C, D). While the CLE25p sequence appeared to be fully conserved

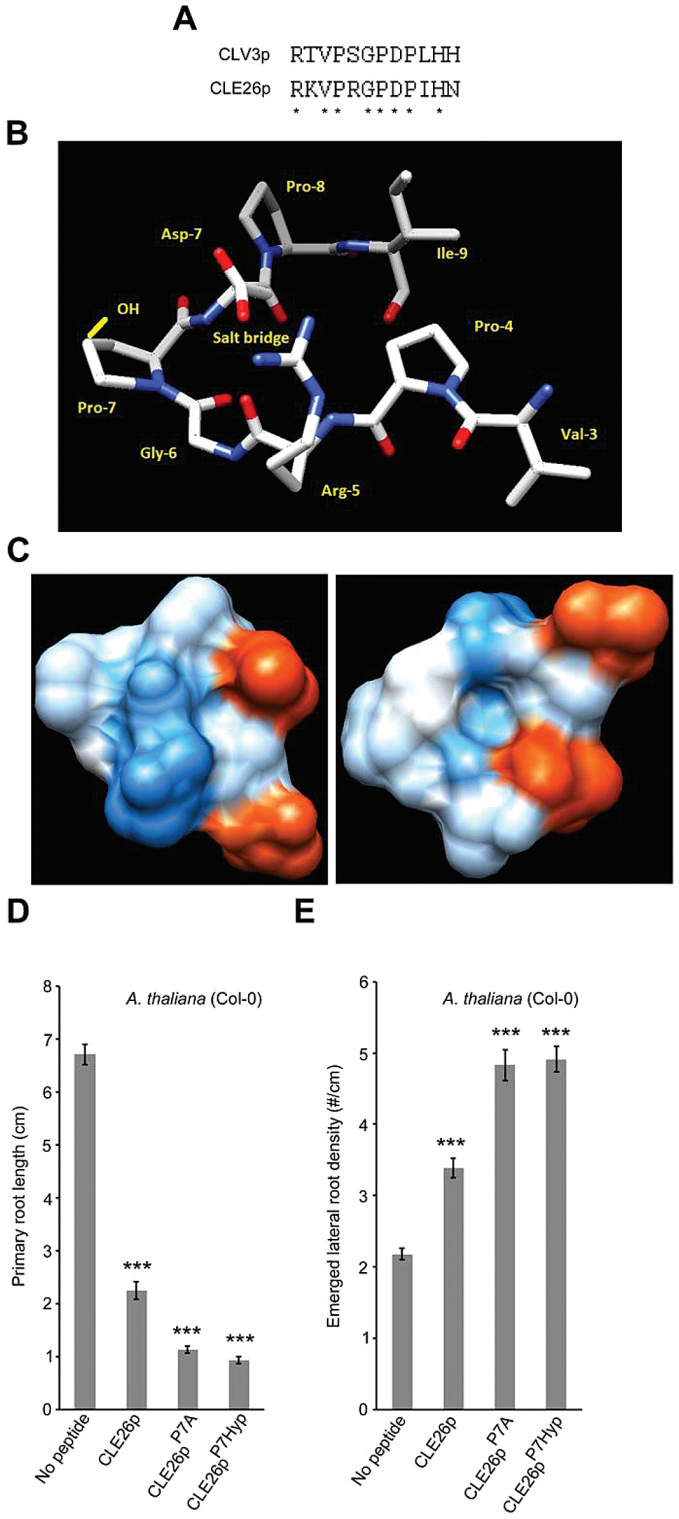


Fig. 5. Sequence and structure versus activity of CLE26p. (A) Conserved residues between CLE26p and CLV3p are denoted by asterisks. (B) The top-ranked predicted structure with amino acids of the cleaved CLE26 peptide named, the position of a potentially stabilizing salt bridge marked, and the hydroxyl group of Pro-7-Hyp (in the 2S, 4S conformation reported from other studies) depicted in yellow. (C) The solvent-accessible surface (left) and solvent-accessible surface of the opposite face of the peptide in (B) (right) coloured in shades of red or blue to indicate the level of acidity or alkalinity, respectively. (D, E) Quantification of primary root length (D) and emerged lateral root density (E) for CLE26p, CLE27p^{P7A} (~mCLE26p A7), and CLE26p^{7Hyp}-treated wild-type seedlings. The graph indicates the mean ±SE. Statistical significance (Student's *t*-test) compared with no peptide treatment is indicated: ***P<0.01.

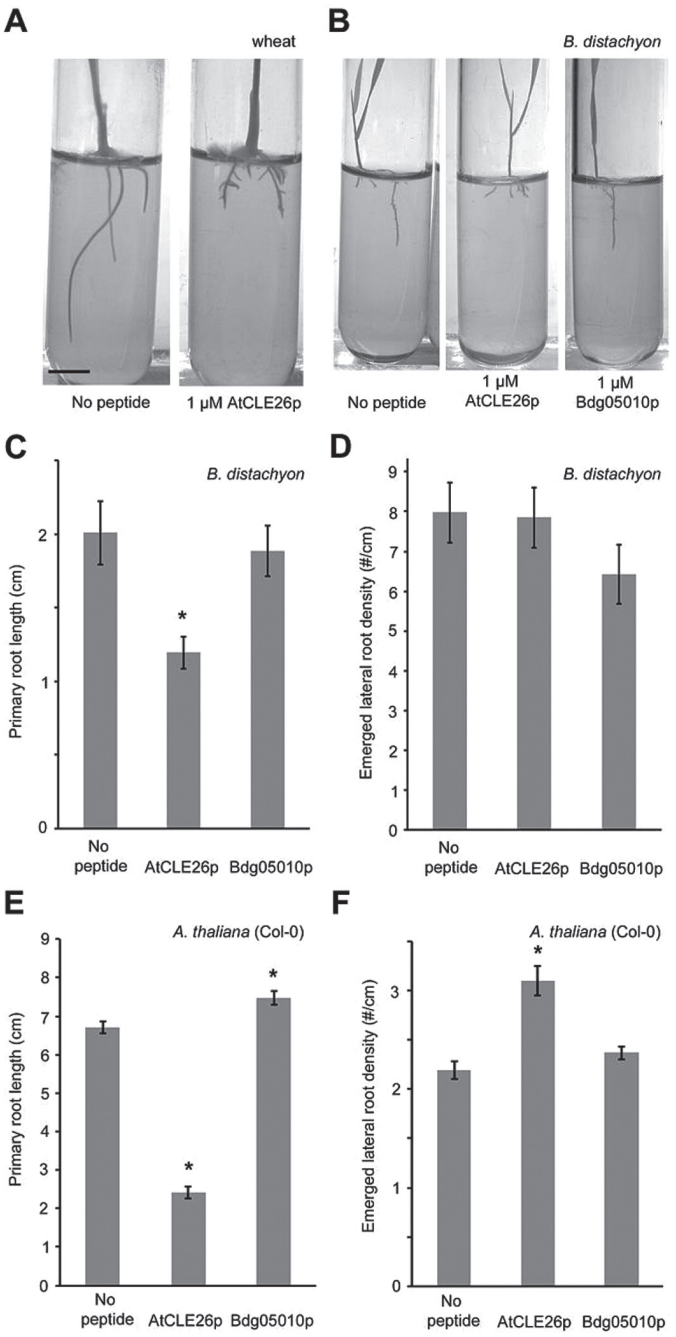


Fig. 6. Effect of AtCLE26p and BdCLE26p on wheat, *B. distachyon,* and *A. thaliana.* (A, B) Representative pictures are shown for wheat (A) and *B. distachyon* (B) at 12 d after germination. (C, D) Quantification of *B. distachyon* seedling primary root length (C) and emerged lateral root density (D). (E, F) Quantification of *A. thaliana* seedling primary root length (C) and emerged lateral root density (D). The bar graphs indicate the mean ±SE. Statistical significance (Student's *t*-test) compared with no peptide treatment is indicated: ***P<0.01. Scale bar=1 cm.

in monocots such as rice and maize, completely conserved CLE26p sequences were not retrieved (Fig. 7C, E). Putative CLE26p-like sequences differed at one or two positions, namely position 2 (arginine instead of lysine) and 5 (asparagine instead of arginine) in *B. distachyon*, *Z. mays* and *O. sativa* (Fig. 7E). According to the blocks substitution matrix 62 (BLOSUM62), these substitutions are conservative amino acid substitutions—the substitution has similar biochemical properties to that of the original—and should,

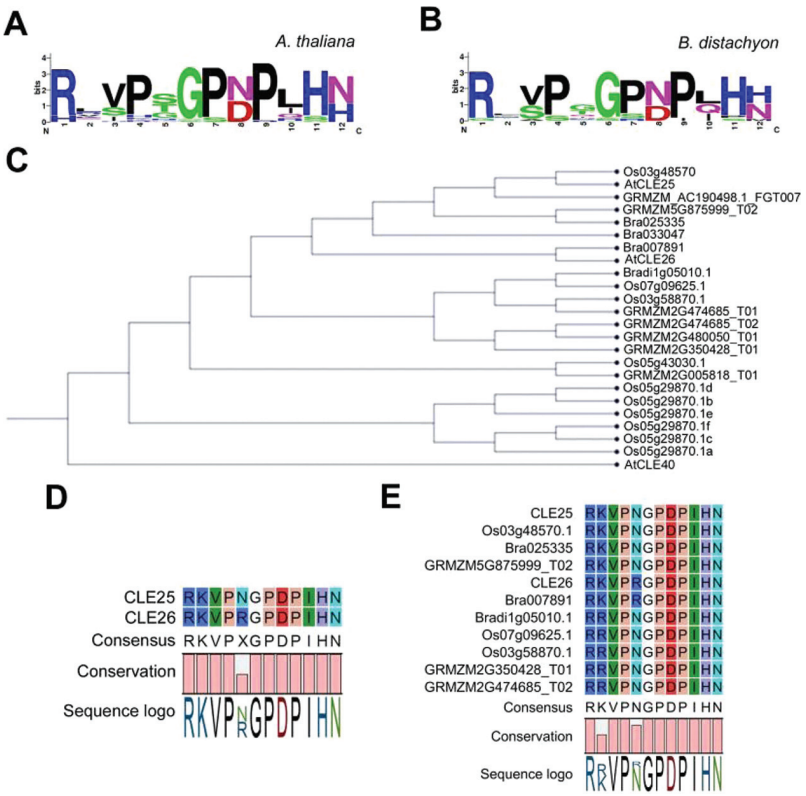


Fig. 7. Phylogenetic analysis of mature CLE25 and CLE26 orthologues. (A, B) Weblogo for *A. thaliana* (A) and *B. distachyon* mature CLE peptide sequences (B). (C) Phylogenetic tree. (D-E) Alignment of the indicated CLE peptide sequences in *Arabidopsis thaliana*, *Oryza sativa* (Os), *Brassica rapa* (Bra), *Zea mays* (GRMZM), and *Brachypodium distachyon* (Bradi). (This figure is available in colour at *JXB* online.)

therefore, not strongly affect the bioactivity of the peptide. However, the CLE26p alanine scan showed that the arginine at position 5 was essential for function in *A. thaliana*, while the lysine at position 2 was not (Fig. 4). Based on these observations, it cannot be ruled out that a non-specific CLE26p effect was observed in wheat and *B. distachyon*, To investigate this further, a synthetic CLEp derived from a *B. distachyon Bradi1g05010*-encoded protein (Bd1g05010p), a CLE25p/CLE26p-related CLE peptide, was applied to *A. thaliana* seedlings. This did not recapitulate the effects observed for the *A. thaliana* CLE26p (Fig. 6E, F), indeed supporting that this peptide is not active in *A. thaliana*. In contrast, Bd1g05010p-treated *A. thaliana* seedlings display a slightly increased primary root length (Fig. 6E), suggesting that Bd1g05010p might act as an antagonistic peptide. Next, Bd1g05010p was applied to *B. distachyon* and the impact on root architecture was evaluated. Interestingly, Bd1g05010p did not reduce primary root length, but slightly decreased lateral root density (Fig. 6C, D). This is opposite to what was observed with the *A. thaliana* CLE26p and to what was previously observed for *A. thaliana* CLE25p (Strabala *et al.*, 2006; Kinoshita *et al.*, 2007). It appears that the change of the conserved amino acid K into R has a strong impact on functionality. While this needs to be explored in more detail, the monocot Bd1g05010p is possibly not a functional orthologue of *A. thaliana* CLE26p or even CLE25p. This may indicate the presence of another (currently unknown) peptide present in *B. distachyon*, which, although less similar in primary sequence to *A. thaliana* CLE26p, is able to form a similar secondary structure, fulfilling the role of CLE26 role in *B. distachyon.*

CLE26 peptide affects auxin response

Since auxin plays a dominant role in primary root growth and lateral root initiation and development (De Smet, 2012; Lavenus *et al.*, 2013; Tian *et al.*, 2014), it was explored whether and potentially where CLE26p would have an influence on auxin response. For this, it was first tested if *CLE26* expression was regulated by auxin. qPCR analyses showed an ~4-fold increase in *CLE26* expression in wild-type seedling roots following 6 h of auxin treatment (Fig. 8A). Subsequently, it was tested whether CLE26p affects the auxin response marker *pDR5::GUS*. At 1 nM CLE26p, a concentration that significantly affected primary root growth, no obvious difference in *pDR5::GUS* expression was observed in the primary root tip (Fig. 8B). However, at a higher concentration (1 µM), the *pDR5::GUS* expression level was significantly reduced (Fig. 8B). Subsequently, the AUX/IAA protein-based auxin sensor *p35S::DII:VENUS* (Vernoux *et al.*, 2011; Brunoud *et al.*, 2012) was tested upon CLE26p treatment. While a mild increase in DII:VENUS fluorescence was observed at 1 nM CLE26p, there was a dramatic increase at 1 µM (Fig. 8C). In agreement with the *pDR5::GUS* results (Fig. 8B), this suggested an altered auxin response in the root tip. These observations are similar to what was recently observed using 10 nM CLE26p on *pDR5::NLS-3xVENUS* for 48 h (Rodriguez-Villalon *et al.*, 2015). Next, to determine if the effect of CLE26p on the auxin response and/or distribution

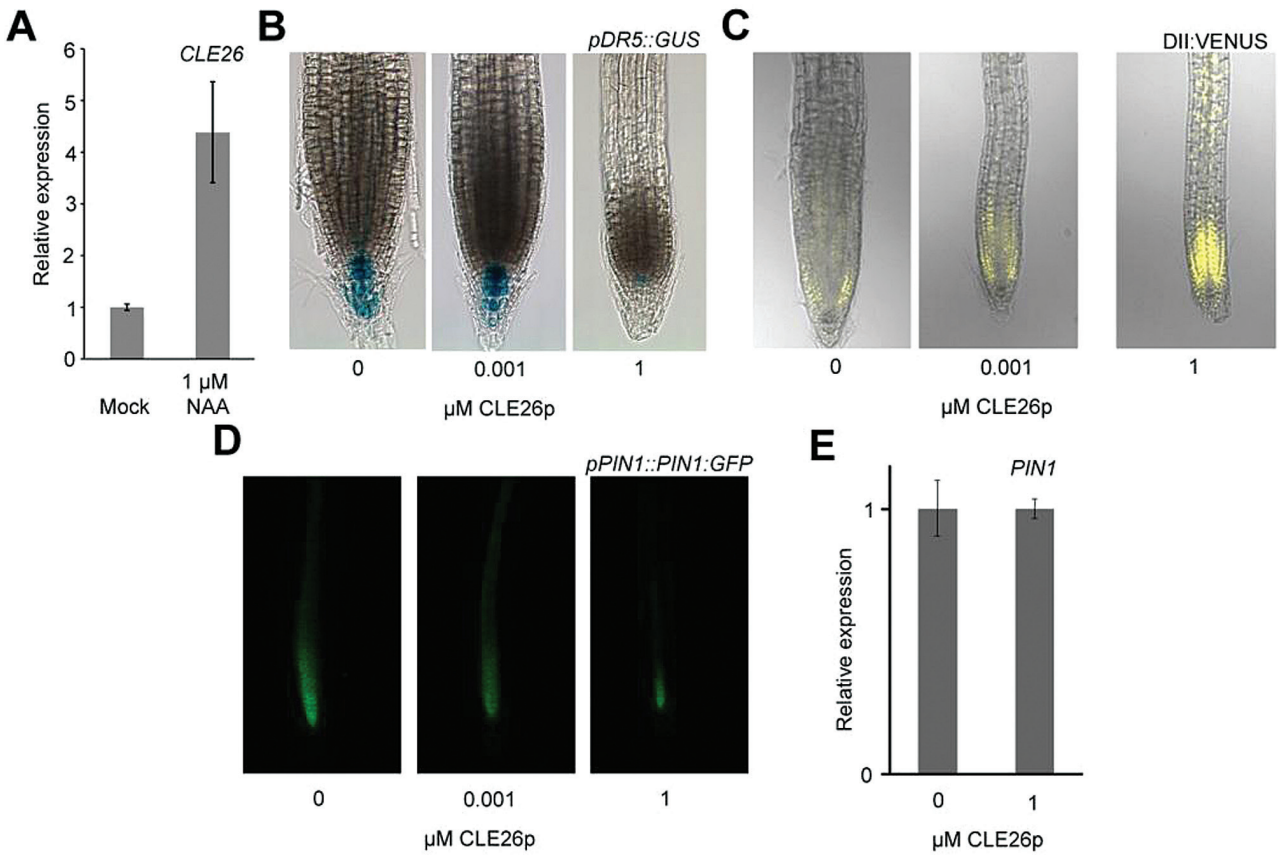


Fig. 8. CLE26 and auxin response/transport. (A) *CLE26* expression level as determined by qPCR in auxin-treated (6 h) 5-day-old wild-type seedlings. (B–D) CLE26p-treated *pDR5::GUS* (B), *35S::DII:VENUS* (C), and *pPIN1::PIN1:GFP* 5-day-old seedlings continuously grown on CLE26p (D). (E) *PIN1* expression level in 7-day-old seedling roots treated with CLE26p for 24 h. The bar graph indicates the mean ±SE.

in the root tip could be related to CLE26p regulation of polar auxin transport, the *pPIN1::PIN1:GFP* marker line was used (Benková *et al.*, 2003). The *pPIN1::PIN1:GFP* marker displayed mildly and strongly reduced fluorescence at 1 nM and 1 μM, respectively (Fig. 8D; Supplementary Fig. S8 at *JXB* online). An even stronger effect on PIN1 fluorescence and localization was observed with 1 nM CLE26p^{P7Hyp} (Supplementary Fig. S8). However, this reduction is in contrast to the qPCR results, where CLE26p treatment did not dramatically affect *PIN1* expression in the root (Fig. 8E). This suggested a possible CLE26p-mediated effect on PIN1:GFP at the protein level, which could explain the reduced auxin response in the root tip.

Finally, it was analysed whether CLE26p acts upstream or downstream of the ARF7–ARF19 module, a major regulator of lateral root development (Lavenus *et al.*, 2013). For this, the impact of CLE26p treatment on *ARF7* and *ARF19* expression was tested using qPCR. In CLE26p-treated roots, the *ARF7* and *ARF19* expression levels are not significantly affected (Fig. 9A). Subsequently, the effect of CLE26p treatment on *arf7arf19* was tested. Interestingly, the lateral rootless *arf7arf19* double mutant was partially insensitive to CLE26p with respect to primary root length, but displayed a limited—often closely grouped—number of lateral roots upon CLE26p treatment (Fig. 9B–E). In conclusion, on the one hand, CLE26p appears to require an ARF7- and ARF19-dependent auxin response for its activity, but, on the other hand, it appears to be able to induce lateral root development in *arf7arf19*. These two—seemingly opposing—effects can possibly be reconciled through a CLE26-mediated perturbation of auxin transport and accumulation.

An Arabidopsis cle26 *mutant affects root architecture*

To explore further the role of CLE26 in mediating root architecture, a T-DNA insertion line, which was named *cle26-1*, was analysed (Fig. 10A). Interestingly, *CLE26* has two splicing variants that are both expressed in the root (Fig. 10A; Supplementary Fig. S9 at *JXB* online). qPCR was performed to examine *CLE26* mRNA transcript levels (using a primer pair that captures both *CLE26.1* and *CLE26.2*) in *cle26-1*, and an ~80% decrease in *CLE26* expression was observed (Fig. 10B). Then the primary root length and lateral root density of *cle26-1* were analysed. This revealed a mild, significant increase with respect to primary root length, and no difference in the level of emerged lateral root density (Fig. 10C–E). Overall, it appears that CLE26 impacts on primary root length and that its effect on lateral root density may be compensated for by other closely related signalling pathways or by genetic redundancy with other CLE peptides.

Conclusion

Taken together, the gain- and loss-of-function data support a role for CLE26 in regulating root architecture. It was

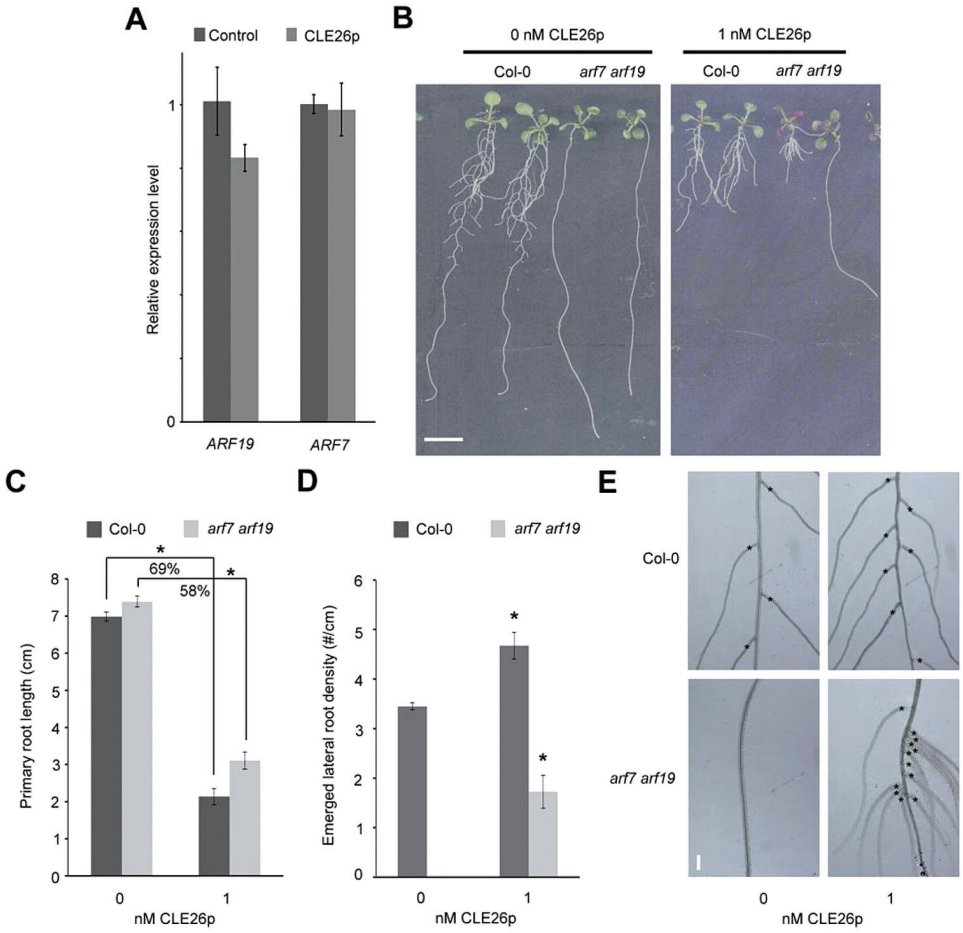


Fig. 9. CLE26p and ARF7–ARF19. (A) *ARF7* and *ARF19* expression as determined by qPCR in 7-day-old seedling roots treated with 1 μM CLE26p for 24 h. The bar graph indicates the mean ±SE. (B–E) Root phenotype of CLE26p-treated Col-0 and *arf7arf19* at 9 d after germination. Representative pictures (B) and quantification of primary root length (C) and emerged lateral root density (D). The bar graphs indicate the mean ±SE. Statistical significance (Student's *t*-test) compared with no peptide treatment: *$P<0.05$. Scale bar=1 cm (B) and 100 μm (E). (E) Detail of lateral root positions (asterisk) and density in Col-0 and *arf7arf19* following peptide treatment. (This figure is available in colour at *JXB* online.)

recently reported that both CLE45 and CLE26 affect primary root protophloem differentiation, which in turn systemically affects root branching (Rodriguez-Villalon *et al.*, 2014, 2015). The present results on CLE26 confirm, and are complementary to, these recently published data on the *CLE26* expression pattern and the CLE26p effect on auxin response and *Arabidopsis* root system architecture. The findings indicate that application of CLE26p decreases the distribution of auxin to the root apical meristem, seemingly by decreasing the abundance of PIN1 through post-translational regulation. Interestingly, it has been reported that localization of PIN1 is responsive to cytokinin signalling (Bishopp *et al.*, 2011). Since CLE14 and CLE20 have previously been demonstrated to be cytokinin responsive (Meng and Feldman, 2010), it will be of interest to determine whether CLE26 interacts with cytokinin signalling, which may indicate a role for CLE26 in mediating localization and/or degradation of PIN1 in response to cytokinin (Marhavy *et al.*, 2014). However, it is also possible that altered CLE26-mediated protophloem differentiation globally affects shoot to root transport and/or protein localization, including PIN1-mediated auxin distribution, but also, for example, the distribution of sugars.

On a structural level, the alanine scanning data indicated a hyperactive proline ($CLE26^{P7}$). Further analysis indicated that the $mCLE26p^{P7A}$ variant mimics the effect on bioactivity of $CLE26p^{P7Hyp}$. The former could affect the position of the arms of the loop, while the latter could achieve the same effect by altering the positions of Arg5 and Asp8. The CLE26 model also suggests that other interactions between amino acids may contribute to the folding process, and thus the bioactivity of CLE26p. In view of a possible antagonistic peptide, a new approach to obtain loss-of-function phenotypes that has, however, some limitations (Song *et al.*, 2013; Czyzewicz *et al.*, 2015), $mCLE26p^{D8A}$ has some potential as it appears to mimic the *cle26-1* phenotype.

In monocot model systems (*Brachypodium* and wheat), synthetic CLE26 application exhibited a similar reduction in primary root length, suggesting an orthologous signalling pathway. However, application of a sequentially orthologous peptide (termed Bd1g05010p) to *Brachypodium* did not induce a short-root phenotype. This suggests that *Brachypodium* may have evolved a separate signalling peptide to fulfil the same role as CLE26, that, although less similar in primary sequence, presumably forms a similar functional secondary structure. Similarly,

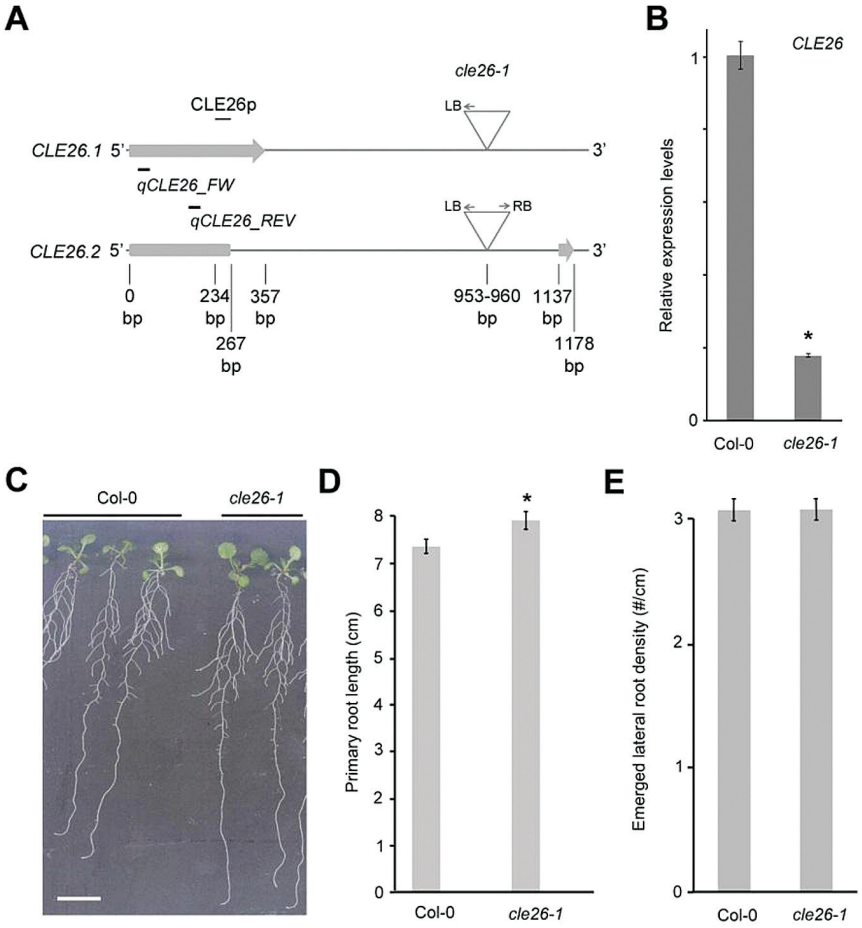


Fig. 10. Characterization of the *cle26-1* mutant. (A) Position of the T-DNA insertion in two splicing variants. Primers used in qPCR are indicated. (B) *CLE26* expression level as determined by qPCR in *cle26-1* roots. (C–E) Root phenotype of *cle26-1* at 9 d after germination. Representative pictures of wild-type and *cle26-1* seedlings (C). (D, E) Quantification of primary root length (D) and emerged lateral root density (E) for *cle26-1* seedlings. The graphs indicate the mean ±SE. Statistical significance (Student's *t*-test) compared with Col-0 is indicated: *$P<0.05$. Scale bar=1 cm. (This figure is available in colour at *JXB* online.)

synthetic Bd1g05010p did not induce a short-root phenotype when applied to *Arabidopsis* at the same concentration as AtCLE26p, indicating that the peptide is either non-functional, or requires a higher concentration in order to stimulate its receptor in both species.

Supplementary data

Supplementary data are available at *JXB* online.

Figure S1. *pCLE::GUS* expression in *Arabidopsis* primary root tip.

Figure S2. *pCLE::GUS* expression during early stages of *Arabidopsis* lateral root development.

Figure S3. *pCLE::GUS* expression during later stages of *Arabidopsis* lateral root development.

Figure S4. *pCLE::GUS* expression in selected stages of lateral root development.

Figure S5. Emerged lateral root numbers corresponding to Figs 2D, E, and 4D.

Figure S6. CLE26p effect on *pAT2G18380::GFP* in primary root tip.

Figure S7. CLE26 consensus secondary structure prediction.

Figure S8. CLE26p effect on PIN1:GFP.

Figure S9. *CLE26* splicing variants in the root.

Figure S10. PSI-BLAST output for CLE26.

Table S1. *pCLE::GUS* lines.

Acknowledgements

We thank Jennifer Fletcher, Anthony Bishopp, and the NASC for providing seeds, and Ruth Cornock and Stephanie Smith for technical support. This work was supported by a BBSRC David Phillips Fellowship (BB_BB/H022457/1) and a Marie Curie European Reintegration Grant (PERG06-GA-2009–256354) to IDS, a BBSRC CASE Studentship co-funded by Bayer CropScience to NC, and grants 13785/F20 and 230849/F20 to MAB, and 348256/F20 to C-LS from the Research Council of Norway. LDV received a VIB International PhD Scholarship in life sciences.

References

Araya T, Miyamoto M, Wibowo J, *et al*. 2014. CLE–CLAVATA1 peptide–receptor signaling module regulates the expansion of plant root systems in a nitrogen-dependent manner. *Proceedings of the National Academy of Sciences, USA* **111,** 2029–2034.

Benková E, Michniewicz M, Sauer M, Teichmann T, Seifertová D, Jürgens G, Friml J. 2003. Local, efflux-dependent auxin gradients as a common module for plant organ formation. *Cell* **115,** 591–602.

Betsuyaku S, Sawa S, Yamada M. 2011. The function of the CLE peptides in plant development and plant–microbe interactions. *Arabidopsis Book* **9,** e0149.

Bidadi H, Matsuoka K, Sage-Ono K, *et al*. 2014. CLE6 expression recovers gibberellin deficiency to promote shoot growth in Arabidopsis. *The Plant Journal* **78,** 241–252.

Bishopp A, Help H, El-Showk S, Weijers D, Scheres B, Friml J, Benková E, Mähönen Ari P, Helariutta Y. 2011. A mutually inhibitory interaction between auxin and cytokinin specifies vascular pattern in roots. *Current Biology* **21,** 917–926.

Brunoud G, Wells DM, Oliva M, *et al*. 2012. A novel sensor to map auxin response and distribution at high spatio-temporal resolution. *Nature* **482,** 103–106.

Butenko MA, Vie AK, Brembu T, Aalen RB, Bones AM. 2009. Plant peptides in signalling: looking for new partners. *Trends in Plant Science* **14,** 255–263.

Butenko MA, Wildhagen M, Albert M, Jehle A, Kalbacher H, Aalen RB, Felix G. 2014. Tools and strategies to match peptide–ligand receptor pairs. *The Plant Cell* **26,** 1838–1847.

Casamitjana-Martinez E, Hofhuis HF, Xu J, Liu CM, Heidstra R, Scheres B. 2003. Root-specific CLE19 overexpression and the sol1/2 suppressors implicate a CLV-like pathway in the control of Arabidopsis root meristem maintenance. *Current Biology* **13,** 1435–1441.

Clark SE, Running MP, Meyerowitz EM. 1995. CLAVATA3 is a specific regulator of shoot and floral meristem development affecting the same processes as CLAVATA1. *Development* **121,** 2057–2067.

Crooks GE, Hon G, Chandonia JM, Brenner SE. 2004. WebLogo: a sequence logo generator. *Genome Research* **14,** 1188–1190.

Czyzewicz N, Wildhagen M, Cattaneo P, *et al.* 2015. Antagonistic peptide technology revisited. *Journal of Experimental Biology* **66,** 5367–5374.

Czyzewicz N, Yue K, Beeckman T, De Smet I. 2013. Message in a bottle: small signalling peptide outputs during growth and development. *Journal of Experimental Biology* **64,** 5281–5296.

Davière J-M, Achard P. 2013. Gibberellin signaling in plants. *Development* **140,** 1147–1151.

Depuydt S, Rodriguez-Villalon A, Santuari L, Wyser-Rmili C, Ragni L, Hardtke CS. 2013. Suppression of Arabidopsis protophloem differentiation and root meristem growth by CLE45 requires the receptor-like kinase BAM3. *Proceedings of the National Academy of Sciences, USA* **110,** 7074–7079.

De Smet I. 2012. Lateral root initiation: one step at a time. *New Phytologist* **193,** 867–873.

De Smet I, Signora L, Beeckman T, Inze D, Foyer CH, Zhang H. 2003. An abscisic acid-sensitive checkpoint in lateral root development of Arabidopsis. *The Plant Journal* **33,** 543–555.

De Smet I, Tetsumura T, De Rybel B, *et al*. 2007. Auxin-dependent regulation of lateral root positioning in the basal meristem of Arabidopsis. *Development* **134,** 681–690.

Ding Z, De Smet I. 2013. Localised ABA signalling mediates root growth plasticity. *Trends in Plant Science* **18,** 533–535.

Duan L, Dietrich D, Ng CH, Chan PM, Bhalerao R, Bennett MJ, Dinneny JR. 2013. Endodermal ABA signaling promotes lateral root quiescence during salt stress in Arabidopsis seedlings. *The Plant Cell* **25,** 324–341.

Dunbrack RL Jr. 2002. Rotamer libraries in the 21st century. *Current Opinion in Structural Biology* **12,** 431–440.

El-Showk S, Ruonala R, Helariutta Y. 2013. Crossing paths: cytokinin signalling and crosstalk. *Development* **140,** 1373–1383.

Fiers M, Golemiec E, Xu J, van der Geest L, Heidstra R, Stiekema W, Liu CM. 2005. The 14-amino acid CLV3, CLE19, and CLE40 peptides trigger consumption of the root meristem in Arabidopsis through a CLAVATA2-dependent pathway. *The Plant Cell* **17,** 2542–2553.

Fletcher JC, Brand U, Running MP, Simon R, Meyerowitz EM. 1999. Signaling of cell fate decisions by CLAVATA3 in Arabidopsis shoot meristems. *Science* **283,** 1911–1914.

Funayama-Noguchi S, Noguchi K, Yoshida C, Kawaguchi M. 2011. Two CLE genes are induced by phosphate in roots of Lotus japonicus. *Journal of Plant Research* **124,** 155–163.

Geier F, Lohmann JU, Gerstung M, Maier AT, Timmer J, Fleck C. 2008. A quantitative and dynamic model for plant stem cell regulation. *PLoS One* **3,** e3553.

Goodstein DM, Shu S, Howson R, *et al*. 2011. Phytozome: a comparative platform for green plant genomics. *Nucleic Acids Research* **40,** D1178–D1186.

Gruber BD, Giehl RF, Friedel S, von Wiren N. 2013. Plasticity of the Arabidopsis root system under nutrient deficiencies. *Plant Physiology* **163,** 161–179.

Guo Y, Han L, Hymes M, Denver R, Clark SE. 2010. CLAVATA2 forms a distinct CLE-binding receptor complex regulating Arabidopsis stem cell specification. *The Plant Journal* **63,** 889–900.

Hellemans J, Mortier G, De Paepe A, Speleman F, Vandesompele J. 2007. qBase relative quantification framework and software for management and automated analysis of real-time quantitative PCR data. *Genome Biology* **8,** R19.

Hirakawa Y, Shinohara H, Kondo Y, *et al*. 2008. Non-cell-autonomous control of vascular stem cell fate by a CLE peptide/receptor system. *Proceedings of the National Academy of Sciences, USA* **105,** 15208–15213.

Hobe M, Muller R, Grunewald M, Brand U, Simon R. 2003. Loss of CLE40, a protein functionally equivalent to the stem cell restricting signal CLV3, enhances root waving in Arabidopsis. *Development Genes and Evolution* **213,** 371–381.

Ito Y, Nakanomyo I, Motose H, Iwamoto K, Sawa S, Dohmae N, Fukuda H. 2006. Dodeca-CLE peptides as suppressors of plant stem cell differentiation. *Science* **313,** 842–845.

Jun J, Fiume E, Roeder AHK, *et al*. 2010. Comprehensive analysis of CLE polypeptide signaling gene expression and overexpression activity in Arabidopsis. *Plant Physiology* **154,** 1721–1736.

Kelley LA, Sternberg MJ. 2009. Protein structure prediction on the Web: a case study using the Phyre server. *Nature Protocols* **4,** 363–371.

Kinoshita A, Nakamura Y, Sasaki E, Kyozuka J, Fukuda H, Sawa S. 2007. Gain-of-function phenotypes of chemically synthetic CLAVATA3/ESR-related (CLE) peptides in Arabidopsis thaliana and Oryza sativa. *Plant and Cell Physiology* **48,** 1821–1825.

Kondo T, Nakamura T, Yokomine K, Sakagami Y. 2008. Dual assay for MCLV3 activity reveals structure–activity relationship of CLE peptides. *Biochemical and Biophysical Research Communications* **377,** 312–316.

Kondo T, Sawa S, Kinoshita A, Mizuno S, Kakimoto T, Fukuda H, Sakagami Y. 2006. A plant peptide encoded by CLV3 identified by *in situ* MALDI-TOF MS analysis. *Science* **313,** 845–848.

Kurup S, Runions J, Kohler U, Laplaze L, Hodge S, Haseloff J. 2005. Marking cell lineages in living tissues. *The Plant Journal* **42,** 444–453.

Lavenus J, Goh T, Roberts I, *et al*. 2013. Lateral root development in Arabidopsis: fifty shades of auxin. *Trends in Plant Science* **18,** 450–458.

Lee JY, Colinas J, Wang JY, Mace D, Ohler U, Benfey PN. 2006. Transcriptional and posttranscriptional regulation of transcription factor expression in Arabidopsis roots. *Proceedings of the National Academy of Sciences, USA* **103,** 6055–6060.

Lim CW, Lee YW, Lee SC, Hwang CH. 2014. Nitrate inhibits soybean nodulation by regulating expression of CLE genes. *Plant Science* **229,** 1–9.

Malamy JE, Benfey PN. 1997. Organization and cell differentiation in lateral roots of Arabidopsis thaliana. *Development* **124,** 33–44.

Marhavy P, Duclercq J, Weller B, *et al*. 2014. Cytokinin controls polarity of PIN1-dependent auxin transport during lateral root organogenesis. *Current Biology* **24,** 1031–1037.

Matsubayashi Y. 2011. Post-translational modifications in secreted peptide hormones in plants. *Plant and Cell Physiology* **52,** 5–13.

Matsuzaki Y, Ogawa-Ohnishi M, Mori A, Matsubayashi Y. 2010. Secreted peptide signals required for maintenance of root stem cell niche in Arabidopsis. *Science* **329,** 1065–1067.

Meng L, Feldman LJ. 2010. CLE14/CLE20 peptides may interact with CLAVATA2/CORYNE receptor-like kinases to irreversibly inhibit cell division in the root meristem of Arabidopsis. *Planta* **232,** 1061–1074.

Miyawaki K, Tabata R, Sawa S. 2013. Evolutionarily conserved CLE peptide signaling in plant development, symbiosis, and parasitism. *Current Opinion in Plant Biology* **16,** 598–606.

Mortier V, De Wever E, Vuylsteke M, Holsters M, Goormachtig S. 2012. Nodule numbers are governed by interaction between CLE peptides and cytokinin signaling. *The Plant Journal* **70,** 367–376.

Murphy E, De Smet I. 2014. Understanding the RALF family: a tale of many species. *Trends in Plant Science* **19,** 664–671.

Murphy E, Smith S, De Smet I. 2012. Small signaling peptides in Arabidopsis development: how cells communicate over a short distance. *The Plant Cell* **24,** 3198–3217.

Ogawa M, Shinohara H, Sakagami Y, Matsubayashi Y. 2008. Arabidopsis CLV3 peptide directly binds CLV1 ectodomain. *Science* **319,** 1150083.

Ohyama K, Shinohara H, Ogawa-Ohnishi M, Matsubayashi Y. 2009. A glycopeptide regulating stem cell fate in Arabidopsis thaliana. *Nature Chemical Biology* **5,** 578–580.

Okamoto S, Ohnishi E, Sato S, Takahashi H, Nakazono M, Tabata S, Kawaguchi M. 2009. Nod factor/nitrate-induced CLE genes that drive HAR1-mediated systemic regulation of nodulation. *Plant and Cell Physiology* **50,** 67–77.

Okushima Y, Fukaki H, Onoda M, Theologis A, Tasaka M. 2007. ARF7 and ARF19 regulate lateral root formation via direct activation of LBD/ASL genes in Arabidopsis. *The Plant Cell* **19,** 118–130.

Parizot B, Laplaze L, Ricaud L, *et al*. 2008. Diarch symmetry of the vascular bundle in Arabidopsis root encompasses the pericycle and is reflected in distich lateral root initiation. *Plant Physiology* **146,** 140–148.

Parizot B, Roberts I, Raes J, Beeckman T, De Smet I. 2012. In silico analyses of pericycle cell populations reinforce their relation with associated vasculature in Arabidopsis. *Philosophical Transactions of the Royal Society B: Biological Sciences* **367,** 1479–1488.

Pearce G, Moura DS, Stratmann J, Ryan CA. 2001. RALF, a 5-kDa ubiquitous polypeptide in plants, arrests root growth and development. *Proceedings of the National Academy of Sciences, USA* **98,** 12843–12847.

Péret B, De Rybel B, Casimiro I, Benková E, Swarup R, Laplaze L, Beeckman T, Bennett MJ. 2009. Arabidopsis lateral root development: an emerging story. *Trends in Plant Science* **14,** 399–408.

Pettersen EF, Goddard TD, Huang CC, Couch GS, Greenblatt DM, Meng EC, Ferrin TE. 2004. UCSF Chimera—a visualization system for exploratory research and analysis. *Journal of Computational Chemistry* **25,** 1605–1612.

Reid DE, Ferguson BJ, Gresshoff PM. 2011. Inoculation- and nitrate-induced CLE peptides of soybean control NARK-dependent nodule formation. *Molecular Plant-Microbe Interactions* **24,** 606–618.

Rodriguez-Villalon A, Gujas B, Kang YH, Breda AS, Cattaneo P, Depuydt S, Hardtke CS. 2014. Molecular genetic framework for protophloem formation. *Proceedings of the National Academy of Sciences, USA* **111,** 11551–11556.

Rodriguez-Villalon A, Gujas B, van Wijk R, Munnik T, Hardtke CS. 2015. Primary root protophloem differentiation requires balanced phosphatidylinositol-4–5-biphosphate levels and systemically affects root branching. *Development* **142,** 1437–1446.

Sawa S, Kinoshita A, Nakanomyo I, Fukuda H. 2006. CLV3/ESR-related (CLE) peptides as intercellular signaling molecules in plants. *Chemical Record* **6,** 303–310.

Schindelin J, Arganda-Carreras I, Frise E, *et al*. 2012. Fiji: an open-source platform for biological-image analysis. *Nature Methods* **9,** 676–682.

Sharma V, Ramirez J, Fletcher J. 2003. The Arabidopsis CLV3-like (CLE) genes are expressed in diverse tissues and encode secreted proteins. *Plant Molecular Biology* **51,** 415–425.

Shinohara H, Matsubayashi Y. 2013. Chemical synthesis of Arabidopsis CLV3 glycopeptide reveals the impact of hydroxyproline arabinosylation on peptide conformation and activity. *Plant and Cell Physiology* **54,** 369–374.

Smith S, De Smet I. 2012. Root system architecture: insights from Arabidopsis and cereal crops. *Philosophical Transactions of the Royal Society B: Biological Sciences* **367,** 1441–1452.

Song XF, Guo P, Ren SC, Xu TT, Liu CM. 2013. Antagonistic peptide technology for functional dissection of CLV3/ESR genes in Arabidopsis. *Plant Physiology* **161,** 1076–1085.

Stahl Y, Grabowski S, Bleckmann A, *et al*. 2013. Moderation of Arabidopsis root stemness by CLAVATA1 and ARABIDOPSIS CRINKLY4 receptor kinase complexes. *Current Biology* **23,** 362–371.

Strabala TJ, O'Donnell PJ, Smit A-M, *et al*. 2006. Gain-of-function phenotypes of many CLAVATA3/ESR genes, including four new family members, correlate with tandem variations in the conserved CLAVATA3/ESR domain. *Plant Physiology* **140,** 1331–1344.

Tian H, De Smet I, Ding Z. 2014. Shaping a root system: regulating lateral versus primary root growth. *Trends in Plant Science* **19,** 426–431.

Vanstraelen M, Benkova E. 2012. Hormonal interactions in the regulation of plant development. *Annual Review of Cell and Developmental Biology* **28,** 463–487.

Vernoux T, Brunoud G, Farcot E, *et al*. 2011. The auxin signalling network translates dynamic input into robust patterning at the shoot apex. *Molecular Systems Biology* **7,** 508.

Wang G, Fiers M. 2010. CLE peptide signaling during plant development. *Protoplasma* **240,** 33–43.

Yoon GM, Kieber JJ. 2013. 1-Aminocyclopropane-1-carboxylic acid as a signalling molecule in plants. *AoB Plants* **5,** plt017.

Zhao C, Craig JC, Petzold HE, Dickerman AW, Beers EP. 2005. The xylem and phloem transcriptomes from secondary tissues of the Arabidopsis root-hypocotyl. *Plant Physiology* **138,** 803–818.

Chapter 4: The Arabidopsis thaliana CLAVATA3/EMBRYO-SURROUNDING REGION 26 (CLE26) peptide is able to alter root architecture of Solanum lycopersicum and Brassica napus

Published as Czyzewicz N and De Smet I (2015) *Plant Signaling and Behavior* 11(1): e1118598, DOI: 10.1080/15592324.2015.1118598

Author Contribution:

I devised and conducted all experiments in the paper.

I wrote the paper, contributed to figures, and was involved in development of the manuscript.

PLANT signaling & behavior

Plant Signaling & Behavior

ISSN: (Print) 1559-2324 (Online) Journal homepage: http://www.tandfonline.com/loi/kpsb20

The Arabidopsis thaliana CLAVATA3/EMBRYO-SURROUNDING REGION 26 (CLE26) peptide is able to alter root architecture of Solanum lycopersicum and Brassica napus

Nathan Czyzewicz & Ive De Smet

To cite this article: Nathan Czyzewicz & Ive De Smet (2016) The Arabidopsis thaliana CLAVATA3/EMBRYO-SURROUNDING REGION 26 (CLE26) peptide is able to alter root architecture of Solanum lycopersicum and Brassica napus, Plant Signaling & Behavior, 11:1, e1118598, DOI: 10.1080/15592324.2015.1118598

To link to this article: http://dx.doi.org/10.1080/15592324.2015.1118598

© 2016 The Author(s). Published with license by Taylor & Francis Group, LLC© Nathan Czyzewicz and Ive De Smet

Accepted author version posted online: 15 Dec 2015.

Submit your article to this journal

Article views: 228

View related articles

View Crossmark data

Full Terms & Conditions of access and use can be found at http://www.tandfonline.com/action/journalInformation?journalCode=kpsb20

Download by: [Bayer Business Services GmbH] **Date:** 07 April 2016, At: 00:41

PLANT SIGNALING & BEHAVIOR
2016, VOL. 11, NO. 1, e1118598 (4 pages)
http://dx.doi.org/10.1080/15592324.2015.1118598

Taylor & Francis
Taylor & Francis Group

SHORT COMMUNICATION

OPEN ACCESS

The *Arabidopsis thaliana* CLAVATA3/EMBRYO-SURROUNDING REGION 26 (CLE26) peptide is able to alter root architecture of *Solanum lycopersicum* and *Brassica napus*

Nathan Czyzewicz[a] and Ive De Smet[a,b,c,d]

[a]Division of Plant and Crop Sciences, School of Biosciences, University of Nottingham, Loughborough LE12 5RD, United Kingdom; [b]Department of Plant Systems Biology, VIB, B-9052, Ghent, Belgium; [c]Department of Plant Biotechnology and Bioinformatics, Ghent University, B-9052, Ghent, Belgium; [d]Centre for Plant Integrative Biology, University of Nottingham, Loughborough, LE12 5RD, United Kingdom

ABSTRACT

Optimal development of root architecture is vital to the structure and nutrient absorption capabilities of any plant. We recently demonstrated that AtCLE26 regulates *A. thaliana* root architecture development, possibly by altering auxin distribution to the root apical meristem via inhibition of protophloem development. In addition, we showed that AtCLE26 application is able to induce a root architectural change in the monocots *Brachypodium distachyon* and *Triticum aestivum*. Here, we showed that application of the synthetic AtCLE26 peptide similarly affects other important agricultural species, such as *Brassica napus* and *Solanum lycopersicum*.

ARTICLE HISTORY
Received 28 October 2015
Accepted 6 November 2015

KEYWORDS
CLAVATA3/EMBRYO-SURROUNDING REGION (CLE) peptide; CLE26; oilseed rape; root architecture; tomato

Downloaded by [Bayer Business Services GmbH] at 00:42 07 April 2016

Optimal development of root architecture is vital to the structure and nutrient absorption capabilities of any plant. Root architecture is inherently plastic to deal with an ever-changing environment.[1,2] Key parts of root architectural development are primary root growth and post-embryonic development of lateral roots, which increase the available surface area for nutrient absorption.[2,3] Understanding the role of signaling elements involved in governing root architecture will enable the future adaptation of crop species to maintain and/or increase yield in areas of stress conditions.

One group of signaling molecules involved in a wide array of physiological and biochemical processes leading to development of tissues and organs are post-translationally modified peptides.[4-6] These relatively short proteins commonly form ligands for receptors and initiate signaling cascades.[5] Signaling peptides exist as 2 main families, cysteine-rich, and post-translationally modified peptides, with CLAVATA3/EMBRYO-SURROUNDING REGION (CLE) peptides belonging to the latter family.[4] Post-translationally modified peptides are expressed as precursor sequences, which are then commonly modified by tyrosine sulfation or hydroxyprolination.[4] Hydroxyprolinated residues can be further modified by addition of l-arabinose, and all of the above modifications are able to modify the activity of the peptide, by altering the secondary structure of the peptide or providing additional surfaces by which interaction between peptide and receptor can occur.[7]

The CLE peptide family has been demonstrated to regulate several aspects of growth and development in *Arabidopsis thaliana*, as well as in several other species, with TRACHEARY ELEMENT DIFFERENTIATION INHIBITORY FACTOR (encoded by CLE41/CLE44), CLE45 and CLE40 being key signals in root architectural development.[5,8-10] It has recently been demonstrated that AtCLE26 regulates *A. thaliana* root architecture development, possibly by altering auxin distribution to the root apical meristem via inhibition of protophloem development.[9,11] In addition, it was shown that AtCLE26 application is able to induce a root architectural change in the monocots *Brachypodium distachyon* and *Triticum aestivum*.[11] Given that enhanced root architecture is key to increasing crop yield, and that the CLE peptide family is present across a broad range of species, we also evaluated if application of the synthetic AtCLE26 peptide was able to similarly affect other important agricultural species.

Brassica napus (oilseed rape), is a crop species closely related to *A. thaliana*, and is an important agricultural species, allowing for the cultivation of oils for both human consumption and biofuel generation.[12,13] Additionally, the meal produced from the seed husks remaining after oil extraction is regularly included in feed for livestock, due to the high protein content (circa 38%).[14] *B. napus* is a hybrid of 2 diploid progenitor species *B. rapa* and *B. oleracea*.[15] In order to determine if AtCLE26p was active on this crop species, we germinated and grew seedlings on media containing 1 μM peptide as detailed previously.[11] This indicated that AtCLE26p is able to inhibit primary root growth and increase lateral root density in *B. napus* (Fig. 1A, C and D), which is phenotypically similar to our previously reported data for AtCLE26 application to *A. thaliana, B. distachyon* and *T. aestivum*.[11]

Since CLE peptide species are present across a broad range of plant species,[11] we also investigated whether AtCLE26 can affect a larger range of crop species than the closely related *B. napus* and cereal crops. A less closely related, but similarly commercially important crop species is tomato (*Solanum lycopersicum*), which is grown and consumed globally, and is a key

CONTACT Ive De Smet ive.desmet@psb.vib-ugent.be

Published with license by Taylor & Francis Group, LLC © Nathan Czyzewicz and Ive De Smet
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. The moral rights of the named author(s) have been asserted.

species in deciphering the signaling pathways involved in fruit ripening.[16] In order to determine if AtCLE26p was active on this crop species, we germinated and grew tomato (M82D) seedlings on media containing 1 μM peptide as detailed previously.[11] Compared with the data reported previously for *A. thaliana, B. distachyon* and *T. aestivum*,[11] and the results for *B. napus* reported here, growth of *S. lycopersicum* on medium containing AtCLE26p resulted in a similar root phenotype (Fig. 1B).

The morphological change upon application of AtCLE26p to root architecture of *B. napus* and *S. lycopersicum* (Fig. 1) resembles that previously reported for *A. thaliana, B. distachyon*, and *T. aestivum*,[11] suggesting that *B. napus* and *S. lycopersicum* contain a homologous AtCLE26-activated signaling module that acts to govern root architecture. It is yet to be determined whether the observed morphological change to crop species results from disruption of phloem auxin transport, as observed in *A. thaliana*.[11] However, given the similarities in root morphology, it is possible that the same process of auxin transport is disrupted in AtCLE26-treated *B. napus*.

Our previous analyses indicated that multiple crop and model species contain putative CLE26 orthologues.[11] However, since the initial phylogeny did not include *S. lycopersicum*, a BLASTp (Phytozome) of *A. thaliana* mature peptide sequences

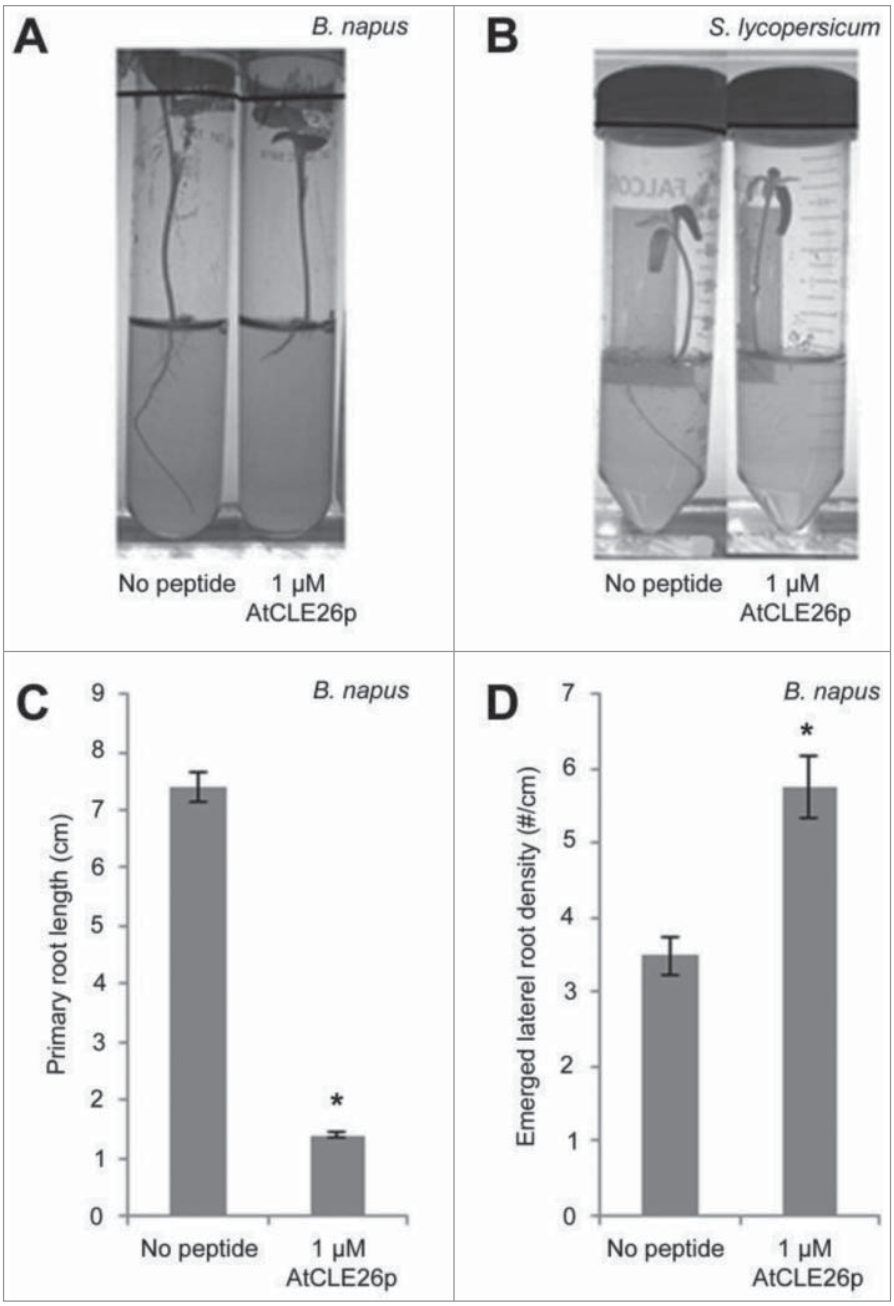


Figure 1. AtCLE26 effect on *B. napus* and *S. lycopersicum* root architecture. (A-B) Representative pictures of *B. napus* (A) and *S. lycopersicum* (B) grown in the absence or presence of 1 μM AtCLE26p. (C-D) Quantification of *B. napus* root phenotypes with respect to primary root length (C) and lateral root density (D) in absence or presence of 1 μM AtCLE26p (n = 18 for no peptide and 26 for 1 μM CLE26). Graphs depict average $\pm$ standard error of indicated sample numbers. *, $p < 0.05$ according to Student's t-test.

Downloaded by [Bayer Business Services GmbH] at 00:42 07 April 2016

Downloaded by [Bayer Business Services GmbH] at 00:42 07 April 2016

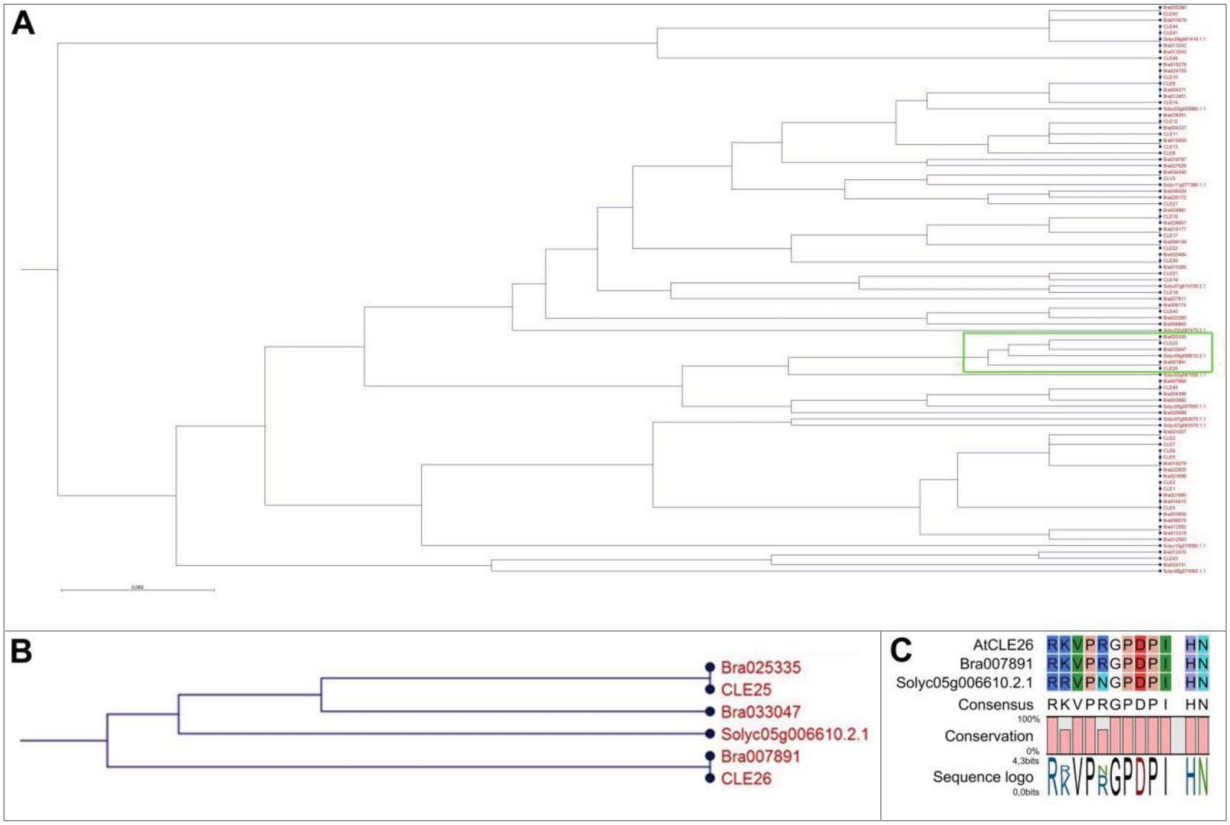


Figure 2. AtCLE26 orthologs in *A. thaliana, B. rapa* and *S. lycopersicum*. (A) Phylogenetic tree of mature CLE peptide sequences. (B) Detail of tree depicted in A, as outlined in green. (C) Sequence alignment of likely AtCLE26 orthologs.

was conducted on the *S. lycopersicum* proteome, which returned 12 putative tomato CLE peptides. Here, we used the annotated proteome data for *B. rapa* instead of *B. napus*, since there is no annotated proteome data for *B. napus*.[13] Mature peptide sequences from *A. thaliana, S. lycopersicum* and *B. rapa* were aligned and arranged into a phylogenetic tree using CLC workbench (Fig. 2A–B). Our results indicated that *B. rapa* contained a protein (Bra007891) with high homology to AtCLE26p and with the mature peptide having an identical amino acid sequence to that of AtCLE26p (RKVPRGPDPIHN) (Fig. 2C), which is in agreement with earlier observations.[11] Since *B. napus* contains the *B. rapa* genome, it is likely that Bra007891 and any potential responsive signaling module represent a homologous CLE26 signaling pathway in *B. napus*. These phylogenetic analyses also revealed that the closest AtCLE26 homolog in *S. lycopersicum* is Solyc05g006610.2.1, with a sequence of RRVPNGPDPIHN, which differs from AtCLE26 at residues 2 and 5, representing a K2R and R5N substitution respectively (Fig. 2C). The Blocks Substitution Matrix (BLOSUM62) indicated that both of these substitutions are likely to be conservative of function (K2R = 2 and R5N = 0).

Taken together with our previous findings,[11] our data indicated that the signaling module initiated by CLE26p (or a functionally related CLE) is conserved across a number of important crop species, suggesting that data generated in the investigation of CLE26 function in *A. thaliana* may potentially impact on a broad range of agriculturally important species. Additionally, further investigation of CLE26 downstream protein effectors may identify putative target proteins for targeted crop improvement, allowing for increased yield of crops in adverse growth conditions.

Disclosure of potential conflicts of interest

No potential conflicts of interest were disclosed.

Acknowledgments

We thank Catherine Thomas, Graham Seymour, and Fereshteh Malekpoor for supplying seeds and Martin Broadley for comments on the manuscript. This work was supported by a BBSRC David Phillips Fellowship (BB_BB/H022457/1) and a Marie Curie European Reintegration Grant (PERG06-GA-2009–256354) to I.D.S, and a BBSRC CASE Studentship co-funded by Bayer CropScience to N.C.

References

1. Pacheco-Villalobos D, Hardke C. Natural genetic variation of root system architecture from Arabidopsis to Brachypodium: towards adaptive value. Philos Trans R Soc Lond B Biol Sci 2012; 367:1552–8.; http://dx.doi.org/10.1098/rstb.2011.0237
2. Smith S, De Smet I. Root system architecture: insights from Arabidopsis and cereal crops. Philos Trans R Soc Lond B Biol Sci 2012; 367:1441–52; PMID:22527386; http://dx.doi.org/10.1098/rstb.2011.0234
3. Postma J, Dathe A, Lynch J. The Optimal Lateral Root Branching Density for Maize Depends on Nitrogen and Phosphorus Availability.

Plant Physiology 2014; 166:590–602; PMID:24850860; http://dx.doi.org/10.1104/pp.113.233916
4. Murphy E, Smith S, De Smet I. Small signaling peptides in Arabidopsis development: how cells communicate over a short distance. Plant Cell 2012; 24:3198–217; PMID:22932676; http://dx.doi.org/10.1105/tpc.112.099010
5. Czyzewicz N, Yue K, Beeckman T, De Smet I. Message in a bottle: small signalling peptide outputs during growth and development. Journal of Experimental Botany 2013; 64:5281–96; PMID:24014870; http://dx.doi.org/10.1093/jxb/ert283
6. Tavormina P, De Coninck B, Nikonorova N, De Smet I, Cammue B. The Plant Peptidome: An Expanding Repertoire of Structural Features and Biological Functions. Plant Cell 2015: 27(8):2095–118; PMID: 26276833; http://dx.doi.org/10.1105/tpc.15.00440
7. Shinohara H, Matsubayashi Y. Chemical synthesis of Arabidopsis CLV3 glycopeptide reveals the impact of hydroxyproline arabinosylation on peptide conformation and activity. Plant Cell Physiology 2013; 54:369–74; PMID:23256149; http://dx.doi.org/10.1093/pcp/pcs174
8. Cho H, Ryu H, Rho S, Hill K, Smith S, Audenaert D, Park J, Han S, Beeckman T, Bennett MJ, et al. A secreted peptide acts on BIN2-mediated phosphorylation of ARFs to potentiate auxin response during lateral root development. Nature Cell Biology 2014; 16:66–76; PMID:24362628; http://dx.doi.org/10.1038/ncb2893
9. Rodriguez-Villalon A, Gujas R, van Wijk R, Munnik T, Hardtke C. Primary root protophloem differentiation requires balanced phosphatidylinositol-4,5-biphosphate levels and systemically affects root branching. Development 2015; 142:1437–46; PMID:25813544; http://dx.doi.org/10.1242/dev.118364
10. Stahl Y, Wink R, Ingram G, Simon R. A Signaling Module Controlling the Stem Cell Niche in Arabidopsis Root Meristems. Current Biology 2009; 19:909–14; PMID:19398337; http://dx.doi.org/10.1016/j.cub.2009.03.060
11. Czyzewicz N, Shi C, Vu L, Van De Cotte B, Hodgman C, Butenko M, De Smet, I. Modulation of Arabidopsis and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide. Journal of Experimental Botany 2015; 66:5229–43; PMID:26188203; http://dx.doi.org/10.1093/jxb/erv360
12. Zapata, Vargas, Reyes, Belmar. Quality of biodiesel and press cake obtained from Euphorbia lathyris, Brassica napus and Ricinus communis. Industrial Crops and Products 2012; 38:1–5.; http://dx.doi.org/10.1016/j.indcrop.2012.01.004
13. Wells R, Trick M, Soumpourou E, Clissold L, Morgan C, Werner P, Gibbard C, Clarke M, Jennaway R, Bancroft I Wells, Trick, Soumpourou, Clissold, Morgan, Werner, et al. The control of seed oil polyunsaturate content in the polyploid crop species Brassica napus. Molecular Breeding 2014; 33:349–62; PMID:24489479; http://dx.doi.org/10.1007/s11032-013-9954-5
14. Pustjens A, de Vries S, Schols H, Gruppen H, Gerrits W, Kabel M. Understanding carbohydrate structures fermented or resistant to fermentation in broilers fed rapeseed (Brassica napus) meal to evaluate the effect of acid treatment and enzyme addition. Poultry Science 2013; 93:926–34.; http://dx.doi.org/10.3382/ps.2013-03519
15. Chalhoub B, Denoeud F, Liu S, Parkin IAP, Tang H, Wang X, Chiquet J, Belcram H, Tong C, Samans B, et al. Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. Science 2014; 345:950–3; PMID:25146293; http://dx.doi.org/10.1126/science.1253435
16. Seymour GB, Chapman NH, Chew BL, Rose JK Seymour, Chapman, Chew, Rose. Regulation of ripening and opportunities for control in tomato and other fruits. Plant Biotechnology Journal 2013; 11:269–78; PMID:22958755; http://dx.doi.org/10.1111/j.1467-7652.2012.00738.x

Downloaded by [Bayer Business Services GmbH] at 00:42 07 April 2016

Chapter 5: Antagonistic Peptide Technology for the Functional Dissection of CLE Peptides Revisited

Published as Czyzewicz N, Wildhagen M, Cattaneo P, Stahl Y, Pinto KG, Aalen RB, Butenko MA, Hardke CS, and De Smet I (2015) *Journal of Experimental Botany* 66(17):5367-5374

Author Contribution:

I was involved with the planning and execution of the CLE/mCLE peptide application root trait analysis.

I contributed to introduction, discussion, and CLE/mCLE peptide functional screening (Figure 4), and was involved in development of the manuscript.

Journal of Experimental Botany, Vol. 66, No. 17 pp. 5367–5374, 2015
doi:10.1093/jxb/erv284 Advance Access publication 30 June 2015
This paper is available online free of all access charges (see http://jxb.oxfordjournals.org/open_access.html for further details)

RESEARCH PAPER

Antagonistic peptide technology for functional dissection of CLE peptides revisited

Nathan Czyzewicz[1], Mari Wildhagen[2], Pietro Cattaneo[3], Yvonne Stahl[4], Karine Gustavo Pinto[4], Reidunn B. Aalen[2], Melinka A. Butenko[2], Rüdiger Simon[4], Christian S. Hardtke[3], Ive De Smet[1,5,6,7,*]

[1] Division of Plant and Crop Sciences, School of Biosciences, University of Nottingham, Loughborough LE12 5RD, UK
[2] Department of Biosciences, Section for Genetics and Evolutionary Biology, University of Oslo, N-0316 Oslo, Norway
[3] Department of Plant Molecular Biology, University of Lausanne, CH-1015, Lausanne, Switzerland
[4] Institute for Developmental Genetics, Heinrich-Heine University, D-40225 Düsseldorf, Germany
[5] Centre for Plant Integrative Biology, University of Nottingham, Loughborough LE12 5RD, UK
[6] Department of Plant Systems Biology, VIB, B-9052 Ghent, Belgium
[7] Department of Plant Biotechnology and Genetics, Ghent University, B-9052 Ghent, Belgium

* To whom correspondence should be addressed. E-mail: ive.desmet@psb.vib-ugent.be

Received 23 February 2015; Revised 10 April 2015; Accepted 20 April 2015

Editor: Thomas Dresselhaus

Abstract

In the *Arabidopsis thaliana* genome, over 1000 putative genes encoding small, presumably secreted, signalling peptides can be recognized. However, a major obstacle in identifying the function of genes encoding small signalling peptides is the limited number of available loss-of-function mutants. To overcome this, a promising new tool, antagonistic peptide technology, was recently developed. Here, this antagonistic peptide technology was tested on selected CLE peptides and the related IDA peptide and its usefulness in the context of studies of peptide function discussed. Based on the analyses, it was concluded that the antagonistic peptide approach is not the ultimate means to overcome redundancy or lack of loss-of-function lines. However, information collected using antagonistic peptide approaches (in the broad sense) can be very useful, but these approaches do not work in all cases and require a deep insight on the interaction between the ligand and its receptor to be successful. This, as well as peptide ligand structure considerations, should be taken into account before ordering a wide range of synthetic peptide variants and/or generating transgenic plants.

Key words: CLE, IDA, peptide structure, peptide variants, root, small signalling peptides.

Introduction

Small signalling peptides are able to elicit a vast array of biological and physiological responses, allowing the plant to develop and adapt to changes in the surrounding environment (Czyzewicz *et al.*, 2013; Murphy *et al.*, 2012). In the *Arabidopsis thaliana* genome, over 1000 putative genes encoding small, presumably secreted, signalling peptides can be recognized (Lease and Walker, 2006). These small signalling peptides are mainly perceived by receptors, such as receptor kinases, and in the *A. thaliana* genome, over 600 genes encoding putative receptor-like kinase (RLK) proteins have been detected (Shiu and Bleecker, 2001*a*, *b*). However, to date, only a small portion of these putative small signalling peptides have been functionally characterized and few have been linked to a receptor (Butenko *et al.*, 2009; Czyzewicz *et al.*, 2013; Lee and Torii, 2012; Murphy *et al.*, 2012).

© The Author 2015. Published by Oxford University Press on behalf of the Society for Experimental Biology.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0/), which permits unrestricted reuse, distribution, and reproduction in any medium, provided the original work is properly cited.

Small signalling peptides consist of usually <20 amino acids in their mature form and rarely >120 amino acids as a full-length precursor. Although there are hardly any data for most small signalling peptides, they are likely often present at very low (nanomolar range) physiological concentrations. Forward and reverse genetic approaches have been employed to study the biological function of genes encoding small signalling peptides. For example, CLAVATA3 (CLV3), a peptide regulating maintenance of plant stem cells, was identified in a forward genetic screen (Clark *et al.*, 1995; Fletcher *et al.*, 1999). The *clv3* mutants have an enlarged shoot apical meristem (SAM) and floral meristems, which generate supernumerary floral organs, suggesting a general role in regulating above-ground meristematic growth (Clark *et al.*, 1996). CLV3 belongs to the family of CLV3/EMBRYO SURROUNDING REGION-related (CLE) peptides, which consists of 31 members in *A. thaliana*. These peptides share a conserved 12–14 amino acid C-terminal domain that is proteolytically released and has been shown to function in various contexts, including shoot and root meristem development, nodulation, embryo and endosperm development, regulation of root architecture in response to nutrients, and vascular development (Araya *et al.*, 2014; Cock and McCormick, 2001; Fiers *et al.*, 2005; Fiume and Fletcher, 2012; Hirakawa *et al.*, 2008; Hobe *et al.*, 2003; Jun *et al.*, 2010; Lim *et al.*, 2011; Mortier *et al.*, 2010; Okamoto *et al.*, 2013; Reid *et al.*, 2011; Stahl *et al.*, 2009). Genetic interaction studies suggested CLV3 to act as a small signalling peptide since mutations in the RLK encoding gene, *CLV1*, had a similar phenotype to *clv3* mutants and the overexpression phenotype of *CLV3* was lost in the *clv1* mutant background (Brand *et al.*, 2000). Indeed, the identification of the mature active CLV3 peptide and biochemical evidence for its interaction with CLV1 was confirmed almost a decade later (Ogawa *et al.*, 2008; Ohyama *et al.*, 2009). This example illustrates some of the difficulties in identifying the mature active form of small signalling peptides in plants and thereafter finding their receptors and/or interacting signalling partners.

One major obstacle in identifying the function of genes encoding small signalling peptides is the limited number of available loss-of-function mutants, since most have no useful T-DNA insertions, partly because small genes are less likely to be targeted by a T-DNA insertion. To complicate matters further, the functional redundancy of some small signalling peptides and RLKs can mask phenotypes when only one family member is successfully disrupted. Although some small signalling peptides have been discovered through screening of T-DNA or transposon insertion mutants—such as INFLORESECENCE DEFICIENT IN ABSCISSION (IDA), TAPETUM DETERMINANT1 (TPD1), CLV3, and CLE40 (Butenko *et al.*, 2003; Fletcher *et al.*, 1999; Hobe *et al.*, 2003; Yang *et al.*, 2003), new approaches and technologies are required to facilitate the functional analyses of genes encoding small signalling peptides and their putative corresponding receptor partners (Butenko *et al.*, 2014; Stes *et al.*, 2015).

To interfere with and unravel endogenous peptide function, antagonistic peptides—such as mutant peptide variants, chemically modified peptides or peptide-like molecules that can affect peptide ligand–receptor (kinase) pathways are an important tool. In this context, structure-function/activity analyses can provide useful information on peptide residues critical for function. With respect to CLE peptides, such analyses were used to test, for example, suppression of nodulation capability in soybean (*Glycine max*) roots of the nodulation-controlling RHIZOBIA-INDUCED CLE1 (GmRIC1) (Reid *et al.*, 2013) or regulation of primary and lateral root growth of various CLE peptides (Czyzewicz *et al.*, 2015; Kondo *et al.*, 2008). Recently, this approach was used to develop a promising new tool, referred to as antagonistic peptide technology, for functional dissection of CLE peptides (Song *et al.*, 2013). Based on transgenic plants carrying CLV3 variants where each of the 12 residues in the core CLE motif were one by one replaced by alanine (Ala), it was shown that the glycine (Gly) to Ala substitution at position six gave a weak *clv3* phenotype. Subsequently, replacing this highly conserved Gly residue with other amino acids revealed that a Gly to threonine (Thr) produced a phenotype most similar to *clv3* mutants. This was further tested using synthetic CLV3 peptide with the Gly to Thr substitution (CLV3p^{6Thr}), which was also able to produce—although less effective—the *clv3* mutant phenotype, and which could compete with wild-type synthetic CLV3 peptide (CLV3p). These exciting observations suggested that the CLV3p^{6Thr} variant could act as an antagonistic peptide. Specifically, a loss-of-function phenotype is suggested to be obtained through competitive inhibition, namely the peptide is proposed to be able to bind to the native receptor, but unable to activate it, since a functionally critical amino acid is mutated. Probably the CLV3p^{6Thr} variant has compromised peptide flexibility leading to stronger interaction with corresponding receptors and to disrupted downstream signal transduction. Taken together, such antagonistic peptides would provide a powerful tool for the functional dissection of CLEs in plants, and might also have the potential to be used for other plant peptides. Based on this assumption and the conserved nature of the Gly at position six (Fig. 1), this technology was applied to CLE8 (giving rise to embryo-lethal phenotype) and CLE22 (giving rise to short root phenotype) (Song *et al.*, 2013).

Here, this antagonistic peptide technology was tested, specifically Gly^6-to-Ala or Gly^6-to-Thr, as used by Song *et al.* (2013), on selected CLE peptides and the related IDA peptide, and its usefulness discussed in the context of studies of peptide function.

Materials and methods

Plant growth conditions

For the work on CLE40 and CLV3, seeds were surface sterilized with chlorine gas and imbibed in 0.1% (w/v) agarose for 2 d at 4 °C before being plated onto 0.5× Murashige and Skoog (MS) medium with Gamborgs No. 5 vitamins (Duchefa), 0.5 g/l 2-(*N*-morpholino) ethanesulfonic acid (MES), 1% (w/v) sucrose, and 1.2% (w/v) plant agar. Plates were incubated vertically in a growth chamber with constant light at 21 °C for 5 d. For peptide-containing plates, synthetic dodecapeptides were added to a final concentration of 1 µM. For the work on CLE1/4, CLE7, CLE26, and CLE27, seeds were surface sterilized by immersion in 70% ethanol for 30 s, and incubated

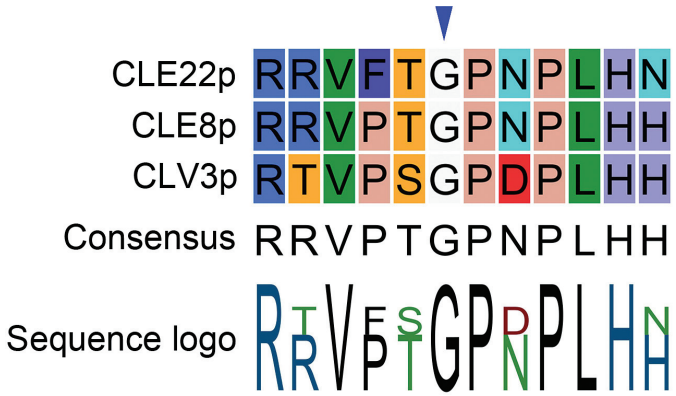


Fig. 1. Alignment of CLE peptides used in Song *et al.* (2013). Conserved glycine (G) at position six is indicated with a blue arrowhead. (This figure is available in colour at *JXB* online.)

in 20% bleach at room temperature for 20 min. Sterile seeds were vernalized in water at 4 °C for 2 d, before being plated onto 0.5× MS medium supplemented with 0.1 g/l Myo-inositol (Sigma Aldrich), 0.5 g/l MES (Sigma Aldrich), and 1% (w/v) bacteriological agar. Plants were incubated vertically under constant light at 21 °C until 12 d after germination. Synthetic CLE was added to a final concentration of 10 µM or 10 nM. The work on CLE45 was essentially performed as previously described (Rodriguez-Villalon *et al.*, 2014).

Starch staining

Starch granules and cell walls in root tips were stained with the mPSPI method and imaged with a confocal microscope as previously described (Truernit *et al.*, 2008).

Oxidative burst experiments

For transient expression, *Agrobacterium tumefaciens* carrying HAESA-LIKE 2 (HSL2) in frame with eGFP in an estradiol-inducible expression vector described previously (Bleckmann *et al.*, 2010), was infiltrated into *Nicotiana benthamiana* leaves according to (Mueller *et al.*, 2012). The oxidative burst experiment was performed as previously described by (Butenko *et al.*, 2014), with the exception that 3 d after infiltration with *A. tumefaciens*, leaf pieces of *N. benthamiana* were induced with 20 µM estradiol before cut. Light emission was measured in a Wallac 1420 VICTOR^{2}™ microplate luminometer (PerkinElmer).

Peptide structure predictions

The recently published solution structure of CLE10p, solved using nuclear magnetic resonance (NMR) (MMDB ID: 125940; PMBID: 2MD), depicts the backbone of the PXGP core (position 4–7) as a smooth curve protruding from the rest of the peptide. To investigate the effect of mutations in this core of the peptides investigated, amino acid sequences with the structure AAA[core]AAA with the core PGGP, PGAP, PGTP, PRGP, PRTP, PSAP, or PSTP were submitted for analysis in PEP-FOLD (http://mobyle.rpbs.univ-paris-diderot.fr/cgi-bin/portal.py?form=PEP-FOLD#forms::PEP-FOLD) using standard settings.

Results and discussion

'Antagonistic' CLE peptides

Among many processes (Cock and McCormick, 2001; Fiume and Fletcher, 2012; Hirakawa *et al.*, 2008; Okamoto *et al.*, 2013), various CLE peptides affect primary and lateral root growth and development (Czyzewicz *et al.*, 2015; Depuydt *et al.*, 2013; Fiers *et al.*, 2005; Hobe *et al.*, 2003; Jun *et al.*, 2010; Rodriguez-Villalon *et al.*, 2014; Rodriguez-Villalon *et al.*, 2015; Stahl *et al.*, 2009). To build on previous work investigating CLE peptides in the context of lateral root development, primary root growth, root apical stem cell maintenance, and vascular development, putative antagonistic versions of CLV3, CLE1/4, CLE7, CLE26, CLE27, CLE40, and CLE45 peptides were designed—based on the findings by Song *et al.* (2013)—to further unravel CLE peptide function (Figs 2A, 3A, 4A). To assess the function of these mutated chemically synthesized CLE peptides with Gly/cysteine (Cys) to Ala or Gly/Cys to Thr substitutions (referred to as mCLEp^{Ala6} or mCLEp^{6Thr}, respectively), a number of biological assays were used.

The antagonistic peptide technology was first applied to CLE45 peptide (CLE45p), which, when applied exogenously, leads to shorter primary roots because it suppresses protophloem differentiation (Depuydt *et al.*, 2013; Rodriguez-Villalon *et al.*, 2014). To explore a potential loss-of-function phenotype, synthetic mCLE45p^{6Thr} peptide was applied and its effect on primary root development upon external application evaluated (Fig. 2A, B). This revealed that at the low nanomolar range mCLE45p^{6Thr} does not have an effect on primary root length as compared with the wild-type CLE45p (Fig. 2B), again confirming that position six is important for peptide activity. However, a higher concentration of 1 µM mCLE45p^{6Thr} had the same effect as the unmodified wild-type CLE45p (Fig. 2B). In addition, this peptide was not able to out-compete the effects of simultaneous CLE45p application (Fig. 2B). Thus, while the mCLE45p^{6Thr} peptide does not act as an antagonistic peptide, a CLE45p variant was obtained, which has identical effects as the wild-type version but required application of higher peptide concentrations. The notion that mCLE45p^{6Thr} is a weak CLE45p, rather than an antagonistic version, was confirmed *in planta* (Rodriguez-Villalon *et al.*, 2014). Plants that express a wild-type *pCLE45::CLE45* transgene are notoriously difficult to create, presumably because of the detrimental effects of increased CLE45 dosage. However, the few lines that were eventually obtained recapitulated the root phenotype observed upon external CLE45p application (Fig. 2C). Specifically, in *pCLE45::CLE45* lines, root growth was impaired, the periclinal division of the sieve element precursor cell was frequently abolished, and protophloem differentiation was often suppressed (Fig. 2D). This phenotype is similar to plants that express a corresponding *pCLE45::CLE45^{6Thr}* transgene, which are much easier to obtain (Rodriguez-Villalon *et al.*, 2014). Thus, the data for both tissue culture assay and *in planta* are consistent with the interpretation that mCLE45p^{6Thr} is a weak rather than an antagonistic version of the CLE45 peptide.

Next, the antagonistic peptide approach for CLE40 was explored (Fig. 3A). It was previously shown that an increasing concentration of synthetic CLE40 peptide reduces stemness and causes differentiation of columella stem cells (CSCs), quiescent centre (QC) cells, and proximal initial (P1) cells in wild-type roots (Fig. 3B, D, H, Supplementary Table S1 available at *JXB* online) (Stahl *et al.*, 2013). Also

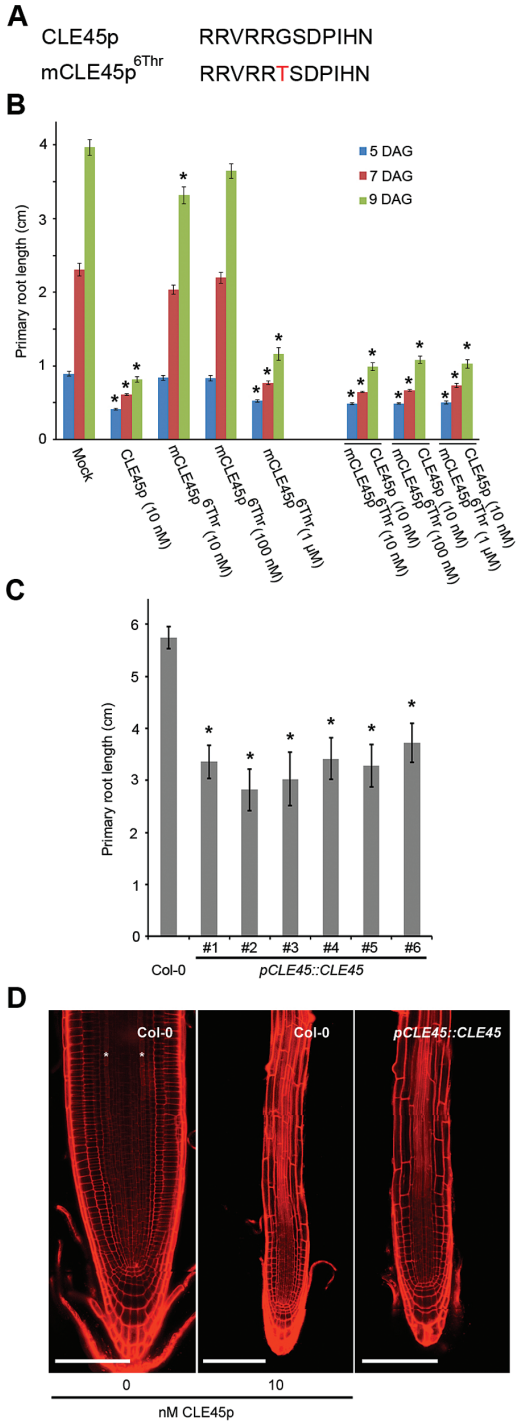


Fig. 2. CLE45 peptide treatment and *pCLE45::CLE45* transgenic lines. (A) Sequence of synthetic CLE45 and mCLE45 peptides used. (B) Primary root length following treatment of wild-type seedlings with indicated concentrations of CLE45p or mCLE45p^{6Thr}. The bar graph indicates the mean ± standard error. Statistical significance (Student's *t*-test) compared with mock is indicated for each time point (DAG, days after germination): * P <0.01. (C) Primary root length of *pCLE45::CLE45* lines. The bar graph indicates the mean ± standard error. Statistical significance (Student's *t*-test) compared with Col-0 is indicated: * P <0.01. (D) Confocal images of primary root meristems of 7-d-old seedlings (propidium iodide-stained; composite images). The asterisks highlight the two protophloem strands that can be distinguished in wild-type (Col-0) grown on mock (left), but that do not develop when grown on 10 nM CLE45p (middle). Protophloem strands also do not develop in wild-type seedlings that express a *pCLE45::CLE45* transgene (right). Scale bar, 100 µm.

synthetic CLV3 peptide acts similarly on the stemness in the root tip (Fig. 3E, G, Supplementary Table S1 available at *JXB* online). In contrast, in the shorter *cle40* mutant roots, differentiation of CSC daughters into CCs was significantly delayed (Fig. 3B, F, H, Supplementary Table S1 available at *JXB* online) (Hobe *et al.*, 2003; Stahl *et al.*, 2009). Wild-type roots carry mostly one (at D1 position) or, after a recent cell division, two layers of CSCs distal to the QC (at D1 and D2 positions), which lack stainable starch granules (Fig. 3B, H, Supplementary Table S1). In *cle40* root tips, additional CSCs in more distal positions (D2) were found (Fig. 3B, C, H, Supplementary Table S1). To assess if synthetic mCLE40p^{6Thr} and mCLV3p^{6Thr} variants could be used as antagonistic peptides to obtain a loss-of-function phenotype, their impact on the distal root stemness was evaluated (Fig. 3A). This revealed a response comparable with the wild-type CLE40p or CLV3p treatments (Fig. 3E, G, H, Supplementary Table S1 available at *JXB* online). Taken together, this suggests that the Gly to Thr substitution in CLE40 and CLV3 does not give rise to an antagonistic peptide.

Finally, while treatment of *A. thaliana* seedlings with 10 µM wild-type CLE1/4p, CLE7p, CLE26p, and CLE27p resulted in a short primary root and more lateral roots (Fig. 4B, C) (Czyzewicz *et al.*, 2015; Depuydt *et al.*, 2013; Kinoshita *et al.*, 2007; Rodriguez-Villalon *et al.*, 2014), this does not necessarily reflect their natural function. However, based on the *CLE1/4*, *CLE7*, *CLE26*, and *CLE27* expression patterns, a role in lateral root development might be expected (Czyzewicz *et al.*, 2015; Jun *et al.*, 2010). In this context, only CLE26p gave rise to a short primary root and increased lateral root density at a concentration of 10 nM (Fig. 4B) (Czyzewicz *et al.*, 2015; Rodriguez-Villalon *et al.*, 2015), further supporting caution when interpreting exogenous peptide application results, especially at higher concentrations. To assess if the above-mentioned CLE peptides have a role in primary and lateral root development, the antagonistic peptide technology was attempted (Fig. 4A). However, analysis of mutated chemically synthesized CLE peptides (mCLEp) at 10 µM revealed that, although mCLE1/4p$^{6Ala/Thr}$ and mCLE7p$^{6Ala/Thr}$ did not induce a primary root shortening or a lateral root density increase—unlike the non-mutated forms of these peptides, mCLE1/4p^{6Thr} and mCLE7p$^{6Ala/Thr}$ were also unable to produce an obvious dominant negative root phenotype, namely an expected longer primary root and/or decrease in lateral root density (Fig. 4B, C). However, for mCLE1/4p^{6Ala}, a subtle increase in primary root length, but no effect on lateral root density was observed (Fig. 1C). It should be pointed out that since the receptor, and the associated loss-of-function phenotype, for these peptides is not known, the expected dominant negative root phenotype remains speculative. Nevertheless, this outcome suggested that for CLE1p, CLE4p, and CLE7p activity, the Gly at position six is essential, but that this mutant form did not appear to act as an antagonistic peptide. In contrast, mCLE26p$^{6Ala/Thr}$ and mCLE27p$^{6Ala/Thr}$ displayed a similar phenotype to the non-mutated forms, namely a significant reduction in primary root length (92–95%) and increased lateral root density (110–151%) (Fig. 4B, C), suggesting that the sixth amino acid in their respective sequences is not critical

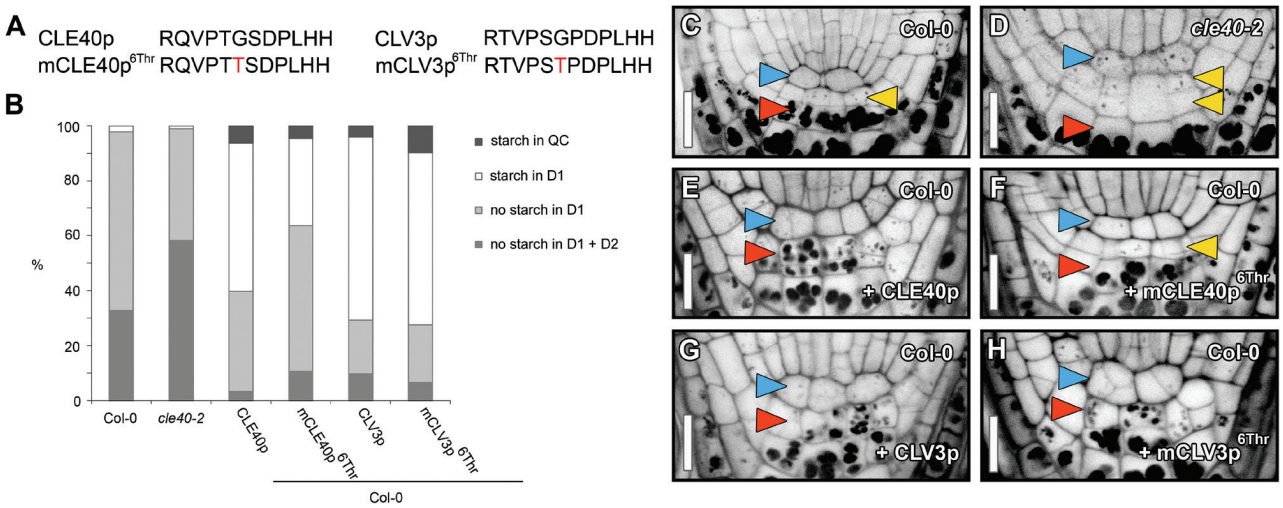


Fig. 3. Distal root phenotypes after antagonistic peptide treatments. (A) Sequence of synthetic CLE and mCLE peptides used. (B–H) Distal root cell fates were analysed by mPSPI staining 5 d after germination in wild-type (Col-0) and *cle40-2* mutant roots (C, D). Representative examples of Col-0 roots grown on media with 1 μM CLE40p (E), mCLE40p^{6Thr} (F), CLV3p (G), and mCLV3p^{6Thr} (H) are shown. Frequency of roots carrying starch granules in the designated domains is shown in (B). Arrowheads: blue, QC position; yellow, CSC position (D1); red, CC position (D2). Double yellow arrowheads indicate CSC fate in D2, whereas the lack of a yellow arrowhead indicates CC fate in D1 position. QC, quiescent centre position; D1, distal layer position one; D2, distal layer position two; CC, columella cell position. Scale bars represent 15 μm.

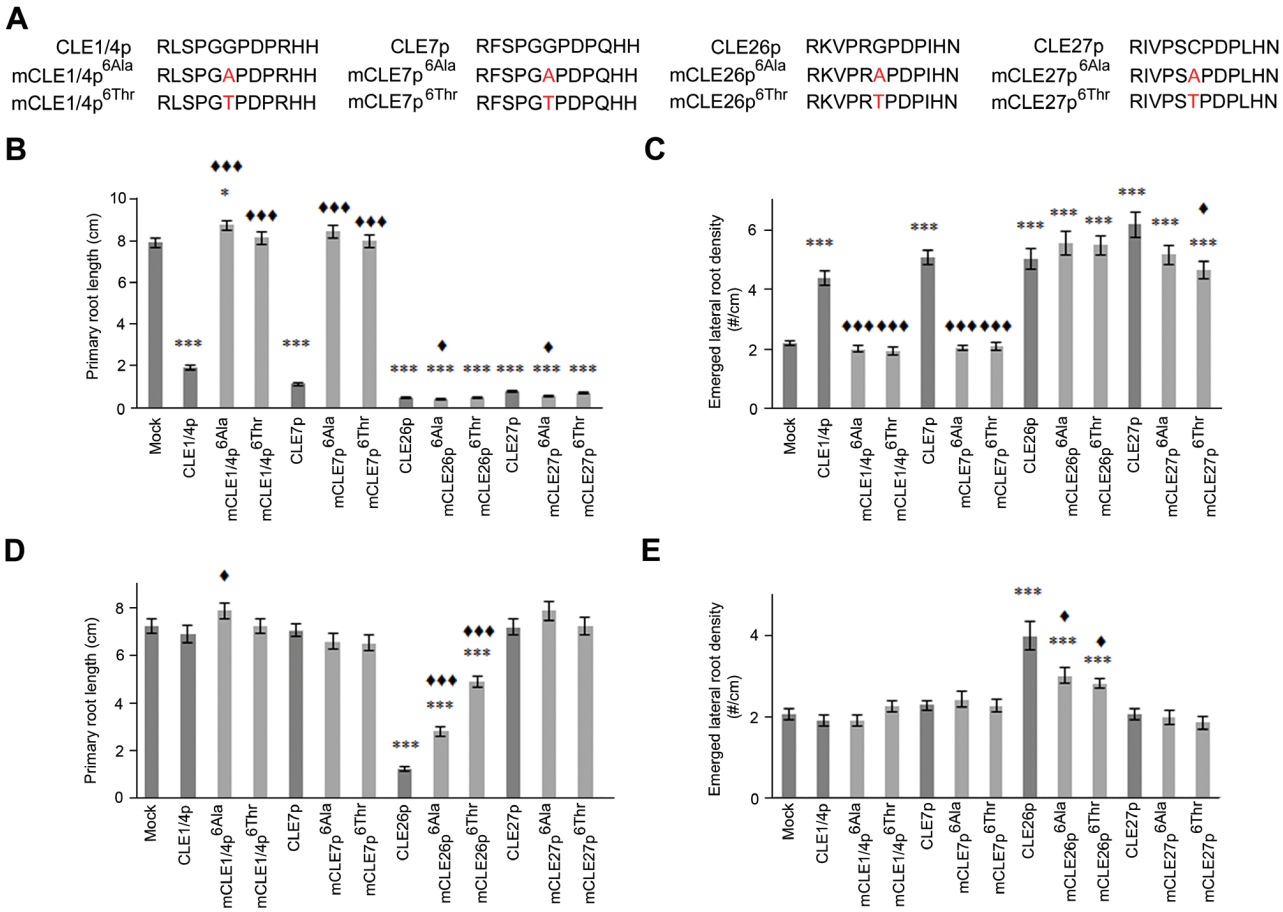


Fig. 4. CLE1/4, CLE7, CLE26, and CLE27 peptide treatment. (A) Sequence of synthetic CLE and mCLE peptides used. (B–E) Treatment of wild-type seedlings with 10 μM (B, C) or 10 nM of CLE or mCLE peptide (D, E). Quantification of primary root length (B, D) and emerged lateral root density (C, E) for CLEp and mCLEp-treated wild-type seedlings. The bar graph indicates the mean ± standard error. Statistical significance (Student's *t*-test) compared with no peptide (*) and to CLEp treatment (♦) is indicated: ***/♦♦♦, P <0.001, */♦, P <0.05. (This figure is available in colour at *JXB* online.)

to their function, and also, did not appear to give rise to an antagonistic peptide when mutated. Intriguingly, at 10 nM, mCLE26p$^{6Ala/Thr}$ retained activity, but was less potent than CLE26p. This suggests that mCLE26p$^{6Ala/Thr}$ is a weak rather than an antagonistic version of the CLE26 peptide, which is in agreement with the results on CLE45. In contrast, most

mCLE1/4p, mCLE7p, and mCLE27p variants had no altered activity compared with the wild-type variant at 10 nM, except mCLE1/4p^{6Ala} (Fig. 4D, E). In general, it appears that also for CLE1/4p, CLE7p, CLE26p, and CLE27p, the antagonistic peptide technology is not easily applicable.

In conclusion, other amino acid mutations are likely required to give rise to (strong) antagonistic CLE1p, CLE4p, CLE7p, CLE26p, CLE27p, CLE40p, and CLE45p peptides, or alternatively, this approach cannot be universally applied with respect to synthetic CLE peptides. A poor effect of synthetic antagonistic peptides could be due to delivery to relevant tissues and/or instability. However, synthetic peptide stability issues were not observed in these assays or with respect to synthetic control peptides, nor was a lack of phenotypes observed when synthetic (antagonistic) peptides were exogenously applied to the root. While the latter can be a non-specific effect in some cases, specific and local phenotypes were also observed.

'Antagonistic' IDA peptides

In addition, the extent the antagonistic peptide technology can be applied to other small signalling peptides was assessed. For this, the IDA and IDA-LIKE (IDL) family were chosen, given their sequence similarity to CLEs (Stenvik *et al.*, 2006). The IDA and IDL1 peptides of 12 amino acids share a common core at positions four to seven [PS(G/A)P] and the C-terminal end [H(N/H)] with CLV3 and some CLE peptides (Figs 5A, 6A). Like CLV3, hydroxylation of the Pro at position seven of the IDA dodecapeptide (IDAp, also referred to as PIPPo) increases the activity of the peptide (Butenko *et al.*, 2014). An oxidative burst response in *Nicotiana benthamiana* can be employed as readout for the RLK HAESA-LIKE2 (HSL2) activation by exogenously applied synthetic IDA peptides (Butenko *et al.*, 2014). Previous results indicated that IDAp binds to HSL2 with a Kd of 20 nM (Butenko *et al.*, 2014). As the wild-type IDA peptide has an Ala at position six corresponding to the Gly at that position in CLV3, and the *ida* mutant phenotype can be fully rescued by IDL1, which has a Gly at this position (Stenvik *et al.*, 2008) (Fig. 6A); both of these small amino acids are evidently compatible with high signalling activity. It was, however, conceivable that substitution to the larger Thr (mIDAp^{6Thr}) (Fig. 5A) could have an effect on receptor binding and/or activation. Therefore, the activity of mIDAp^{6Thr} in comparison with the activity of synthetic IDAp was assessed in an oxidative burst assay. For all peptide concentrations tested, mIDAp^{6Thr} gave the same response as IDAp in the presence of its receptor HSL2 (Fig. 5B), indicating that the mutated peptide was just as active as its wild-type counterpart. In conclusion, this mutation neither produced a ligand with weaker activity, nor a peptide with antagonistic effect.

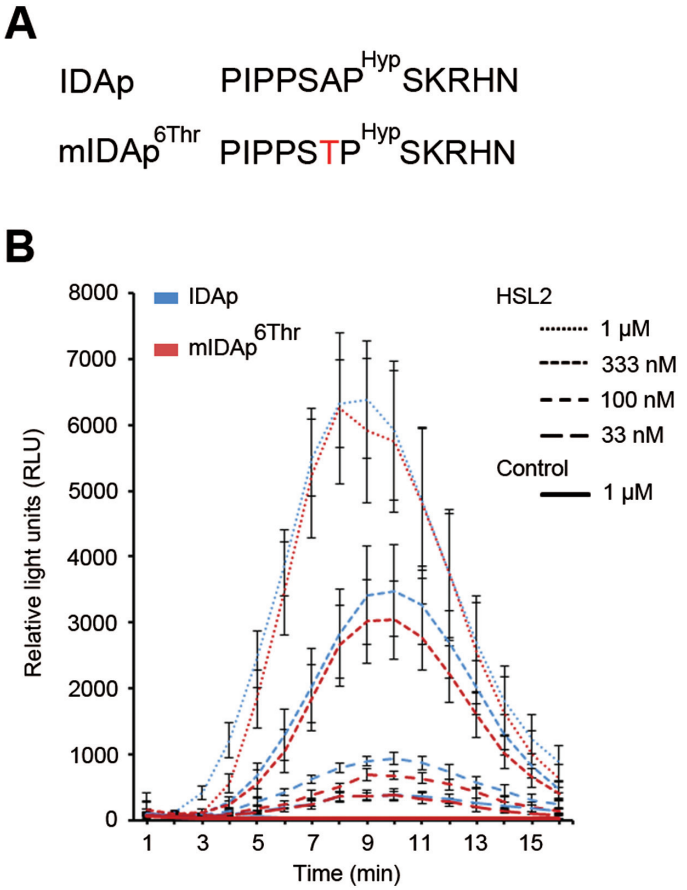


Fig. 5. IDA peptide treatment. (A) Sequence of synthetic IDA peptides used. (B) *N. benthamiana* leaf pieces expressing *HSL2* were exposed to various concentrations of peptides as indicated. Oxidative burst by the luminol-based assay was monitored over time as relative light units (RLU). Leaf pieces infiltrated with *Agrobacterium* without HSL2 were exposed to 1 µM of both peptides and used as control. Error bars indicate standard error of *n*=3 or 4 replicates.

Conclusion

Information collected using antagonistic peptide approaches (in the broad sense) can be very useful, but these approaches do not work in all cases and require a deep insight on the interaction between the ligand and its receptor to be successful. While the antagonistic peptide approach might work in a number of cases, as described by Song *et al.* (2013) and Xu *et al.* (2015), its universal applicability remains to be determined. Initial data were presented for CLV3, CLE8, and CLE22, and recently for CLE19 but in the absence of the pertinent wild-type control transgenes and genetic knockout lines, it remains difficult to judge whether the phenotypes triggered by *mCLE8^{6Thr}*, *mCLE19^{6Thr}*, and *mCLE22^{6Thr}* transgenes are antagonistic or not. Importantly, in view of the results presented here, and in agreement with the results of Song *et al.* (2013), it appears that the antagonistic peptide technology cannot be easily applied to synthetic CLE peptides and—at least—requires expressing mutant variants to deliver dominant peptides to their endogenous locations. However, as was shown with the *CLE45^{6Thr}* transgene, the latter also does not always work. Nevertheless, it can provide novel insight that can lead to other tools to dissect peptide activity, as— for example—the weakened activity of mCLE45^{6Thr} could be used to functionally characterize CLE45. In addition, it also does not appear to be straightforward to translate this approach to other peptide families, as exemplified

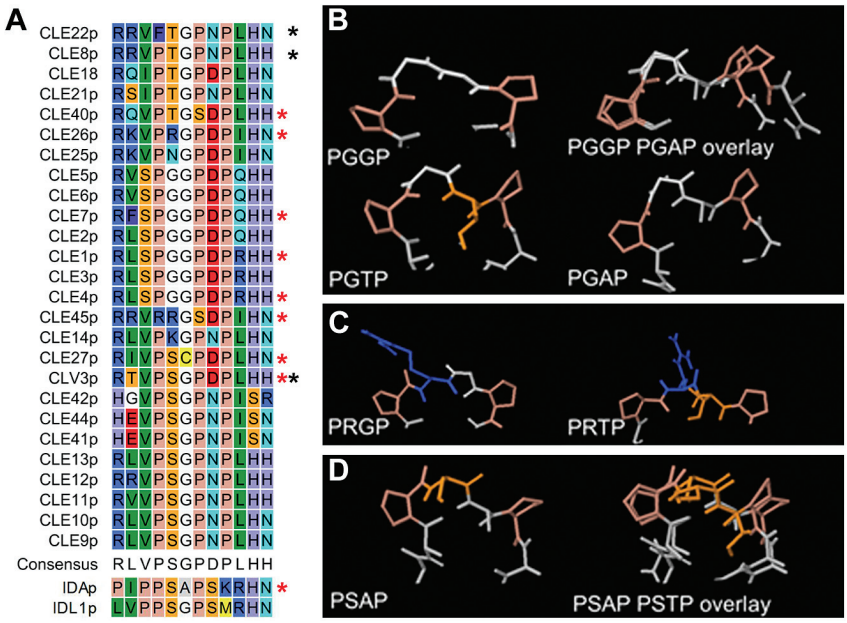


Fig. 6. Peptide structure. (A) Manually adjusted alignment of the 12 amino acids of CLE peptides, with IDA and IDL1 for comparison. Red stars mark peptides used in the present study, black stars those tested by Song *et al.* (2013). (B–D) Examples of structures of the PXXP core predicted by PEP-FOLD. (B) PGGP. The larger Thr might interfere with receptor binding, and substitution of Gly6 with Ala6 may change the angles between the Pro residues. (C) PRGP. The side chain of Arg may change direction when the Gly6 is exchanged with a Thr. (D) PSAP. A change from Ala to Thr in position six may not result in major conformational changes when Ser is present in the core. (This figure is available in colour at *JXB* online.)

through analyses on IDA. In general, it was observed that whether the mutations have an effect or not, seems dependent on the context, with differential sensitivity to conformational changes (Fig. 6A and Supplementary Table S2 available at *JXB* online). CLE1/4p and CLE7p are highly similar peptides with the same PGGP core at position four to seven, and both lose activity when the Gly at position six is mutated to Ala or Thr. Structure prediction for the peptides may suggest that a mutation in this context, with the small Gly at position five, easily changes the peptide conformation (Fig. 6B). Alternatively, all size increases in the side chain of the amino acid at position six could interfere with binding of the putative receptor(s) of CLE1, CLE4, and CLE7. CLE26p and CLE45p both have an Arg in the core sequence (PRGP and RRGS, respectively) and react similarly to the introduced mutations, namely weaker activity when the Gly at position six is mutated. The long side chain of Arg might change direction in the mutant peptides, which might reduce its binding affinity for a receptor (Fig. 6C). In contrast, mutation of Ala at position six to Thr did not reduce the activity of the IDA peptide, which has a PSAP core, suggesting that the serine (Ser) residue might stabilize the peptide structure (Fig. 6D).

In conclusion, the antagonistic peptide approach can be a useful tool to study the function of some *CLE* genes (Song *et al.*, 2013; Xu *et al.*, 2015), but not the ultimate means to overcome redundancy or lack of loss-of-function lines (Rodriguez-Villalon *et al.*, 2014; this study). However, while the approach described by Song *et al.* (2013), when applied to synthetic CLE peptide variants, did not work—for the peptides selected in this study and with respect to the phenotypes investigated, it does not preclude there being any other substitution, modification, or combination thereof or a transgene that may induce the desired effects. This, as well as structure considerations, should be taken into account before ordering a wide range of synthetic peptide variants and/or generating transgenic plants.

Supplementary data

Supplementary data are available at *JXB* online.

Supplementary Table S1. Quantification of distal root phenotypes after antagonistic peptide treatments.

Supplementary Table S2. Summary of mutations and phenotypes.

Acknowledgements

This work was supported by a BBSRC David Phillips Fellowship (BB_BB/H022457/1) and a Marie Curie European Reintegration Grant (PERG06-GA-2009–256354) to IDS, a BBSRC CASE Studentship co-funded by Bayer CropScience to NC, and a Swiss National Science Foundation grant (310030B_147088) to CSH. This work was supported by Grants 13785/F20, 218735, and 204756 to MAB, MW, and RBA, and 230849/F20 and 225299 to MAB from the Research Council of Norway. Work by RS, YS, and KGP was supported by the German excellence initiative (CEPLAS, EXC1028).

References

Araya T, Miyamoto M, Wibowo J, *et al*. 2014. CLE-CLAVATA1 peptide-receptor signaling module regulates the expansion of plant root systems in a nitrogen-dependent manner. *Proceedings of the National Academy of Sciences USA* **111,** 2029–2034.

Bleckmann A, Weidtkamp-Peters S, Seidel CAM, Simon R. 2010. Stem Cell Signaling in *Arabidopsis* Requires CRN to Localize CLV2 to the Plasma Membrane. *Plant Physiology* **152,** 166–176.

Brand U, Fletcher JC, Hobe M, Meyerowitz EM, Simon R. 2000. Dependence of stem cell fate in *Arabidopsis* on a feedback loop regulated by CLV3 activity. *Science* **289,** 617–619.

Butenko MA, Patterson SE, Grini PE, Stenvik GE, Amundsen SS, Mandal A, Aalen RB. 2003. Inflorescence deficient in abscission controls floral organ abscission in *Arabidopsis* and identifies a novel family of putative ligands in plants. *The Plant Cell* **15,** 2296–2307.

Butenko MA, Vie AK, Brembu T, Aalen RB, Bones AM. 2009. Plant peptides in signalling: looking for new partners. *Trends in Plant Science* **14,** 255–263.

Butenko MA, Wildhagen M, Albert M, Jehle A, Kalbacher H, Aalen RB, Felix G. 2014. Tools and Strategies to Match Peptide-Ligand Receptor Pairs. *The Plant Cell* **26,** 1838–1847.

Clark SE, Running MP, Meyerowitz EM. 1995. CLAVATA3 is a specific regulator of shoot and floral meristem development affecting the same processes as CLAVATA1 Development **121,** 2057–2067.

Clark SE, Jacobsen SE, Levin JZ, Meyerowitz EM. 1996. The CLAVATA and SHOOT MERISTEMLESS loci competitively regulate meristem activity in *Arabidopsis*. *Development* **122,** 1567–1575.

Cock JM, McCormick S. 2001. A large family of genes that share homology with CLAVATA3. *Plant Physiology* **126,** 939–942.

Czyzewicz N, Yue K, Beeckman T, De Smet I. 2013. Message in a bottle: small signalling peptide outputs during growth and development. *Journal of Experimental Botany* **64,** 5281–5296.

Czyzewicz N, Shi C, Vu LD, Van De Cotte B, Butenko MA, De Smet I. 2015. Modulation of *Arabidopsis* and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide. *Journal of Experimental Botany* **66,** 5229–5243.

Depuydt S, Rodriguez-Villalon A, Santuari L, Wyser-Rmili C, Ragni L, Hardtke CS. 2013. Suppression of *Arabidopsis* protophloem differentiation and root meristem growth by CLE45 requires the receptor-like kinase BAM3. *Proceedings of the National Academy of Sciences USA* **110,** 7074–7079.

Fiers M, Golemiec E, Xu J, van der Geest L, Heidstra R, Stiekema W, Liu CM. 2005. The 14-amino acid CLV3, CLE19, and CLE40 peptides trigger consumption of the root meristem in *Arabidopsis* through a CLAVATA2-dependent pathway. *The Plant Cell* **17,** 2542–2553.

Fiume E, Fletcher JC. 2012. Regulation of *Arabidopsis* embryo and endosperm development by the polypeptide signaling molecule CLE8. *The Plant Cell* **24,** 1000–1012.

Fletcher JC, Brand U, Running MP, Simon R, Meyerowitz EM. 1999. Signaling of cell fate decisions by CLAVATA3 in *Arabidopsis* shoot meristems. *Science* **283,** 1911–1914.

Hirakawa Y, Shinohara H, Kondo Y, *et al*. 2008. Non-cell-autonomous control of vascular stem cell fate by a CLE peptide/receptor system. *Proceedings of the National Academy of Sciences USA* **105,** 15208–15213.

Hobe M, Muller R, Grunewald M, Brand U, Simon R. 2003. Loss of CLE40, a protein functionally equivalent to the stem cell restricting signal CLV3, enhances root waving in *Arabidopsis*. *Development Genes and Evolution* **213,** 371–381.

Jun J, Fiume E, Roeder AH, *et al*. 2010. Comprehensive analysis of CLE polypeptide signaling gene expression and overexpression activity in *Arabidopsis*. *Plant Physiology* **154,** 1721–1736.

Kinoshita A, Nakamura Y, Sasaki E, Kyozuka J, Fukuda H, Sawa S. 2007. Gain-of-function phenotypes of chemically synthetic CLAVATA3/ESR-related (CLE) peptides in *Arabidopsis thaliana* and *Oryza sativa*. *Plant and Cell Physiology* **48,** 1821–1825.

Kondo T, Nakamura T, Yokomine K, Sakagami Y. 2008. Dual assay for MCLV3 activity reveals structure-activity relationship of CLE peptides. *Biochemical and Biophysical Research Communications* **377,** 312–316.

Lease KA, Walker JC. 2006. The *Arabidopsis* unannotated secreted peptide database, a resource for plant peptidomics. *Plant Physiology* **142,** 831–838.

Lee JS, Torii KU. 2012. A tale of two systems: peptide ligand-receptor pairs in plant development. *Cold Spring Harbor Symposia on Quantitative Biology* **77,** 83–89.

Lim CW, Lee YW, Hwang CH. 2011. Soybean nodule-enhanced CLE peptides in roots act as signals in GmNARK-mediated nodulation suppression. *Plant and Cell Physiology* **52,** 1613–1627.

Mortier V, Den Herder G, Whitford R, Van de Velde W, Rombauts S, D'Haeseleer K, Holsters M, Goormachtig S. 2010. CLE peptides control *Medicago truncatula* nodulation locally and systemically. *Plant Physiology* **153,** 222–237.

Mueller K, Bittel P, Chinchilla D, Jehle AK, Albert M, Boller T, Felix G. 2012. Chimeric FLS2 receptors reveal the basis for differential flagellin perception in *Arabidopsis* and tomato. *The Plant Cell* **24,** 2213–2224.

Murphy E, Smith S, De Smet I. 2012. Small signaling peptides in *Arabidopsis* development: how cells communicate over a short distance. *The Plant Cell* **24,** 3198–3217.

Ogawa M, Shinohara H, Sakagami Y, Matsubayashi Y. 2008. *Arabidopsis* CLV3 peptide directly binds CLV1 ectodomain. *Science* **319,** 294.

Ohyama K, Shinohara H, Ogawa-Ohnishi M, Matsubayashi Y. 2009. A glycopeptide regulating stem cell fate in *Arabidopsis thaliana*. *Nature Chemical Biology* **5,** 578–580.

Okamoto S, Shinohara H, Mori T, Matsubayashi Y, Kawaguchi M. 2013. Root-derived CLE glycopeptides control nodulation by direct binding to HAR1 receptor kinase. *Nature Communications* **4,** 2191.

Reid DE, Ferguson BJ, Gresshoff PM. 2011. Inoculation- and nitrate-induced CLE peptides of soybean control NARK-dependent nodule formation. *Molecular Plant-Microbe Interactions* **24,** 606–618.

Reid DE, Li D, Ferguson BJ, Gresshoff PM. 2013. Structure-function analysis of the GmRIC1 signal peptide and CLE domain required for nodulation control in soybean. *Journal of Experimental Botany* **64,** 1575–1585.

Rodriguez-Villalon A, Gujas B, Kang YH, Breda AS, Cattaneo P, Depuydt S, Hardtke CS. 2014. Molecular genetic framework for protophloem formation. *Proceedings of the National Academy of Sciences USA* **111,** 11551–11556.

Rodriguez-Villalon A, Gujas B, van Wijk R, Munnik T, Hardtke CS. 2015. Primary root protophloem differentiation requires balanced phosphatidylinositol-4,5-biphosphate levels and systemically affects root branching. *Development* **142,** 1437–1446.

Shiu SH, Bleecker AB. 2001*a*. Plant receptor-like kinase gene family: diversity, function, and signaling. *Science Signaling 2001* , re22.

Shiu SH, Bleecker AB. 2001*b*. Receptor-like kinases from *Arabidopsis* form a monophyletic gene family related to animal receptor kinases. *Proceedings of the National Academy of Sciences USA* **98,** 10763–10768.

Song XF, Guo P, Ren SC, Xu TT, Liu CM. 2013. Antagonistic peptide technology for functional dissection of CLV3/ESR genes in *Arabidopsis*. *Plant Physiology* **161,** 1076–1085.

Stahl Y, Wink RH, Ingram GC, Simon R. 2009. A signaling module controlling the stem cell niche in *Arabidopsis* root meristems. *Current Biology* **19,** 909–914.

Stahl Y, Grabowski S, Bleckmann A, *et al*. 2013. Moderation of *Arabidopsis* root stemness by CLAVATA1 and ARABIDOPSIS CRINKLY4 receptor kinase complexes. *Current Biology* **23,** 362–371.

Stenvik GE, Butenko MA, Urbanowicz BR, Rose JK, Aalen RB. 2006. Overexpression of INFLORESCENCE DEFICIENT IN ABSCISSION activates cell separation in vestigial abscission zones in *Arabidopsis*. *The Plant Cell* **18,** 1467–1476.

Stenvik GE, Tandstad NM, Guo Y, Shi CL, Kristiansen W, Holmgren A, Clark SE, Aalen RB, Butenko MA. 2008. The EPIP peptide of INFLORESCENCE DEFICIENT IN ABSCISSION is sufficient to induce abscission in *Arabidopsis* through the receptor-like kinases HAESA and HAESA-LIKE2. *The Plant Cell* **20,** 1805–1817.

Stes E, Gevaert K, De Smet I. 2015. Phosphoproteomics-based peptide ligand-receptor kinase pairing. Commentary on: "A peptide hormone and its receptor protein kinase regulate plant cell expansion". *Frontiers in Plant Science* **6,** 224.

Truernit E, Bauby H, Dubreucq B, Grandjean O, Runions J, Barthelemy J, Palauqui JC. 2008. High-resolution whole-mount imaging of three-dimensional tissue organization and gene expression enables the study of phloem development and structure in *Arabidopsis*. *The Plant Cell* **20,** 1494–1503.

Xu T-T, Ren S-C, Song X-F, Liu C-H. 2015. *CLE19* expressed in the embryo regulates both cotyledon establishment and endosperm development in *Arabidopsis*. *Journal of Experimental Botany* **66,** 5217–5227.

Yang SL, Xie LF, Mao HZ, Puah CS, Yang WC, Jiang L, Sundaresan V, Ye D. 2003. Tapetum determinant1 is required for cell specialization in the *Arabidopsis* anther. *The Plant Cell* **15,** 2792–2804.

Chapter 6: CLE26 (Phospho)proteomics Screening Reveals Putative Effectors of CLE26 Signalling

Author Contribution:

I was involved with planning and I prepared samples for completion of the CLE26 differential phosphoproteomics screen.

I wrote this chapter and compiled all diagrams except where otherwise noted.

Chapter 6: CLE26 (Phospho)proteomics Screening Reveals Putative Effectors of CLE26 Signalling

Abstract:

Having established CLE26 as a potent inhibitor of protophloem differentiation, resulting in a severe short root phenotype in *Arabidopsis* and several agriculturally important crop models, it was considered prudent to probe into the potential mechanism of CLE26 signalling using a (phospho)proteomics approach. In this chapter, several putative effectors of CLE26 signalling (PECS) are identified using this approach, and their potential for transducing the CLE26 signal is discussed in view of the available literature.

6.1 Short background

In the previous chapters it was established that CLE26 is a potent inhibitor of primary root growth in Arabidopsis and a number of commercially important crop species. The primary effect of CLE26 appears to be inhibition of protophloem identity, which leads to altered distribution of auxin in the root apical meristem, inhibition of primary root growth and increased lateral root density (Czyzewicz, et al., 2015; Rodriguez-Villalon, et al., 2015). However, it is currently unknown how the CLE26 signal is perceived and which downstream effectors of CLE26 signalling are involved.

Previously, it was shown that phosphoproteomics is a powerful approach to identify receptors for small signalling peptides and downstream targets (for example RALF1 was paired with the

receptor kinase FERONIA (Haruta, et al., 2014)). Additionally, this approach also enables analysis of differentially regulated proteins, which may provide some insight into the mechanics of CLE26 signalling further downstream than phosphorylation. To address the afore-mentioned gap in our CLE26 knowledge, a similar approach was employed. Proteins identified in this manner will provide insights into CLE26 signalling machinery.

6.2 Results and Discussion

(Phospho)proteomics Analysis Indicates Multiple Putative Effectors of CLE26 Signalling

(Phospho)proteomics samples were prepared and analysed as detailed in materials and methods. 5 DAG liquid cultured seedlings were subjected to 10 minutes of peptide treatment by adjusting the concentration of the liquid MS to 1 µM CLE26p or mock (water) control. Samples were snap frozen and proteins isolated and digested, and peptides were purified by passing through a C18 column. Samples were then split into two equal fractions, one of which was enriched for phosphopeptides using a TiO_2 column. Both phosphoenriched and proteome samples were then dried and resuspended in analysis buffer prior to analysis by LC-MS/MS (Figure 1).

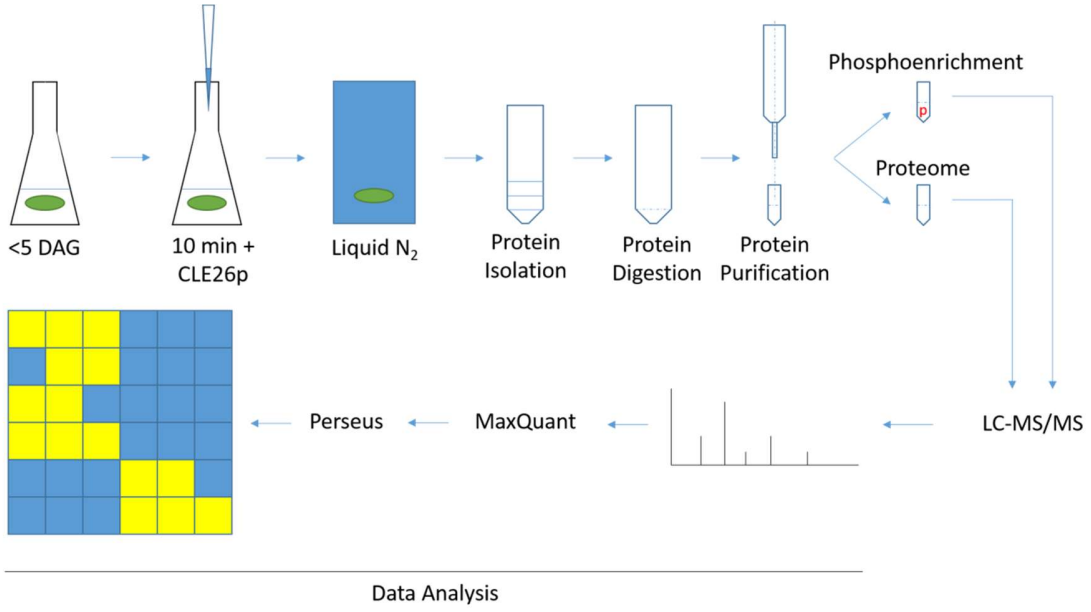


Figure 1: A schematic method of differential (phospho)proteomics methodology.

CLE26-mediated Differential Regulation

LC-MS/MS based proteomics analysis indicated 18 proteins that are >2 fold up- or down-regulated in response to CLE26 treatment (Figure 2). Cross-referencing of this data against the UniProt database suggested a significant amount of background noise including metabolic and photosystem enzymes, and ribosomes, which were excluded prior to literature searches, due to the unlikelihood of their direct involvement in signalling processes. However, there are five potentially interesting putative effectors of CLE26 signalling, which I will discuss in more detail below, based on published literature: AT5G49760, DWF1 (AT3G19820), AT3G20370, GRF7/14-3-3v (AT3G02520), and P4H6 (AT3G28490).

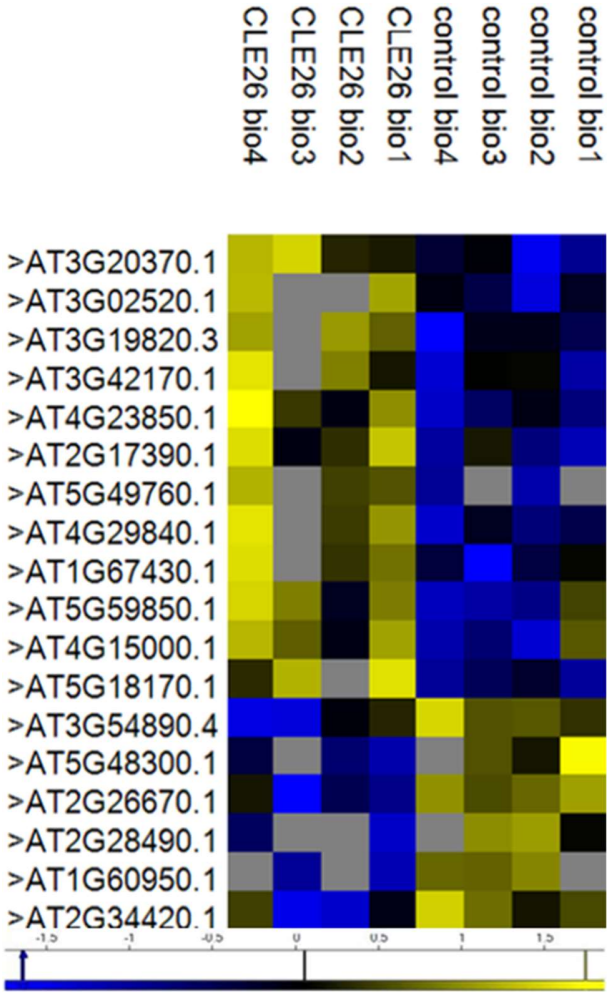


Figure 2: Differential proteomics analysis indicates differential regulation of proteins in CLE26 treated samples compared with untreated samples following statistical analysis (P <0.05 according to Student's T-Test). Yellow denotes increased abundance of proteins (<2-fold increase), blue denotes decreased abundance of proteins (<2-fold decrease).

Upregulated PECS

AT5G49760 (LRR-RLK)

AT5G49760 is a leucine-rich repeat receptor-like kinase (LRR-RLK) of unknown function, and is upregulated in response to CLE26 treatment (Figure 2). LRR-RLKs are a class of proteins commonly responsible for perception and transduction of ligand-based signalling, and generally, ligand binding initiates a signalling cascade allowing a specific developmental or defence response (De Smet, et al., 2009). As such, it may be tempting to speculate that AT5G49760 represents a receptor capable of interpreting and transducing CLE26 signalling. Interestingly, perception of FLAGELLIN by FLAGELLIN-SENSING 2 (FLS2) induces internalisation and degradation of the receptor (Robatzek, et al., 2006). Increased abundance of AT4G49760 may therefore indicate CLE26 treatment is able to inhibit degradation of AT4G49760 by inhibiting a similar mechanism of degradation. However, given that binding of ligand to receptor often results in autophosphorylation (Schlesinger, 2002; Wang, et al., 2005), and no phosphorylation events are detected in AT5G49760 by the corresponding differential phosphoproteomics approach, it is unlikely that CLE26 and AT4G49760 form a ligand/receptor pair.

From this perspective, it will be important to determine whether transcription, translation or degradation are affected by CLE26p treatment.

AT3G19820 (DWF1)

AT3G19820 encodes DELTA(24)-STEROL REDUCTASE/DIMINUTIO/DWARF1/CABBAGE1/ ENHANCED VERY-LOW-FLUENCE RESPONSE1 (DIM/DWF1/CBB1/EVE1), an enzyme involved in

brassinosteroid (BR) production, which is upregulated in response to CLE26 treatment (Figure 2). Interestingly, *dwf1* mutants display decreased primary root length compared to wild-type, suggesting that BRs are required for root elongation (Müssig, et al., 2003). Correspondingly, brassinosteroid insensitive mutants *brassinosteroid insensitive-like 1*, *brassinosteroid insensitive-like 3*, and *brassinosteroid insensitive 1* have increased numbers of differentiated phloem at the expense of differentiated xylem in the RAM, and similarly demonstrate a short root phenotype (Caño-Delgado, et al., 2004). From this perspective it is interesting to note that restoration of BR sensitivity in the protophloem alone is sufficient to restore correct vascular development in root tissues, as *bri1 brl1 brl3* complimented with protophloem-specific expression of *BRI1* restores a wild-type root (Kang, et al., 2017). Taken together, this suggests that perception of BR by the phloem lineage inhibits their differentiation, but simultaneously upregulates an effector of protoxylem differentiation, which is consistent with current knowledge of TRACHEARY ELEMENT DIFFERENTIATION INHIBITORY FACTOR (TDIF), being a phloem-derived inhibitor of xylem differentiation (Hirakawa, et al., 2008).

Given the putative role of CLE26 in the upregulation of brassinosteroid synthesis, it is interesting to note that brassinosteroids are not thought to undergo long-distance transport (Symons & Reid, 2004), and the reporter *pBRL3::GUS* shows that the BRL3 brassinolide receptor has a very similar protophloem-localised expression pattern to that of *pCLE26::GUS* (Caño-Delgado, et al., 2004; Czyzewicz, et al., 2015). In addition, although BR application has been demonstrated to inhibit primary root growth, at low concentrations of BR (0.04 nM), an increase to primary root length is observed (Müssig, et al., 2003), similar to the dose-response curve of applied CLE26 (Czyzewicz, et al., 2015). Thus, it is tempting to speculate that CLE26 regulates protophloem differentiation

through localised activation of BR synthesis, and that the short-root phenotype observed previously may directly result from increased inhibition of protophloem differentiation, leading to restricted bulk flow of auxin from shoot to root (Figure 3).

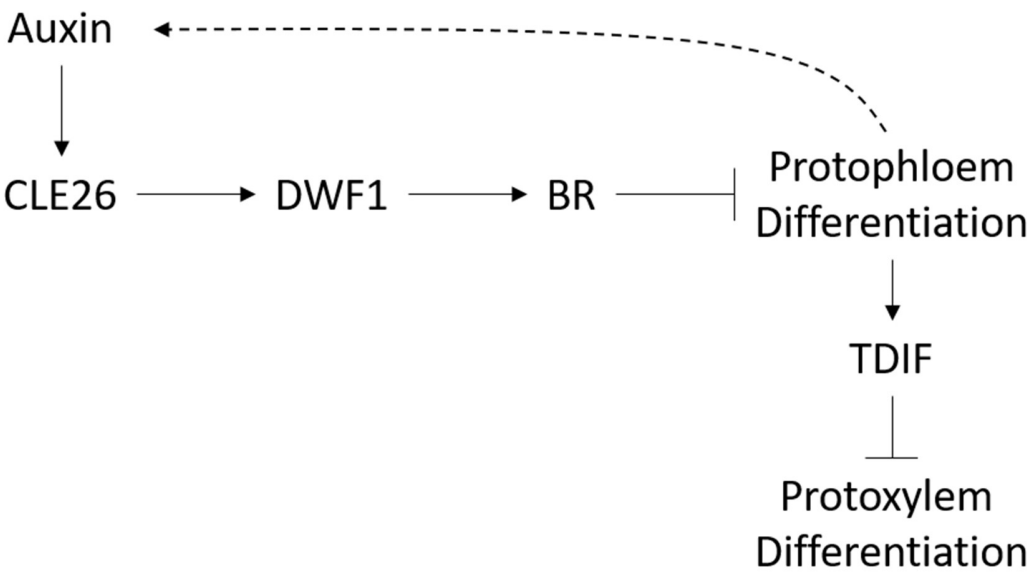


Figure 3: A hypothetical model for CLE26-mediated induction of brassinosteroid signalling. *CLE26* expression is induced by auxin (Czyzewicz, et al., 2015), and increased CLE26 results in increased abundance of DWF1 (Figure 2), which is a key enzyme in brassinosteroid (BR) biosynthesis. Increased BR synthesis results in activation of BR signalling machinery, which regulates differentiation of protophloem, resulting in decreased bulk flow of auxin to the RAM. Since TDIF is synthesised by protophloem, and diffuses through the stele to inhibit protoxylem differentiation (Hirakawa, et al., 2008), identification of DWF1 as an effector of CLE26 signalling may indicate CLE26 as a "master signal" for regulation of vascular development.

AT3G20370 (TRAF-like)

AT3G20370 encodes a TUMOUR RECEPTOR ASSOCIATED FACTOR-LIKE family protein of unknown function. Interestingly, another member of the TRAF-like family, SEVEN IN ABSENTIA 2 (SINA2) is involved in inferring drought tolerance in response to abscisic acid signalling (Bao, et al., 2014). Increased abundance of AT3G20370 in CLE26p treated samples may therefore suggest that CLE26 signalling forms a molecular link between phytohormone and stress tolerance. Further

characterisation of *AT3G20370* and *CLE26* expression using a qPCR-based approach may reveal whether these signalling elements are similarly regulated by phytohormone signals and/or stressors.

AT3G02520 (GRF7/14-3-3v)

AT3G02520 encodes GENERAL REGULATORY FACTOR 7/14-3-3-LIKE PROTEIN GF14 NU (GRF7/14-3-3v, respectively). Interestingly, 14-3-3v has been indicated to interact with the SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE1 (SERK1)/BRASSINOSTEROID INSENSITIVE1 (BRI1) complex in *Arabidopsis,* which is involved in perception of brassinosteroid (BR) signalling (Karlova, et al., 2006). 14-3-3 family members are able to regulate the nuclear or cytoplasmic localisation of their binding partners in a phosphorylation dependent manner (Muslin & Xing, 2000). In the case of BR signalling, it has been indicated that 14-3-3v sequesters two downstream effectors of BR signalling – *bri1*-EMS SUPPRESSOR1 (BES1) and BRASSINOZOLE RESISTANT1 (BZR1) – in the cytoplasmic compartment (Karlova, et al., 2006; Clouse, 2011). Upon perception of BR by the SERK1/BRI1 receptor complex, the associated BR-SIGNALING KINASE1 (BSK1) activates the phosphatase BRI SUPPRESSOR1 (BSU1), causing dephosphorylation – and deactivation – of the cytoplasmic kinase BRASSINOSTEROID INSENSITIVE2 (BIN2) (Clouse, 2011). Inhibited in this BR-dependent manner, BIN2 is no longer able to phosphorylate the transcription factors BES1 and BZR1. As a result, PROTEIN PHOSPHATASE2A (PP2A) activity dephosphorylates BES1 and BZR1, resulting in dissociation of 14-3-3v, and relocalisation of BES1 and BZR1 to the nucleus, where they induce expression of BR response genes (Clouse, 2011). Since 14-3-3v activity causes both cytoplasmic localisation and their degradation by the 26S proteasome

(Clouse, 2011; Karlova, et al., 2006), and the increased abundance of DWF1 discussed previously, it is tempting to speculate that the increased abundance of 14-3-3v observed in CLE26-treated samples may be representative of BR-mediated dissociation from substrate proteins, resulting in decreased 26S proteasome-mediated degradation.

Downregulated PECS

AT3G28490 (P4H6)

AT3G28490 encodes PROBABLE PROLYL 4-HYDROXYLASE 6 (P4H6), which catalyses the post-translational formation of 4-hydroxyproline in –Xaa-Pro-Gly- sequences in proline rich peptides, and is downregulated in response to CLE26 treatment. Hydroxyprolination plays such an important role in peptide signalling. By introducing a charged OH^- group, hydroxyprolination alters the conformation of peptides in a similar way to phosphorylation (Shinohara & Matsubayashi, 2013). Downregulation of P4H6 in CLE26-treated samples may therefore indicate that CLE26 has its effect through modification of other peptides and proteins via hydroxyprolination, thus affecting their activity.

Interestingly, P4H enzymes appear to be involved in a number of processes, including modulation of CLV3 activity (Kondo, et al., 2006), iron sensing, (Vigani, et al., 2013), hypoxia, anoxia and mechanical wounding, (Vlad, et al., 2007), and root hair expansion (Velasquez, et al., 2015). Intriguingly, previous observations made in CLE26p-treated WAVE131Y roots indicated potential involvement of CLE26 in root hair development (Figure 4). The observed disruption to root hair regulation included growth of root hairs closer to the RAM, and occasionally branching in root

hairs was observed in CLE26p-treated samples. This was not yet quantified, therefore to get an accurate idea of whether CLE26p treatment and *cle26* are able to effect root hair development, further analysis is required.

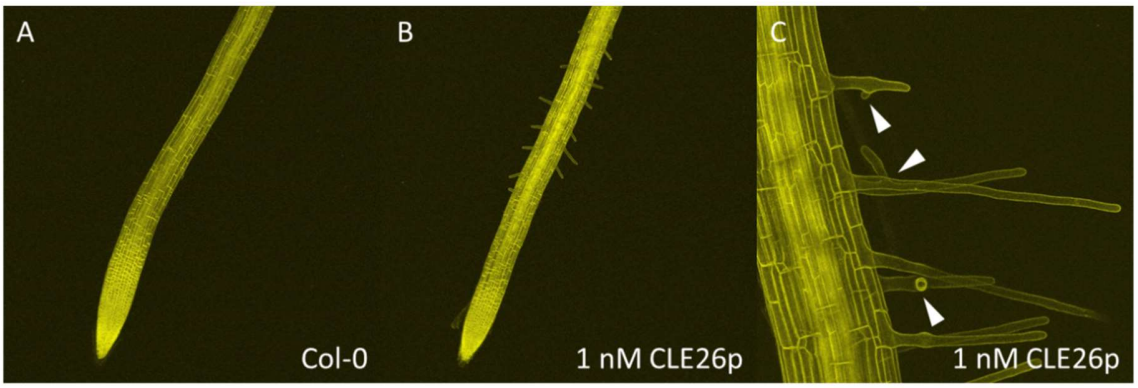


Figure 4: 1 nM CLE26p treatment was observed to affect root hair development in WAVE131Y roots, increasing proximity to the RAM (A and B), and occasionally root hair branching was observed (C).

Expression of *P4H6* remains stable in response to wounding, as well as hypoxic and anoxic stress (Vlad, et al., 2007), suggesting that P4H6 may be involved in perceiving stress from a different stimulus. Given that there are several putative effectors in this screen involved in mediating or regulating the drought stress response, it is possible that CLE26/CYP63 mediated signalling is able to trigger a response to drought stress. Alternatively, since CLE26 itself is likely to be hydroxyprolinated, and hydroxyprolination at CLE26^{P7HYP} increases bioactivity (Czyzewicz, et al., 2015), downregulation of P4H6 may represent a feedback loop, decreasing the activity of CLE26 itself.

CLE26-mediated Differential Phosphorylation

Analysis of differential phosphorylation (Figure 5) indicated two proteins that are phosphorylated in response to CLE26 treatment (AT5G51200 and AT1G67730), and three further proteins (AT4G18780, AT3G63400 and AT1G47740) that are dephosphorylated under the same conditions. It is to be noted that the phosphopeptide score calculated in Perseus for these differentially phosphorylated proteins was very low (<30) and none would usually pass the stringent statistical analyses. However, since phosphorylation remains significantly different between CLE26p and mock treatment, it is possible that this preliminary screen may indicate some putative effectors of CLE26 signalling (PECS), and several are therefore discussed below based on published literature. Phosphorylated PECS may represent direct targets of CLE26/receptor signalling, while dephosphorylated PECS may represent targets further downstream from activation of the receptor. Alternatively, if the CLE26 receptor is inactivated by binding CLE26, the reverse may also be true, with dephosphorylated targets being more direct effectors of CLE26 signalling than those which are phosphorylated. Since phosphorylation and dephosphorylation events of specific proteins are often key to translation of ligand–receptor signalling, and result in differential regulation or activity of effector proteins, both groups of data may indicate PECS.

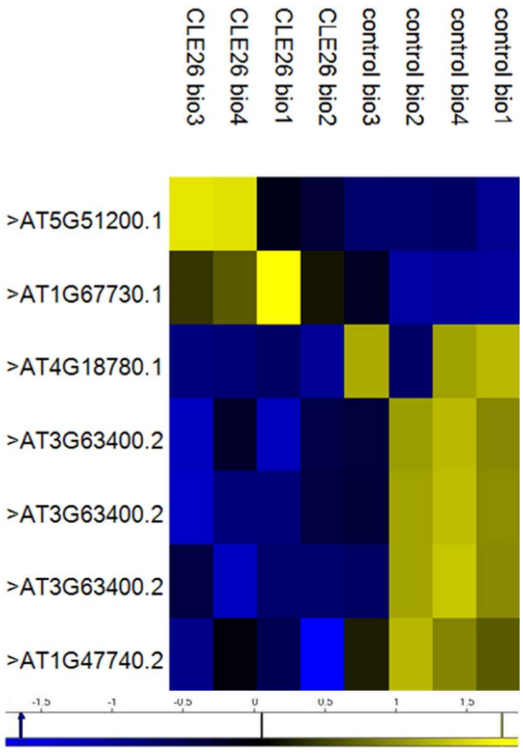


Figure 5: LC-MS/MS analysis of phosphorylation indicates differential phosphorlyation of 5 proteins in CLE26 treated samples compared with untreated samples following statistical analysis (P <0.05 according to Student's T-Test). Yellow denotes increased phosphorylation of proteins (<2-fold increase), blue denotes decreased phosphorylation of proteins (<2-fold decrease).

Phosphorylated PECS

AT1G67730 (KCR1)

AT1G67730 encodes VERY-LONG-CHAIN 3-OXOACYL-COA REDUCTASE 1 (KCR1), which is a ß-ketoacyl-coenzyme A reductase involved in production of very long chain fatty acids (VLCFAs) (Beaudoin, et al., 2009). This may suggest that CLE26 signalling is capable of regulating VLCFA biosynthesis.

Interestingly, although *KCR1* expression is detected in the stele throughout the root, knockdown of *KCR1* results in decreased lateral root emergence, while primary root growth remains unaffected (Beaudoin, et al., 2009). Additionally, it has been observed that VLCFA-derived signals synthesised in the leaf epidermis are able to inhibit vascular differentiation, by reducing cytokinin availability in the vasculature through downregulation of *ADENOSINE PHOSPHATE-ISOPENTENYLTRANSFERASE 3 (IPT3)* (Nobusawa, et al., 2013). Furthermore, decreased VLCFA signalling causes internalisation of PIN-FORMED 1, similar to that observed for cytokinin and CLE26p treatments (Roudier, et al., 2010).

Taken together, it is possible that CLE26-mediated phosphorylation of KCR1 inhibits its activity, resulting in decreased VLCFA-mediated signalling and increased local cytokinin availability. From this perspective, the normal expression pattern of *CLE26* may restrict VLCFA biosynthesis in protophloem tissues, enabling their differentiation to phloem by removing inhibition of cytokinin biosynthesis in these tissues (Aloni, et al., 2006; Nobusawa, et al., 2013). Subsequently, exogenous application of CLE26p may increase cytokinin biosynthesis throughout the root, thus increasing cytokinin-mediated inhibition of primary and lateral root growth (Laplaze, et al., 2007).

If this model is correct, it is possible that the roots previously observed emerging perpendicular to the primary root in CLE26p-treated *Arabidopsis* are in fact newly-emerged adventitious roots, which do not require cytokinin signalling for development, and would therefore be unaffected by increased abundance of cytokinin (Kuroha, et al., 2006).

Dephosphorylated PECS

AT4G18780 (IRX1)

AT4G18780 encodes IRREGULAR XYLEM 1/CELLULOSE SYNTHASE A CATALYTIC SUBUNIT 8 (IRX1/CESA8) which is involved in secondary cell wall formation, and is required, together with *IRX3,* for correct deposition of cellulose in the xylem and interfasicular tissues (Turner & Somerville, 1997; Taylor, et al., 2000). The *irx1* mutant demonstrates a severe reduction to deposition of cellulose in xylem cells, causing these vessels to collapse (Taylor, et al., 2000). CLE26-mediated dephosphorylation of IRX1 may therefore indicate a role for CLE26 in regulation of cellulose deposition.

Interestingly however, IRX1/CESA8 has been indicated to be able to interact with both primary (CESA2, CESA3 and CESA6), and secondary (CESA7) cellulose synthases, as well as forming homodimers (Li, et al., 2013). This may suggest that IRX1 can additionally interact with primary CESA enzymes to regulate primary cell wall synthesis, although since no primary cell wall phenotype is observed in *cesa8*, any potential interaction is likely redundant with other CESA enzymes.

Since cell wall loosening occurs during lateral root emergence (Péret, et al., 2009), requires the presence of EXPANSIN 14 (EXP14) (Lee, et al., 2013), and is a result of cellulose digestion resulting from xyloglucan endotransglucosylase and xyloglucan hydrolase activity (Van Sandt, et al., 2007), it is possible that during this period of cell wall remodelling, cellulose synthases may additionally be inhibited. Interestingly, *cesa3* and *cesa6* display lateral root growth on repressive media containing sucrose, KNO_3, and NH_4NO_3, while wild type does not (Roycewicz & Malamy, 2014), suggesting that when cell wall synthesis is inhibited, lateral root emergence is less restricted. Given that emerged lateral root density is increased in CLE26p-treated plants, it is possible that CLE26-mediated dephosphorylation inactivates IRX1, and therefore may indicate that CLE26p treatment is able to regulate a complimentary signalling cascade capable of inhibiting cellulose synthesis, assisting endotransglucosylase and hydrolase activity in loosening cell walls for lateral root emergence.

However, since expression of *pCLE26::GUS* is observed in protophloem and was not observed in lateral roots until initiation of vasculature formation, and LRD was unaffected in *cle26* (Czyzewicz, et al., 2015), it seems more likely that native-expressed CLE26p may act to inhibit the activity of IRX1 in developing protophloem. Since IRX1 is expressed in the xylem and interfasicular cells that bracket phloem tissues, and *irx1* results in defects to secondary cell wall development in both tissues (Taylor, et al., 2003; Taylor, et al., 2000), it is possible that CLE26-mediated dephosphorylation of IRX1 in the developing (proto)phloem acts as a “safeguard”, preventing secondary cell wall formation in the phloem tissues during vascular development by inhibition of IRX1 activity (Figure 6).

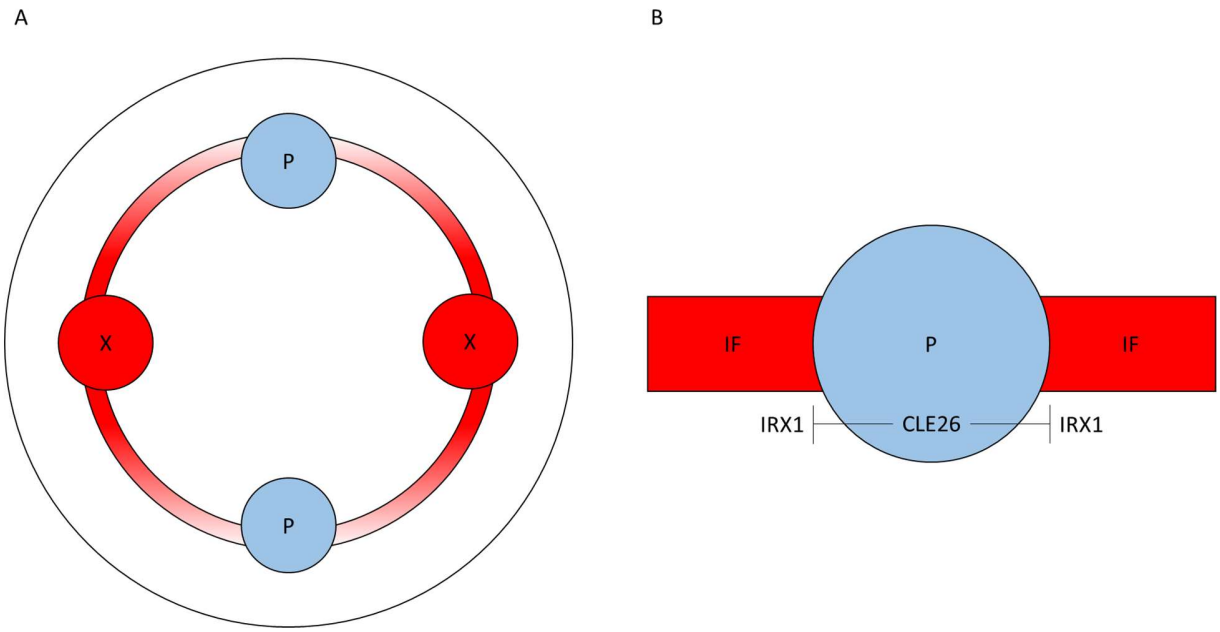


Figure 6: A hypothetical model for CLE26-mediated inhibition of IRX1. A) A schematic of the root illustrating expression domains of CLE26 (blue) and IRX1 (red). B) CLE26 expression (blue) in the developing phloem (P) may prevent secondary cell wall formation in developing phloem (P) by "safeguarding" the phloem against neighbouring interfascicular cell (IF) IRX1 expression (red).

AT3G63400 (CYP63)

AT3G63400 encodes PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CYCLOPHILIN 63/CYCLOPHILIN LIKE PROTEIN CYPRS64 (CYP63/CYPRS64), a peptidyl-prolyl cys-trans isomerase (PPIase) involved in protein folding. CLE26-mediated dephosphorylation of CYP63 may therefore indicate a potential role for CLE26 signalling in regulating the correct folding of proteins for complex formation.

Given their role in protein folding by catalysis of the cis-trans isomerisation of proline imidic peptide bonds, PPIases have been indicated in a number of different processes, from protein

trafficking to alternative splicing (Fruman, et al., 1994; He, et al., 2004; Patterson, et al., 2000). As a potential indicator of function it is interesting to note that yeast 2-hybrid approaches using CYP63 as bait identified multiple interactions with small nuclear ribonucleoprotein (snRNP)-specific proteins, as well as serine/arginine rich proteins which are responsible for intron recognition and spliceosome assembly, suggesting that CYP63 may be involved in the regulation of alternative splicing (Lorković, et al., 2004; Lorković, et al., 2005). Additionally, it is interesting to note that interaction of CYP63 is enhanced by phosphorylation of the substrate spliceosome proteins SERINE/ARGININE-RICH-SPLICING FACTOR SR34 (SR34) and SERINE/ARGININE-RICH SC35-LIKE SPLICING FACTOR SCL30 (SCL30) (Lorković, et al., 2004). Given that CYP63 interacts with spliceosome specific proteins, but is not directly involved in RNA splicing, it was predicted that CYP63 may serve to facilitate formation of, and/or stabilise the spliceosome complex, suggesting that CLE26-mediated dephosphorylation of CYP63 may be able to regulate production of alternatively spliced proteins, or modulate translation of genes via RNA-mediated interference (RNAi) (Lorković, et al., 2004), though how this would have a specific effect on root architecture or protophloem development remains unclear.

Interestingly another PPIase, PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PIN1 (Pin1At) - named because it is 53% identical in sequence to the *H. sapiens* PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA-INTERACTING 1 (PIN1) (Landrieu, et al., 2000)) – has been demonstrated to directly catalyse the cys-trans isomerization of a synthetic form of phosphorylated residues in the central hydrophilic loop of PIN-FORMED 1 (PIN1) (Xi, et al., 2016). This change accelerates the rate of the conformational change responsible for defining apical PIN1 localisation induced by PINOID (PID) phosphorylation, and thus regulates root gravotropism (Xi, et al., 2016).

Given the evidence for CYP63 interaction with the spliceosome, it is tempting to speculate that CLE26-mediated dephosphorylation of CYP63 may be able to regulate expression of other proteins via modulation of RNAi, which may in turn present a model for the differential regulation of proteins discussed below. However, given that PIN1 polarisation is disrupted in CLE26 treated lines, and the ability of Pin1At to directly affect PIN1 polarisation, the possibility that CLE26-mediated CYP63 signalling is also able to affect PIN1 localisation in a manner distinct from its role in spliceosome stabilisation should not be prematurely ruled out.

AT1G47740 (Thiol Peptidase)

AT1G47740 encodes a putative thiol peptidase. There are several subfamilies of thiol peptidases (also known as cysteine proteases) present in *Arabidopsis,* and are involved in a diverse range of physiological processes, including immunity, mobilization of seed resources and senescence (Shindo, et al., 2012; Grudkowska & Zagdanska, 2004). To which group of thiol peptidases AT1G47740 may belong is unclear, however, it is unlikely to belong to the papain family, since they characteristically contain a C-terminal KDEL endoplasmic reticulum retention signal, involved in vesicle formation and vacuolar transport (Okamoto, et al., 2003), and an ERFNIN autoinhibitory domain at the N-terminus (Beers, et al., 2004), neither of which appear to be present in AT1G47740. Given the diverse range of functions exhibited by this group of proteins, it is difficult to assign a putative role for CLE26-mediated dephosphorylation of an uncharacterised member.

Interestingly, in *Oryza sativa,* the thiol peptidase OsEP3A is regulated by multiple mechanisms, including hormonal regulation in germinating seeds, spatiotemporal regulation in vegetative

tissues, and is upregulated in response to nitrogen stress in callus-derived suspension cells (Ho, et al., 2000). The involvement of a thiol peptidase in these processes may represent the mobilization and/or recycling of resources in periods of nutrient stress (Ho, et al., 2000). From this perspective, it is possible that CLE26-mediated dephosphorylation of such an enzyme may represent a molecular “switch” for adaptation of root morphology between conservation of nutrients in stress and growth in non-stress conditions (Figure 7).

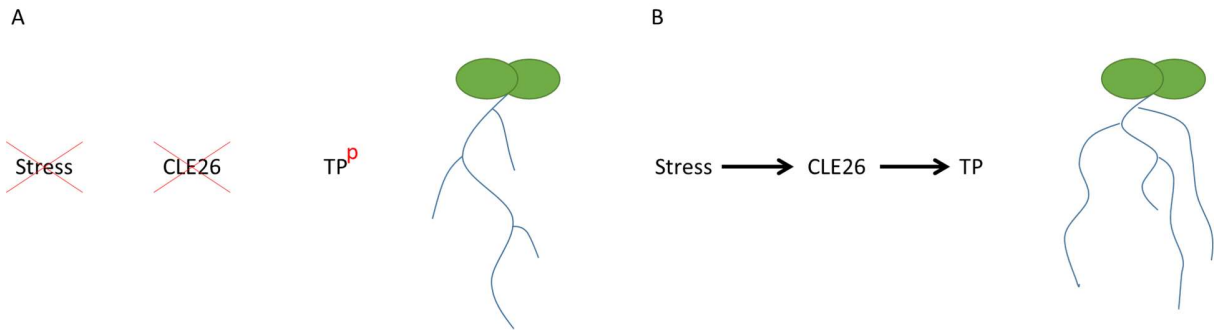


Figure 7: CLE26 expression may act as a molecular "switch" allowing adaptation to stress and non-stress conditions. TP = thiol peptidase, ^{P} = phosphorylation.

6.3 Conclusions

Proteomics screening revealed a number of potentially interesting targets that may be involved in the transduction of the CLE26 signal. Of particular interest, given the CLE26 application and *cle26* phenotypes, is DWF1, which is involved in governing root architectural traits upon which CLE26 treatment appears to have an effect. Given the similarities in localisation for both CLE26 and BRL3, and the CLE26-mediated upregulation of DWF1 it is likely that CLE26 is involved in localised regulation of brassinolide synthesis responsible for regulating protophloem differentiation (Czyzewicz, et al., 2015). Further analysis of CLE26 activity using BR reporters may provide more insight into the intricacies of this mechanism.

An interesting question, is how relevant the protein abundance data is, given that the treatment period with CLE26 or mock was restricted to 10 minutes. From this perspective, there are three distinct points at which the abundance of proteins can be moderated; expression, translation, and degradation.

On average, proteins have a half-life of 3.1-3.5 days (Ishihara, et al., 2015). However, this half-life varies greatly, especially for signalling elements, which are often subject to rapid turnover following induction, as continuous signalling would likely induce stress in the affected tissues. An example of rapid turnover is 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE, which has a half-life of 58 minutes following induction (Kim & Yang, 1992). Half-life may further be affected by the original abundance of the protein, a more highly expressed protein would likely have a greater half-life than that of one less highly expressed, as a greater number of molecules would require degradation to remove half from the system under analysis. From this

perspective, it is possible that the 10 minute treatment with CLE26p may result in the observed decrease to abundance of P4H6 from degradation events.

Furthermore, it is important to address the rate of transcription and translation. A previous analysis (Haruta, et al., 2014) identified significant increased phosphorylation events and differential regulation of proteins after 5 minutes treatment with peptide, suggesting that phosphorylation and downstream regulation events are very rapid. Considering that speed of transcription and translation in *E. coli* were approximated to 40-80 bp/sec and 10-20 AA/sec respectively at 37^{o}C (Dennis & Young, 1974; Young & Bremer, 1976), equating to approximately 2400-4800 bp/min and 600-1200 AA/min it is possible to approximately calculate time required for transcription and translation. Using the receptor kinase AT5G49760 as an example of a protein differentially regulated in response to CLE26, it is possible to approximate the time frame over which the protein will be expressed (Table 1).

Table 1: Determination of time frame for transcription and translation of AT5G49760 accounting for kinetics caused by difference in growth temperature between *E. coli* and *A. thaliana*. A) Time for transcription of AT5G49760. B) Time for translation of AT5G49760. * denotes hypothetical min/max transcription/translation rate based on reaction kinetics.

A

Temperature (°C)	Min/Max Rate	Rate of Transcription (b/min)	Length of Genomic Sequence (bp)	Time for Transcription (min)
21	Min*	900*	4901	5.4
21	Max*	1800*	4901	2.7
37	Min	2400	4901	2.0
37	Max	4800	4901	1.0

B

Temperature (°C)	Min/Max Rate	Rate of Translation (AA/min)	Length of Protein Sequence (AA)	Time for Translation (min)
21	Min*	225*	953	4.2
21	Max*	450*	953	2.1
37	Min	600	953	1.6
37	Max	1200	953	0.8

Given that E. coli is grown at 37°C, and Arabidopsis is grown at 21°C, a difference of 16°C, and chemical kinetics dictates a doubling of reaction rate with an increase of 10°C, it is likely that the rate of synthesis in *Arabidopsis* is approximately 0.375 x that in *E. coli* due to differences in temperature. Therefore, it would take between 2.7 and 5.4 minutes to transcribe AT5G49760, and an additional 2.1-4.2 minutes to translate the mRNA sequence into a protein, giving a total time of 4.8-9.6 minutes for both processes, which is within the 10-minute window between treatment and harvesting. This model does not account for speed of signalling or rate of transport of mRNA from nucleus to endoplasmic reticulum, however, since evolution commonly selects for the most efficient proteins for a given environmental niche (Packer & Liu, 2015), it is likely that the hypothetical maximum rate of transcription for *Arabidopsis* is more accurate than the minimum value, which would allow time for signal transduction and mRNA transport.

Additionally, given that CLE26 signalling is indicated by this phosphoproteomics screen to dephosphorylate CYP63, it is possible that alterations to protein abundance are a result of CLE26-mediated regulation of RNAi. From this perspective, it is certainly possible that the changes in protein concentration observed are a result of differential regulation of expression. Western analysis can additionally be used to determine quantity and phosphorylation status of PECs, and use of proteasome inhibitors and *argonaute7* may help to decipher if downregulation is due to protein degradation or RNAi, respectively in CLE26p treated roots.

Continued characterisation of PECS may reveal novel regulators of root architecture, and provide further insight into the regulation of expression and activity for those previously known to affect root growth. This may eventually lead to identification of suitable protein motifs for targeted crop adaptation, further facilitating their use in improving yield and adaptation to stress conditions, thus contributing to the continued effort to alleviate world hunger.

6.4 Future Work

While differential proteomics gives a good indication of PECS, the phosphorylation score for the PECS identified in the phosphoproteomics screen was very low. To increase confidence in the differential phosphorylation data, the screen must be repeated with a larger number of samples, and a more stringent threshold for phosphorylation events.

Furthermore, the differentially regulated PECS identified by this screen must be characterized in order to confirm the effect of CLE26 signalling observed in the above screen. It is most important to establish the expression pattern of PECS using a GFP reporter construct and determine if there is any overlap with the CLE26 expression domain. Furthermore, it will be necessary to conduct mutant and overexpression analyses for each individual PECS, and identify if there is a corresponding root architectural trait with that of the CLE26 treatment or *cle26-1* mutant. Should any of these PECS result in a CLE26-related root morphology, it may be indicative that the PECS is involved in mediating the CLE26 signal. In addition, once characterised, these mutants may be grown on CLE26p containing medium to determine sensitivity to CLE26 signalling. Additionally, comparing root architectural traits between *pecs* and *cle26* in a broad spectrum abiotic stress screen may also aid in characterisation of CLE26 and PECS function.

Since several PECS are involved in hormone signalling, it may be of interest to determine whether CLE26 treatment or PECS mutation/overexpression results in modulation of other hormones than auxin. To accomplish this, response factors for other hormones can be analysed by qPCR to determine up- or downregulation in response to CLE26 application as well as in the *cle26* mutant

line. Similarly, analysis of available reporter constructs may indicate any perturbed hormonal fluxes present in *cle26* and *pecs* mutants as well as overexpression lines.

Furthermore, there remain several questions pertaining to CLE26 characterisation. it would be interesting to apply CLE26p to brassinolide insensitive mutants and *dwf1* and determine if these mutants are also insensitive to CLE26 signalling. It may similarly be informative to apply BR to the pAT2G18380::GFP marker used previously (Czyzewicz, et al., 2015) and compare to CLE26p treatment to investigate whether BR shows similar changes in protophloem differentiation to CLE26-treated plants.

Additionally, it would be useful to definitively indicate whether the "lateral" roots observed in CLE26-treated plants are true laterals, or stress-induced adventitious roots. To this end, it would be informative to observe the effect of CLE26 treatment on *root initiation defective1,* which lacks the ability to form adventitious roots (Verstraeten, et al., 2014).

It would also be interesting to determine regulatory events leading to *CLE26* expression via a qPCR or reporter line based approach, to determine hormonal and/or environmental conditions that cause differential regulation of *CLE26*. Alternatively, a yeast 1-hybrid approach may be employed to determine transcription factors capable of upregulating *CLE26*.

Finally, given the potential that CLE26 signalling may form a master signal for regulating vascular growth, it may be informative to investigate the effect of CLE26 treatment on xylem development. This could be accomplished using protoxylem specific reporter lines, such as *pIRX3::IRX3:YFP,* (Kubo, et al., 2005), or using an RNAseq approach to determine if any effectors of xylem development are differentially regulated in response to CLE26 treatment. Additionally,

it may be possible to visualise differences to xylem development in *cle26* or CLE26p-treated lines using propidium iodide staining.

References

Aloni, R., Aloni, E., Langhans, M. & Ullrich, C., 2006. Role of Cytokinin and Auxin in Shaping Root Architecture: Regulating Vascular Differentiation, Lateral Root Initiation, Root Apical Dominance and Root Gravitropism. *Annals of Botany,* 97(5), pp. 883-893.

Bao, Y. et al., 2014. The tumor necrosis factor receptor-associated factor (TRAF)-like family protein SEVEN IN ABSENTIA 2 (SINA2) promotes drought tolerance in an ABA-dependent manner in Arabidopsis. *New Phytologist,* 202(1), pp. 174-187.

Beaudoin, F. et al., 2009. Functional characterization of the Arabidopsis beta-ketoacyl-coenzyme A reductase candidates of the fatty acid elongase. *Plant Physiology,* 150(3), pp. 1174-1191.

Beers, E., Jones, A. & Dickerman, A., 2004. The S8 serine, C1A cysteine and A1 aspartic protease families in Arabidopsis. *Phytochemistry,* 65(1), pp. 43-58.

Caño-Delgado, A. et al., 2004. BRL1 and BRL3 are novel brassinosteroid receptors that function in vascular differentiation in Arabidopsis. *Development,* 131(21), pp. 5341-5351.

Clouse, S., 2011. Brassinosteroid Signal Transduction: From Receptor Kinase Activation to Transcriptional Networks Regulating Plant Development. *Plant Cell,* 23(4), pp. 1219-1230.

Czyzewicz, N. et al., 2015. Modulation of Arabidopsis and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide. *Journal of Experimental Botany,* 66(17), pp. 5229-5243.

De Smet, I., Voß, U., Jürgens, G. & Beeckman, T., 2009. Receptor-like kinases shape the plant. *Nature Cell Biology,* Volume 11, pp. 1166-1173.

Dennis, P. & Young, R., 1974. Differential rate of ribosomal protein synthesis in Escherichia coli. *Journal of Molecular Biology,* Volume 84, pp. 407-422.

Fruman, D., Burakoff, S. & Bierer, B., 1994. Immunophilins in protein folding and immunosuppression. *Federation of the American Societies for Experimental Biology Journal,* 8(6), pp. 391-400.

Grudkowska, M. & Zagdanska, B., 2004. Multifunctional Role of Plant Cysteine Proteinases. *Acta Biochimica Polonica,* 51(3), pp. 609-624.

Haruta, M. et al., 2014. A peptide hormone and its receptor protein kinase regulate plant cell expansion. *Science,* 343(6169), pp. 408-411.

He, Z., Li, L. & Luan, S., 2004. Immunophilins and Parvulins. Superfamily of Peptidyl Prolyl Isomerases in Arabidopsis. *Plant Physiology,* 134(4), pp. 1248-1267.

Hirakawa, Y. et al., 2008. Non-cell-autonomous control of vascular stem cell fate by a CLE peptide/receptor system. *Proceedings of the National Academy of Sciences of the United States of America,* 105(39), pp. 15208-15213.

Ho, S., Tong, W. & Yu, S., 2000. Multiple Mode Regulation of a Cysteine Proteinase Gene Expression in Rice. *Plant Physiology,* Volume 122, pp. 57-66.

Ishihara, H. et al., 2015. Quantifying Protein Synthesis and Degradation in Arabidopsis by Dynamic 13CO2 Labeling and Analysis of Enrichment in Individual Amino Acids in Their Free Pools and in Protein. *Plant Physiology,* 168(1), pp. 74-93.

Kang, Y., Breda, A. & Hardtke, C., 2017. Brassinosteroid signaling directs formative cell divisions and protophloem differentiation in Arabidopsis root meristems. *Development,* Volume 144, pp. 272-280.

Karlova, R. et al., 2006. The Arabidopsis SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE1 Protein Complex Includes BRASSINOSTEROID-INSENSITIVE1. *Plant Cell,* 18(3), pp. 626-638.

Kim, W. & Yang, S., 1992. Turnover of 1-Aminocyclopropane-1-Carboxylic Acid Synthase Protein in Wounded Tomato Fruit Tissue. *Plant Physiology,* 100(3), pp. 1126-1131.

Kondo, T. et al., 2006. A Plant Peptide Encoded by CLV3 Identified by in Situ MALDI-TOF MS Analysis. *Science,* 313(5788), pp. 845-848.

Kubo, M. et al., 2005. Transcription switches for protoxylem and metaxylem vessel formation. *Genes & Development,* 19(16), pp. 1855-1860.

Kuroha, T., Ueguchi, C., Sakakibara, H. & Satoh, S., 2006. Cytokinin receptors are required for normal development of auxin-transporting vascular tissues in the hypocotyl but not in adventitious roots. *Plant Cell Physiology,* 47(2), pp. 234-243.

Kwak, S. & Schiefelbein, J., 2008. A Feedback Mechanism Controlling SCRAMBLED Receptor Accumulation and Cell-Type Pattern in Arabidopsis. *Current Biology,* 18(24), pp. 1949-1954.

Landrieu, I. et al., 2000. The Arabidopsis thaliana PIN1At gene encodes a single-domain phosphorylation-dependent peptidyl prolyl cis/trans isomerase. *Journal of Biological Chemistry,* 275(14), pp. 10577-10581.

Laplaze, L. et al., 2007. Cytokinins Act Directly on Lateral Root Founder Cells to Inhibit Root Initiation. *Plant Cell,* 19(12), pp. 3889-3900.

Lee, H. et al., 2013. LBD18 acts as a transcriptional activator that directly binds to the EXPANSIN14 promoter in promoting lateral root emergence of Arabidopsis. *Plant Journal,* 73(2), pp. 232-224.

Li, S., Lei, L. & Gu, Y., 2013. Functional analysis of complexes with mixed primary and secondary cellulose synthases. *Plant Signaling and Behavior,* 8(3), p. doi: 10.4161/psb.23179.

Lorković, Z., Lehner, R., Forstner, C. & Barta, A., 2005. Evolutionary conservation of minor U12-type spliceosome between plants and humans. *RNA,* 11(7), pp. 1095-1107.

Lorković, Z. et al., 2004. Interactions of Arabidopsis RS Domain Containing Cyclophilins with SR Proteins and U1 and U11 Small Nuclear Ribonucleoprotein-specific Proteins Suggest Their Involvement in Pre-mRNA Splicing. *Journal of Biological Chemmistry,* Volume 279, pp. 33890-33898.

Muslin, A. & Xing, H., 2000. 14-3-3 proteins: regulation of subcellular localization by molecular interference. *Cellular Signalling,* 12(11-12), pp. 703-709.

Müssig, C., Shin, G. & Altman, T., 2003. Brassinosteroids Promote Root Growth in Arabidopsis. *Plant Physiology,* 133(3), pp. 1261-1271.

Nobusawa, T. et al., 2013. Restriction of cell proliferation in internal tissues via the synthesis of very-long-chain fatty acids in the epidermis. *Plant Signaling and Behavior,* 8(8), p. DOI:10.4161/psb.25232.

Okamoto, T. et al., 2003. C-Terminal KDEL Sequence of A KDEL-Tailed Cysteine Proteinase (Sulfhydryl-Endopeptidase) Is Involved in Formation of KDEL Vesicle and in Efficient Vacuolar Transport of Sulfhydryl-Endopeptidase. *Plant Physiology,* 132(4), pp. 1892-1900.

Packer, M. & Liu, D., 2015. Methods for the directed evolution of proteins. *Nature Reviews Genetics,* Volume 16, p. 379–394.

Patterson, C., Schaub, T., Coleman, E. & Davis, E., 2000. Developmental Regulation of FKBP65 An ER-localized Extracellular Matrix Binding-Protein. *Molecular Biology of the Cell,* 11(11), pp. 3925-3935.

Péret, B., Larrieu, A. & Bennett, M., 2009. Lateral root emergence: a difficult birth. *Journal of Experimental Botany,* 60(13), pp. 3637-3643.

Robatzek, S., Chinchilla, D. & Boller, T., 2006. Ligand-induced endocytosis of the pattern recognition receptor FLS2 in Arabidopsis. *Genes and Development,* 20(5), pp. 537-542.

Rodriguez-Villalon, A. et al., 2015. Primary root protophloem differentiation requires balanced phosphatidylinositol-4,5-biphosphate levels and systemically affects root branching. *Development,* Volume 142, pp. 1437-1446.

Roudier, F. et al., 2010. Very-Long-Chain Fatty Acids Are Involved in Polar Auxin Transport and Developmental Patterning in Arabidopsis. *Plant Cell,* 22(2), pp. 364-375.

Roycewicz, P. & Malamy, J., 2014. Cell wall properties play an important role in the emergence of lateral root primordia from the parent root. *Journal of Experimental Botany,* 65(8), pp. 2057-2069.

Schlesinger, J., 2002. Ligand-Induced, Receptor-Mediated Dimerization and Activation of EGF Receptor. *Cell,* 110(6), pp. 669-672.

Shindo, T. et al., 2012. A Role in Immunity for Arabidopsis Cysteine Protease RD21, the Ortholog of the Tomato Immune Protease C14. *Public Library of Science One,* 7(1), p. e29317.

Shinohara, H. & Matsubayashi, Y., 2013. Chemical synthesis of Arabidopsis CLV3 glycopeptide reveals the impact of hydroxyproline arabinosylation on peptide conformation and activity. *Plant Cell Physiology,* 54(3), pp. 369-374.

Symons, G. & Reid, J., 2004. Brassinosteroids Do Not Undergo Long-Distance Transport in Pea. Implications for the Regulation of Endogenous Brassinosteroid Levels. *Plant Physiology,* 135(4), pp. 2196-2206.

Taylor, N. et al., 2003. Interactions among three distinct CesA proteins essential for cellulose synthesis. *Proceedings of the National Academy of Sciences of the United States of America,* 100(3), pp. 1450-1455.

Taylor, N., Laurie, S. & Turner, S., 2000. Multiple Cellulose Synthase Catalytic Subunits Are Required for Cellulose Synthesis in Arabidopsis. *Plant Cell,* 12(12), pp. 2529-2539.

Turner, S. & Somerville, C., 1997. Collapsed Xylem Phenotype of Arabidopsis Identifies Mutants Deficient in Cellulose Deposition in the Secondary Cell Wall. *Plant Cell,* 9(5), pp. 689-701.

Van Sandt, V., Suslov, D., Verbelen, J. & Vissenberg, K., 2007. Xyloglucan Endotransglucosylase Activity Loosens a Plant Cell Wall. *Annals of Botany,* 100(7), pp. 1467-1473.

Velasquez, S. et al., 2015. Complex Regulation of Prolyl-4-Hydroxylases Impacts Root Hair Expansion. *Molecular Plant,* 8(5), pp. 734-746.

Verstraeten, I., Schotte, S. & Geelen, D., 2014. Hypocotyl adventitious root organogenesis differs from lateral root development. *Frontiers in Plant Science,* 5(495), p. doi: 10.3389/fpls.2014.00495.

Vigani, G., Morandini, P. & Murgia, I., 2013. Searching iron sensors in plants by exploring the link among 2'-OG-dependent dioxygenases, the iron deficiency response and metabolic adjustments occurring under iron deficiency. *Frontiers in Plant Science,* 4(169), p. doi: 10.3389/fpls.2013.00169.

Vlad, F. et al., 2007. Arabidopsis prolyl 4-hydroxylases are differentially expressed in response to hypoxia, anoxia and mechanical wounding. *Physiologia Plantarum,* 130(4), pp. 471-483.

Wang, X. et al., 2005. Identification and Functional Analysis of in Vivo Phosphorylation Sites of the Arabidopsis BRASSINOSTEROID-INSENSITIVE1 Receptor Kinase. *Plant Cell,* 17(6), pp. 1685-1703.

Xi, W. et al., 2016. Pin1At regulates PIN1 polar localization and root gravotropism. *Nature Communications,* Volume 7, p. doi:10.1038/ncomms10430.

Young, R. & Bremer, H., 1976. Polypeptide-chain-elongation rate in Escherichia coli B/r as a function of growth rate. *Biochemical Journal,* 160(2), pp. 185-194.

Chapter 7: The Growing Story of (ARABIDOPSIS)CRINKLY4

Published as Czyzewicz N, Nikonorova N, Meyer MR, Sandal P, Shah S, Vu LD, Gevaert K, Rao AG, and De Smet I (2016) *Journal of Experimental Botany* 67(16):4835-4847

Author Contribution: I wrote a section on the roles of ACR4 in plant growth and development, and I contributed to, and was involved in editing, sections on protein activity and stability, protein-protein interactions and targets, (auto)phosphorylation and outstanding questions sections. I also contributed to the construction of figures 3, 4 and 5, and was involved in development of the manuscript.

Journal of Experimental Botany Advance Access published May 21, 2016

Journal of Experimental Botany
doi:10.1093/jxb/erw192

REVIEW PAPER

The growing story of (ARABIDOPSIS) CRINKLY 4

Nathan Czyzewicz[1], Natalia Nikonorova[2,3], Matthew R. Meyer[4,#], Priyanka Sandal[4], Shweta Shah[4], Lam Dai Vu[2,3,5,6], Kris Gevaert[5,6], A. Gururaj Rao[4,$] and Ive De Smet[1,2,3,7,$,*]

[1] Division of Plant and Crop Sciences, School of Biosciences, University of Nottingham, Loughborough, LE12 5RD, UK
[2] Department of Plant Systems Biology, VIB, B–9052 Ghent University, Belgium
[3] Department of Plant Biotechnology and Bioinformatics, Ghent University, B–9052 Ghent, Belgium
[4] Roy J. Carver Department of Biochemistry Biophysics and Molecular Biology, Iowa State University, Ames, IA, 50011, USA
[5] Medical Biotechnology Center, VIB, 9000 Ghent, Belgium
[6] Department of Biochemistry, Ghent University, 9000 Ghent, Belgium
[7] Centre for Plant Integrative Biology, University of Nottingham, Loughborough, LE12 5RD, UK
[#] Current address: Donald Danforth Plant Science Center, St. Louis, MO 63132, USA
[$] These authors contributed equally to this manuscript

*Correspondence: ive.desmet@psb.vib-ugent.be

Received 16 February 2016; Accepted 21 April 2016

Editor: Christine Raines, University of Essex

Abstract

Receptor kinases play important roles in plant growth and development, but only few of them have been functionally characterized in depth. Over the past decade CRINKLY 4 (CR4)-related research has peaked as a result of a newly discovered role of ARABIDOPSIS CR4 (ACR4) in the root. Here, we comprehensively review the available (A)CR4 literature and describe its role in embryo, seed, shoot, and root development, but we also flag an unexpected role in plant defence. In addition, we discuss ACR4 domains and protein structure, describe known ACR4-interacting proteins and substrates, and elaborate on the transcriptional regulation of *ACR4*. Finally, we address the missing knowledge in our understanding of ACR4 signalling.

Key words: ACR4, Arabidopsis, embryo, epidermis, flower, maize, receptor kinase, root, rice, seed.

Introduction

Cell-to-cell communication plays a crucial role in plant growth and development and relies to a large extent on peptide ligand−receptor kinase signalling mechanisms (De Smet, *et al.*, 2009; Murphy, *et al.*, 2012; Czyzewicz, *et al.*, 2013; Murphy and De Smet, 2014; Tavormina, *et al.*, 2015). Over 600 receptor-like kinase genes have been identified in *Arabidopsis thaliana* and similar or even higher numbers have been found in other plant species (Shiu and Bleecker, 2001, 2003; Liu, *et al.*, 2002; Shiu, *et al.*, 2004; Lehti-Shiu, *et al.*, 2009). Mutations in receptor kinases often lead to obvious and crucial defects as they are involved in various developmental and environmental responses, such as maintenance of root and shoot apical meristems (De Smet, *et al.*, 2009; Stahl and Simon, 2012; Wierzba and Tax, 2013; Soyars, *et al.*, 2016).

One such receptor kinase is ARABIDOPSIS CRINKLY4 (ACR4, AT3G59420), which belongs to the CRINKLY4 (CR4) family of receptor-like kinases. CR4 was first identified in maize (*Zea mays*), where the *cr4* mutation affects leaf epidermis differentiation (Becraft, *et al.*, 1996). So far, CR4 family members have been identified and characterized in several vascular plants, supporting the importance of this

© The Author 2016. Published by Oxford University Press on behalf of the Society for Experimental Biology. All rights reserved.
For permissions, please email: journals.permissions@oup.com

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

family of receptor kinases (Jin, *et al.*, 2000; Pu, *et al.*, 2012; Nikonorova, *et al.*, 2015). While it seems that this family, with all its domains (see section below), only emerged in land plants (Fig. 1), it cannot – at the moment – be ruled out that multicellular algae also contain CR4 family members, due to a lack of full genome information.

Since its initial description two decades ago, ACR4 has been shown to be involved in a wide range of biological processes. Here, we comprehensively review the CR4 family-related literature and summarize insights on the genetic, biochemical, and signalling level. For this, we mainly focus on (A)CR4, the founding member of this receptor kinase family, but we also flag up a few observations relating to other CR4 family members.

Key protein domains

The 895-amino-acid Arabidopsis ACR4 protein has a signal peptide, an extracellular domain, a single transmembrane helix, and an intracellular kinase domain; and it is similar in all architectural features to mammalian receptor tyrosine (Tyr) kinases (RTKs) and plant receptor-like kinases (RLKs) that are predominantly serine (Ser)/threonine (Thr) kinases (Becraft, *et al.*, 1996; Shiu and Bleecker, 2001) (Fig. 2A, B). Orthologs in rice (OsCR4), maize (ZmCR4), and several other plant species share the same features (Tanaka, *et al.*, 2002; Cao, *et al.*, 2005; Nikonorova, *et al.*, 2015).

The extracellular domain of ACR4, a putative ligand binding domain, contains seven repeat regions approximately 39 amino acids in length, followed by three cysteine (Cys)-rich regions similar to the TUMOR NECROSIS FACTOR RECEPTOR (TNFR) ligand binding domain, and is distantly related to REGULATOR OF CHROMATIN CONDENSATION 1 (RCC1) (McCarty and Chory, 2000; Gifford, *et al.*, 2005). Three-dimensional modelling of the ACR4 extracellular domain based on the high-resolved crystal structure of the Arabidopsis photoreceptor UVB-RESISTANCE 8 (UVR8), but also on structural homologues in other species, indicates a distinctive seven-bladed β-propeller, similar to structure models of CR4 family members in other green plants (McCarty and Chory, 2000; Gifford, *et al.*, 2005; Nikonorova, *et al.*, 2015) (Fig. 3A). The model shows conserved, regularly spaced Cys residues in the repeats that probably contribute to structural stability in the oxidizing environment of the extracellular space by formation of disulphide bonds (Fig. 3A). Proteins in the β-propeller domain family display huge functional diversity and play particularly important roles in protein–protein and protein–ligand interactions (Chen, *et al.*, 2011).

A single alpha helix spanning the membrane connects the ACR4 extracellular domain to the intracellular, active serine/threonine kinase domain (Fig. 3B). The kinase catalytic domain comprises approximately 250–300 amino acids and, based on numerous structural and biochemical studies, can be separated into 11 distinct subdomains that house roughly 10 highly conserved residues and/or motifs that contribute to the activity and stability of the molecule (Hanks and Hunter, 1995) (Fig. 3C). The kinase domain folds into a highly conserved structure with an N-terminal lobe that is comprised predominantly of β-sheets and a C-terminal lobe that is mostly α-helical (Fig. 3B). The tertiary structure produced at the interface of the N- and C-terminal domains creates a pocket that serves as the active site of the enzyme. Conserved features include the glycine (Gly)-rich motif (P-loop) between β-strands 1 and 2 of the N-lobe (subdomain I), which function to help bind and stabilize the α and β phosphates of the bound ATP molecule (Fig. 3C). The essential lysine (Lys) residue at position 540 in β-strand 3 of the ACR4 N-lobe (subdomain II) also helps to stabilize these α and β phosphates and forms a salt bridge with the invariant glutamic acid (Glu) residue in helix-C (subdomain III) (Fig. 3B, C). Not surprisingly, in general a mutation of this invariant Lys residue in subdomain II abolishes kinase activity (Hanks and Hunter, 1995). Interestingly, however, a mutation of the analogous site in the kinase domain of CR4 in rice does not appear to entirely abolish kinase activity (Pu, *et al.*, 2012). The C-lobe of the kinases harbours a conserved HRD motif, termed the catalytic loop (subdomain VI B), in which the aspartic acid serves as the catalytic base during the phosphotransfer reaction and chelates

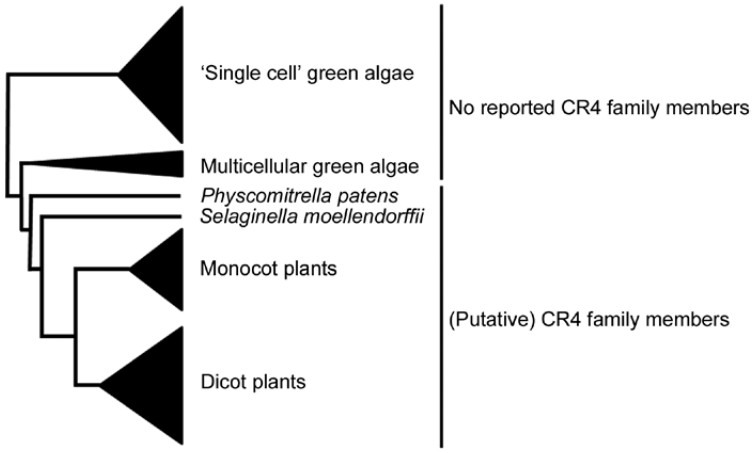


Fig. 1. Schematic phylogenetic tree to indicate absence or presence of CR4 family members in indicated clades. Collapsed tree based on detailed results in Nikonorova *et al.* (2015).

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

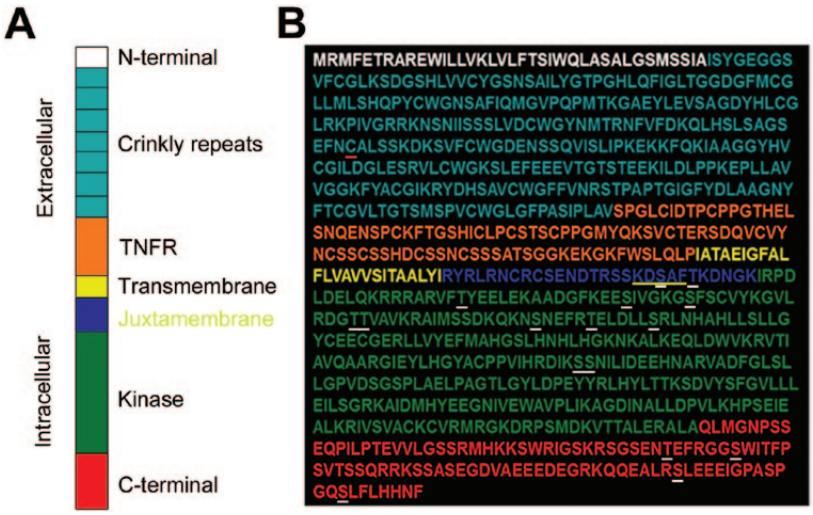


Fig. 2. Details of the ACR4 protein. (A) Schematic of the subdomains of the ACR4 protein. In the extracellular region: the 'Crinkly' repeats (light blue) and the TUMOR NECROSIS FACTOR RECEPTOR (TNFR)-like domain (orange); in the intracellular region: the juxtamembrane domain (purple), the kinase domain (green), and the C-terminal domain (red). A transmembrane helix (yellow) connects the extracellular and intracellular portions of the protein. (B) The 895-amino acid sequence of ACR4. The sequence is color-coded as in (A). The signal sequence for membrane targeting is highlighted (white). The CRINKLY domain cysteine (Cys) residue (at position 180) critical for ACR4 function is underscored in red. Key residues that can be phosphorylated *in vitro* are underscored in white. The KDSAF motif is underscored in yellow.

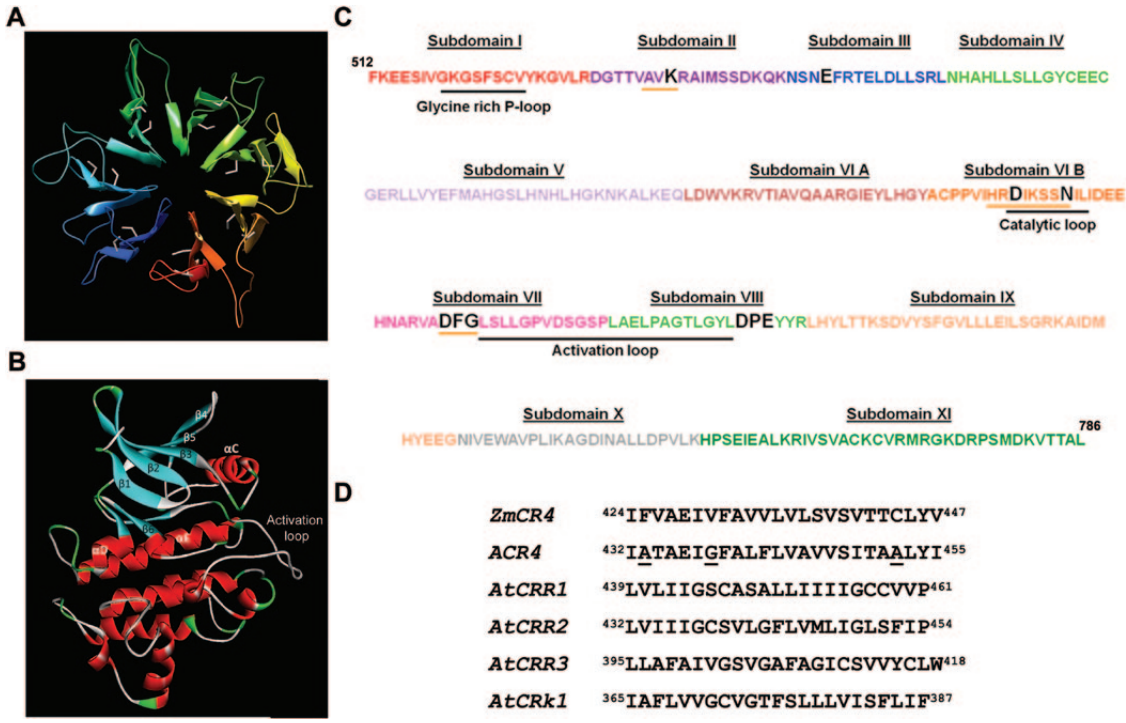


Fig. 3. (A) 3-D-structure model of ACR4, based on the 1.7 Å crystal structure of the Arabidopsis UVR8 photoreceptor (PDB: 4D9S). Visualization was performed using Chimera 1.10.2 (Pettersen, *et al.*, 2004). Conserved cysteine (Cys) residues are indicated as grey sticks. (B) General structure of a kinase domain. The model for the ACR4 kinase domain (residues 512–786 of the RLK sequence) was built by homology modelling using Discovery Studio (Biovia, San Diego, USA) and visualized on the same platform, as described in Meyer *et al.* (2013). The kinase domain forms a bilobal structure with an N-lobe (blue) and a C-lobe (red). The N-lobe is primarily comprised of β-sheets, whereas the C-lobe is predominantly α-helical. Secondary structures surrounding the active site are labeled. (C) The subdomain architecture of the ACR4 kinase domain. The 11 subdomains of the ACR4 kinase domain are indicated in varying colors. Residues essential to catalytic activity are highlighted (black, bold). Regions involved in kinase activation and catalysis are underlined in black. Underlined regions in orange indicate Arabidopsis AXK, HRDIKSSN and DFG conserved motifs important to kinase activity, as determined by Pu and Sun (2012). (D) Transmembrane (TM) domains of maize CR4 (ZmCR4), Arabidopsis CR4 (ACR4) and Arabidopsis homologs (CRR). Residues in ACR4 that impact the stability are underlined.

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

a Mg^{2+} ion that bridges the α and γ phosphates (Fig. 3C). In general, loss of this amino acid results in complete inactivity of the kinase. The activation loop of the CR4 kinases is slightly downstream of the catalytic loop and located between two conserved DFG and DPE motifs (APE in most kinases) (subdomains VII to VIII) that serve as hinge points for activation loop movement (Fig. 3B, C). The aspartic acid (Asp) in the DFG motif functions to chelate a Mg^{2+} ion that stabilizes the β and γ phosphates of ATP. The APE motif serves a structural role in stabilizing the C-lobe (Zheng, *et al.*, 1993; Hanks and Hunter, 1995; Nolen, *et al.*, 2004). These conserved features work to co-ordinate the efficient transfer of phosphate from ATP to the appropriate target.

Transmembrane (TM) domains in membrane-bound proteins are typically ~20–30 residues in length and consist predominantly of hydrophobic residues that adopt an α-helical conformation. They span the lipid bilayer and demarcate the extracellular and cytoplasmic domains of the membrane-anchored protein. Whereas much is known about the biochemical and structural properties of the extracellular and cytoplasmic domains of several receptors, the exact mechanism of signal transduction from the outside to the inside is not fully understood. Clearly, interactions within the membrane milieu are a particularly important aspect of the overall mechanism. In RTKs, evidence indicates that TM domains function in a dynamic fashion and have the intrinsic capacity to drive receptor dimerization (Tanner and Kyte, 1999; You, *et al.*, 2005). Interestingly, naturally occurring mutations have been identified in the TM regions of at least two RTKs that lead to constitutive activation in the absence of a ligand (Gadella and Jovin, 1995; Mischel, *et al.*, 2002). In the rat growth factor receptor Neu, a valine (Val) to Glu mutation leads to an active dimer that is stabilized by hydrogen-bonds, which renders the more stable mutant protein oncogenic (Sternberg and Gullick, 1989). The TM domain in the CR4 family comprises ~24 amino acids (Fig. 3D). While TM domains of ACR4 and CR4 share ~50% identity there is little sequence similarity in this region with the other CR4-RELATED (CRR) proteins. The propensity of the TM helices of the CR4, ACR4, and ACR4 homologs (AtCRRs) to dimerize has been studied by a modified TOXCAT assay (Russ and Engelman, 1999). The TOXCAT assay is an elegant method that facilitates an *in vivo* analysis of the strength of the interaction between TM domains. In brief, a chimeric protein consisting of the TM domain of interest fused to a dimerization-dependent protein (transcription factor ToxR) and a monomeric protein (maltose-binding protein, MBP) is expressed in the inner membrane of *E. coli* cells. Any interaction between the α-helices of the TM domain induces the dimerization of the ToxR protein, which then activates the reporter gene, chloramphenicol acetyltransferase (CAT). A quantitative assessment of CAT activity in an *in vitro* assay is then correlated to the strength of the TM dimer, i.e. the greater the activity, the higher the propensity for TM dimerization. The TM domains of the receptors vary in their ability to homodimerize, with Arabidopsis CRR1 possessing the highest propensity to dimerize and the ACR4 TM showing the lowest potential (Stokes and Rao, 2008). Further mutagenesis studies have also demonstrated the important role of specific amino acids within the TM helix of CR4 and ACR4 that profoundly affect dimer formation (Stokes and Rao, 2010) (Fig. 3D).

In RTKs, flanking regions of the molecule, such as the juxtamembrane (JM) and carboxy-terminal domains, can regulate kinase activity (He, *et al.*, 1996; Wybenga-Groot, *et al.*, 2001; Hubbard, 2004; Thiel and Carpenter, 2007; Sengupta, *et al.*, 2009; Endres, *et al.*, 2013). *In vivo*, the kinase domain is anchored to the phospholipid bilayer and structure–function studies with RTKs such as EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR) suggest that intramolecular interactions with the membrane bilayer can influence the allosteric regulation of kinase activity by the juxtamembrane domain (Jura, *et al.*, 2009; Sengupta, *et al.*, 2009). Importantly, the intrinsic dimerization capacity of the TM domain in ACR4, and its dynamic role in receptor dimerization, adds a layer of complexity that is not considered in structure–function studies of recombinant kinase domains. This is exemplified by observations that the TM domain of ACR4 is important for heteromerization with CLV1 (Stahl, *et al.*, 2013).

Protein activity and stability

ACR4 has been shown to undergo rapid turnover and internalization via a BFA-sensitive pathway (Gifford, *et al.*, 2005). Furthermore, ACR4 appears to respond similarly to CLAVATA/EMBRYO-SURROUNDING REGION 40 (CLE40) signalling as CLAVATA1 (CLV1), namely internalization and removal to the lytic vacuole (Stahl, *et al.*, 2013). With respect to its trafficking, it seems that SUPERNUMERARY ALEURONE LAYERS 1 (SAL1) could be involved in the internalization and degradation of CR4, since CR4 is internalized by SAL1-positive endosomes (Shen, *et al.*, 2003; Tian, *et al.*, 2007).

Furthermore, function, stability, and localization of ACR4 *in planta* appear to be mediated by several regions within the protein. Gifford *et al.* (2005) have examined the role of the extracellular domain, the intracellular domain, and their constituent sub-domains by expressing various deletion constructs with C-terminally fused GREEN FLUORESCENT PROTEIN (GFPs) and by complementation assays in *acr4* mutant plants. Remarkably, a truncation construct created by deletion of 4.5 of the seven crinkly repeats was unable to compliment *acr4*, indicating that the extracellular crinkly repeat domain is essential for ACR4 function. Furthermore, the same study identified that the $ACR4^{C180Y}$ mutation at the sole Cys residue in the fourth repeat of the propeller domain (Fig. 2B) similarly caused a loss of function, as the *pACR4::ACR4*^{C180Y}*:GFP* construct was also unable to compliment the *acr4* mutant phenotype. Interestingly, given the importance of the Cys residue in disulfide bridging and protein stability, its mutation did not, however, appear to compromise the stability of the $ACR4^{C180Y}$:GFP protein, which expressed and localized to the plasma membrane in the root epidermal cells and other tissues. Similarly, deletion of the

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

TNFR sub-domain abolished function even though the protein localized to the same membrane as the wild-type protein. Analogous deletion experiments performed within the cytoplasmic domain indicated that removal of the kinase domain and the C-terminal extension resulted in an unstable product with little or no detectable protein. In contrast, constructs containing either the C-terminal deletion or the inactive kinase domain were fully functional in a complementation assay with relatively uncompromised protein expression and localization. The Gifford *et al.* (2005) study points to the critical role of the extracellular (putative ligand-binding) domain in the function of ACR4 while simultaneously suggesting that the kinase domain may be dispensable.

While ACR4 has all the typical domains of a receptor kinase, some data in Arabidopsis suggest that neither the C-terminal domain nor its kinase activity is required for ACR4 signalling (Gifford, *et al.*, 2005). A study by Pu and Sun (2012) identifies three distinct conserved CR4 motifs in rice, maize, and Arabidopsis. The AXK motif is thought to be essential for kinase activity, HRDLKXXN is predicted to contain a catalytic base facilitating transfer of phosphate to target proteins, and the DFG motif is thought to be involved in chelation of positive ions, enabling the correct orientation of the γ-phosphate of ATP for kinase activity (Hanks and Hunter, 1995; Pu and Sun, 2012). Substitutions of $CR4^{D652A}$ in maize and $ACR4^{K540M}$ in Arabidopsis are mutations of the DFG and AXK motifs, respectively, and both mutations abolish kinase activity (Jin, *et al.*, 2000; Gifford, *et al.*, 2003), although the corresponding AXK motif mutation in rice ($OsCR4^{K532E}$) did not affect autophosphorylation to the same extent. However, there are two AXK motifs present in OsCR4 (and in ZmCR4), which probably explains why the $OsCR4^{K532E}$ variant did not completely abolish kinase activity (Pu and Sun, 2012). Interestingly, Jin *et al.* (2000) reported that another maize point mutation (*cr4-651*) immediately N-terminal of the DFG motif results in a similarly strong *cr4* phenotype, indicating that the mutant phenotype may be due to steric hindrance of the DFG motif. However, the role of the kinase domain, vis-à-vis its activity or lack of activity, needs further verification in the context of the observations of Pu and Sun (2012), who showed that in rice CR4 the conserved Lys residue (K532) is not essential for *in vitro* kinase activity, but that the OsCR4 Lys mutant still shows a reduced level of kinase activity. This suggests that the point mutant produced by Gifford *et al.* (2005) may potentially possess residual kinase activity that could exert some influence in their complementation assays, or that in rice alternative CR4 AXK domains may be important to conformation and activity of the kinase (Pu and Sun, 2012). In contrast, it seems that the extracellular domain of ACR4 is necessary for its function (Gifford, *et al.*, 2005).

Protein–protein interactions and targets

There is increasing evidence that the classical paradigm of RTK function involving a single receptor−single ligand interaction may be an over-simplified model and that heteromeric interactions play a significant role in expanding the signalling potential (Saito, *et al.*, 2001; Pfeiffer, *et al.*, 2002; Schulze, *et al.*, 2005; Morgillo, *et al.*, 2006; Wieduwilt and Moasser, 2008). Additionally, atypical RTKs with kinase-inactive domains can signal through heterodimerization with active RTKs (Kroiher, *et al.*, 2001; Wieduwilt and Moasser, 2008; Hynes and MacDonald, 2009). In plants, RLKs such as FLAGELLIN SENSITIVE 2 (FLS2) and BRASSINOSTEROID INSENSITIVE 1 (BRI1) ASSOCIATED RECEPTOR KINASE 1 (BAK1) (Chinchilla, *et al.*, 2007; Kemmerling, *et al.*, 2011), CLAVATA2 (CLV2) (Guo and Clark, 2010), BRASSINOSTEROID INSENSITIVE 1 (BRI1) (Clouse, 2011; Ye, *et al.*, 2011), the SOMATIC EMBRYOGENESIS RECEPTOR KINASE (SERK) family (Albrecht, *et al.*, 2008), and the 5-member ethylene receptor family participate in signal transduction pathways via heteromeric interactions (Gao and Schaller, 2009). In Arabidopsis, the two RLKs CLV1 and ACR4 co-express in the distal root meristem and form a heteromeric complex in the plasma membrane that profoundly impacts on root stemness (Stahl, *et al.*, 2013). ACR4 and CLV1 form homomeric and heteromeric complexes depending on local concentration differences and local environments/subcellular localizations. It seems that CLV1 moderates ACR4-dependent signalling by binding to ACR4. However, another pathway is likely active in the absence of CLV1 (Stahl, *et al.*, 2013).

Genetic and cell biology analyses suggest that the Arabidopsis CR4 family of receptors, including ACR4, CRINKLY 4 RELATED 1 (CCR1 or CRR1, AT3G09780), CCR2 (or CRR2, AT2G39180), CCR3 (or CRR3, AT3G55950), and CCR4/CRINKLY 4-RELATED KINASE 1 (CRK1, AT5G47850), may act in the same genetic pathway through functional redundancy based upon gene duplication and/or through activation of signalling cascades via receptor heterodimerization (Cao, *et al.*, 2005; Gifford, *et al.*, 2005; De Smet, *et al.*, 2008). Further support for potential *in vivo* interactions among members of the ACR4 family comes from *in vitro* studies demonstrating interactions between the intracellular domains of ACR4 and the CRRs using various techniques, which are perhaps mediated through a conserved KDSAF motif among these proteins (Meyer, *et al.*, 2015) (Fig. 2B). It is entirely possible that heteromeric interactions can promote preferred binding of specific ligands to the extracellular domain(s) and initiate a diverse array of signalling pathways with differential outputs. The same study also showed *in vitro* evidence for the interaction of ACR4 kinase with WUSCHEL-RELATED HOMEOBOX 5 (WOX5), a transcription factor implicated in the regulation of ACR4 signalling (Meyer, *et al.*, 2015) (Fig. 4A). Although the physiological relevance of this interaction is yet to be established, such focused *in vitro* studies nevertheless can drive new hypothesis-driven biological investigations.

Recently, the ACR4 interactome pinpointed a number of likely putative interactors (Yue, *et al.*, 2016). A very strong and biologically relevant candidate protein to emerge from this study, particularly in the context of reversible protein phosphorylation – which is a key element in the fidelity of signal transduction processes – is the catalytic subunit of the

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

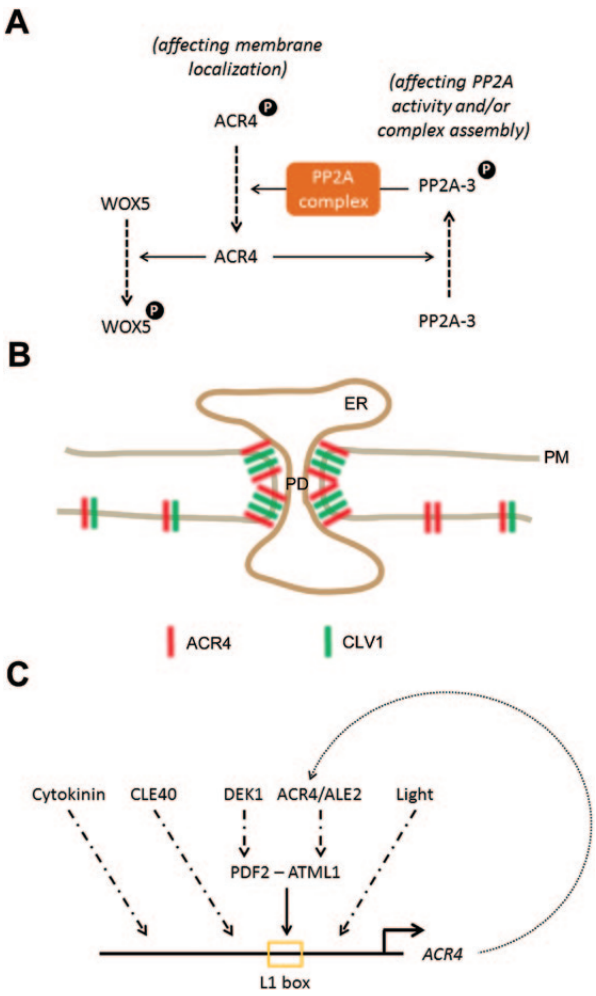


Fig. 4. Aspects of ACR4 regulation and targets. (A) Schematic representation of ACR4 interactions with the PP2A holoenzyme complex and WOX5. ACR4 is able to interact with and phosphorylate WOX5 (*in vitro*) and PP2A-3 (*in vivo/in vitro*), which forms part of the PP2A holoenzyme complex, which in turn dephosphorylates ACR4. These interactions impact on localization and/or activity. (B) Simplified representation of ACR4 and CLV1 interacting (and possibly acting) at plasmodesmata. PM, plasma membrane; ER, endoplasmic reticulum; PD, plasmodesma. (C) Regulation of *ACR4* expression in Arabidopsis and/or maize, and relevant inputs. The dash-dotted arrows indicate that (probably) one or more intermediate steps are required. The dotted arrow indicates the steps from expression to protein. The L1 box is indicated.

PROTEIN PHOSPHATASE 2A family (PP2A-3 and PP2A-4). In a study encompassing cell biology, genetics, and *in vitro* biochemical approaches, compelling evidence is provided for the interaction between ACR4 with the PP2A-3 catalytic subunit (Fig. 4A). *In vitro* assays clearly demonstrate that PP2A-3 is in fact a substrate for ACR4 kinase and is phosphorylated on at least nine sites (as determined by mass spectrometry) of which five are at serine, three are at threonine and one is at tyrosine (Yue, *et al.*, 2016).

(Auto)phosphorylation

Like other RLKs, such as BRI1 (Oh, *et al.*, 2011) and Xa21 (Liu, *et al.*, 2002), the ACR4 kinase domain undergoes autophosphorylation via an intramolecular mechanism with at least 16 phosphorylation sites distributed across the juxtamembrane, kinase, and carboxy-terminal domains (Fig. 2B). Of particular note is the phosphorylation of two serine residues within the activation loop sequence of the kinase domain (Meyer, *et al.*, 2011). It is well known that phosphorylation of residues within the activation segment triggers a regulatory step necessary for kinase activity in many kinases belonging to the Ser/Thr family and the Tyr kinase family (Johnson, *et al.*, 1996; Johnson and Lewis, 2001; Shah, *et al.*, 2001; Wang, *et al.*, 2005; Burza, *et al.*, 2006). This is a characteristic feature of kinases belonging to the RD family [which refers to arginine (Arg, R) and aspartic acid (Asp, D) residues], which contain an Arg residue preceding the invariant catalytic Asp and are critical elements of a mechanism that stabilizes a conformation for optimal kinase activity following phosphorylation in the activation segment.

Presumably, multiple phosphorylations induce conformational changes that regulate binding sites for ATP, substrates, and interaction partners involved in downstream signal transduction. Indeed, in RTKs it has been demonstrated that phosphorylated residues create docking sites for the modification-dependent recruitment of interacting proteins that initiate multifarious downstream signalling events (Holland, *et al.*, 1997; Huse and Kuriyan, 2002; Schulze, *et al.*, 2005). Insofar as very few RLKs have been characterized in detail at the molecular level, the biological functions of several RLKs (Shiu and Bleecker, 2001; Haffani, *et al.*, 2004; Afzal, *et al.*, 2008; Tang, *et al.*, 2008; Kim, *et al.*, 2009) suggest that activation of the kinase domain also elicits an amplification of the extracellular signal via recruitment of cytoplasmic downstream protein targets and their subsequent phosphorylation. The phosphorylated effector proteins can then act to modulate transcriptional activity in the nucleus. In an effort to dissect the functional role of phosphorylated residues in ACR4 as potential sites of interactions with other proteins, a combinatorial phage-peptide library screening approach to identify peptide sequences/motifs interacting with the phosphorylated Ser residue in the JM domain of the kinase has been used (Meyer, *et al.*, 2013). This study identified the motif LxxLL as a recognition motif that is present within the kinase domain of ACR4, and it presumably participates in a regulatory intramolecular interaction between the JM and the N-terminal lobe of the kinase domain. Intriguingly, the LxxLL motif has been demonstrated to be central to protein–protein interactions among many proteins in both plants and animals, particularly in a number of the LRRIII subfamily of the leucine-rich repeat (LRR) RLKs and mammalian receptor signalling proteins (Cubas, *et al.*, 1999; Dong, *et al.*, 2004; Savkur and Burris, 2004; Plevin, *et al.*, 2005; Kim, *et al.*, 2009). More importantly, inasmuch as the LxxLL motif occurs in at least one of the ACR4 homologs and is also present in many other RLKs, phosphatases, and transcription factors involved in plant growth and development, a compelling case could be put forward for ACR4-mediated signal transduction driven by cross-talk and heteromeric protein–protein interactions. It has been speculated that protein–protein interactions between transmembrane (TM) regions of ACR4 and CRR2

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

may facilitate the observed phosphorylation of the inactive kinase domain of CRR2 (Cao, *et al.*, 2005; Stokes and Rao, 2008, 2010). Further, it has recently been demonstrated that the LLSLL motif present in the ACR4 kinase domain is able to bind a KDSAF motif in CRR3 using peptide interactions and hydrogen–deuterium exchange (Meyer, *et al.*, 2015). Since interactions between Arabidopsis TM domains are relatively weak compared to interactions of maize CR4 TM domains, it is possible that the LxxLL motif present in the JM domain (Meyer, *et al.*, 2013) serves to further stabilise protein–protein interactions between ACR4 and interacting proteins in order for phosphorylation to occur.

Interestingly, *in vitro* phosphorylation analyses indicate that intracellular domains of ABNORMAL LEAF SHAPE 2 (ALE2) and ACR4 are able to mutually trans-phosphorylate; potentially indicating dimerization of the two domains and formation of a receptor complex involved in defining epidermal identity during ovule development (Tanaka, *et al.*, 2007; Lemmon and Schlessinger, 2010).

Previously, through the lack of interaction with KINASE-ASSOCIATED PROTEIN PHOSPHATASE (KAPP), it was suggested that dephosphorylation is not a major means of down-regulating ACR4 or CR4 (Braun, *et al.*, 1997; Gifford, *et al.*, 2005). However, recently it has been shown that PP2A (or at least the human variant) is able to dephosphorylate ACR4. Furthermore, the ACR4 phospho-status seems to affect its membrane localization (Yue, *et al.*, 2016). Overall, the Yue *et al.* (2016) study has defined a hypothesis involving a balance between the phosphorylation and dephosphorylation processes in regulating the membrane localization of ACR4 (Fig. 4A).

Localization at plasmodesmata

Interestingly, next to its membrane localization, ACR4 has been shown to localize to plasmodesmata, potentially indicating that ACR4−CLV1 heteromeric complexes may act to restrict mobility of signalling molecules responsible for maintenance of stem-cell fate from the quiescent centre to the surrounding columella stem cells via the plasmodesmata (Stahl, *et al.*, 2013; Williams and De Smet, 2013; Stahl and Faulkner, 2016) (Fig. 4B). Similarly, in *in vitro* grown maize endosperm tissue, expression of the *γ-Zein::CR4:HA:FLAG:AcGFP* construct is detected in the membrane and endosomes of endosperm cells, specifically concentrating at plasmodesmata on the anticlinal intersection between aleurone cells (Tian, *et al.*, 2007).

Expression and transcriptional regulation

ACR4 is expressed in different cells and organs in the plant, suggesting it functions in multiple developmental processes. In this section, we summarize this and include aspects of *ACR4* transcriptional regulation.

In the Arabidopsis root, *ACR4* has three important expression domains: in the stem cell niche, in the epidermis, and during lateral root initiation. *ACR4* is specifically expressed in the small daughter cells after the first asymmetric pericycle cell division (De Smet, *et al.*, 2008). This expression pattern is associated with formative cell divisions, as no *ACR4* expression is observed when pericycle cells are proliferating (De Smet, *et al.*, 2008, 2010). In the root apical meristem, *ACR4* is expressed in the columella and other initials (De Smet, *et al.*, 2008; Stahl, *et al.*, 2009; Stahl and Simon, 2012). Finally, *ACR4* is also expressed in the root epidermis, but no clear role for ACR4 in this tissue has been described so far (Gifford, *et al.*, 2005). Immunostaining of wild-type maize root sections with antibodies raised against the extracellular domain of CR4 indicate that *CR4* is also expressed in maize roots, where it localizes to the plasma membrane and endosomes (Tian, *et al.*, 2007).

In Arabidopsis, *ACR4* expression is observed in the L1 layer of the developing embryo, inflorescence and floral meristems, sepal margins, and additionally in the inner and outer integuments, funiculus, and endothelium of mature ovules (Gifford, *et al.*, 2003). In maize, RT-PCR indicates expression in the leaf, ear, tassel, and stalk tissues (Jin, *et al.*, 2000; Kang, *et al.*, 2002). Additionally, *in situ* hybridization of the *CR4* transcript indicates expression in the shoot apical meristem and young leaf primordia, and in the epidermis, vasculature, and leaf margins of mature leaves (Becraft, *et al.*, 2001).

Very little is known about the transcriptional regulation of *ACR4*, but it seems that a network structure where *ACR4* expression is regulated by ATML1 and PDF2 in a negative feedback model is important for epidermal identity (San-Bento, *et al.*, 2014). In this context, it seems that the L1 box is required for normal epidermal expression of *ACR4* during embryogenesis (San-Bento, *et al.*, 2014), and this is in line with earlier work where it was suggested that ATML1 and PDF2 positively regulate *ACR4* expression via the L1 box (Tanaka, *et al.*, 2002; Abe, *et al.*, 2003) (Fig. 4C). However, other results also suggest a negative regulation of *ACR4* expression by ATML1 and PDF2 (San-Bento, *et al.*, 2014). Interestingly, *in situ* hybridization indicates decreased expression of *ATML1* in *ale2* embryos (Tanaka, *et al.*, 2007). Given that the ACR4 and ALE2 intracellular domains interact *in vitro*, ACR4−ALE2-mediated regulation of *ATML1* may potentially reflect a feedback loop capable of regulating *ACR4* expression (Tanaka, *et al.*, 2007) (Fig. 4C).

In addition to this, *ACR4* expression is up-regulated by CLE40 (Stahl, *et al.*, 2009), but at the moment it is not clear what the transcription factors involved are. Interestingly, *CRK1* expression is negatively regulated by the plant hormones auxin, ABA, and cytokinin (Schäfer and Schmülling, 2002). Especially with respect to cytokinin, there is an important role for okadaic acid-sensitive phosphatases (such as PP2A) (Schäfer and Schmülling, 2002). However, Chang *et al.* (2015) have shown that while cytokinin-deficient plants display reduced *ACR4* expression, *ACR4* does not appear to be a primary cytokinin response gene. Furthermore, an RT-PCR based analysis of leaf tissues indicates that expression of *CR4* in maize aerial tissues is only observed after 24 hours of light induction in 7-day dark-germinated seedlings, indicating that *CR4* expression may be light-induced in these tissues (Kang, *et al.*, 2002). Additionally, no expression of *ACR4* is detected

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

in the *dek1* mutant embryos (Johnson, *et al.*, 2005) suggesting that DEK1 is required for *ACR4* expression and subsequent determination of epidermal cell fate, which is further evidenced by reduced *ACR4* transcript presence and apparent loss of epidermal identity in *DEK1* RNAi lines (Johnson, *et al.*, 2005). Finally, a recent study in *Populus trichocarpa* showed that an *ACR4* orthologue is down-regulated by treatment with the HISTONE DEACETYLASE-specific inhibitor trichostatin A (TSA), suggesting that the acetylation status of histones may provide further control over *ACR4* expression (Ma, *et al.*, 2016).

Roles of (A)CR4 in plant growth and development

In this section, we describe the key processes in which (A)CR4 is involved during plant growth and development (Fig. 5).

Root development

In columella stem cells (CSCs), ACR4 is implicated in regulating asymmetric cell division, as *acr4* displays a disorganized and/or irregularly differentiating columella (De Smet, *et al.*, 2008; Stahl, *et al.*, 2013). While ACR4 is required for CLE40 signalling activity (Stahl, *et al.*, 2009), it remains to be shown that CLE40 directly binds ACR4. Nevertheless, given the genetic data it seems clear that both act in the same pathway (together with CLV1) regulating columella stem cell differentiation by regulation of *WOX5* expression (Fig. 5C). A possible mechanism is that ACR4 relays the CLE40 signal and also sequesters CLE40 to protect the quiescent centre (QC), around which the stem cells are located, from too much peptide (Stahl and Simon, 2009).

During early lateral root initiation, ACR4 (in a redundant way with other family members) similarly influences formative asymmetric cell division, which normally results in daughter cells of different identities that give rise to the cell lineages required for lateral root formation (De Smet, *et al.*, 2008). This results in lateral roots being initiated close to each other and often in the normally excluded opposite positions, and in stretches of two-layered pericycle or fused primordia (De Smet, *et al.*, 2008). Thus, ACR4 appears to be involved in preventing surrounding cells from dividing, and also in the initiation itself.

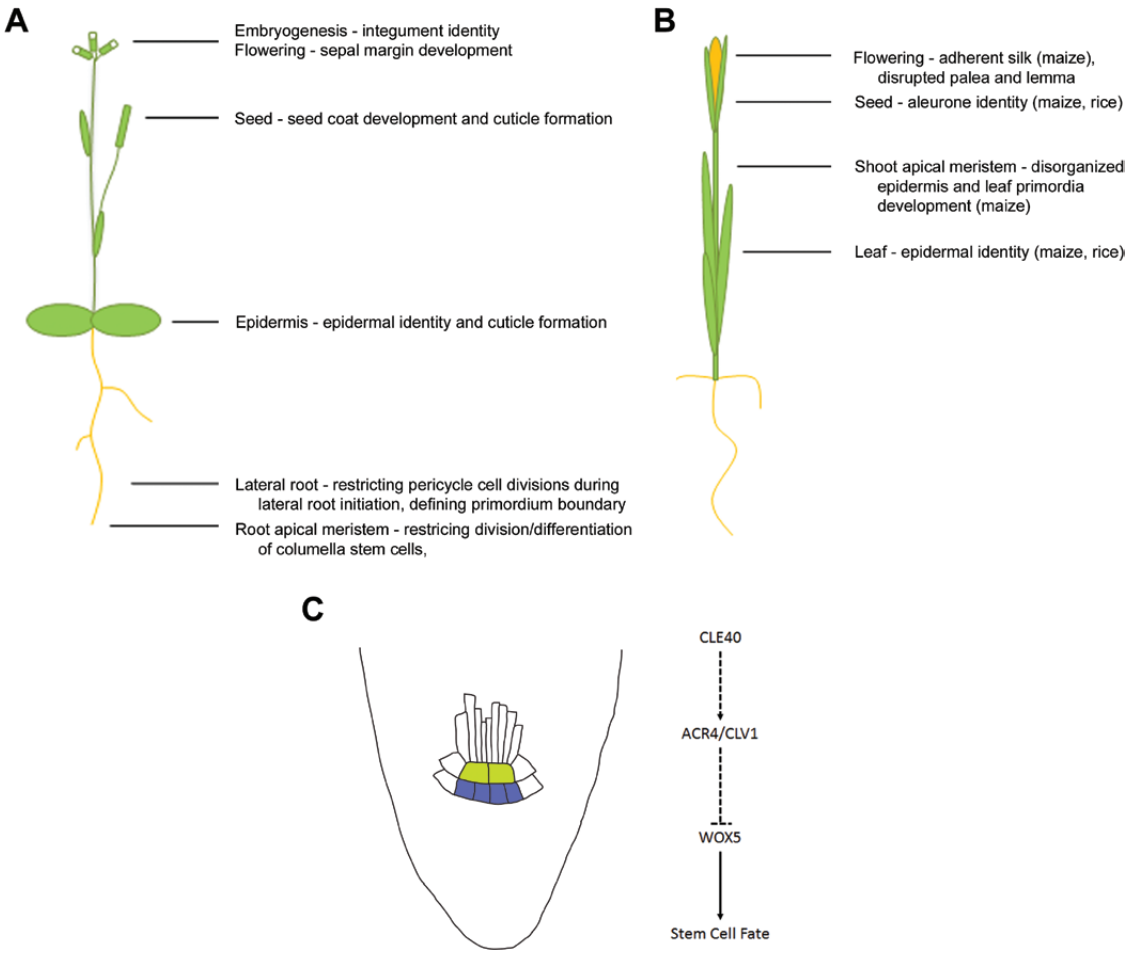


Fig. 5. Roles of ACR4 in plants. (A, B) Schematic overview of roles of (A)CR4 in (A) dicot and (B) monocot plants. (C) Root apical meristem with the quiescent centre (yellow/green, upper cells) and columella stem cells (blue, lower cells). The (possible) signalling cascade regulating Arabidopsis columella stem cell fate is shown.

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

Shoot epidermis development

(A)CR4 also functions to define epidermal identity during the vegetative phase of plant growth (Fig. 5A, B). In maize, abnormal expansion and overabundant division of cells in regions of the shoot apical meristem epidermis in the *cr4* lineage leads to a disorganized structure on the cellular scale, which becomes visible at the macro scale as the irregularities in the cellular structure give rise to the characteristic short 'crinkly' leaves (Jin, *et al.*, 2000; Becraft, *et al.*, 2001; Kang, *et al.*, 2002). This is, however, not the only effect observed on the aerial tissues of maize, since wart-like growths are also observed in the leaves of *cr4* mutants, which cross-sectional analysis reveals as masses of large, undifferentiated and disorganized cell structures, similar to tumour growths (Jin, *et al.*, 2000). In addition to the effect observed in leaf epidermal tissues, *cr4* mutants display abnormalities in trichome, bulliform, and mesophyll cells, suggesting that CR4 signalling in the epidermis is able to affect neighbouring tissues (Jin, *et al.*, 2000; Becraft, *et al.*, 2001; Cao, *et al.*, 2005). Interestingly, cross-sectional analysis reveals that the cell wall structure of the maize *cr4* leaf epidermis is irregular, varying in thickness several fold over a few microns (Jin, *et al.*, 2000), demonstrating a similar epidermal tissue phenotype to that observed in the aleurone layer of seeds (see below) (Becraft and Asuncion-Crabb, 2000; Cao, *et al.*, 2005), suggesting that *CR4* regulates formative divisions of the epidermis and is responsible for maintaining an organized structure.

In Arabidopsis, there is no visible alteration to *acr4* aerial tissues on the macro scale; however, microscopic analysis indicates extrusion of epidermal cells from the leaf tips, and toluidine blue staining indicates decreased deposition of cuticle on the leaf surface (Watanabe, *et al.*, 2004). This suggests that – similar to its role of signalling in the seed coat – ACR4 is responsible for determination of epidermal cell fate in Arabidopsis leaves.

Embryo and seed development

In addition to the role of regulation of division of meristematic tissues during the vegetative phase of growth, (A)CR4 is also involved in embryonic development (Becraft and Asuncion-Crabb, 2000; Gifford, *et al.*, 2003; Watanabe, *et al.*, 2004; Cao, *et al.*, 2005; Johnson, *et al.*, 2005; Tian, *et al.*, 2007). In the *acr4* background, there are several development defects during embryonic development, which lead to increased rates (40–85%) of seed abortion (Gifford, *et al.*, 2003; Watanabe, *et al.*, 2004). This observation was further supported by Tanaka *et al.* (2007), who additionally observed a compounded effect on seed sterility in the *acr4 ale2* double-mutant. The *ale2* siliques contained no seeds and were unable to be rescued by the presence of wild-type ACR4. However, the decreased seed production observed in the *ale2*/+ heterozygous mutant was further decreased in the *acr4 ale2*/+ background (Tanaka, *et al.*, 2007). Scanning electron microscopy images of the seed coat reveal an irregular, rough surface structure of *acr4* seeds compared with a smooth surface in the wild-type, potentially due to the disrupted organization of the integument cell lineage in the *acr4* background, which is occasionally severe enough to leave the nucellus exposed (Gifford, *et al.*, 2003; Watanabe, *et al.*, 2004; Cao, *et al.*, 2005). Additionally, cross-sections of *acr4* ovules reveal that the internal structure is similarly disorganized, with irregular cell layers and fused ovules being the causative factors leading to seed abortion (Gifford, *et al.*, 2003; Watanabe, *et al.*, 2004). Disorganized ovule development is also observed in *ale2* mutants, and this disruption is further increased in the *acr4 ale2* background, suggesting that both proteins act on the same or overlapping pathways responsible for determining epidermal identity during embryogenesis (Tanaka, *et al.*, 2007). Application of the hydrophilic toluidine blue stain indicated that the surface of *acr4* seeds is water permeable, suggesting disrupted production of cuticle (Watanabe, *et al.*, 2004). Extrapolating from this it is possible that ACR4 is required to retain integument epidermal identity (Watanabe, *et al.*, 2004).

Similar disorganization in seed coat development is observed in the maize *cr4* background. In these plants, differentiation of the endosperm into aleurone and starchy endosperm is partially disrupted, forming mosaic patches of starchy endosperm instead of aleurone at the seed surface (Becraft and Asuncion-Crabb, 2000; Cao, *et al.*, 2005). Interestingly, the *defective kernel 1* (*dek1*) mutant lineage in maize forms no aleurone, and does not express *CR4* in the embryo, suggesting that DEK1 is responsible for governing CR4 activity (Becraft and Asuncion-Crabb, 2000; Johnson, *et al.*, 2005).

In maize *cr4* mutants, silk development is also disrupted, since mutants exhibit short, deformed papillar hairs, and in more severe mutations multiple silks fuse together, suggesting a loss of epidermal identity (Jin, *et al.*, 2000).

In rice *CR4* RNAi (*OsCR4i*) lines, seed development is disrupted by two mechanisms: not only is the aleurone layer disrupted similar to that of maize, but the development of the palea and lemma structures encasing the developing seed is also disrupted (Pu, *et al.*, 2012). The interlock does not form correctly between the palea and lemma, resulting in an open-hull spikelet exposing the fragile inner floral organ before pollination, and later the developing seed (Pu, *et al.*, 2012). This leads to a large number of unpollinated gynoecia, and also increases risk of damage during post-fertilization development, which causes increased numbers of pollinated seed to fill incorrectly, resulting in turn in a very low viable seed yield (Pu, *et al.*, 2012). Structural analysis of the palea and lemma structures reveals wart-like protrusions of large undifferentiated cells on the inner surface, suggestive of disrupted control of division and loss of epidermal cell identity in these cells (Pu, *et al.*, 2012).

Other roles

In addition to being an important developmental regulator, ACR4 also appears to play a role – directly or indirectly – in plant defence, since *acr4* displays increased resistance to *Botrytis* infection. This is thought to be due to increased expression of *LIPOXYGENASE2*, an essential enzyme for

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

jasmonic acid (JA) synthesis (Zereen and Ingram, 2012). Since application of JA is able to affect root architecture, producing a short-root phenotype (Wasternack and Hause, 2013), it is possible that downstream effectors of *ACR4* signalling may be involved in localized regulation of JA synthesis.

Outstanding questions

While (A)CR4 has an extracellular domain that is a putative ligand binding domain, a ligand has yet to be identified. Notwithstanding that CLE40 has been put forward in this context (Stahl, *et al.*, 2009), there is no conclusive biochemical data to support this. Future analyses will have to determine if ACR4 on its own is ligand binding and/or if this requires an interacting partner, such as CLV1 – and if this is the case, what the nature of the ligand is. Additionally, while *CLE40* is involved in regulation of CSC division in the root apical meristem, there is no expression observed in lateral root primordia, suggesting the possibility that multiple ligands are able to trigger *ACR4* signalling in a tissue-specific manner, a situation that may be facilitated by heteromeric interactions with different co-receptors. Further to this, although *WOX5* is regulated by CLE40−ACR4 signalling, little is known about the immediate downstream targets of ACR4 or the signalling pathway responsible for regulating *WOX5* expression. In this context, (A)CR4 localization at plasmodesmata, the model of ACR4 regulating a stemness factor (Stahl and Simon, 2013) together with the mobility of WOX5 (Pi, *et al.*, 2015), and the fact that ACR4 can phosphorylate WOX5 (*in vitro*) (Meyer, *et al.*, 2015) offers exciting leads to further explore this.

Also in a more general context, the molecular and biochemical pathways on which ACR4 signalling impacts have not been uncovered. Importantly, from a molecular standpoint, a comprehensive *in vitro* biochemical and biophysical study of the entire recombinant receptor should provide valuable clues towards an understanding of *in vivo* physiological functions. Despite recent studies on the properties of the juxtamembrane domain, the kinase domain, and the transmembrane domain (Stokes and Rao, 2008, 2010; Meyer, *et al.*, 2013, 2015), important questions regarding the role of the subdomains and the role of the phosphorylation sites remain to be answered. Ultimately, the three-dimensional structure of the ACR4 kinase domain, in the phosphorylated and unphosphorylated state, will provide a better understanding of the finer aspects of kinase activity and its regulation. More importantly, elucidation of the crystal structure of the extracellular domain of ACR4 can catalyse the identification of ligand(s), the molecular basis for ligand binding, activation of the receptor, and concomitant activation of the intracellular kinase domain. In addition, the identification of components of the downstream signalling pathway is essential. The recent identification of the catalytic subunit of the protein phosphatase PP2A-3 as an interacting protein and a regulator of *in vivo* ACR4 function (Yue, *et al.*, 2016) opens up the opportunity to delve further into the biochemical properties of the PP2A holoenzyme, phosphatase activity, and mechanistic aspects of regulation of kinase activity.

Thus far, little is known about the role of the C-terminal domain (CTD) in kinase autoregulation and activation. It is common among RTKs to have their CTDs phosphorylated at tyrosine residues in response to receptor activation. These sites can then recruit Src Homology 2 (SH2) or Phosphotyrosine Binding (PTB) domain-containing target proteins. As exemplified in the four-member EGF receptor family, multiple sites within their respective CTDs are phosphorylated and act to attract downstream targets (Schulze, *et al.*, 2005; Jones, *et al.*, 2006). Therefore, we can invoke the likelihood that some of the autophosphorylation sites in the CTD could serve to recruit downstream signalling targets. Furthermore, the intrinsic dimerization capacity of the TM domain and molecular details of its dynamic role in affecting receptor function are yet to be ascertained. As mentioned earlier, Stokes and Rao (2008, 2010) have demonstrated the differential dimerization propensities of the TM domains of the ACR4 family and Stahl *et al.* (2013) have shown that, *in vivo*, the TM domain in ACR4 is important for heteromerization with CLV1. The development of the Nanodisc technology (Bayburt and Sligar, 2003, 2010) now facilitates the reconstitution of receptor kinases in a membrane environment and provides a tool to examine the mechanism of receptor activation *in vitro*. Particularly exciting will be the ability to delineate the role of TM domains in the formation of homomeric and heteromeric complexes in a membrane-bound environment, and to further understand kinase activity and protein–protein interaction in the context of the TM domain.

Finally, in the future, it will be interesting to explore the role(s) of CR4 family members and assess to what extent their function is evolutionary conserved. Recently, this was already initiated in Physcomitrella patens demonstrating the involvement of CR4 in developmental control of gametophytic and sporophytic organs (Demko *et al.*, 2016).

ACKNOWLEDGEMENTS

This work was supported by a BBSRC David Phillips Fellowship (BB_BB/H022457/1) and a Marie Curie European Reintegration Grant (PERG06-GA-2009–256354) to I.D.S., a BBSRC CASE Studentship co-funded by Bayer CropScience to N.C., and L.D.V. is the recipient of a VIB International PhD program fellowship.

References

Abe M, Katsumata H, Komeda Y, Takahashi T. 2003. Regulation of shoot epidermal cell differentiation by a pair of homeodomain proteins in Arabidopsis. Development **130,** 635–643.

Afzal A, Wood A, Lightfoot D. 2008. Plant receptor-like serine threonine kinases: roles in signaling and plant defense. Molecular Plant-Microbe Interactions **21,** 507–517.

Albrecht C, Russinova E, Kemmerling B, Kwaaitaal M, Sacco C, de Vries SC. 2008. Arabidopsis SOMATIC EMBRYOGENESIS RECEPTOR KINASE proteins serve brassinosteroid-dependent and -independent signaling pathways. Plant Physiology **148,** 611–619.

Bayburt T, Sligar S. 2003. Self-assembly of single integral membrane proteins into soluble nanoscale phospholipid bilayers. Protein Science **12,** 2476–2481.

Bayburt T, Sligar S. 2010. Membrane protein assembly into Nanodiscs. Federation of European Biochemical Societies Letters **584,** 1721–1727.

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

Becraft P, Asuncion-Crabb Y. 2000. Positional cues specify and maintain aleurone cell fate in maize endosperm development. Development **127,** 4039–4048.

Becraft P, Kang S, Suh S. 2001. The maize CRINKLY4 receptor kinase controls a cell-autonomous differentiation response. Plant Physiology **127,** 486–496.

Becraft P, Stinard P, McCarty D. 1996. CRINKLY4: A TNFR-like receptor kinase involved in maize epidermal differentiation. Science **273,** 1406–1409.

Braun D, Stone J, Walker J. 1997. Interaction of the maize and Arabidopsis kinase interaction domains with a subset of receptor-like protein kinases: implications for transmembrane signaling in plants. Plant Journal **12,** 83–95.

Burza A, Pekala I, Sikora J, Siedlecki P, Małagocki P, Bucholc M, Koper L, Zielenkiewicz P, Dadlez M, Dobrowolska G. 2006. *Nicotiana tabacum* osmotic stress-activated kinase is regulated by phosphorylation on Ser-154 and Ser-158 in the kinase activation loop. Journal of Biological Chemistry **281,** 34299–34311.

Cao X, Li K, Suh SG, Guo T, Becraft PW. 2005. Molecular analysis of the CRINKLY4 gene family in *Arabidopsis thaliana*. Planta **220,** 645–657.

Chang L, Ramireddy E, Schmülling T. 2015. Cytokinin as a positional cue regulating lateral root spacing in Arabidopsis. Journal of Experimental Botany **66,** 4759–4768.

Chen C, Chan N, Wang A. 2011. The many blades of the β-propeller proteins: conserved but versatile. Trends in Biochemical Sciences **36,** 553–561.

Chinchilla D, Zipfel C, Robatzek S, Kemmerling B, Nürnberger T, Jones JD, Felix G, Boller T. 2007. A flagellin-induced complex of the receptor FLS2 and BAK1 initiates plant defence. Nature **448,** 497–500.

Clouse S. 2011. Brassinosteroids. The Arabidopsis Book **9,** e0151. doi: 10.1199/tab.0151.

Cubas P, Lauter N, Doebley J, Coen E. 1999. The TCP domain: a motif found in proteins regulating plant growth and development. Plant Journal **18,** 215–222.

Czyzewicz N, Yue K, Beeckman T, De Smet I. 2013. Message in a bottle: small signalling peptide outputs during growth and development. Journal of Experimental Botany **64,** 5281–5296.

De Smet I, Lau S, Voss U, *et al*. 2010. Bimodular auxin response controls organogenesis in Arabidopsis. Proceedings of the National Academy of Science, USA **107,** 2705–2710.

De Smet I, Vassileva V, De Rybel B, *et al*. 2008. Receptor-like kinase ACR4 restricts formative cell divisions in the Arabidopsis root. Science **322,** 594–597.

De Smet I, Voβ U, Jϋrgens G, Beeckman T. 2009. Receptor-like kinases shape the plant. Nature Cell Biology **11,** 1166–1173.

Demko V, Ako E, Perroud PF, Quatrano R, Olsen OA. 2016. The phenotype of the CRINKLY4 deletion mutant of Physcomitrella patens suggests a broad role in developmental regulation in early land plants. Planta. PMID: 27100110.

Dong X, Challis J, Lye S. 2004. Intramolecular interactions between the AF3 domain and the C-terminus of the human progesterone receptor are mediated through two LXXLL motifs. Journal of Molecular Endocrinology **32,** 843–857.

Endres N, Das R, Smith AW, *et al*. 2013. Conformational coupling across the plasma membrane in activation of the EGF receptor. Cell **152,** 543–556.

Gadella TJ, Jovin T. 1995. Oligomerization of epidermal growth factor receptors on A431 cells studied by time-resolved fluorescence imaging microscopy. A stereochemical model for tyrosine kinase receptor activation. Journal of Cell Biology **129,** 1543–1558.

Gao Z, Schaller G. 2009. The role of receptor interactions in regulating ethylene signal transduction. Plant Signaling and Behavior **4,** 1152–1153.

Gifford M, Dean S, Ingram G. 2003. The Arabidopsis ACR4 gene plays a role in cell layer organisation during ovule integument and sepal margin development. Development **130,** 4249–4248.

Gifford M, Robertson F, Soares D, Ingram G. 2005. ARABIDOPSIS CRINKLY4 function, internalization, and turnover are dependent on the extracellular crinkly repeat domain. Plant Cell **17,** 1154–1166.

Guo Y, Clark S. 2010. Membrane distributions of two ligand-binding receptor complexes in the CLAVATA pathway. Plant Signaling and Behavior **5,** 1442–1445.

Haffani Y, Silva N, Goring D. 2004. Receptor kinase signalling in plants. Canadian Journal of Botany **82,** 1–15.

Hanks S, Hunter T. 1995. Protein kinases 6. The eukaryotic protein kinase superfamily: kinase (catalytic) domain structure and classification. Federation of American Societies for Experimental Biology Journal **9,** 576–596.

He W, Craparo A, Zhu Y, O'Neill TJ, Wang LM, Pierce JH, Gustafson TA. 1996. Interaction of insulin receptor substrate-2 (IRS-2) with the insulin and insulin-like growth factor I receptors. Evidence for two distinct phosphotyrosine-dependent interaction domains within IRS-2. Journal of Biological Chemistry **271,** 11641–11645.

Holland S, Gale NW, Gish GD, Roth RA, Songyang Z, Cantley LC, Henkemeyer M, Yancopoulos GD, Pawson T. 1997. Juxtamembrane tyrosine residues couple the Eph family receptor EphB2/Nuk to specific SH2 domain proteins in neuronal cells. EMBO Journal **16,** 3877–3888.

Hubbard S. 2004. Juxtamembrane autoinhibition in receptor tyrosine kinases. *Nature Reviews.* Molecular Cell Biology **5,** 464–471.

Huse M, Kuriyan J. 2002. The conformational plasticity of protein kinases. Cell **109,** 275–282.

Hynes N, MacDonald G. 2009. ErbB receptors and signaling pathways in cancer. Current Opinion in Cell Biology **21,** 177–184.

Jin P, Guo T, Becraft P. 2000. The maize CR4 receptor-like kinase mediates a growth factor-like differentiation response. Genesis **27,** 104–116.

Johnson K, Degnan K, Walker J, Ingram G. 2005. AtDEK1 is essential for specification of embryonic epidermal cell fate. Plant Journal **44,** 114–127.

Johnson L, Lewis R. 2001. Structural basis for control by phosphorylation. Chemical Reviews **101,** 2209–2242.

Johnson L, Noble M, Owen D. 1996. Active and inactive protein kinases: structural basis for regulation. Cell **85,** 149–158.

Jones R, Gordus A, Krall J, MacBeath G. 2006. A quantitative protein interaction network for the ErbB receptors using protein microarrays. Nature **439,** 168–174.

Jura N, Endres NF, Engel K, Deindl S, Das R, Lamers MH, Wemmer DE, Zhang X, Kuriyan J. 2009. Mechanism for activation of the EGF receptor catalytic domain by the juxtamembrane segment. Cell **137,** 1293–1307.

Kang S, Lee H, Suh S. 2002. The maize *Crinkly4* gene is expressed spatially in vegetative and floral organs. Journal of Plant Biology **45,** 219–224.

Kemmerling B, Halter T, Mazzotta S, Mosher S, Nürnberger T. 2011. A genome-wide survey for Arabidopsis leucine-rich repeat receptor kinases implicated in plant immunity. Frontiers in Plant Science **2,** 88.

Kim J, Li X, Roden JA, *et al*. 2009. Xanthomonas T3S effector XopN suppresses PAMP-triggered immunity and interacts with a tomato atypical receptor-like kinase and TFT1. Plant Cell **21,** 1305–1323.

Kroiher M, Miller M, Steele R. 2001. Deceiving appearances: signaling by "dead" and "fractured" receptor protein-tyrosine kinases. BioEssays **23,** 69–76.

Lehti-Shiu M, Zou C, Hanada K, Shiu S. 2009. Evolutionary history and stress regulation of plant receptor-like kinase/pelle genes. Plant Physiology, **150,** 12–26.

Lemmon M, Schlessinger J. 2010. Cell signaling by receptor-tyrosine kinases. Cell, **141,** 1117–1134.

Liu G, Pi LY, Walker JC, Ronald PC, Song WY. 2002. Biochemical characterization of the kinase domain of the rice disease resistance receptor-like kinase XA21. Journal of Biological Chemistry **277,** 20264–20269.

Ma X, Zhang C, Zhang B, Yang C, Li S. 2016. Identification of genes regulated by histone acetylation during root development in *Populus trichocarpa*. BioMed Central Genomics **17,** 96.

McCarty D, Chory J. 2000. Conservation and innovation in plant signaling pathways. Cell **103,** 201–209.

Meyer M, Lichti C, Townsend R, Rao A. 2011. Identification of *in vitro* autophosphorylation sites and effects of phosphorylation on the Arabidopsis CRINKLY4 (ACR4) receptor-like kinase intracellular domain: insights into conformation, oligomerization, and activity. Biochemistry **50,** 2170–2186.

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

Meyer M, Shah S, Rao A. 2013. Insights into molecular interactions between the juxtamembrane and kinase subdomains of the Arabidopsis Crinkly-4 receptor-like kinase. Archives of Biochemistry and Biophysics **535,** 101–110.

Meyer M, Shah S, Zhang J, Rohrs H, Rao AG. 2015. Evidence for intermolecular interactions between the intracellular domains of the Arabidopsis receptor-like kinase ACR4, its homologs and the Wox5 transcription factor. PLOS One **10,** e0118861.

Mischel P, Umbach JA, Eskandari S, Smith SG, Gundersen CB, Zampighi GA. 2002. Nerve growth factor signals via preexisting TrkA receptor oligomers. Biophysical Journal **83,** 968–976.

Morgillo F, Woo JK, Kim ES, Hong WK, Lee HY. 2006. Heterodimerization of insulin-like growth factor receptor/epidermal growth factor receptor and induction of survivin expression counteract the antitumor action of erlotinib. Cancer Research **66,** 10100–10111.

Murphy E, De Smet I. 2014. Understanding the RALF family: a tale of many species. Trends in Plant Science **19,** 664–671.

Murphy E, Smith S, De Smet I. 2012. Small signaling peptides in Arabidopsis development: how cells communicate over a short distance. Plant Cell **24,** 3198–3217.

Nikonorova N, Vu LD, Czyzewicz N, Gevaert K, De Smet I. 2015. A phylogenetic approach to study the origin and evolution of the CRINKLY4 family. Frontiers in Plant Science **6,** 880.

Nolen B, Taylor S, Ghosh G. 2004. Regulation of protein kinases: controlling activity through activation segment conformation. Molecular Cell **15,** 661–675.

Oh M, Wu X, Clouse S, Huber S. 2011. Functional importance of BAK1 tyrosine phosphorylation in vivo. Plant Signaling and Behavior **6,** 400–405.

Pettersen E, Goddard TD, Huang CC, Couch GS, Greenblatt DM, Meng EC, Ferrin TE. 2004. UCSF Chimera--a visualization system for exploratory research and analysis. Journal of Computational Chemistry **25,** 1605–1612.

Pfeiffer M, Koch T, Schröder H, Laugsch M, Höllt V, Schulz S. 2002. Heterodimerization of somatostatin and opioid receptors cross-modulates phosphorylation, internalization, and desensitization. Journal of Biological Chemistry **277,** 19762–19772.

Pi L, Aichinger E, van der Graaff E, Llavata-Peris CI, Weijers D, Hennig L, Groot E1, Laux T. 2015. Organizer-derived WOX5 signal maintains root columella stem cells through chromatin-mediated repression of CDF4 expression. Developmental Cell **33,** 576–588.

Plevin M, Mills M, Ikura M. 2005. The LxxLL motif: a multifunctional binding sequence in transcriptional regulation. Trends in Biochemical Sciences **30,** 66–69.

Pu C, Ma Y, Wang J, Zhang YC, Jiao XW, Hu YH, Wang LL, Zhu ZG, Sun D, Sun Y. 2012. Crinkly4 receptor-like kinase is required to maintain the interlocking of the palea and lemma, and fertility in rice, by promoting epidermal cell differentiation. Plant Journal **70,** 940–953.

Pu C, Sun Y. 2012. Rice Crinkly4 receptor-like kinase positively regulates culm elongation and amino acid K532 is not essential for its kinase activity. Plant Signaling and Behavior **7,** 1062–1064.

Russ W, Engelman D. 1999. TOXCAT: A measure of transmembrane helix association in a biological membrane. Proceedings of the National Academy of Sciences, USAa **96,** 863–868.

Saito Y, Haendeler J, Hojo Y, Yamamoto K, Berk BC. 2001. Receptor heterodimerization: essential mechanism for platelet-derived growth factor-induced epidermal growth factor receptor transactivation. Molecular and Cell Biology **21,** 6387–6394.

San-Bento R, Farcot E, Galletti R, Creff A, Ingram G. 2014. Epidermal identity is maintained by cell-cell communication via a universally active feedback loop in *Arabidopsis thaliana*. Plant Journal **77,** 46–58.

Savkur R, Burris T. 2004. The coactivator LXXLL nuclear receptor recognition motif. Journal of Peptide Research **63,** 207–212.

Schäfer S, Schmülling T. 2002. The CRK1 receptor-like kinase gene of tobacco is negatively regulated by cytokinin. Plant Molecular Biology **50,** 155–166.

Schulze W, Deng L, Mann M. 2005. Phosphotyrosine interactome of the ErbB-receptor kinase family. Molecular Systems Biology **1, doi:** 10.1038/msb4100012.

Sengupta P, Bosis E, Nachliel E, Gutman M, Smith SO, Mihályné G, Zaitseva I, McLaughlin S. 2009. EGFR juxtamembrane domain, membranes, and calmodulin: kinetics of their interaction. Biophysical Journal **96,** 4887–4895.

Shah K, Vervoort J, de Vries S. 2001. Role of threonines in the *Arabidopsis thaliana* somatic embryogenesis receptor kinase 1 activation loop in phosphorylation. Journal of Biological Chemistry **276,** 41263–41269.

Shen B, Li C, Min Z, Meeley RB, Tarczynski MC, Olsen OA. 2003. sal1 determines the number of aleurone cell layers in maize endosperm and encodes a class E vacuolar sorting protein. Proceedings of the National Academy of Science, USA **100,** 6552–6557.

Shiu S, Bleecker A. 2001. Plant receptor-like kinase gene family: diversity, function, and signaling. Science. Signalling Transduction Knowledge Environment **113,** re22.

Shiu S, Bleecker A. 2003. Expansion of the receptor-like kinase/Pelle gene family and receptor-like proteins in Arabidopsis. Plant Physiology **132,** 530–543.

Shiu S, Karlowski WM, Pan R, Tzeng Y-H, Mayer KFX, Lia W-H. 2004. Comparative analysis of the receptor-like kinase family in Arabidopsis and rice. Plant Cell **16,** 1220–1234.

Soyars C, James S, Nimchuk Z. 2016. Ready, aim, shoot: stem cell regulation of the shoot apical meristem. Current Opinion in Plant Biology **29,** 163–168.

Stahl Y, Faulkner C. 2016. Receptor complex mediated regulation of symplastic traffic. Trends in Plant Science in press. doi:10.1016/j.tplants.2015.11.002.

Stahl Y, Grabowski S, Bleckmann A, *et al*. 2013. Moderation of Arabidopsis root stemness by CLAVATA1 and ARABIDOPSIS CRINKLY4 receptor kinase complexes. Current Biology **23,** 362–371.

Stahl Y, Simon R. 2009. Is the Arabidopsis root niche protected by sequestration of the CLE40 signal by its putative receptor ACR4? Plant Signaling and Behavior **4,** 634–635.

Stahl Y, Simon R. 2012. Peptides and receptors controlling root development. Philosophical Transactions of the Royal Society of London. Series B, Biological Science **367,** 1453–1460.

Stahl Y, Simon R. 2013. Gated communities: apoplastic and symplastic signals converge at plasmodesmata to control cell fates. Journal of Experimental Botany **64,** 5237–5241.

Stahl Y, Wink R, Ingram G, Simon R. 2009. A signaling module controlling the stem cell niche in Arabidopsis root meristems. Current Biology **19,** 909–914.

Sternberg M, Gullick W. 1989. Neu receptor dimerization. Nature **339,** 587.

Stokes K, Rao A. 2008. Dimerization properties of the transmembrane domains of Arabidopsis CRINKLY4 receptor-like kinase and homologs. Archives of Biochemistry and Biophysics **477,** 219–226.

Stokes K, Rao A. 2010. The role of individual amino acids in the dimerization of CR4 and ACR4 transmembrane domains. Archives of Biochemistry and Biophysics **502,** 104–111.

Tanaka H, Watanabe M, Sasabe M, Hiroe T, Tanaka T, Tsukaya H, Ikezaki M, Machida C, Machida Y. 2007. Novel receptor-like kinase ALE2 controls shoot development by specifying epidermis in Arabidopsis. Development **134,** 1643–1652.

Tanaka H, Watanabe M, Watanabe D, Tanaka T, Machida C, Machida Y. 2002. ACR4, a putative receptor kinase gene of *Arabidopsis thaliana*, that is expressed in the outer cell layers of embryos and plants, is involved in proper embryogenesis. Plant Cell Physiology **43,** 419–428.

Tang W, Kim TW, Oses-Prieto JA, Sun Y, Deng Z, Zhu S, Wang R, Burlingame AL, Wang ZY. 2008. BSKs mediate signal transduction from the receptor kinase BRI1 in Arabidopsis. Science **321,** 557–560.

Tanner K, Kyte J. 1999. Dimerization of the extracellular domain of the receptor for epidermal growth factor containing the membrane-spanning segment in response to treatment with epidermal growth factor. Journal of Biological Chemistry **274,** 35985–35990.

Tavormina P, De Coninck B, Nikonorova N, De Smet I, Cammue BP. 2015. The plant peptidome: an expanding repertoire of structural features and biological functions. Plant Cell **27,** 2095–2118..

Thiel K, Carpenter G. 2007. Epidermal growth factor receptor juxtamembrane region regulates allosteric tyrosine kinase activation. Proceedings of the National Academy of Sciences, USA **104,** 19238–19243.

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

Tian Q, Olsen L, Sun B, *et al*. 2007. Subcellular localization and functional domain studies of DEFECTIVE KERNEL1 in maize and Arabidopsis suggest a model for aleurone cell fate specification involving CRINKLY4 and SUPERNUMERARY ALEURONE LAYER1. Plant Cell **19,** 3127–3145.

Wang X, Goshe MB, Soderblom EJ, Phinney BS, Kuchar JA, Li J, Asami T, Yoshida S, Huber SC, Clousea SD. 2005. Identification and functional analysis of *in vivo* phosphorylation sites of the Arabidopsis BRASSINOSTEROID-INSENSITIVE1 receptor kinase. Plant Cell **17,** 1685–1703.

Wasternack C, Hause B. 2013. Jasmonates: biosynthesis, perception, signal transduction and action in plant stress response, growth and development. An update to the 2007 review in Annals of Botany. Annals of Botany **111,** 1021–1058.

Watanabe M, Tanaka H, Watanabe D, Machida C, Machida Y. 2004. The ACR4 receptor-like kinase is required for surface formation of epidermis-related tissues in *Arabidopsis thaliana*. Plant Journal **39,** 298–308.

Wieduwilt M, Moasser M. 2008. The epidermal growth factor receptor family: biology driving targeted therapeutics. Cellular and Molecular Life Sciences **65,** 1566–1584.

Wierzba M, Tax F. 2013. Notes from the underground: receptor-like kinases in Arabidopsis root development. Journal of Integrative Plant Biology **55,** 1224–1237.

Williams E, De Smet I. 2013. Development: CLAVATA1 joins the club of root stem cell regulators. Current Biology **23,** R245-R247.

Wybenga-Groot L, Baskin B, Ong SH, Tong J, Pawson T, Sicheri F. 2001. Structural basis for autoinhibition of the Ephb2 receptor tyrosine kinase by the unphosphorylated juxtamembrane region. Cell **106,** 745–757.

Ye H, Li L, Yin Y. 2011. Recent advances in the regulation of brassinosteroid signaling and biosynthesis pathways. Journal of Integrative Plant Biology **53,** 455–468.

You M, Li E, Wimley W, Hristova K. 2005. Forster resonance energy transfer in liposomes: measurements of transmembrane helix dimerization in the native bilayer environment. Analytical Biochemistry **340,** 154–164.

Yue K, Sandalc P, Williams EL, *et al*. 2016. PP2A-3 interacts with ACR4 and regulates formative cell division in the Arabidopsis root. PNAS **113,** 1447–1452.

Zereen J, Ingram G. 2012. A possible involvement of ACR4, a receptor like kinase, in plant defense mechanism. Bangladesh Pharmaceutical Journal **15,** 127–130.

Zheng J, Knighton DR, ten Eyck LF, Karlsson R, Xuong N, Taylor SS, Sowadski JM. 1993. Crystal structure of the catalytic subunit of cAMP-dependent protein kinase complexed with MgATP and peptide inhibitor. Biochemistry **32,** 2154–2161.

Downloaded from http://jxb.oxfordjournals.org/ at University of Nottingham on August 5, 2016

Chapter 8: Yeast 2-Hybrid and Co-Immunoprecipitation Reveal Novel Putative ACR4 Interacting Proteins

Author Contribution:

I was involved with planning and executed all experiments in this chapter except Y2H screening, which was conducted under contract with Hybrigenics.

I wrote this chapter and compiled all diagrams except where otherwise noted.

Chapter 8: Putative ACR4 Interacting Proteins

Abstract:

ARABIDOPSIS CRINKLY4 (ACR4) is a receptor-like protein kinase implicated in regulation of asymmetric cell division in both root apical meristem and lateral root primordia. Although it has been established that ACR4 suppresses *WUSCHEL-RELATED HOMEOBOX5 (WOX5)* expression in the root apical meristem, and is able to phosphorylate, and subsequently be dephosphorylated by the PROTEIN PHOSPHATASE 2A holoenzyme complex, little else is known about the downstream mechanics of ACR4 activity in regulating asymmetric cell division. This chapter presents several novel putative ACR4 interacting proteins (PAIPs) identified by yeast 2-hybrid and co-immunoprecipitation approaches, and reviews their potential involvement in ACR4-mediated signal transduction based on available literature.

8.1 Introduction

Previously, it was established that ACR4 is a key regulator of formative divisions in both the root apical meristem (RAM) and during lateral root primordium (LRP) development (De Smet, et al., 2008; Stahl, et al., 2009). *ACR4* is expressed in the RAM, epidermal tissues of the basal meristem and in the small daughter cells of lateral root primordia. *acr4* and higher order mutants display decreased regulation of asymmetric cell division in both columella and LR primordia tissues, resulting in disorganised cellular structure. At present, knowledge on ACR4 *in-vivo* protein-protein interactions and downstream signalling is limited. It has previously been reported that

homo- and hetero-dimerisation of ACR4 family members and CLAVATA1 (CLV1) are able to precieve the CLAVATA/EMBRYO SURROUNDING REGION 40 (CLE40) ligand, resulting in downregulation of *WUSCHEL-RELATED HOMEOBOX5 (WOX5)*, a nuclear expressed protein responsible for maintaining the RAM quiescent centre (QC) niche (Stahl, et al., 2009; Stahl, et al., 2013). Furthermore, recently *in-vitro* approaches have indicated that ACR4 interacts with and phosphorylates PROTEIN PHOSPHATASE 2A-SUBUNIT3 (PP2A-3), and is in turn dephosphorylated by the active PP2A holoenzyme, which appears to affect the membrane localisation of ACR4 (Yue, et al., 2016). Interestingly, the PP2A holoenzyme complex is involved in activation of the brassinosteroid response (Tang, et al., 2011), and has additionally been indicated as a critical enzyme in governing PIN-FORMED 1 (PIN1) phosphostatus, and therefore regulating PIN1 basal/apical polarisation (Ballesteros, et al., 2013), potentially indicating a role for ACR4 in regulation of polar auxin transport. Additionally, ACR4 has been indicated to interact with ABNORMAL LEAF SHAPE 2 (ALE2) – a receptor-like kinase (RLK) responsible for defining epidermal identity during ovule development – and this interaction triggers transphosphorylation of both kinases *in-vitro* (Tanaka, et al., 2007). These interactions indicate multiple proteins are able to form complexes with ACR4*,* potentially allowing the perception of alternative ligands and activation of alternative signalling pathways dependent on which interaction partner is co-expressed with *ACR4*. These notable interactions aside, it remains unclear how ACR4-mediated signalling is transduced, resulting in regulation of *WOX5* expression.

To address this gap in knowledge, two parallel proteomics screens were employed in order to identify novel interactors of ACR4 potentially responsible for signal transduction. A Yeast-2-Hybrid screen was conducted on the intracellular domain of ACR4, and a Co-Immunoprecipitation

(Co-IP) screen on the full length ACR4:YFP fusion protein. Putative interacting proteins identified by these screens were subsequently analysed for root architectural traits potentially relevant to the *acr4* phenotype.

8.2 Results and Discussion

Yeast 2-Hybrid Analysis Reveals Six Novel Putative ACR4 Interacting Proteins

The high throughput yeast-2-hybrid screen conducted on the intracellular domain of ACR4 (published in Yue et al 2016 – Appendix 1) indicated 4 PUTATIVE ACR4 INTERACTING PROTEINs (PAIPs) with a high level of confidence, and a further two PAIPs with lower confidence, due to lower clone survival on selection medium. However, since yeast colony growth depends upon two halves of split GAL4 being brought into proximity with *IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (HIS3)* by bait and prey proteins, resulting in expression of HIS3, and allowing growth on media lacking in histidine, these proteins remain possible interactors of ACR4 nonetheless (Table 1).

Table 1: Yeast-2-Hybrid screening (Hybrigenics) identified six putative ACR4 interacting proteins, for which descriptions were retrieved from the UniProt database.

AGI Code	Protein Name	Number of Clones
At1g49840	Protein of Unknown Function	2
At5g01020	Serine/threonine-protein kinase At5g01020 - membrane	11
At1g70070	DEVH-box ATP-dependent RNA helicase ISE2, chloroplastic	11
At1g06800	Phospholipase A1-Igamma1, chloroplastic	13
At2g30550	Phospholipase A1-Igamma2, chloroplastic	8
At3g11130	Clathrin Heavy Chain 1	1

Co-Immunoprecipitation Reveals Additional Novel PAIPs

Method Optimisation

In order to probe deeper into the ACR4 interactome, a co-immunoprecipitation (Co-IP) approach was employed using an *ACR4:YFP* fusion construct and GFP-Trap (ChromoTek). In order to optimise the experiment, it was first necessary to determine if ACR4:YFP could be detected via Western blotting techniques following immunoprecipitation using HRP conjugated anti-GFP (Abcam). Detection of ACR4:YFP was not initially possible with the *pACR4::ACR4:YFP* or *35S::ACR4:YFP* native promoter and overexpression lines respectively, though the control (PIN1:GFP) could be detected by anti-GFP, therefore alternative extraction buffers were trialled. Adjustments to salt and detergent compound and quantity were ineffective at increasing ACR4:YFP available for detection, however increasing the pH of the extraction buffer to pH 9.5 (From pH 7.5) allowed for detection of ACR4:YFP in the overexpression line (Figure 1). This is likely due to the fact that integral membrane proteins often have higher pI values than cytoplasmic proteins, allowing for increased stability in the acidic environment of the extracellular matrix (Schwartz, et al., 2001). In addition, many membrane proteins contain hydrophobic α-helices, causing precipitation at their isoelectric point, making detection of rare membrane proteins difficult (Komatsu, et al., 2007).

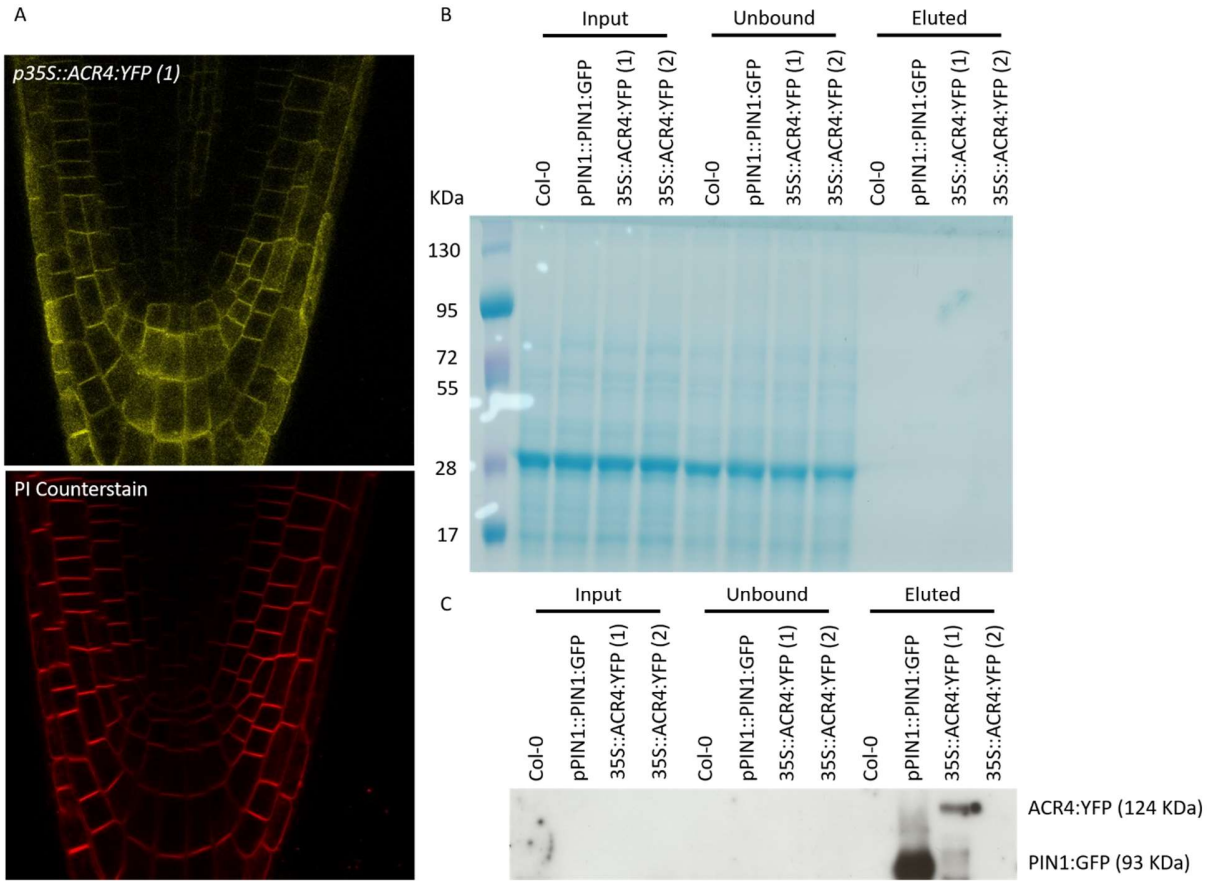


Figure 1: Detection of immunoprecipitated ACR4:YFP using HRP-conjugated anti-GFP primary antibody following total protein extraction using an alkaline extraction buffer (pH 9.5). Col-0 and *pPIN1::PIN1:GFP* seedlings were used as negative and positive controls (respectively) for GFP detection, and protein samples were analysed following extraction (input), after immunoprecipitation (unbound), and following elution from GFP-trap agarose beads (eluted). A) Confocal analysis of *p35S::ACR4:YFP (1)* confirms ACR4:YFP fusion protein is present in transformed roots. B) Coomassie stain of SDS-PAGE protein samples showing even loading/concentration of protein. C) Western blot analysis demonstrates presence of ACR4:YFP and PIN1:GFP control in the eluted fraction, which are not detectable in the input or unbound fractions, indicating significant concentration of these proteins by GFP-trap immunoprecipitation.

Western analysis following extraction of protein using pH 9.5 extraction buffer and subsequent immunoprecipitation indicates that both PIN1:GFP and ACR4:YFP are significantly concentrated following immunoprecipitation, since neither protein was detected in the input or unbound fractions, but was present in the eluted fraction. This indicates that the immunoprecipitation is effective at concentrating these proteins from a dilute solution, and should therefore be efficacious in isolating putative interacting proteins.

LC-MS/MS Analysis of Co-Immunoprecipitated Proteins Indicates Additional Novel PAIPs

Once *35S::ACR4:YFP(1)* was confirmed as a good line for ACR4:YFP pulldown, demonstrating optimisation of the extraction and precipitation techniques, quadruplicate total protein samples were prepared from the *35S::ACR4:YFP*and Col-0 background lines, precipitated using GFP-trap beads (ChromoTek), and interacting proteins were identified by LC-MS/MS analysis following on-bead digestion of protein (as described in Materials and Methods, Figure 2).

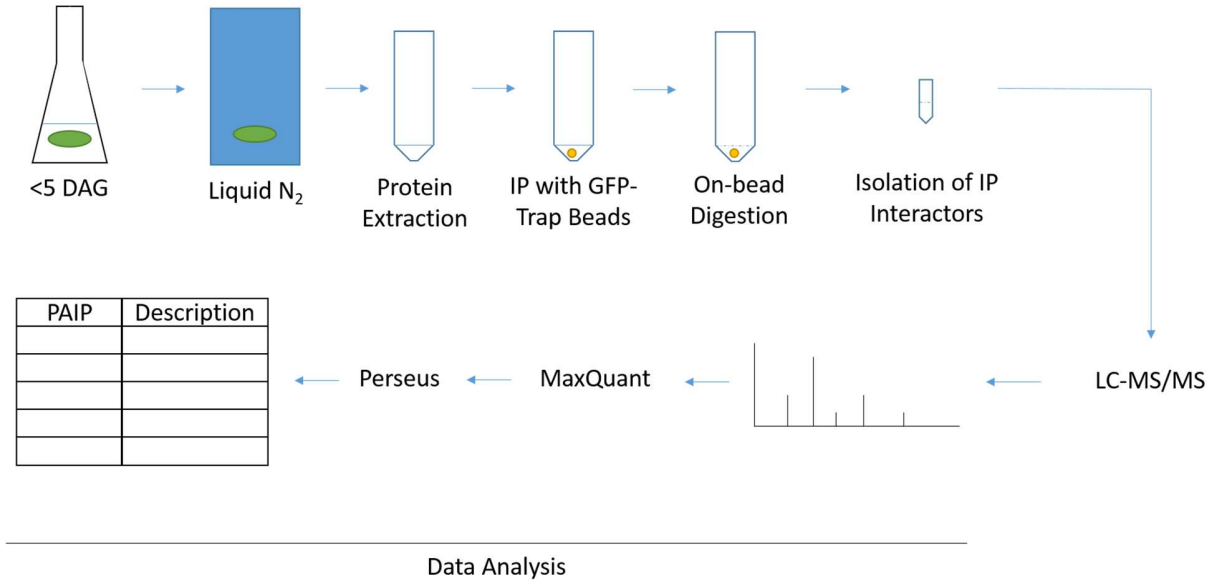


Figure 2: A schematic representation of Co-IP methodology.

This indicated 277 putative ACR4 interacting proteins (Appendix 2), of which 52 were over 10-fold more concentrated in the immunoprecipitation samples than in Col-0. Contaminants (e.g. keratin, trypsin) were omitted, and the remaining results were filtered for proteins potentially involved in signalling or transport processes and stress responsive genes. Screening in this manner resulted in 14 further PAIPs potentially involved in ACR4 signalling and/or processing (Table 2).

Table 2: 14 PAIPs were identified by Co-IP, with potential for involvement in root architectural development.

Name (Identifier)	Fold Change in 35S::ACR4:YFP vs Col-0	Description
(At3g20820)	107.1	Leucine-rich repeat-containing protein
TUBB5 (At1g20010)	63.7	Tubulin beta-5 chain
CHC2;CHC1 (At3g08530;At3g11130)	54.6	Clathrin heavy chain 2;Clathrin heavy chain 1
SHM4 (At4g13930)	41.9	Serine hydroxymethyltransferase 4
(At1g29310; At2g34250)	41.8	Putative Uncharacterised Protein; Putative uncharacterized protein
APM1 (At4g33090)	38.4	Aminopeptidase M1
Alpha-COP2; Alpha-COP1 (At2g21390;At1g62020)	35.1	Coatomer subunit alpha-2;Coatomer subunit alpha-1
RPT5B;RPT5A (At1g09100;At3g05530)	26.4	26S protease regulatory subunit 6A homolog B;26S protease regulatory subunit 6A homolog A
PIP1B (AT2G45960)	23.7	Aquaporin PIP1B
T1G11.19 (At1g04560)	19.7	AWPM-19-like family protein
T15B16.17a:T15B16.17b (At4g01610)	14.8	Cathepsin B-like cysteine protease
Probable LRR-RLK;Probable LRR-RLK (At3g14840;At1g53440)	12.6	Probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840;Probable LRR receptor-like serine/threonine-protein kinase At1g53440
RPN11 (At5g23540)	10.4	26S proteasome non-ATPase regulatory subunit 14
RD21B (At5g43060)	10.2	Probable cysteine protease RD21B

Attempts to Establish an acr4 Root Architectural Baseline Reveals Inconsistency in Phenotype Between Analyses

ACR4 is an important regulatory kinase, responsible for restricting asymmetric cell division in primary and lateral root meristematic tissues, thus shaping the correct development of these tissues. Although there are more primordia formed in the *acr4* background comparative to wild-type, lateral root emergence is decreased, indicating increased abortion of lateral root development. From this perspective, any *paips* displaying similar or corresponding root architectural traits to that of *acr4* are more likely to be of biological relevance.

In order to establish a baseline root trait for comparison with *paips, acr4-2* (De Smet, et al., 2008), and a novel pentuple mutant (*acr4-crr1-crr2-crr3-crr4*) (Appendices 3 & 7) were analysed for root architectural traits comparative to wild-type *Arabidopsis* (Col-0). T-DNA insert locations were confirmed by PCR-based genotyping and sequencing as described in materials and methods, and qPCR analysis indicated knockdown of all *ACR4* homologues (Figure 3 A and B). Interestingly – in contrast to the findings of De Smet *et al.* – root trait analysis of *acr4* indicated increased lateral root emergence, while the higher order mutant demonstrated increased primary root length, and a subtle, but not statistically significant increase to lateral root density (Figure 3 C-E). This apparent contrast in root architecture may be due to differences in media composition and/or growth conditions, and warrants further investigation of the effect of mineral availability on root architectural development in *acr4.* For the purposes of this investigation, root traits will be compared to the published data for *acr4,* as the observed differences may be due to age or the number of times the *acr4* mutant lines had been bulked, or differences in growth or assay conditions between laboratories. Since the *paip* mutants were seed-bulked twice in isolated

conditions (once following isolation of homozygous seedlings and once further for generation of large numbers of seed), it is unlikely that there was any introduction of downstream gene silencing or random mutations following genotyping.

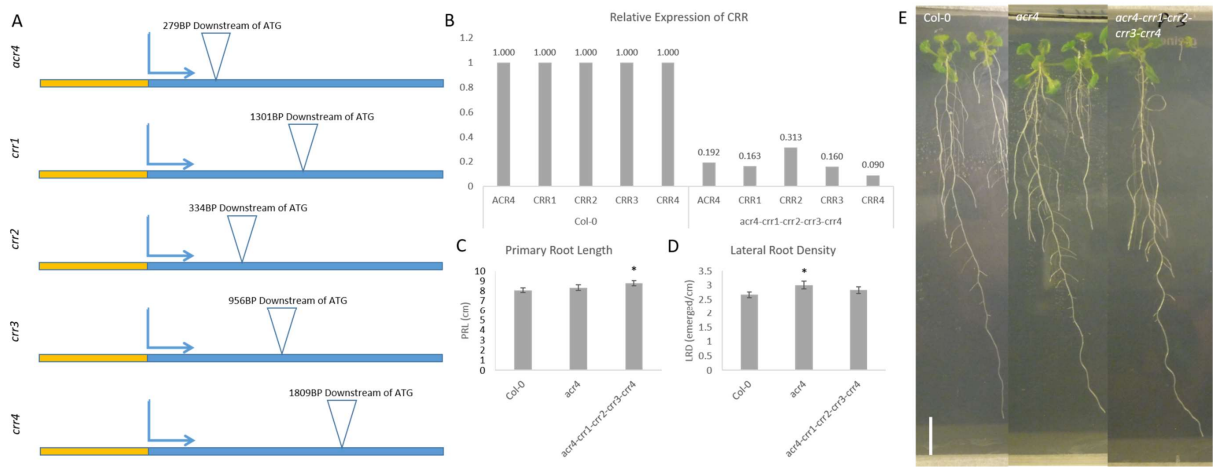


Figure 3: Characterisation of *acr4* and *acr4-crr1-crr2-crr3-crr4*. A) T-DNA insert locations were identified by sequencing of PCR products. B) qPCR analysis indicates decreased expression of *ACR4* and *CRR1-4* in the pentuple mutant. C-E) Root trait analysis indicates that *acr4* has increased emerged lateral root density, with no significant change to primary root length, and *acr4-crr1-crr2-crr3-crr4* indicates increased primary root length, but no change to emerged lateral root density, compared to wild-type Arabidopsis (Col-0). Error bars represent standard error, * = P<0.05, scale bar = 1 cm.

UNK Characterisation Reveals a Novel Regulator of Lateral Root Density

AT1G49840 Encodes a Protein of Unknown Function

The UniProt entry for *AT1G49840* indicates that it encodes an uncharacterised protein of unknown function (UNK). The presence of a protein of unknown function in the Y2H screen is intriguing, as most signalling elements such as kinases and phosphatases can be easily identified by the conserved enzymatic domains present within the protein sequence. UNK however, does not appear to contain any domains of known function by which a putative function may be assigned, instead containg a single domain of unknown function (DUF620). Therefore, how the domain functions and whether UNK/ACR4 interactions have an impact on development is unclear.

An in-silico Approach Provides Hints to Potential UNK Function

In order to investigate putative functions for UNK, a BLASTp search (Phytozome 11) was conducted against *Arabidopsis* in order to determine similarity to other proteins of known function. This approach revealed a small family of 9 similar proteins in *Arabidopsis*, all of which are of unknown function, and contain domain of unknown function (DUF620) domains (Figure 4). Cross-referencing these genes with the Uniprot database did not reveal any putative function, and submission of the UNK protein sequence into the InterProScan 5 database similarly yielded no results for domains of known function.



Views	Defline	Score	E	Query View
G B	AT1G49840.1 Protein of unknown function (DUF620)	942.6	0.0	1-494
G B	AT3G19540.1 Protein of unknown function (DUF620)	725.7	0.0	1-494
G B	AT1G27690.1 Protein of unknown function (DUF620)	497.3	2E-172	72-449
G B	AT5G05840.1 Protein of unknown function (DUF620)	363.6	3.5E-120	134-479
G B	AT1G79420.1 Protein of unknown function (DUF620)	358.6	1.5E-118	85-442
G B	AT5G06610.1 Protein of unknown function (DUF620)	310.1	2.3E-100	86-443
G B	AT5G66740.1 Protein of unknown function (DUF620)	308.1	1.4E-99	78-443
G B	AT3G55720.1 Protein of unknown function (DUF620)	302.0	2.3E-96	78-442
G B	AT1G75160.1 Protein of unknown function (DUF620)	292.4	3.4E-93	141-444

Figure 4: A Phytozome 11 BLASTp search of UNK indicates a small family of 9 homologous proteins in *Arabidopsis.*

BLASTp results were aligned using Jalview (TCoffee with defaults – Appendix 4). This alignment indicated multiple stretches of highly conserved amino acid sequence according to the BLOSUM62 matrix, suggesting that members of this family may serve a similar function. However, none of the 9 UNK family members have been assigned a putative function, therefore potentially indicating a novel family of signalling effectors. Since ACR4 family members are also unusual, containing a cysteine-rich CRINKLY repeat domain in place of the more common leucine-rich repeat receptor domain, UNK/ACR4 interaction may indicate a previously uncharacterised signalling module capable of regulating asymmetric cell division.

To probe further into putative UNK function, a second, broader, BLASTp search was performed against the UniProt database using the BLOSUM62 matrix, revealing 691 proteins with homologous amino acid sequences (Appendix 5). Uncharacterised proteins, unannotated proteins and fragments were filtered from the search, and the remaining proteins were aligned in CLC workbench, and a phylogenetic tree was constructed. Proteins clustering with the outgroup were then omitted and remaining proteins were realigned, resulting in 14 annotated proteins aligned with the 9 UNK family members from *Arabidopsis* (Figure 5).

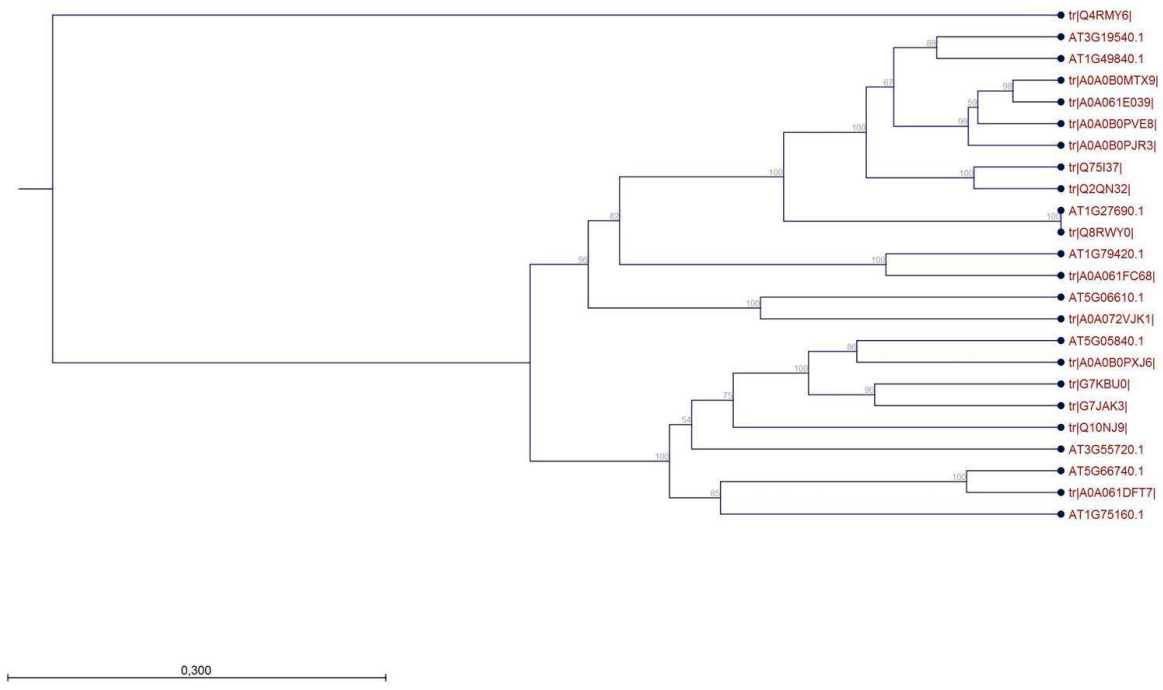


Figure 5: A phylogeny constructed from a BLAST search of the UniProt database indicates closely related proteins from across the plant kingdom.

The resulting phylogeny indicates primarily that orthologues of UNK are restricted to the plant kingdom, suggesting that UNK and its orthologous proteins evolved after plants and animals diverged from their last common ancestor. The closest orthologues to UNK are a group of predicted glutamyl-tRNA amidotransferase subunits in *Gossypium arborium* (A0A0B0PVE8, A0A0B0PJR3, A0A0B0MTX9), and a predicted soluble secretory phospholipase A2 receptor in *Theobroma cacao* (A0A061E039). Alignment of these proteins with UNK indicates significant sequence homology (Appendix 6) for all proteins, therefore it remains difficult to assign a putative function to UNK without additional experimental evidence.

Interestingly, there is evidence that another glutamine amidotransferase, GAT1_2.1 (AT1G15040) suppresses branching in the Arabidopsis shoot (Zhu & Kranz, 2012), suggesting that

members of this family may play a role in lateral organ development; however, the mechanism by which GAT1_2.1 inhibits shoot branching remains unclear.

Intriguingly, given that membrane anchored receptors are one of the main areas of investigation in plant models, little is known about soluble secretory phospholipase receptors in *Arabidopsis.* In mouse and human model organisms however, evidence suggests that soluble secretory phospholipase receptors are able to bind PHOSPHOLIPASE A2, which severely inhibits the activity of the latter molecule (Higashino, et al., 2002; Ancian, et al., 1995). TMHMM indicates there are no transmembrane sequences in UNK (Figure 6), therefore it is likely that *UNK* is located in the cytosol, or is secreted. If UNK does belong to this family of proteins, it may represent a novel form of regulation for phospholipase mediated signalling in *Arabidopsis*. Interaction of such a molecule with ACR4 may allow altered regulation of bioactive lipid derived signalling.

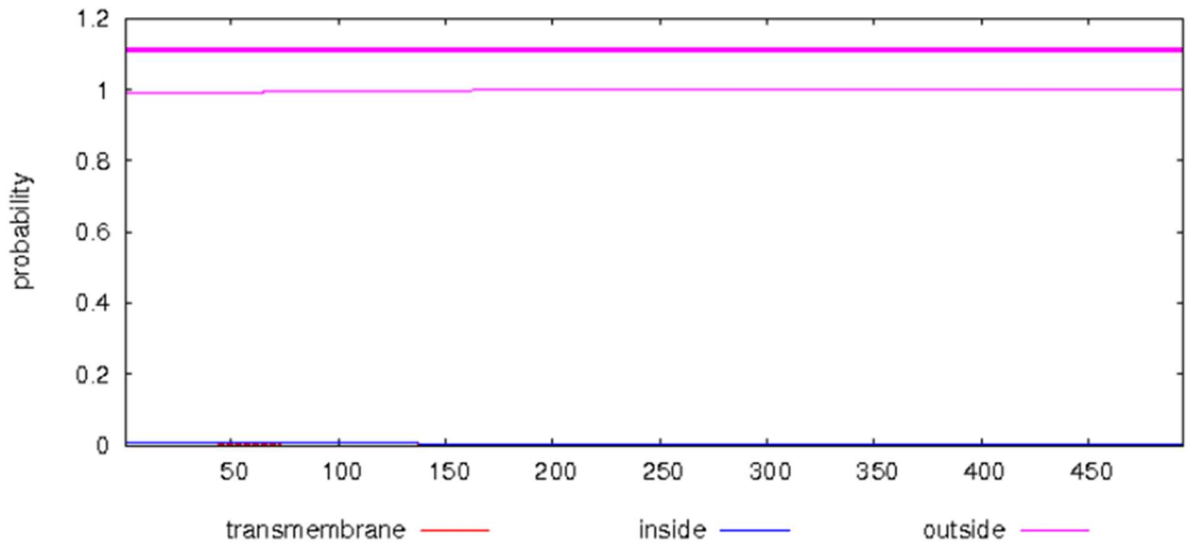


Figure 6: TMHMM analysis of UNK suggests no transmembrane helices are present in the protein sequence, therefore it is likely that this protein is located in the cytoplasm.

Finally, the closest annotated relative in *Arabidopsis* (Q8RWY0/AT1G27690) is a putative lipase (by similarity), according to UniProt annotation. If UNK does indeed belong to this class of molecule, this interaction may provide further evidence for ACR4 mediated regulation of the production of bioactive lipids.

Interestingly, *ACR4* has previously been indicated in regulation of bioactive lipid production, as expression of *LIPOXYGENASE 2 (LOX2)* – an essential enzyme for jasmonic acid (JA) production – is increased in *acr4* (Zereen & Ingram, 2012). If UNK does indeed belong to either the lipase or soluble phospholipase receptor families, the interaction indicated by the Y2H screen may potentially indicate a novel mechanism for ACR4-mediated regulation of bioactive lipid synthesis.

In order to further characterise the nature of UNK/ACR4 interactions, translational fusion and mutant lines were examined in order to determine localisation and root architectural traits.

Analysis of pUNK::UNK:GFP Reveals a Membrane Localised, Meristem-specific Expression Pattern.

To determine tissue specificity and subcellular localisation of UNK, the construct *pUNK::UNK:GFP* was transformed into *Arabidopsis* (as described in materials and methods). Confocal analysis of *pUNK::UNK:GFP* expression indicates that *UNK* is expressed in the root apical and basal meristem tissues, and in the lateral root primordium from stage 1 until emergence (Figure 7). Expression of pUNK::UNK:GFP is retained in the mature lateral root, where it is observed in the basal meristem region. Surprisingly, given that UNK contains no putative transmembrane domains (Figure 6), confocal microscopy also indicated that UNK:GFP is partially membrane localised

(Figure 7). Since the yeast 2-hybrid analysis indicates that UNK and ACR4 are able to interact *in-vitro*, it is possible that the membrane localisation observed is due to interaction with ACR4 on the plasma membrane.

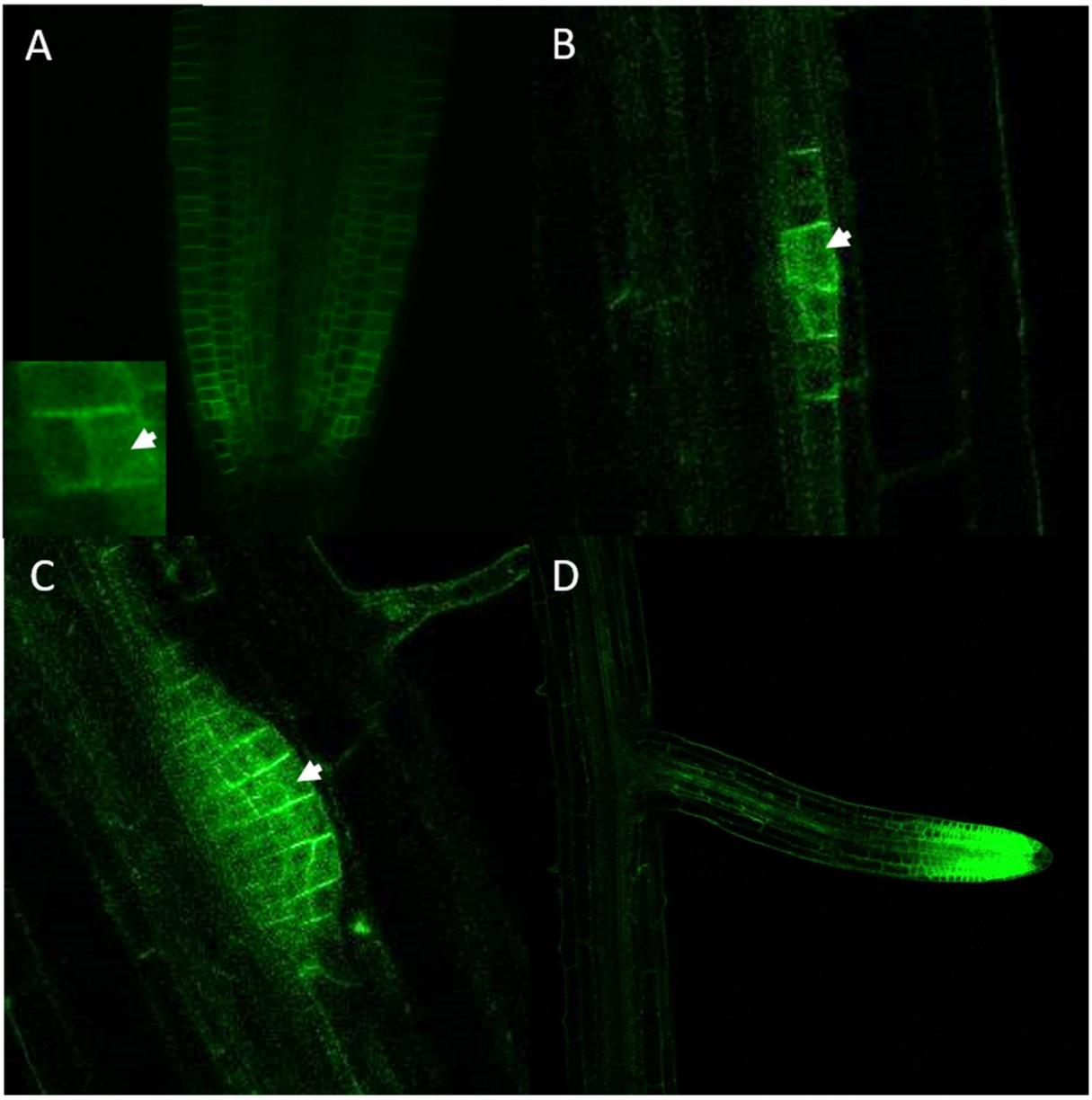


Figure 7: Confocal analysis of *pUNK::UNK:GFP* indicates membrane associated expression in the root apical meristem (A), lateral root primordia from early (B) to late (C) stages of development, and expression is retained by

the basal meristem region of the mature emerged lateral root (D). Additionally, closer analysis of UNK:GFP localisation potentially indicates a cytoplasmic population of UNK:GFP (A – inset, arrowheads).

Interestingly, UNK:GFP is not observed in the columella tissues, therefore it is unlikely that it interacts with ACR4 in this region. However, *ACR4* expression has also been observed in the epidermal cells of the basal meristem (De Smet, et al., 2008), therefore it is possible that the interaction indicated by the Y2H screen may occur here. It is additionally interesting to note that UNK:GFP appears only partially membrane localised, potentially indicating that interactions with ACR4 may mediate the transition between membrane bound and cytosolic localisation. At this point the nature of the putative interaction between UNK and ACR4, and how this interaction may influence root architecture remains unclear. However, since ACR4 is responsible for defining epidermal identity in the leaf, it is possible that a similar role is fulfilled in the root epidermis, and UNK may be involved in downstream signalling.

unk T-DNA Insertion Mutant Displays Decreased Emerged Lateral Root Density

To determine the effect of *unk* on root architecture, a SAIL T-DNA insertion line was sourced (NASC/ABRC – Appendices 3 & 7). Insert location was confirmed by PCR-based genotyping and sequencing as described in methods and materials, and qPCR determined that *UNK* expression was decreased by 97.1% in the mutant line (Figure 8 A & B).

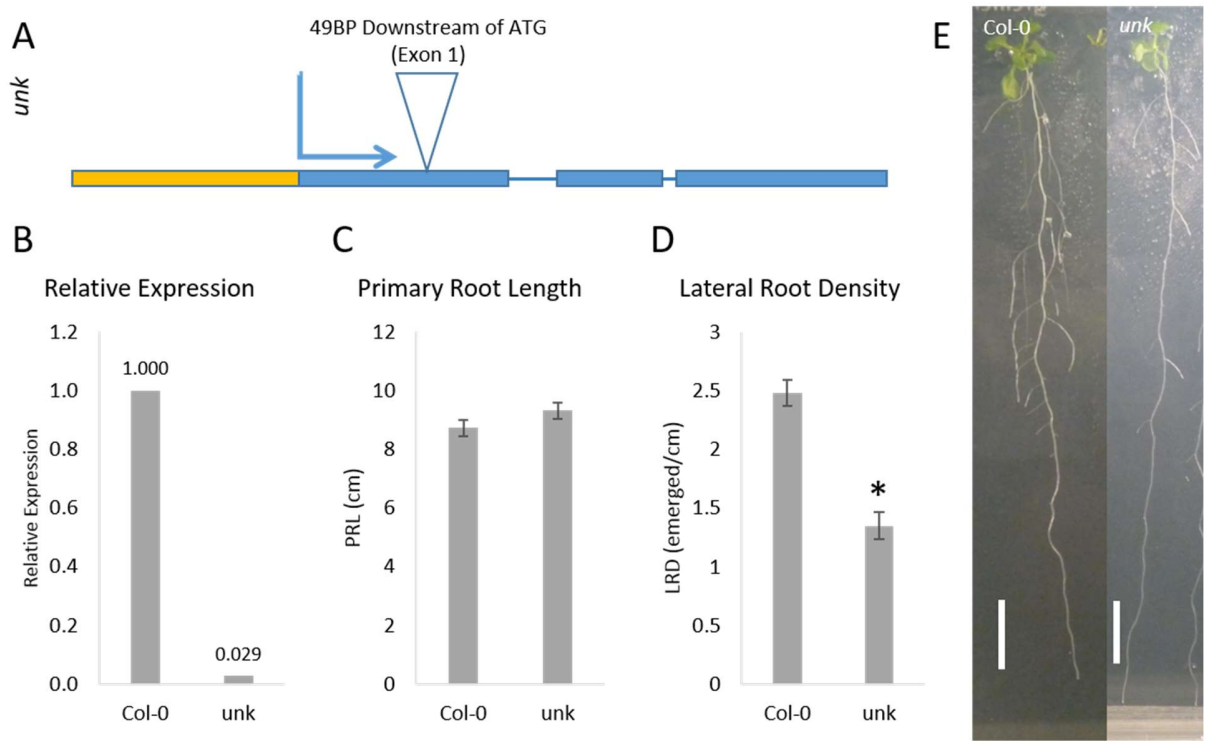


Figure 8: Characterisation of the *unk* mutant. A) PCR-based genotyping and sequencing located the T-DNA insert in the exon 1 of *unk*. B) qPCR analysis indicates 97.1% knockdown of *UNK* expression in the mutant line. C – E) Root trait analysis indicates that *unk* has a similar primary root length, but significantly decreased lateral root density compared to wild-type Arabidopsis (Error bars = standard error, * = P<0.05, scale bars = 1 cm).

Root architectural trait analysis of *unk* indicates decreased emerged lateral root density when compared to wild-type Arabidopsis, but *unk* maintains similar primary root growth, as there is no significant difference in primary root length (Figure 8 C - E). The observed phenotype is phenotypically similar to that published for ACR4 (De Smet, et al., 2008), suggesting that UNK may act as a downstream effector of ACR4 signalling.

Together with the meristem-specific expression pattern of UNK:GFP, the decreased lateral root density observed in *unk* may indicate that UNK is involved in regulating differentiation in meristematic regions. Since *unk* mutation alone exhibits a significant alteration to root architecture compared to the wild-type, functional redundancy – at least within the root - seems unlikely, suggesting either that members of this family are subject to strict spatiotemporal regulation, with individual members being regulated appropriately in response to activation of distinct signalling modules; or alternatively, different family members may be involved in regulation of other lateral organ development (eg. Adventitious roots, leaves, floral meristems).

UNK May Represent a Novel Effector of ACR4-Mediated Bioactive Lipid Regulation

In-silico analysis of UNK indicates that it may encode a number of proteins potentially involved in developmental processes. Although it is not currently possible to rule out the potential that UNK may belong to the glutamine amidotransferase family, it is intriguing to note that a number of orthologous proteins are involved in regulation of bioactive lipid production. Bioactive lipids govern a large number of signalling and regulatory processes (Hannun & Obeid, 2008). Very-long-

chain fatty acids (discussed in Chapter 6) are one group of bioactive signals capable of regulating root architectural development, however, previous evidence has indicated that ACR4 signalling may be involved with regulating biosynthesis of another lipid-derived signal – jasmonic acid (JA) – via regulation of *LOX2* (Zereen & Ingram, 2012; Wasternack & Xie, 2010).

Since JA has previously been shown to increase lateral root emergence (Raya-González, et al., 2012), and *acr4* exhibits increased expression of *LOX2* (Zereen & Ingram, 2012), as well as increased lateral root initiation, but decreased emergence (De Smet, et al., 2008), it is possible that ACR4/UNK interactions may restrict JA production in specific cells. Given that the action of JA has been indicated to stimulate auxin production in lateral root primordia via the JA-responsive ETHYLENE RESPONSE FACTOR 109 (ERF109), which results in the up-regulation of two enzymes involved in auxin synthesis, *ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1 (ASA1)*, and *INDOLE-3-PYRUVATE MONOOXYGENASE YUCCA2 (YUC2)* (Cai, et al., 2014), it is tempting to speculate that the localised action of ACR4/UNK signalling may restrict JA production, thus dampening auxin production and causing a perturbance in the auxin:cytokinin ratio on a cellular scale. This effective increase in cytokinin signalling may allow the differentiation of key tissues during lateral root development. Taking into account that *ACR4* is required for correct epidermal development in leaf cuticle (Watanabe, et al., 2004), it is possible that it performs a similar function during lateral root development, and that definition of the epidermal layer via localised regulation of JA production is critical for the correct development and emergence of lateral root primordia.

PLA-Iγ2 Characterisation Reveals a Novel Role in Regulation of Lateral Root Density

AT1G06800 and AT2G30550 Encode Phospholipases Involved in JA Synthesis

AT1G06800/PHOSPHOLIPASE A1-Iγ1 (PLA-Iγ1) and AT2G30550/PHOSPHOLIPASE A1-Iγ2 (PLA-Iγ2), are two highly homologous constitutively expressed chloroplast related phospholipases responsible for catalysing the hydrolysis of phosphatidylcholine at the *sn*-1 position (Seo, et al., 2009). Both PLAs are comparatively polygamous, accepting not only phosphatidylcholine as a substrate *in-vitro*, but also monogalactosyldiacylglycerol, digalactosyldiacylglycerol and triacylglycerol (Seo, et al., 2009). Previous analyses have indicated that *pla-Iγ1* has reduced jasmonic acid (JA) accumulation in the early stages of wound response, and *pla-Iγ2* has decreased basal levels of JA, indicating that these PLA proteins may contribute to JA synthesis by hydrolysis of phospholipids, creating a pool of precursor lipid molecules (Ellinger, et al., 2010; Ruduś, et al., 2014). Given that *pla-iγ2* showed no reduction to wound induced JA responsiveness, but decreased basal levels of JA (Ellinger, et al., 2010), it is tempting to speculate that this enzyme may be involved in production of JA precursors for growth and development. In this respect, it is possible that ACR4 may be able to regulate JA biosynthesis both basally and during wound response.

pla-iγ2 Displays a Significant Change to Root Architecture

pla-iγ2 was analysed for root architectural traits similarly to *unk,* as described in materials and methods (Appendices 3 & 7). PCR-based genotyping and sequencing determined SALK T-DNA insertion was located in the promoter region, 246 bp upstream of ATG (Figure 9 A). qPCR analysis

indicated that the T-DNA insertion resulted in a knockdown of 98.8% of *PLA-Iγ2* expression (Figure 9 B). Finally, root trait analysis indicates that *pla-iγ2* significantly increases primary root length and lateral root density compared to wild-type *Arabidopsis* (Figure 9 C - E).

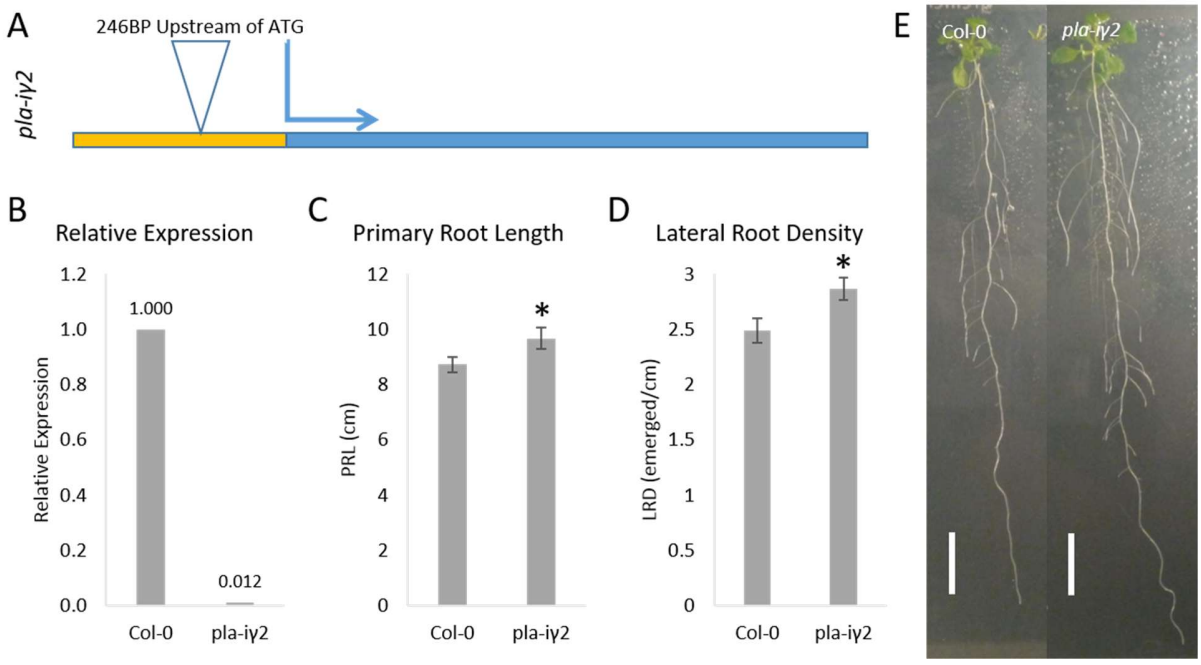


Figure 9: Characterisation of the *pla-iγ2* mutant. A) PCR-based genotyping and sequencing located the T-DNA insert in the promoter region of *pla-iγ2*. B) qPCR analysis indicates 98.2% knockdown of *PLA-Iγ2* expression in the mutant line. C – E) Root trait analysis indicates that *pla-iγ2* has significantly increased primary root length and lateral root density compared to wild-type Arabidopsis (Error bars = standard error, * = P<0.05, scale bars = 1 cm).

PLA-Iγ2 Interaction with ACR4 Further Implicates a Role for ACR4 in Regulation of Bioactive Lipid Synthesis

pla-iγ2 exhibits a root architectural phenotype opposite to that published for *acr4* (De Smet, et al., 2008). Given it has previously been demonstrated that *pla-iγ2* has decreased basal levels of JA (Ellinger, et al., 2010), and that JA has been described to promote lateral root emergence by upregulation of auxin biosynthesis in lateral root primordia (Cai, et al., 2014), it initially appears

strange that lateral root density is increased in *pla-iγ2* – a trait normally associated with increased auxin or JA. However, primary root length is also increased, in contrast to the physiological trait normally attributed to overexpression of auxin and JA (Cai, et al., 2014; Staswick, et al., 1992). This may suggest that the decreased basal level of JA present in *pla-iγ2* in turn decreases localised auxin synthesis globally, but given the comparatively isolated nature of lateral root primordia, they may be affected more than tissues with less restricted access to auxin. Hypothetically, therefore, it is possible that the presence of cytokinin surrounding the diminished auxin maxima primordia results in a perturbed auxin:cytokinin ratio, increasing differentiation of lateral root tissues, which may result in the observed increase to emerged lateral root density.

At this point, it is interesting to note that while *acr4* displays fewer emerged lateral roots, increased lateral root initiation occurs, but due to lack of regulation of asymmetric cell division, the boundaries of many primordia are poorly defined, leading to abortion of lateral root development (De Smet, et al., 2008). This may suggest that the presence of auxin is able to initiate lateral root primordia formation in *acr4,* but due to decreased regulation of JA by ACR4, the fine tuning of localised auxin biosynthesis is disrupted on a cellular level, preventing the correct differentiation into specific cell lineages responsible for correct lateral root development. Given its role in epidermal differentiation in the aerial tissues (Czyzewicz, et al., 2016), it is possible that ACR4 fulfils a similar role in defining the epidermal layer during lateral root development, and that this layer produces further signals which are capable of regulating continued development of the primordium into an emerged lateral root.

Since PLA-Iγ2 is a chloroplast related protein (Seo, et al., 2009), it is unlikely that it regulates root architecture except possibly via regulating global availability of JA precursors, although it remains

possible that *PLA-Iγ2* may also be expressed in plastids, since previous analyses were conducted on protoplasts isolated from rosette tissue (Seo, et al., 2009). However, this hypothesis does not explain the divergent subcellular localisation of ACR4 and PLA-Iγ2, being membrane and chloroplast localised respectively. Interestingly, it has been indicated that chloroplast expressed proteins can be exported during periods of biotic and abiotic stress (Kwon, et al., 2013). From this perspective, given that JA is also upregulated in response to wounding, it is possible that upon induction of stress, a cytosolic population of PLA-Iγ2 may be established that is capable of interaction with ACR4. The putative interaction of ACR4 with PLA-Iγ1 and PLA-Iγ2 therefore provides additional evidence for ACR4-mediated regulation of JA synthesis.

Knockdown of STPK is Insufficient to Induce a Change to Root Architecture

AT5G01020 Encodes a Serine/Threonine Protein Kinase

AT5G01020 is a serine/threonine protein kinase (STPK) of unknown function. Protein kinases are an important group of phosphotransferase enzymes involved in protein signalling due to their ability to define conformation of proteins by transferring a phosphate group from ATP to specific amino acid residues. Serine/threonine protein kinases, as the name suggests, specifically target serine and threonine residues on substrate proteins. Cytosolic protein kinases commonly act as intermediary signals in signalling cascades, as they are not membrane bound, and therefore are capable of transducing signals from membrane bound receptor kinases to downstream effectors. From this perspective, it is possible that STPK represents such an element capable of transducing ACR4 signalling.

TMHMM Analysis Indicates STPK is Unlikely to Contain a Transmembrane Helix

TMHMM analysis of STPK indicates that it is unlikely to contain any transmembrane helix domains, suggesting that STPK is located in the cytoplasm (Figure 10). This may indicate that STPK is a kinase involved in transducing ACR4 signalling to downstream effectors.

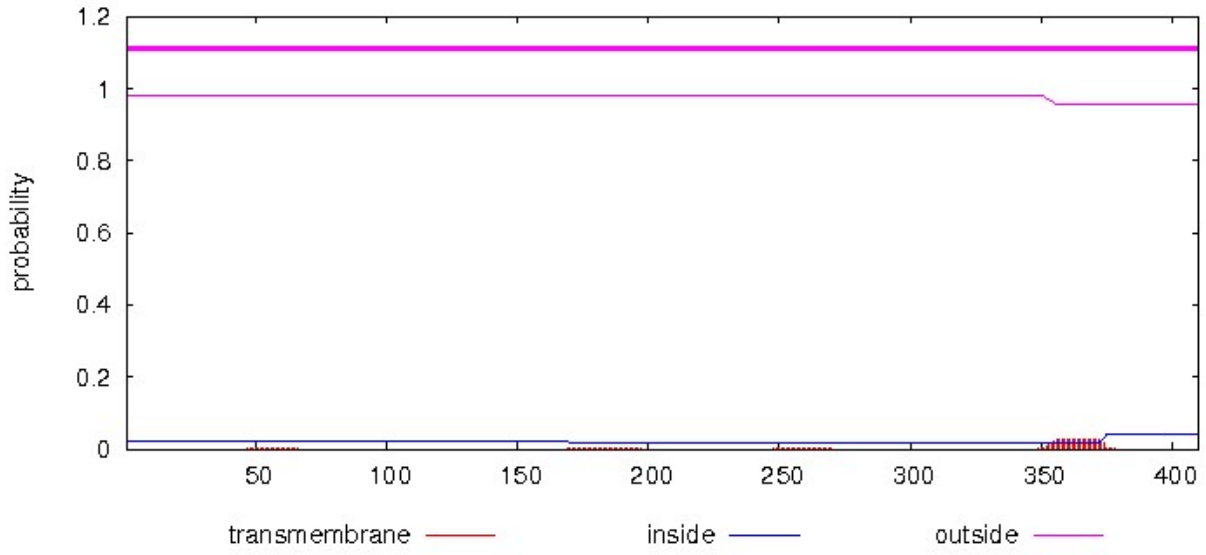


Figure 10: TMHMM analysis indicates STPK is unlikely to contain any transmembrane domains, therefore is likely to be located in the cytoplasm.

stpk does not Demonstrate any Significant Change to Root Morphology

stpk was analysed for root architectural traits similarly to *unk* and *pla-iγ2,* as described in materials and methods (Appendices 3 & 7). PCR-based genotyping and sequencing determined SALK T-DNA insertion was located in the promoter region, 111 bp upstream of ATG (Figure 11 A). qPCR analysis indicated that the T-DNA insertion resulted in a knockdown of 35.3% of *STPK*

expression (Figure 11 B). Finally, root trait analysis indicates that the isolated *stpk* mutant has no significant effect on root architectural development (Figure 11 C - E).

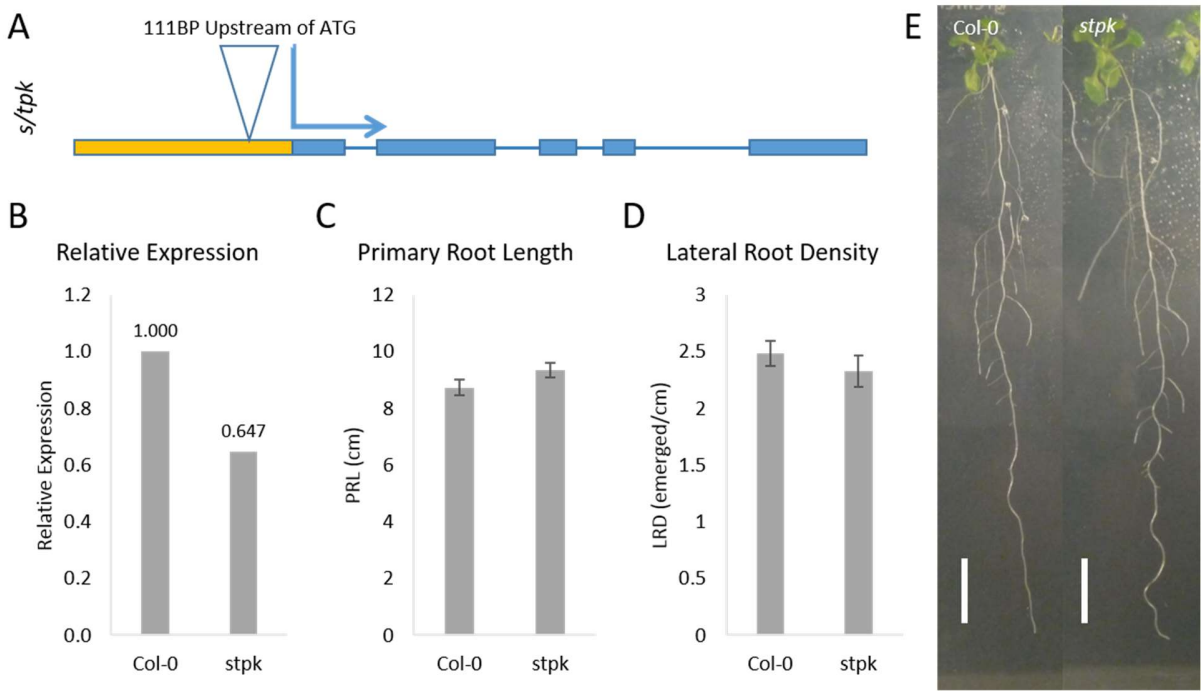


Figure 11: Characterisation of the *stpk* mutant. A) PCR-based genotyping and sequencing located the T-DNA insert in the promoter region of *stpk*. B) qPCR analysis indicates 35.3% knockdown of *STPK* expression in the mutant line. C – E) Root trait analysis indicates that *stpk* shows no significant change in root morphology compared to wild-type *Arabidopsis* (Error bars = standard error, * = P<0.05, scale bars = 1 cm).

stpk May Represent a Novel Mediator Capable of Mediating ACR4-derived Signalling

Although no significant architectural traits were observed in *stpk,* it is possible that this is due to functional redundancy with other kinase enzymes potentially associated with ACR4. Alternatively, since expression of *STPK* is not as strongly decreased as that of *UNK* or *PLA-Iγ2* in

their respective mutant lines, it remains possible that the T-DNA insert location does not disrupt promoter activity enough to induce a phenotype in the isolated line.

Interestingly, STPK was identified as a target for N-myristoylation by N-myristoyltransferase *in-vitro* (Boisson, et al., 2003; Pierre, et al., 2007). Myristoylation is the process by which a myristoyl group (derived from the 14-carbon myristic acid) is covalently bonded to a glycine residue at the n-terminus of a protein following methionine excision (Boisson, et al., 2003). N-terminal modification in this manner causes membrane targeting of the protein, and is additionally thought to allow additional protein-protein interactions (Boisson, et al., 2003; Pierre, et al., 2007). Interestingly, the activity of another *Arabidopsis* kinase complex – SNF1-related protein kinase (SnRK1) – is thought to be regulated by myristoylation, since substitution of the glycine residue modified by the myristoyl group in the β-subunit ($SnRK1\beta^{G2A}$) of SnRK1 leads to relocalisation of the complex to the nucleus (Pierre, et al., 2007), a phenomenon which is also observed in SNF-INTERACTING PROTEIN 2 in yeast (Lin, et al., 2003). Since the modification of glycine by myristoylation is irreversible, it is unclear how (or if) membrane localisation may be reversed, except via proteolytic cleavage/degradation. In this example, SnRK1 activity is inhibited by sequestration at the membrane (Pierre, et al., 2007), however, it remains possible that other proteins may indeed be activated by membrane targeting, and/or via interactions with other membrane proteins. Extrapolating from this, it is possible that STPK localisation to the membrane by N-myristoylation, and subsequent interaction with ACR4 may result in phosphorylation of *STPK,* resulting in altered downstream signalling. Alternatively, it is possible that STPK may act in a similar manner to CORYNE (CRN) with CLAVATA2 (CLV2), inasmuch as CRN is inactive as a kinase, but is required for the correct localisation of CLV2 to the plasma membrane (Bleckmann,

et al., 2010). From this perspective, STPK may represent an interesting novel mediator of ACR4 signalling.

Further Putative ACR4 Interacting Proteins

The remaining PAIPs identified by Y2H and Co-IP techniques were broadly classified into two groups, those potentially involved in signalling, protein transport and degradation, and uncharacterised proteins.

Signalling Proteins

The PAIPs investigated above represent only a small fraction of those identified by the Y2H and Co-IP screens. Several further PAIPs may potentially be involved in signalling processes with ACR4, and the potential relevance to ACR4 signalling is discussed below.

INCREASED SIZE EXCLUSION LIMIT 2 (ISE2)

AT1G70070 encodes INCREASED SIZE EXCLUSION LIMIT 2 (ISE2), a DEVH box ATP-dependent RNA helicase involved in regulating the development of secondary plasmodesmata – ie those plasmodesmata created between cells of different parental lineages, rather than resultant from cell proliferation (Lee & Sieburth, 2010; Kim, et al., 2002). Given that ACR4 has previously been described to localise to co-localise with CLV1 at plasmodesmata in the RAM, where it acts to maintain the meristematic niche (Stahl, et al., 2013), the presence of ISE2 in the Y2H screen is intriguing, and may represent a novel method of ACR4-mediated control over meristematic development.

ISE2 was originally identified by screening mutant embryos for plasmodesmata transport defects using fluorescent tracers. 8-Hydroxypyrene-1,3,6-trisulfonic acid (HTPS) ≈ 0.5 kDa and Fluoroscein isothiocyanate (FITC)-conjugated dextran ≈ 10 kDa were loaded into embryos and movement of these fluorescent tracers was monitored. In wt, the HTPS tracer revealed that all cells are connected via the symplast, and observing the diffusion of the FITC tracer indicated plasmodesmatal diameter is decreased during and after the torpedo stage of embryonic development (Kim, et al., 2002). In *ise2* mutant lines, diffusion of the FITC tracer was unaffected during and after the torpedo stage, indicating that the plasmodesmata aperture is not decreased in these lines (Kim, et al., 2002). Since ISE2 is required for intron splicing and RNA metabolism, it seems likely that RNA interference is the effector of ISE2 signalling responsible for regulating plasmodesmatal development (Carlotto, et al., 2016; Kobayashi, et al., 2007). Indeed, in *ise2* lines, post-transcriptional gene silencing is decreased (Kobayashi, et al., 2007), and expression of *CELLULOSE SYNTHASE A (CESA)* catalytic subunits *1, 2,* and *8* alters several-fold (Burch-Smith, et al., 2011).

Interestingly, ISE2 has been repeatedly indicated to localise to chloroplasts by signal peptide target prediction (Emanuelsson, et al., 2007; Ichikawa, et al., 2006), microscopic analyses (Burch-Smith, et al., 2011), and proteomics analyses of isolated chloroplasts (Olinares, et al., 2010; Zybailov, et al., 2008), although *ISE2* expression has also been observed in the root tissues, which are characteristically devoid of chloroplasts (Kobayashi, et al., 2007). This may suggest that ISE2 is involved in an alternative signalling pathway, or that it is plastid-localised in roots, and is capable of regulating plasmodesmatal development in the root tissues. Recently, an ISE2 orthologue has been indicated to be involved in nodulation in *M. truncatula*. According to

microarray data, *MtISE2* is upregulated in response to infection by *B. japonicum* (Breakspear, et al., 2014), potentially indicating that decreasing plasmodesmatal aperture is able to limit the spread of infection. Seemingly supporting this theory, *PLASMODESMATA LOCATED PROTEIN 5 (PDLP5)/CYSTEINE-RICH REPEAT SECRETORY PROTEIN 2 (CRRSP2)/HOPW1-1INDUCED1 (HWI1),* is also upregulated in response to regulation of plasmodesmatal aperture in response to *P. syringae* infection (Lee, et al., 2008). Subsequent analysis of PDLP5 indicates that *P. syringae* growth in *pdlp5* is increased, and correspondingly decreases in *35S::PDLP5* overexpression constructs, and corresponds to relative plasmodesmatal permeability, suggesting a key role of plasmodesmatal aperture control in innate immunity to infection (Lee, et al., 2011). Given the similarity in function between ISE2 and PDPL5, it is possible that ACR4/ISE2 interactions in the root may be involved in pathogenic resistance. From this perspective – taking into account that ACR4/CLV1 homo/heterodimers have been observed to aggregate around plasmodesmata (Stahl, et al., 2013) – it is possible that the activity of ISE2 is able to modulate the expression of a ligand or cofactor involved in ACR4 signalling resulting in regulation of plasmodesmatal aperture, although a direct link between ACR4 and plasmodesmata aperture is yet to be determined. This hypothesis additionally does not take into account the incongruous localisation of ISE2, or the physical interaction with ACR4 indicated by this Y2H screen.

Interestingly, it has been previously demonstrated that GFP expressed in the chloroplast is released during periods of oxidative and biotic stress, indicating that export of chloroplastic proteins occurs under these conditions (Kwon, et al., 2013). Furthermore, ISE2 - while chloroplast localised - has also been demonstrated to aggregate in cytoplasmic stress granules (Kobayashi, et al., 2007). Stress granules are cytosolic aggregations of protein and RNA formed by interactions

between molecular chaperones, and are involved in temporary sequestration and protection of RNA and proteins in periods of stress (Löw, et al., 2000; Forreiter, et al., 1997). This may suggest that ISE2 can be released into the cytoplasm during periods of stress induced by reactive oxygen species and biotic stress. Given this evidence, it is tempting to speculate that ISE2 may be involved in post-transcriptional regulation of nuclear-encoded genes during periods of stress, which may in turn allow interaction with ACR4, or affect ACR4 signalling, resulting in decreased plasmodesmatal aperture, though this is purely conjectural. Finally, at this stage, it remains unclear how or why ISE2 directly interacts with ACR4, rather than localising to the nucleus for involvement in post-transcriptional regulation of transcripts involved in regulation of plasmodesmatal aperture.

Leucine-Rich Repeat (LRR) Containing Proteins

At3g20820, At3g14840 and *At1g53440* encode uncharacterised LRR domain containing proteins. LRR domains are 20-29 amino acids long, and contain a number of leucine residues structured into a conserved LxxLxLxx(N/C)xL motif (Padmanabhan, et al., 2009; Kobe & Kajava, 2001). When these LRR domains are repeated concurrently, they form a hydrophobic surface capable of a wide range of protein-protein interactions (Padmanabhan, et al., 2009; Kobe & Kajava, 2001).

An example of LRR-RLK protein interactions is that of BRASSINOSTEROID INSENSITIVE 1 (BRI1) and its co-receptor BRI1-ASSOCIATED RECEPTOR KINASE 1 (BAK1). Both BRI1 and BAK1 are LRR-RLKs, and act together to interpret brassinosteroid signalling (Li, et al., 2002). Demonstrating the broad interactivity of LRR-repeat proteins, BAK1 is also able to interact with the LRR-containing protein BAK1-LIKE 1/SOMATIC EMBRYOGENESIS RECEPTOR KINASE 1 (BKK1/SERK4), whereby it plays a role in perception of peptide pathogen-associated molecular patterns elf18 and flg22,

triggering an immune response in *Arabidopsis* (Roux, et al., 2011). Since LRR-RLKs commonly act as receptors or co-receptors in *Arabidopsis* signalling pathways, it is possible that this is the role of the putative interaction between ACR4 and these AT3G14840 and AT1G53440.

Interestingly however, although AT3G14840 and AT1G53440 are predicted to contain an C-terminal kinase domain, AT3G20820 does not. Intriguingly, this does not necessarily dictate a lack of involvement in signalling, as the LRR-containing CLV2 similarly contains no kinase domain, and interacts with CORYNE (CRN) – a membrane associated kinase. This partnership facilitates membrane localisation of CLV2, and allows formation of heteromers of CLV1, CLV2 and CRN in order to perceive the CLV3 signal for meristem maintenance (Bleckmann, et al., 2010). It is therefore possible that AT3G20820 is able to act in a similar manner as CLV2, enabling perception of CLE40 in conjunction with ACR4. From this perspective, although STPK does not contain a transmembrane domain, it is possible that the N-myristoylation facilitates membrane localisation and STPK/AT3G20820 interactions may further facilitate ACR4 signalling.

PLASMA MEMBRANE INTRINSIC PROTEIN 1B (PIP1B/PIP1;2)

AT2G45960 encodes the aquaporin PLASMA MEMBRANE INTRINSIC PROTEIN 1B (PIP1B/PIP1;2). PIP1 aquaporins are primarily involved in water transport, and contribute to both hydrostatic pressure and transpiration, making them key players in drought and salt tolerance (Postaire, et al., 2010). Aquaporins are both downregulated and internalised in response to salt stress, representing a long- and short-term response instrumental in preventing water loss respectively (Boursiac, et al., 2005), and overexpression of PIP1B increases plant vigour in optimal conditions, but – perhaps predictably – decreases the length of time for the plant to wilt in drought conditions, and decreases fresh weight gain under salt stress (Aharon, et al., 2003). In recent

years, it has been demonstrated that, while the primary function of aquaporins is in water transport, they are not limited to this role. PIP1B is also implicated in regulation of CO_2 transport, as *pip1b* mutants show a ≈40% decrease in CO_2 conductance, and expression of PIP1B in yeast increased CO_2 triggered intracellular acidification by approximately 4x (Heckwolf, et al., 2011). More recently still, it has become apparent that aquaporins are involved in lateral root development, as both *pip2;1* mutants and *PIP2;1* overexpression lines display delayed emergence of lateral roots (Péret, et al., 2012). Additionally, tonoplast localised aquaporins have been demonstrated to play a role in lateral root emergence, as *tip1;1 tip1;2 tip2;1* triple mutants display significantly reduced lateral root emergence, which was rescued by expression of *TIP2* under control of its native promoter, and indicates that PIPs and TIPs work synergistically to maintain the turgor pressure necessary for lateral root emergence (Reinhardt, et al., 2016). Interestingly, phosphorylation status of PIP2A has previously been described to affect water transport in *Arabidopsis* rosettes, as PIP2;1 phosphorylation at S280 and S283 is required for hydraulic conductivity in darkness (Prado, et al., 2013). Furthermore, the phosphorylation of PIP2;1 S283 has been indicated to be necessary for plasma membrane localisation (Prak, et al., 2008), and phosphorylation of *Spinacia oleracea* aquaporin PM28A at S115 and S274 has been demonstrated to activate the water transport capability of this protein in *Xenopus* oocytes (Johansson, et al., 1998). This may suggest that phosphorylation regulates both aperture and localisation of aquaporins. From this perspective, it is possible that the putative interaction of PIP1B with ACR4 may enable additional regulation of lateral root emergence by controlling water transport via regulating the distribution or aperture of PIP1B.

SERINE HYDROXYMETHYLTRANSFERASE 4 (SHM4)

AT4G13930 encodes SERINE HYDROXYMETHYLTRANSFERASE 4 (SHM4), a serine hydroxymethyltransferase belonging to a family of 5 members in *Arabidopsis,* The SHM family is split into two groups, SHM1-3 and SHM4-5, based on intron positions (McClung, et al., 2000). SHM4 is expressed strongly in the root tissues, where it is involved in methyl donor recycling for the C1 metabolism, using serine as a donor molecule (McClung, et al., 2000; Camargo, et al., 2014). SHM1 has been implicated in salt tolerance, since the *shm1* mutant is hypersensitive to the presence of 50mM NaCl comparative to Col-0, and SHM1 is stabilised by the activity of ubiquitin specific protease 16 (UBP16) (Zhou, et al., 2012). Although the *shm4* mutant shows no significant difference to salt tolerance compared to Col-0 (Zhou, et al., 2012), it is possible that SHM4 is involved in mediating alternative stress responses through interaction with ACR4. Interestingly, SHM4 has recently been demonstrated to be significantly upregulated in response to nitrogen stress (Camargo, et al., 2014). This may suggest a role for ACR4/SHM4 interactions in regulation of nitrogen recycling during periods of nitrogen stress.

AMINOPEPTIDASE M1 (APM1)

AT4G33090 encodes AMINOPEPTIDASE M1 (APM1), a membrane localised metalloprotease involved in hydrolysis of N-1-naphthylphthalamic acid (NPA), an inhibitor of polar auxin transport (Peer, et al., 2009). Both catalytic and protein/protein interaction domains are required for APM1 activity, indicating that homo- or heterodimerization is likely necessary for enzymatic activity (Hosein, et al., 2010). Gravotropism and polar auxin transport are disrupted in *apm1*, and definition of the quiescent centre is abolished in the mutant line (Peer, et al., 2009). Interestingly, ACR4 has previously been implicated in regulation of polar auxin transport, as ACR4

phosphorylates PP2A-3, a subunit of the PP2A holoenzyme responsible for dephosphorylating the central hydrophilic loop in PIN1, the conformation of which determines basal or apical localisation (Yue, et al., 2016; Xi, et al., 2015). The putative ACR4/APM1 interaction may therefore indicate a novel PP2A-independent role for ACR4 in regulation of polar auxin transport.

Transport and Degradation Proteins

Proteins associated with transport and degradation are unlikely to be directly involved with signalling processes, however Gifford *et al.* report that ACR4:GFP is rapidly cycled between cytosol and membrane by vesicular transport as the GFP signal co-localises with that of FM4-64, using a BFA-inducible system. Other vesicles were observed to contain ACR4:GFP without FM4-64 and were insensitive to BFA, but demonstrated decreased fluorescence in response to cycloheximide treatment, suggesting that these are exocytic vesicles containing newly synthesised ACR4:GFP (Gifford, et al., 2005). From this perspective, PAIPs potentially involved in these processes may provide insight into ACR4 recycling.

TRANSPORT-RELATED PAIPS

Transport-related PAIPs were identified in both Y2H and Co-IP screens. *AT3G11130* encodes CLATHRIN HEAVY CHAIN 1 (CHC1), and *AT3G08530* encodes CHC2. CHCs are a major component of the clathrin coat on coated pits and vesicles, forming a triskelion cage, and are key proteins for mediation of endocytosis (Kitakura, et al., 2011). *AT1G62020* and *AT2G21390* encode ALPHA-COP1 and ALPHA-COP2, respectively. Similarly to CHC1 and CHC2, ALPHA-COP1 and ALPHA-COP2 are proteins associated with vesicular transport (Lee & Goldberg, 2010).

Since ACR4 has previously been described as being rapidly cycled between membrane and internal vesicles (Gifford, et al., 2005), it is likely that this process is facilitated by clathrin coated vesicles, and the putative interaction of ACR4 with vesicular transport proteins would provide further evidence in support of this mode of regulation. Vesicular transport of ACR4 may represent movement to a different subcellular compartment for signalling and/or degradation. Interestingly however, this data contrasts with that of Gifford, et al., who report that the extracellular domain is absolutely required for ACR4 internalisation, since only the intracellular domain was used for interaction screening in the Y2H screen, and shows interaction with proteins involved in intracellular transport.

Vesicular transport may also facilitate localisation of ACR4 to specific areas of membrane, as there is evidence of plasmodesmatal localisation in *Nicotiana benthamiana* transiently expressing *pACR4::ACR4:GFP* (Stahl, et al., 2013), and it was also indicated that ACR4:GFP localises to the lateral and basal cell surfaces in *Arabidopsis* leaf epidermis (Watanabe, et al., 2004). It would be interesting to investigate where ACR4 and individual vesicular transport proteins co-localise, as this may be informative in determining whether these proteins facilitate trafficking to alternate destinations for ACR4.

DEGRADATION-RELATED PAIPS

A number of enzymes potentially involved in protein degradation were indicated as PAIPs by the Co-IP screen. *AT3G05530* and *AT1G09100* encode 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG A (RPT5A) and RPT5B, which are predicted to be responsible for the ATP-dependent degradation of ubiquitinated proteins (Cho, et al., 2006). Similarly, *AT5G23540* encodes 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 14 HOMOLOG (RPN11), also potentially

involved in degradation of ubiquitinated proteins, but is not ATP dependent. Furthermore, AT4G01610, AT5G43060 and AT1G04560 encode predicted cysteine-protease-like enzymes CATHEPSIN B-LIKE CYSTEINE PROTEASE (T15B16.17A:T15B16.17B), PROBABLE CYSTEINE PROTEASE RD21B (RD21B), and AWPM-19-LIKE FAMILY PROTEIN (T1G11.19) which may be involved in protein catabolism.

The rapid cycling of ACR4 between membrane and vesicular transport systems reported by Gifford, *et al.* is likely to include the eventual degradation of ACR4 following internalisation in endocytic vesicles. From this perspective, it is possible that these proteins are involved in the degradation of ACR4.

UNCHARACTERISED PROTEINS

Finally, a peptide corresponding to sequences in the putative uncharacterised proteins *AT1G29310* and *AT2G34250* was identified by the Co-IP screen. While the lack of functional or predicted data on these PAIPs is limiting in assigning a putative role in relation to ACR4 signalling, it is interesting to note that both are comprised of a number of predicted transmembrane domains, of which *AT1G29310* contains 10, and *AT2G34250* contains 9. This may suggest that these proteins form large pores in the membrane in which they are located, possibly allowing transport of signalling molecules or proteins from one cell - or compartment thereof - to another. The putative interaction with ACR4 may therefore fulfil a similar potential role as for PIP1B, inasmuch as ACR4-mediated phosphorylation may dictate whether the pore is open or closed, or may regulate subcellular localisation of *AT1G29310* and *AT2G34250*.

Phylogenetic Analyses of PAIPs with Root Traits Reveals Orthologous Proteins in Commercially Important Crop Species

Having identified two proteins involved in regulating root architecture, it was important to determine if the knowledge gained from studies of *Arabidopsis* had potential for translation into commercially important crop species, with the aim of increasing yield and/or stress tolerance by altering root architecture. In order to investigate the presence of orthologous proteins in crops, UNK and PLA-Iγ2 protein sequences were submitted as a BLAST search in Phytozome, and the top hit for each species was aligned in a phylogenetic tree using CLC Workbench.

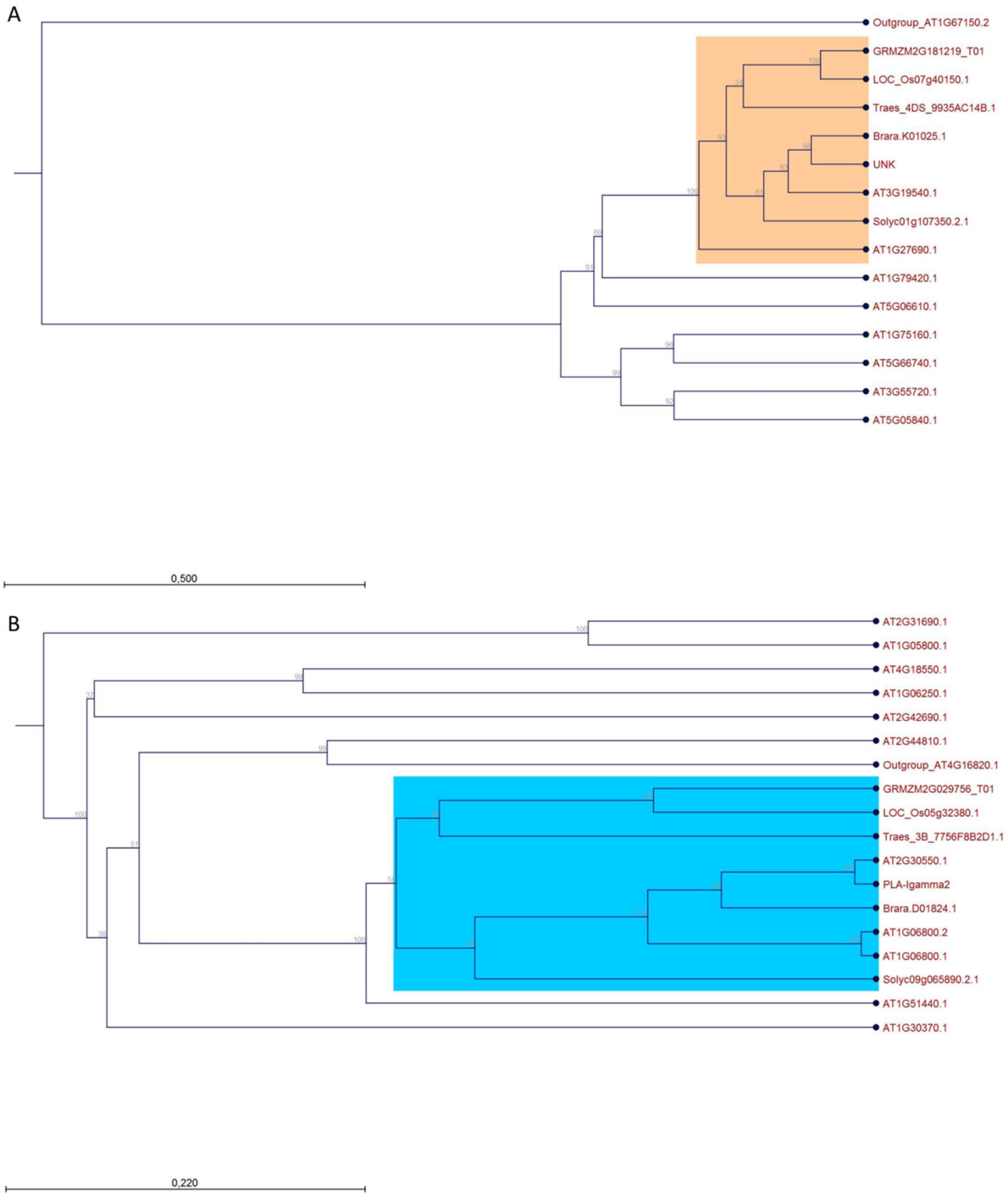


Figure 12: Phylogenetic analysis of PAIPs UNK (A) and PLA-Iγ2 (B) reveals orthologous proteins are present in commercially viable crop species (shaded regions).

Phylogenetic analysis of UNK and PLA-Iγ2 protein sequences (Figure 12) revealed the presence of orthologous species in multiple commercially important crop species. In both cases, the closest homologue was in *B. rapa,* which is unsurprising, since it is the most closely related crop species to *Arabidopsis.* However, orthologous proteins were also observed for both UNK and PLA-Iγ2 in less closely related species, including *S. lycopersicum, T. aestivum, O. sativa,* and *Z. mays*, indicating that knowledge gained in studying UNK and PLA-Iγ2 in *Arabidopsis* can be transferred to a broad range of crop species for use in targeted crop improvement, and development of root architecture to increase nutrient absorption.

8.3 Conclusions

Experiments discussed in this chapter represent a contribution to the early stages of deciphering the ACR4 initiated signalling cascade that regulates lateral root development. Y2H and Co-IP techniques revealed a number of PAIPs, and two mutants - *unk* and *pla-iγ2* - were further implicated in regulation of *Arabidopsis* root architecture. Although it remains possible that these proteins may affect root architecture independently of any interaction with ACR4, further investigation of *pUNK::UNK:GFP* reveals that the expression pattern of UNK partially overlaps with that published for ACR4 (De Smet, et al., 2008) in the basal meristem epidermis and lateral root primordia, suggesting that interaction in these regions may be possible. Furthermore, both PAIPs with root traits are likely involved in regulating bioactive lipid production. Since *acr4* has previously been demonstrated to have increased global levels of JA (Zereen & Ingram, 2012), it is possible that the putative interaction of ACR4 with UNK and PLA-Iγ2 may indicate a more direct

route of ACR4-mediated regulation of JA. Finally, phylogenetics analysis indicates that *UNK* and PLA-Iγ2 orthologues are present in a number of commercially viable crop species. This potentially indicates that any knowledge gained in characterising these proteins further may be directly transferrable to crops for targeted crop improvement.

A Potential Model for ACR4 Mediated Regulation of JA Biosynthesis

pla-iγ2 and *unk* display seemingly opposite root architectural traits. Since PLA-Iγ2 is a phospholipase indicated in JA synthesis, and UNK may be a soluble secretory phospholipase receptor that appears partially membrane associated, it is tempting to speculate that via the interaction indicated by the Y2H screen, binding of ligand to ACR4 results in UNK activation, leading to sequestration of PLA-Iγ2 or a functionally similar phospholipase. This would theoretically have the effect of decreasing local availability of JA, promoting the correct formation of lateral root primordia (Figure 13). Since JA is upregulated in *acr4,* yet *acr4* displays decreased emerged lateral root density, it is possible that ACR4/UNK interactions may act in a localised manner to inhibit JA signalling, resulting in regulation of division/differentiation on a cellular scale.

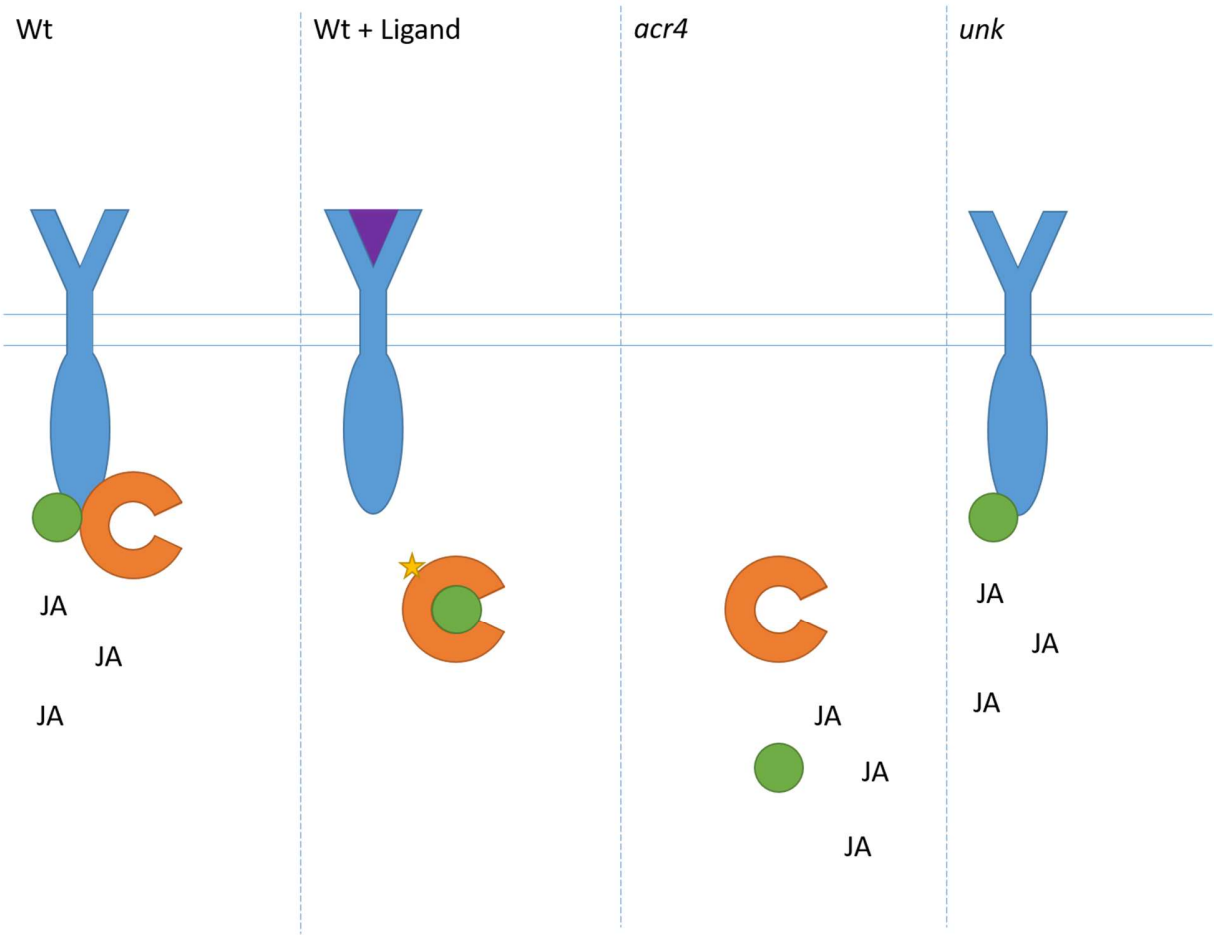


Figure 13: Potential interactions of ACR4, UNK, and PLA-Iγ2 may represent a signalling network capable of regulating lateral root emergence by regulation of local JA production. In this model, binding of ligand to ACR4 triggers activation of UNK – since ACR4 is a kinase, this would likely be via phosphorylation. Activation of UNK allows sequestration of PLA-Iγ2, and inhibits local production of JA in primordia, enabling lateral root emergence. Blue = ACR4, Orange = UNK, Green = PLA-Iγ2, Yellow star = Phosphorylation.

The evidence for this model is far from conclusive, however, given the partial localisation of UNK:GFP to the membrane, it is tempting to speculate that UNK exists in both membrane associated and cytosolic form, which may be regulated by ACR4-mediated phosphorylation.

Creation of fluorescent translational fusion constructs will allow co-localisation analysis, and, if the correct fluorescent protein pairs are used – eg. GFP/RFP (Shcherbo, et al., 2009) – FRET analysis may give an indication whether these proteins interact *in-vivo.* Additionally, analysis of intracellular pH in lateral root primordia by microinjection with 8-Hydroxypyrene-1,3,6-trisulfonic acid or a similar fluorescent pH sensor may give some indication of meristem localised perturbences in JA concentration in mutant and/or overexpression lines.

8.4 Future Work

Each of the PAIPs mentioned above has the potential to play a role in root development, thus making these screens important ground work for targeted crop improvement. Continued characterisation of these PAIPs and their downstream effectors may indicate one or more key regulators of lateral root organogenesis or emergence, potentially allowing for targeted genetic engineering for increased yield or stress tolerance, which may allow for improvements to be made to feeding the global populace, despite the increasingly adverse growth conditions observed as a result of global warming.

Although several PAIPs have been identified by the two screens discussed in this chapter, it remains to be confirmed by independent techniques whether these PAIPs truly interact with ACR4, and, in most cases, what the downstream effect of mutation and overexpression is on root architecture. Several molecular techniques may prove useful to provide further insight into the putative protein-protein interactions between ACR4 and the PAIPs identified by these screens.

In order to further characterise these putative interactions, it will be necessary to create transcriptional and translational fusion constructs to determine whether these PAIPs co-localise with ACR4. It would also be prudent to compliment these interaction screens with fluorescence resonance imaging transfer and/or split-YFP analysis, in order to determine if these proteins interact with ACR4 *in-vivo*. Proteins with indicated or predicted function may also benefit from more target specific approaches, such as phosphosite analyses for the LRR-containing proteins, and exposure to different forms of biotic and abiotic stress for SHM4, UNK and PLA-Iγ1 overexpression and mutant backgrounds, to determine if these proteins are involved in stress responses other than salt stress.

In the case of enzymes identified by the Y2H or Co-IP screens, it may also be informative to compare enzymatic activity in ACR4 and PAIP mutant and overexpression lines, and compare with wild-type *Arabidopsis*.

In order to determine any differences in JA production, qPCR could be used to determine comparative regulation of JA-responsive genes in *acr4, pla-iγ1, pla-iγ2, unk;* their respective overexpression lines, and wild-type *Arabidopsis*. A more informative approach however, given the potential for altered spatiotemporal regulation and/or transport of JA, would be to use a JA reporter such as Jas9-VENUS (Larrieu, et al., 2015) to transform the above lineages, following which relative fluorescence can be analysed to visualise differential JA responsiveness in the root tissues. These reporters can also be grown on media deficient in specific nutrients – mimicking abiotic stress conditions – to determine if there is any differential JA response in these lineages as a result of abiotic stress. Similarly, a stress screen of *paips* using media containing

increased/decreased amounts of specific nutrients or altered osmotic potential may reveal whether any play a role in abiotic stress conditions.

Furthermore, *in-silico* prediction of putative phosphorylation sites and subsequent generation of putative phosphosite mutants may reveal if any PAIPs are putative targets for ACR4 phosphorylation. Determination of differential phosphorylation may also be possible by transient co-expression of *ACR4* and *STPK* in *N. benthamiana,* and subsequent phosphosite analysis by LC-MS/MS.

Finally, in order to determine if UNK is an ACR4 downstream effector, it would be interesting to determine whether *unk,* like *acr4*, similarly exhibits elongated/fused primordia, resulting in the decreased emergence of lateral roots observed in *unk.* Since UNK remains comparatively obscure in terms of function, it would be beneficial to determine any other potential interactors of UNK, using Co-IP, which may provide further evidence as to UNK function.

References

Aharon, R. et al., 2003. Overexpression of a Plasma Membrane Aquaporin in Transgenic Tobacco Improves Plant Vigor under Favorable Growth Conditions but Not under Drought or Salt Stress. *Plant Cell,* 15(2), pp. 439-447.

Ancian, P., Lambeau, M. M. & Lazdunski, M., 1995. The human 180-kDa receptor for secretory phospholipases A2. Molecular cloning, identification of a secreted soluble form, expression, and chromosomal localization. *Journal of Biological Chemistry,* 270(15), pp. 8963-8970.

Ballesteros, I. et al., 2013. Specialized functions of the PP2A subfamily II catalytic subunits PP2A-C3 and PP2A-C4 in the distribution of auxin fluxes and development in Arabidopsis. *Plant Journal,* 73(5), pp. 862-872.

Bleckmann, A., Weidtkamp-Peters, S., Seidel, C. & Simon, R., 2010. Stem cell signaling in Arabidopsis requires CRN to localize CLV2 to the plasma membrane. *Plant Physiology,* 152(1), pp. 166-176.

Boisson, B., Giglione, C. & Meinnel, T., 2003. Unexpected protein families including cell defense components feature in the N-myristoylome of a higher eukaryote. *Journal of Biological Chemistry,* 278(44), pp. 43418-43429.

Boursiac, Y. et al., 2005. Early Effects of Salinity on Water Transport in Arabidopsis Roots. Molecular and Cellular Features of Aquaporin Expression. *Plant Physiology,* 139(2), pp. 790-805.

Breakspear, A. et al., 2014. The Root Hair “Infectome” of Medicago truncatula Uncovers Changes in Cell Cycle Genes and Reveals a Requirement for Auxin Signaling in Rhizobial Infection. *Plant Cell,* 26(12), pp. 4680-4701.

Burch-Smith, T., Brunkard, J., Choi, Y. & Zambryski, P., 2011. Organelle–nucleus cross-talk regulates plant intercellular communication via plasmodesmata. *Proceedings of the National Academy of Science of the United States of America,* 108(51), p. E1451–E1460.

Cai, X. et al., 2014. Arabidopsis ERF109 mediates cross-talk between jasmonic acid and auxin biosynthesis during lateral root formation. *Nature Communications,* 5(5833), p. doi: 10.1038/ncomms6833.

Camargo, E. et al., 2014. Contrasting nitrogen fertilization treatments impact xylem gene expression and secondary cell wall lignification in Eucalyptus. *BioMed Central Plant Biology,* 14(256), pp. doi: 10.1186/s12870-014-0256-9.

Carlotto, M. et al., 2016. The chloroplastic DEVH-box RNA helicase INCREASED SIZE EXCLUSION LIMIT 2 involved in plasmodesmata regulation is required for group II intron splicing. *Plant, Cell & Environment,* 39(1), pp. 165-173.

Cho, Y., Yoo, S. & Sheen, J., 2006. Regulatory functions of nuclear hexokinase1 complex in glucose signaling. *Cell,* Volume 127, pp. 579-589.

Czyzewicz, N. et al., 2016. The growing story of (ARABIDOPSIS) CRINKLY 4. *Journal of Experimental Botany,* p. doi: 10.1093/jxb/erw192.

De Smet, I. et al., 2008. Receptor-like kinase ACR4 restricts formative cell divisions in the Arabidopsis root. *Science,* 322(5901), pp. 594-597.

Ellinger, D. et al., 2010. DONGLE and DEFECTIVE IN ANTHER DEHISCENCE1 lipases are not essential for wound- and pathogen-induced jasmonate biosynthesis: redundant lipases contribute to jasmonate formation. *Plant Physiology,* 153(1), pp. 114-127.

Emanuelsson, O., Brunak, S., von Heijne, G. & Nielsen, H., 2007. Locating proteins in the cell using TargetP, SignalP and related tools. *Nature Protocols,* 2(4), pp. 953-971.

Forreiter, C., Kirschner, M. & Nover, L., 1997. Stable transformation of an Arabidopsis cell suspension culture with firefly luciferase providing a cellular system for analysis of chaperone activity in vivo. *Plant Cell,* 9(12), pp. 2171-2181.

Gifford, M., Robertson, F., Soares, D. & Ingram, G., 2005. ARABIDOPSIS CRINKLY4 Function, Internalisation and Turnover are Dependent on the Extracellular Crinkly Domain. *Plant Cell,* 17(4), pp. 1154-1166.

Gifford, M., Robertson, F., Soares, D. & Ingram, G., 2005. ARABIDOPSIS CRINKLY4 Function, Internalisation and Turnover are Dependent on the Extracellular Crinkly Repeat Domain. *Plant Cell,* 17(4), pp. 1154-1166.

Hannun, Y. & Obeid, L., 2008. Principles of bioactive lipid signalling: lessons from sphingolipids. *Nature Reviews: Molecular Cell Biology,* 9(2), pp. 139-150.

Heckwolf, M., Pater, D., Hanson, D. & Kaldenhoff, R., 2011. The Arabidopsis thaliana aquaporin AtPIP1;2 is a physiologically relevant CO2 transport facilitator. *The Plant Journal,* 67(5), pp. 795-804.

Higashino, K. et al., 2002. Identification of a Soluble Form Phospholipase A2 Receptor as a Circulating Endogenous Inhibitor for Secretory Phospholipase A2. *Journmal of Biological Chemistry,* 277(16), pp. 13583-13588.

Hosein, F., Bandyopadhyay, A., Peer, W. & Murphy, A., 2010. The Catalytic and Protein-Protein Interaction Domains Are Required for APM1 Function. *Plant Physiology,* 152(4), pp. 2158-2172.

Ichikawa, T. et al., 2006. The FOX hunting system: An alternative gain-of-function gene hunting technique. *The Plant Journal,* 48(6), pp. 974-985.

Johansson, I. et al., 1998. Water Transport Activity of the Plasma Membrane Aquaporin PM28A Is Regulated by Phosphorylation. *Plant Cell,* 10(3), pp. 451-459.

Kim, I. et al., 2002. Identification of a developmental transition in plasmodesmatal function during embryogenesis in Arabidopsis thaliana. *Development,* 129(5), pp. 1261-1272.

Kitakura, S. et al., 2011. Clathrin Mediates Endocytosis and Polar Distribution of PIN Auxin Transporters in Arabidopsis. *Plant Cell,* 23(5), pp. 1920-1931.

Kobayashi, K. et al., 2007. INCREASED SIZE EXCLUSION LIMIT2 Encodes a Putative DEVH Box RNA Helicase Involved in Plasmodesmata Function during Arabidopsis Embryogenesis. *Plant Cell,* 19(6), pp. 1885-1897.

Kobe, B. & Kajava, A., 2001. The leucine-rich repeat as a protein recognition motif. *Current Opinion in Structural Biology,* 6(1), pp. 725-732.

Komatsu, S., Konishi, H. & Hashimoto, M., 2007. The proteomics of plant cell membranes. *Journal of Experimental Botany,* 58(1), pp. 103-112.

Kwon, K. et al., 2013. Release of Proteins from Intact Chloroplasts Induced by Reactive Oxygen Species during Biotic and Abiotic Stress. *Public Library of Science One,* 8(6), p. http://dx.doi.org/10.1371/journal.pone.0067106.

Larrieu, A. et al., 2015. A fluorescent hormone biosensor reveals the dynamics of jasmonate signalling in plants. *Nature Communications,* 6(6043), p. doi:10.1038/ncomms7043.

Lee, C. & Goldberg, J., 2010. Structure of Coatomer Cage Proteins and the Relationship among COPI, COPII, and Clathrin Vesicle Coats. *Cell,* 142(1), pp. 123-132.

Lee, D. & Sieburth, L., 2010. Plasmodesmata Formation: Poking Holes in Walls With ise. *Current Biology,* 20(11), pp. R488-R490.

Lee, J. et al., 2011. A Plasmodesmata-Localized Protein Mediates Crosstalk between Cell-to-Cell Communication and Innate Immunity in Arabidopsis. *Plant Cell,* 23(9), pp. 3353-3373.

Lee, M., Jelenska, J. & Greenberg, J., 2008. Arabidopsis proteins important for modulating defense responses to Pseudomonas syringae that secrete HopW1-1. *The Plant Journal,* 54(3), pp. 452-465.

Li, J. et al., 2002. BAK1, an Arabidopsis LRR Receptor-like Protein Kinase, Interacts with BRI1 and Modulates Brassinosteroid Signaling. *Cell,* 110(2), pp. 213-222.

Lin, S., Manchester, J. & Gordon, J., 2003. Sip2, an N-Myristoylated beta subunit of Snf1 kinase, regulates aging in Saccharomyces cerevisiae by affecting cellular histone kinase activity, recombination at rDNA loci, and silencing. *Journal of Biological Chemistry,* Volume 278, pp. 13390-13397.

Löw, D., Brändle, K., Nover, L. & Forreiter, C., 2000. Cytosolic heat-stress proteins Hsp17.7 class I and Hsp17.3 class II of tomato act as molecular chaperones in vivo. *Planta,* 211(4), pp. 575-582.

McClung, C. et al., 2000. Integrated temporal regulation of the photorespiratory pathway. Circadian regulation of two Arabidopsis genes encoding serine hydroxymethyltransferase. *Plant Physiology,* 123(1), pp. 381-392.

Olinares, P., Ponnala, L. & van Wijk, K., 2010. Megadalton complexes in the chloroplast stroma of Arabidopsis thaliana characterized by size exclusion chromatography, mass spectrometry, and hierarchical clustering. *Molecular and Cellular Proteomics,* 9(7), pp. 1594-1615.

Padmanabhan, M., Cournoyer, P. & Dinesh-Kumar, S., 2009. The leucine-rich repeat domain in plant innate immunity: a wealth of possibilities. *Cellular Microbiology,* 11(2), pp. 191-198.

Peer, W. et al., 2009. Mutation of the Membrane-Associated M1 Protease APM1 Results in Distinct Embryonic and Seedling Developmental Defects in Arabidopsis. *Plant Cell,* 21(6), pp. 1693-1721.

Péret, B. et al., 2012. Auxin regulates aquaporin function to facilitate lateral root emergence. *Nature Cell Biology,* Volume 14, pp. 991-998.

Pierre, M. et al., 2007. N-Myristoylation Regulates the SnRK1 Pathway in Arabidopsis. *Plant Cell,* Volume 19, pp. 2804-2821.

Postaire, O. et al., 2010. A PIP1 aquaporin contributes to hydrostatic pressure-induced water transport in both the root and rosette of Arabidopsis. *Plant Physiology,* 152(3), pp. 1418-1430.

Prado, K. et al., 2013. Regulation of Arabidopsis Leaf Hydraulics Involves Light-Dependent Phosphorylation of Aquaporins in Veins. *Plant Cell,* 25(3), pp. 1029-1039.

Prak, S. et al., 2008. Multiple Phosphorylations in the C-terminal Tail of Plant Plasma Membrane Aquaporins Role in Subcellular Trafficking of AtPIP2;1 in Response to Salt Stress. *Molecular and Cellular Proteomics,* Volume 7, pp. 1019-1030.

Raya-González, J., Pelagio-Flores, R. & López-Bucio, J., 2012. The jasmonate receptor COI1 plays a role in jasmonate-induced lateral root formation and lateral root positioning in Arabidopsis thaliana. *Plant Physiology,* 169(14), pp. 1348-1358.

Reinhardt, H. et al., 2016. Tonoplast Aquaporins Facilitate Lateral Root Emergence. *Plant Physiology,* 170(3), pp. 1640-1654.

Roux, M. et al., 2011. The Arabidopsis Leucine-Rich Repeat Receptor–Like Kinases BAK1/SERK3 and BKK1/SERK4 Are Required for Innate Immunity to Hemibiotrophic and Biotrophic Pathogens. *Plant Cell,* 23(6), pp. 2440-2455.

Ruduś, I. et al., 2014. Wound-induced expression of DEFECTIVE IN ANTHER DEHISCENCE1 and DAD1-like lipase genes is mediated by both CORONATINE INSENSITIVE1-dependent and independent pathways in Arabidopsis thaliana. *Plant Cell Reports,* 33(6), pp. 849-860.

Schwartz, R., Ting, C. & King, J., 2001. Whole Proteome pI Values Correlate with Subcellular Localizations of Proteins for Organisms within the Three Domains of Life. *Genome Research,* Volume 11, pp. 703-709.

Seo, Y., Kim, E., Kim, J. & Kim, W., 2009. Enzymatic characterization of class I DAD1-like acylhydrolase members targeted to chloroplast in Arabidopsis. *Federation of European Biochemical Societies Letters,* 583(13), pp. 2301-2307.

Shcherbo, D. et al., 2009. Practical and reliable FRET/FLIM pair of fluorescent proteins. *BioMed Central Biotechnology,* 9(24), pp. 1472-6750.

Stahl, Y. et al., 2013. Moderation of Arabidopsis root stemness by CLAVATA1 and ARABIDOPSIS CRINKLY4 receptor kinase complexes. *Current Biology,* 23(5), pp. 362-371.

Stahl, Y., Wink, R., Ingram, G. & Simon, R., 2009. A Signaling Module Controlling the Stem Cell Niche in Arabidopsis Root Meristems. *Current Biology,* 19(11), pp. 909-914.

Staswick, P., Su, W. & Howell, S., 1992. Methyl jasmonate inhibition of root growth and induction of a leaf protein are decreased in an Arabidopsis thaliana mutant. *Proceedings of the National Academy of Sciences of the United States of America,* 89(5), pp. 6837-6840.

Tanaka, H. et al., 2007. Novel receptor-like kinase ALE2 controls shoot development by specifying epidermis in Arabidopsis. *Development,* 134(9), pp. 1643-1652.

Tang, W. et al., 2011. PP2A activates brassinosteroid-responsive gene expression and plant growth by dephosphorylating BZR1. *Nature Cell Biology,* 13(2), pp. 124-131.

Wasternack, C. & Xie, D., 2010. The genuine ligand of a jasmonic acid receptor: Improved analysis of jasmonates is now required. *Plant Signaling & Behavior,* 5(4), pp. 337-340.

Watanabe, M. et al., 2004. The ACR4 receptor-like kinase is required for surface formation of epidermis-related tissues in Arabidopsis thaliana. *The Plant Journal,* Volume 39, pp. 298-308.

Watanabe, M. et al., 2004. The ACR4 receptor-like kinase is required for surface formation of epidermis-related tissues in Arabidopsis thaliana. *Plant Journal,* 39(3), pp. 298-308.

Xi, W. et al., 2015. Pin1At regulates PIN1 polar localization and root gravitropism. *Nature Communications,* Volume 7, p. doi:10.1038/ncomms10430 .

Yue, K. et al., 2016. PP2A-3 interacts with ACR4 and regulates formative cell division in the Arabidopsis root. *PNAS,* p. in press.

Zereen, J. & Ingram, G., 2012. A possible involvement of ACR4, a receptor like kinase, in plant defense mechanism. *Bangladesh Pharmaceutical Journal,* 15(2), pp. 127-130.

Zhou, H. et al., 2012. UBIQUITIN-SPECIFIC PROTEASE16 Modulates Salt Tolerance in Arabidopsis by Regulating Na+/H+ Antiport Activity and Serine Hydroxymethyltransferase Stability. *Plant Cell,* 24(12), pp. 5106-5122.

Zhu, H. & Kranz, R., 2012. A Nitrogen-Regulated Glutamine Amidotransferase (GAT1_2.1) Represses Shoot Branching in Arabidopsis. *Plant Physiology,* Volume 160, pp. 1770-1780.

Zybailov, B. et al., 2008. Sorting Signals, N-Terminal Modifications and Abundance of the Chloroplast Proteome. *PLOS ONE,* 3(4), p. e1994.

Chapter 9: Materials and Methods

Materials and Methods

Materials and methods relating to publications are included with individual papers. Other materials and methods used in the unpublished sections of this thesis are detailed here.

Yeast 2-Hybrid Screen

Yeast 2-hybrid screens were performed by Hybrigenics (Paris). Full length ACR4 cDNA was supplied in the pCR8/GW/TOPO vector, and this was used to amplify the intracellular juxtamembrane, kinase and c-terminal domains of ACR4 for cloning into a bait vector, and >50 million interactions were screened using an *Arabidopsis* seedling library. Results were collated into an Excel spreadsheet, inclusive of a confidence score based on clone survival. Known experimental artefacts and unscored clones were omitted from the final dataset.

Peptide Stock Creation

Peptides were synthesised by Genscript. Lipophilised stocks were reconstituted to 10 mM stock solutions in sterile distilled water, and stored at -20^{o}C, according to manufacturer's instructions. Working concentrations were sequentially diluted from the 10mM stock solutions before addition to medium (see below).

Arabidopsis Plant Culture

Arabidopsis seeds were surface sterilised by immersion in 70% ethanol for 30 seconds, before replacing the ethanol with 4% sodium hypochlorite solution and incubation at room temperature

with gentle agitation for 15 mins. Surface sterilised seeds were then rinsed three times in sterile distilled water, and incubated in water for 2 nights in the dark at 4^{o}C to vernalise.

Sterile, vernalised seeds were placed onto 50 ml ½ Murashige and Skoog medium (1 L: 2.154 g Murashige and Skoog Salts, 0.5 g n-Morpholino ethanesulphonic acid, 0.1 g Myo-inositol, pH to 5.7 ± 0.1 using 4M sodium hydroxide) containing 1% agar in 12 x 12 cm square petri plates for genotyping, qPCR and root architectural analyses. For growth on ½ MS agar containing peptide, media was first cooled to 50^{o}C, before adjusting to the required concentration of peptide. All seedlings were grown at 21^{o}C, constant light until analysis.

For phosphoproteomics and co-immunoprecipitation analyses, 30-50 mg sterile, vernalised seeds were inoculated into 100 ml ½ MS liquid medium in sealed 250 ml Erlenmeyer flasks, and incubated at 100 RPM, 21^{o}C, constant light until analysis. Liquid cultures containing peptide treatment were adjusted to 1 µM peptide for 10 mins prior to harvesting.

For amplification of seed, individual plants were transferred from plates to soil pots (Levington M3) following genotyping. If large numbers of seeds were required, confirmed homozygous lines were germinated directly on soil. All individual lines were contained within separate bags to prevent cross-contamination.

Differential Phosphoproteomics

Protein Preparation

Following treatment, seedlings were collected in a sterile sieve, blotted dry and snap frozen in liquid nitrogen. Frozen tissue was ground in a pre-chilled pestle and mortar, and 1g of material

was used to extract protein, and methanol/chloroform precipitation was used to isolate protein from the supernatant. Precipitated protein was resuspended in 6M guanidinium chloride in 50 mM TEAB and reduced with tris(2-carboxyethyl)phosphine (TCEP) pH8 and alkylated by addition of 30 mM iodoacetamide (IAA). Samples were digested twice, first using endo lys-c (Sigma), and second with Trypsin Gold (Promega). To arrest digestion, samples were acidified to <pH3 with trifluoroacetic acid, and purified on SampliQ C18 columns (Agilent), eluting in a final volume of 2ml. Samples were divided into two aliquots at this point, those to be used in proteomics analysis and those to be enriched for phosphopeptides. Samples for proteomic analysis were dried using a vacuum concentrator, and stored at -70^{o}C. Samples for phosphoproteomic analysis were first enriched for phosphopeptides using Ti-IMAC beads (ReSyn Biosciences), before drying using a vacuum concentrator and storage at -70^{o}C.

Mass Spectrometry

For MS analysis, samples were resuspended in 20-50 µl injection solvent (2% acetonitrile, 0.1% TFA), and analysed via LC-MS/MS on an Ultimate 3000 RSLC nano LC (Thermo Fisher Scientific) in-line connected to a Q Exactive mass spectrometer (Thermo Fisher Scientific). Peptides were identified by searching each spectrum against the TAIR10 database with the MaxQuant software (Cox, et al., 2014; Cox, et al., 2011). Downstream data analysis and statistics on the (phospho)proteomics were performed using the label-free quantification workflow embedded in the Perseus software (www.perseusframework.org/). The label-free quantification algorithm of MaxQuant determines a quantification intensity value for every identified phosphopeptide or

protein, which can be further processed and visualised with Perseus. To provide sufficient statistical power to the label-free quantification of the proteome, all assays were performed four times. For statistical analyses, only phosphopeptides/proteins that were detected in a minimum of three out of four biological replicates were retained. Log2 values of the phosphopeptide/protein intensities were normalised by subtracting the median of the entire set of phosphopeptide/protein intensities per sample.

Co-Immunoprecipitation

Protein Preparation

Cultures of *Arabidopsis* seedlings (50 mg seed, 100 ml ½ Murashige and Skoog medium) were prepared, and grown on a rotary shaker at 90-100 RPM until 5 DAG. Seedlings were then harvested, excess medium was removed, and seedlings were snap frozen in liquid nitrogen. Frozen tissue was ground in a pre-chilled pestle and mortar, and 1 g of material was used to extract protein. 5 ml extraction buffer (150 mM Tris-HCl (pH 9.5), 150 mM NaCl, 10% Glycerol, 10 mM EDTA pH 8.0, 15 mM DTT, 1% NP-40, 1% Protease inhibitor cocktail (Sigma)) was added to the tissue, and the sample was sonicated at 10% amplitude for 30s on ice to fully disrupt tissue. Sonicated samples were incubated at 4^{o}C for 1 hour with gentle agitation, and cell debris was removed by centrifugation at 18000 x g 4^{o}C for 30 minutes. Supernatant was removed to a fresh 15 ml falcon tube [1], and of 50 µl GFP Trap agarose beads (ChromoTek - prepared according to manufacturer's instructions) were added to each sample, and incubated overnight at 4^{o}C with gentle agitation. Samples were then centrifuged at 10000 x g, 4^{o}C for 2 minutes to pellet the beads, and supernatant removed [2]. Beads were washed three times (1 ml 1 x TBS + 0.05% NP40),

snap frozen in liquid nitrogen and stored at -80°C for proteomics analysis or eluted for use on a Western blot. Samples for Western analyses were eluted by addition of 50 µl 1 x SDS loading dye (100 mM Tris-HCl pH6.8, 4% SDS, 0.2% Bromophenol Blue, 20% Glycerol, 20 mM DTT). Samples for Western blot analysis were heated to 70°C for 20 minutes to denature bound proteins, and residual agarose beads were removed by centrifugation at 12000 x g for 1 minute at room temperature.

[1] 50 µl of cleared supernatant was removed for use as input sample in western blot analyses.

[2] 50 µl of supernatant was retained for use as unbound fraction in western blot analyses.

Western blot Analyses

Input, unbound fraction and eluted fraction samples (prepared as detailed above) were loaded onto an SDS PAGE gel and separated at 100 V constant voltage until the dye front reached the end of the gel. PVDF membrane was cut to size and prepared for use by washing in methanol for 30 seconds, washing briefly in sterile water, and then was allowed to equilibrate in transfer buffer (0.025M Tris, 0.025M Glycine, 10% v/v methanol) for at least 10min. Protein was then transferred from the gel to the membrane by electrophoresing at 400mA for 2 hours in transfer buffer. Following transfer of proteins to the membrane, the membrane was blocked in 5% milk solution in PBST (0.01M phosphate buffer, 0.15M NaCl 0.01% Tween 20). The membrane was then exposed to conjugated anti-GFP/HRP (1:2000) in 1% milk solution in PBST overnight at 4°C on a rolling shaker. The membrane was washed 3 times in PBST for 15 minutes, and once in PBS for 30 seconds. ECL reagents (GE Lifesciences) were then mixed 1:1 and applied to the membrane,

and incubated at room temperature for 5 min, before draining and exposing the blot on photographic film.

Proteomics Analyses

50 µl of 50 mM TEAB pH8 was added to resuspend the GFP Trap beads. 1 µl of 1 µg/µl Lysyl Endopeptidase was added and samples were incubated at 37^{o}C for 4 hours with gentle agitation. 1 µl of 1 µg/ul Trypsin Gold was added and samples were incubated at 37^{o}C overnight with gentle agitation to complete digestion. After digestion was complete, beads were removed by centrifugation at 10000 x g for 2 minutes and the samples were adjusted to pH 3 using 10% trifluoroacetic acid to stop the digest. Digested peptides were dried by vacuum centrifugation and stored at -80^{o}C prior to analysis by LC-MS/MS. For MS analysis, samples were resuspended in 20-50 µl injection solvent (2% acetonitrile, 0.1% TFA), and analysed via LC-MS/MS on an Ultimate 3000 RSLC nano LC (Thermo Fisher Scientific) in-line connected to a Q Exactive mass spectrometer (Thermo Fisher Scientific). Peptides were identified by searching each spectrum against the TAIR10 database with the MaxQuant software (Cox, et al., 2014; Cox, et al., 2011). Downstream data analysis and statistics on the proteomics were performed using the label-free quantification workflow embedded in the Perseus software (www.perseusframework.org/). The label-free quantification algorithm of MaxQuant determines a quantification intensity value for every identified peptide, which can be further processed and visualised with Perseus. To provide sufficient statistical power to the label-free quantification of the proteome, all assays were performed four times. For statistical analyses, only peptides that were detected in a minimum of

three out of four biological replicates were retained. Log2 values of the peptide intensities were normalised by subtracting the median of the entire set of peptide intensities per sample. A student's t-test was carried out to determine the significance of the effect of treatment compared with untreated samples.

Genotyping Analyses

Genotyping was performed using a PCR based approach following growth on ½ Murashige and Skoog agar (see above). Gene-specific primers were acquired for each seed line (Appendix 3), and SALK or SAIL LBb primers were used to detect insertion of T-DNA. PCR products amplified by SALK or SAIL primers in combination with the gene specific reverse primer were isolated using a GeneJET gel extraction kit (Thermo Fisher) according to manufacturer's instructions. Resulting purified PCR products were sequenced (Eurofins) in order to determine the precise location of the insert. Homozygous mutant lines were transferred to soil (as detailed above) in order to bulk seed.

qPCR Analyses

Total RNA was isolated from 4 10-12 DAG seedlings using an RNeasy plant mini kit (Qiagen) according to manufacturer's instructions. 10 µg RNA was digested using DNAse I (New England Biolabs) according to manufacturer's instructions, in order to remove any potential contamination from gDNA prior to cDNA synthesis. cDNA was created using Superscript II reverse transcriptase kit (Thermo Fisher Scientific) according to the manufacturer's instructions and stored at -80^{o}C until required for analysis. qPCR reactions were conducted using SYBR Master Mix

– Low ROX (Origene) using gene specific primers (Appendix 3) on a LightCycler 480 (Roche) and normalised to expression of TRANSLATION ELONGATION FACTOR EEF-1 ALPHA CHAIN. Ct values were exported to excel and used to calculate ΔΔCt using Equation 1.

$$\Delta\Delta Ct = \big(Ct(Am) - Ct(Bm)\big) - \big(Ct(Ac) - Ct(Bc)\big)$$

Equation 1: Calculation of ΔΔCt for relative quantification of mRNA transcripts by qPCR. A = Target gene, B = Reference gene c = control, m = mutant.

Root Architectural Trait Analyses

Seedlings for root architectural analyses were grown vertically on 12 x 12 cm square petri plates (as detailed above) until 10-12 DAG, at which point primary root length and emerged lateral root density was analysed. Seedlings were photographed using a Panasonic Lumix DMC-FX37 camera on a camera mount, primary roots were measured using FIJI software (Schindelin, et al., 2012). Emerged lateral root number was determined by counting emerged lateral roots for each plant using a dissection microscope (Zeiss Stemi SV 6). Data was analysed using Excel, and Equation 2 was used to calculate lateral root density.

$$Lateral\ Root\ Density = \frac{Emerged\ Lateral\ Roots}{Primary\ Root\ Length}$$

Equation 2: Calculation for determination of lateral root density in *Arabidopsis.*

All data was analysed in triplicate, using 3 technical and three biological repeats (3 plates of 10 seeds per biological repeat, 3 biological repeats), and the mean primary root length and lateral root density was used to construct graphs. Standard error was used to illustrate deviation from the mean within the dataset, and a student's t-test was used to determine the significance of the observed root architectural traits.

In silico Analyses

Protein sequences were retrieved from UniProt entries, and BLAST searches were performed in Phytozome 11 (phytozome.jgi.doe.gov) using the BLOSUM62 comparison matrix to interrogate the *Arabidopsis thaliana TAIR10, Oryza sativa v7_JGI, Zea mays Ensembl-18, Solanum lycopersicum iTAG2.3, Brassica rapa FPsc v1.3,* and *Triticum aestivum v2.2* annotated proteome data with an expected (E) threshold of -1. BLAST searches were also carried out, querying the complete UniProtKB database with the BLOSUM62 matrix using an E threshold of 10. These proteins were filtered to remove uncharacterised proteins, unannotated proteins and fragments before further analysis. Resulting proteins were aligned in CLC workbench and phylogenetic trees were created using Neighbour Joining – Jukes Cantor algorithm. TMHMM analyses were carried out on the TMHMM server (www.cbs.dtu.dk/services/TMHMM/) using FASTA format protein sequences retrieved from the UniProt database.

UNK Construct Creation

UNK Cloning

Total RNA was isolated using an RNeasy miniprep kit (Qiagen), and cDNA was created from total RNA using Superscript II (Thermo Fisher Scientific), according to manufacturer's instructions. gDNA was isolated using a GenElute Plant Genomic DNA Miniprep Kit (Sigma-Aldrich) according to manufacturer's instructions. Phusion High-Fidelity DNA Polymerase (Thermo Fisher Scientific) and gene specific primers (Appendix 3) were used to amplify UNK sequences from cDNA and gDNA as detailed in Table 1.

Table 1: List of sequences and constructs used to create *UNK* transcriptional and translational fusions

Construct	Vector	UNK Sequence	+/- STOP	+/- GFP Tag
35S::UNK	pGWB5	AT1G49840 cDNA	+	-
35S::UNK:GFP	pGWB5	AT1G49840 cDNA	-	+
pUNK::UNK	pGWB4	AT1G49840 gDNA + 2004 bp of 5' Sequence	+	-
pUNK::UNK:GFP	pGWB4	AT1G49840 gDNA + 2004 bp of 5' Sequence	-	+
pUNK::GFP	pGWB4	2004 bp of 5' Sequence	N/A	+

The resultant PCR fragments were isolated by gel purification using a GeneJET plasmid miniprep kit (Thermo Fisher Scientific) according to manufacturer's instructions, and fragments were adenine tailed by incubation with dATP and Taq Polymerase for 20 min (Per Reaction: 16.1 µl Purified DNA, 2 µl 10x NH_4 buffer, 1 µl $MgCl_2$, 0.4 µl dATP, 0.5 µl Taq Polymerase).

A-tailed fragments were cloned into pCR8/GW/TOPO according to manufacturer's instructions, and 2 µl of each construct was transformed into DH5α chemically competent *E. coli* by heat shock

treatment (30 minutes on ice, 45 seconds at 42^{o}C in a water bath, 2 minutes on ice), following which, 450 µl room-temperature LB broth was added and *E. coli* was incubated at 37^{o}C for 1.5 hours in order to facilitate recovery. 100 and 200 µl of each transformant was plated out on LB agar containing 50 µg/ml spectinomycin, and plates were incubated overnight at 37^{o}C. Following incubation, colonies were checked for the presence of inserts using colony PCR and M13 primers. PCR fragments demonstrating the correct insert length sequenced (EuroFins) to confirm correct orientation and that no errors in sequence had been introduced during previous PCR reactions. Following confirmation of insert orientation and sequence, vectors containing the correctly orientated insert were amplified by overnight culture at 37^{o}C in 5ml LB broth containing 50 µg/ml spectinomycin. Entry clones amplified in this manner were purified using a GeneJET Plasmid Miniprep kit (Thermo Fisher Scientific), and 150 ng entry clone and 150 ng respective pGWB destination vector (Nakagawa, et al., 2007) were used with LR Clonase II (Invitrogen) to transfer the UNK sequences to the appropriate destination vector (Table 1) according to manufacturer's instructions. Destination vectors were transformed into chemically competent DH5α *E. coli* as detailed previously, and plated on 50 µg/ml kanamycin selective LB agar. Colony PCR was performed as described previously using a combination of 35S, GFP, and gene specific primers (

Table 2) to confirm insertion of UNK inserts in the destination vectors.

Table 2:List of primers used for confirmation of insert presence in destination vectors for sequences see Appendix 3.

Construct	Forward Primer	Reverse Primer
35S::UNK:GFP	35S	GFP
35S::UNK	35S	cUNK_R + Stop
pUNK::GFP	pUNK_F	GFP
pUNK::UNK	pUNK_F	cUNK_R + Stop
pUNK::UNK:GFP	pUNK_F	GFP

Following confirmation of insert presence in destination vectors, constructs were amplified by overnight culture in 5 ml LB broth containing 50 µg/ml kanamycin and purified using a GeneJET plasmid miniprep kit according to manufacturer's instructions.

Transformation of Agrobacterium tumefaciens

Agrobacterium tumefaciens was transformed by mixing 1 µg purified destination vector with the *Agrobacterium* cells, and electroporation using a Biorad MicroPulser electroporation unit and a 1 mm gap cuvette. Following electroporation, cells were allowed to recover in LB broth for 2 hours at 28^{o}C, before transfer to 5 ml LB broth containing 50 µg/ml kanamycin and overnight incubation at 28^{o}C at 200 RPM to increase bacterial count for use in *Arabidopsis* transformations.

Transformation of Arabidopsis Plants

Flowering *Arabidopsis* (Col-0) plants grown on soil were transformed using the floral dip technique (Clough & Bent, 1998). Overnight cultures of transformed *Agrobacterium* was diluted to 50 ml (OD ≈ 0.8) in 5% sucrose solution, and the solution was adjusted to contain 0.05% Silwet

L-77 immediately prior to dipping the plants. Aboveground organs were immersed in the *Agrobacterium* suspension, and wrapped individually in Saran film to prevent cross-contamination of plants with other vectors. Dipped plants were grown to seed, and transformed seeds were selected for by growth on ½ Murashige and Skoog agar containing 50 µg/ml kanamycin.

Confocal Microscopy

Confocal microscopy was performed on a Zeiss 710 or Leica TCS SP5 confocal microscope, using settings optimised for GFP and Propidium Iodide detection (4% argon laser, excitation wavelength 488/568 nm, detection wavelength 509/617 nm respectively).

Appendix 1: PP2A-3 interacts with ACR4 and regulates formative cell division in the Arabidopsis root

Published as Kun Yue, Priyanka Sandal, Elisabeth L. Williams, Evan Murphy, Elisabeth Stes, Natalia Nikonorova, Priya Ramakrishna, Nathan Czyzewicz, Laura Montero-Morales, Robert Kumpf, Zhefeng Lin, Brigitte van de Cotte, Mudassar Iqbal, Michiel Van Bel, Eveline Van De Slijke, Matthew R. Meyer, Astrid Gadeyne, Cyril Zipfel, Geert De Jaeger, Marc Van Montagu, Daniël Van Damme, Kris Gevaert, A. Gururaj Rao, Tom Beeckman, and Ive De Smet (2015) *PNAS*; 113(5):1447-1452

Author Contribution:

I was involved with method optimisation for ACR4 western blotting, and contributed Yeast 2Hybrid interactome data.

PP2A-3 interacts with ACR4 and regulates formative cell division in the *Arabidopsis* root

Kun Yue[a,b,1], Priyanka Sandal[c,1], Elisabeth L. Williams[d,1], Evan Murphy[d], Elisabeth Stes[a,b,e,f], Natalia Nikonorova[a,b], Priya Ramakrishna[d], Nathan Czyzewicz[d], Laura Montero-Morales[a,b], Robert Kumpf[a,b], Zhefeng Lin[d], Brigitte van de Cotte[a,b], Mudassar Iqbal[g,2], Michiel Van Bel[a,b], Eveline Van De Slijke[a,b], Matthew R. Meyer[h], Astrid Gadeyne[a,b], Cyril Zipfel[i], Geert De Jaeger[a,b], Marc Van Montagu[a,b,3], Daniël Van Damme[a,b], Kris Gevaert[e,f], A. Gururaj Rao[c,4], Tom Beeckman[a,b,4], and Ive De Smet[a,b,d,j,3,4]

[a]Department of Plant Systems Biology, VIB, B-9052 Ghent, Belgium; [b]Department of Plant Biotechnology and Bioinformatics, Ghent University, B-9052 Ghent, Belgium; [c]Roy J. Carver Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State University, Ames, IA 50011; [d]Division of Plant and Crop Sciences, School of Biosciences, University of Nottingham, Loughborough LE12 5RD, United Kingdom; [e]Department of Medical Protein Research, VIB, B-9000 Ghent, Belgium; [f]Department of Biochemistry, Ghent University, B-9000 Ghent, Belgium; [g]Multidisciplinary Centre for Integrative Biology, School of Biosciences, University of Nottingham, Loughborough LE12 5RD, United Kingdom; [h]Department of Medicine, Washington University School of Medicine, St. Louis, MO 63130; [i]The Sainsbury Laboratory, Norwich Research Park, Norwich NR4 7UH, United Kingdom; and [j]Centre for Plant Integrative Biology, University of Nottingham, Loughborough LE12 5RD, United Kingdom

Contributed by Marc Van Montagu, December 22, 2015 (sent for review June 4, 2015; reviewed by Joanne Chory, Idan Efroni, Kimberly L. Gallagher, and Zhi-Yong Wang)

In plants, the generation of new cell types and tissues depends on coordinated and oriented formative cell divisions. The plasma membrane-localized receptor kinase ARABIDOPSIS CRINKLY 4 (ACR4) is part of a mechanism controlling formative cell divisions in the *Arabidopsis* root. Despite its important role in plant development, very little is known about the molecular mechanism with which ACR4 is affiliated and its network of interactions. Here, we used various complementary proteomic approaches to identify ACR4-interacting protein candidates that are likely regulators of formative cell divisions and that could pave the way to unraveling the molecular basis behind ACR4-mediated signaling. We identified PROTEIN PHOSPHATASE 2A-3 (PP2A-3), a catalytic subunit of PP2A holoenzymes, as a previously unidentified regulator of formative cell divisions and as one of the first described substrates of ACR4. Our in vitro data argue for the existence of a tight posttranslational regulation in the associated biochemical network through reciprocal regulation between ACR4 and PP2A-3 at the phosphorylation level.

stem cells | columella | phosphorylation | kinase | phosphatase

Plants rely on coordinated formative cell division for the formation of new cell types and tissues (1). For example, in the *Arabidopsis* primary root tip, columella stem cells—upon formative cell division—give rise to new stem cells and daughter cells that will differentiate (2) (*SI Appendix*, Fig. S1*A*). Several plant hormones and proteins that play a role in this process have been identified, and small regulatory networks have been proposed (3–11). However, our knowledge of the mechanisms and signaling networks mediating formative cell divisions is sparse and is largely derived from transcriptional data (12).

Reversible protein phosphorylation represents a major mechanism regulating cell signaling (13), and several kinases have been shown to play a role in primary root development (5, 6, 14). For example, the evolutionarily conserved plasma membrane-localized receptor-like kinase ARABIDOPSIS CRINKLY 4 (ACR4) marks the plasma membrane in the primary root tip columella and is part of a mechanism controlling formative cell divisions in the *Arabidopsis* root (5, 6, 15). ACR4 possesses an extracellular ligand-binding domain, a transmembrane helix, and an intracellular domain that contains the juxtamembrane and the C-terminal subdomains, which flank the core kinase domain with serine/threonine kinase activity (Fig. 1*A*). The intracellular juxtamembrane domain is a likely recruitment site for interacting proteins and essential to facilitate downstream signaling (16, 17). *ACR4* is expressed throughout plant development in specific cells and tissues, such as protoderm, columella, and stage I lateral roots, and ACR4 preferentially localizes at plasmodesmata (6, 18–20). In addition to its primary and lateral root phenotypes, *Arabidopsis* loss-of-function *acr4* mutants are affected in maintaining epidermal cell identity, including disorganized cell layers in the ovule integument (18, 20). Although ACR4 was the first receptor kinase to be assigned a role in root development (5), our knowledge about its signaling pathway in the root remains limited (6, 8).

In addition to posttranslational modifications such as phosphorylation, developmental programs and cellular functions largely rely on interactions between proteins, forming complex networks to control biological processes (21). Although membrane proteins play a crucial role in many biological processes, knowledge of the in planta membrane interactome is limited (21). Notwithstanding the recent progress with respect to global analyses of membrane protein interactions, so far ACR4 has not been represented in a membrane-linked *Arabidopsis* interactome (22). Therefore, the objective of this study was to use

Significance

Plant growth and development are mediated through a wide range of proteins, including receptor kinases and phosphatases. The receptor kinase ARABIDOPSIS CRINKLY 4 (ACR4) is part of a mechanism controlling formative cell divisions in the *Arabidopsis* root. However, the regulation of ACR4 signaling and how it affects cell divisions remains completely unknown. We discovered that ACR4 phosphorylates the PROTEIN PHOSPHATASE 2A-3 (PP2A-3) catalytic subunit of the PP2A phosphatase holoenzyme and that PP2A dephosphorylates ACR4. These data exposed a tightly regulated point in the associated biochemical network regulating formative cell divisions in plant roots.

Author contributions: E.L.W., G.D.J., M.V.M., D.V.D., K.G., A.G.R., T.B., and I.D.S. designed research; K.Y., P.S., E.L.W., E.M., E.S., N.N., P.R., N.C., L.M.-M., R.K., B.v.d.C., M.I., M.V.B., E.V.D.S., M.R.M., and I.D.S. performed research; Z.L., A.G., and C.Z. contributed new reagents/analytic tools; K.Y., P.S., E.L.W., G.D.J., D.V.D., K.G., A.G.R., T.B., and I.D.S. analyzed data; and K.Y., P.S., E.S., D.V.D., K.G., A.G.R., T.B., and I.D.S. wrote the paper.

Reviewers: J.C., The Salk Institute for Biological Studies and Howard Hughes Medical Institute; I.E., New York University; K.L.G., University of Pennsylvania; and Z.-Y.W., Carnegie Institution for Science.

The authors declare no conflict of interest.

[1]K.Y., P.S., and E.L.W. contributed equally to this work.

[2]Present address: Faculty of Life Sciences, University of Manchester, Manchester M13 9PL, United Kingdom.

[4]A.G.R., T.B., and I.D.S. contributed equally to this work.

[3]To whom correspondence may be addressed. Email: ive.desmet@psb.vib-ugent.be or marc.vanmontagu@ugent.be.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1525122113/-/DCSupplemental.

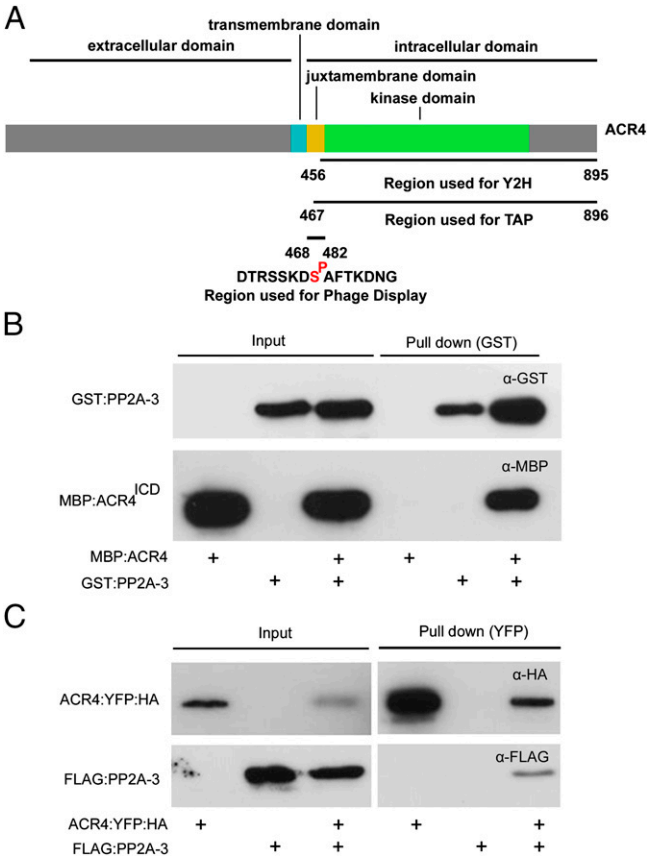


Fig. 1. ACR4 interacts with PP2A-3. (*A*) Schematic representation of ACR4 with key domains and regions used for protein–protein interaction studies. (*B*) In vitro GST pull-down experiment using GST:PP2A-3 and MBP:ACR4^{ICD} according to indicated combinations (+). PP2A-3 and ACR4^{ICD} were detected by Western blotting with anti-GST and anti-MBP antibodies, respectively. (*C*) In planta YFP pull-down experiment using ACR4:YFP:HA and FLAG:PP2A-3 transiently coexpressed in tobacco leaves by *Agrobacterium* infiltration according to indicated combinations (+). PP2A-3 and ACR4 were detected by Western blotting with anti-FLAG and anti-HA antibodies, respectively.

ACR4-centered, protein-focused systems biology approaches to gain insight into the ACR4-signaling cascade and to identify new potential regulators of formative cell division.

Results and Discussion

Mapping Putative ACR4 Interactions. To identify regulators of formative cell division in *Arabidopsis*, we combined, in silico, tandem affinity purification (TAP), yeast two-hybrid (Y2H), and phage display approaches to define potential ACR4-interacting proteins. Given the technical difficulties associated with plasma membrane proteins, we focused on intracellular ACR4 domains for our in vitro and in vivo studies (Fig. 1*A*). We first interrogated available protein–protein interaction (PPI) databases for experimental and predicted interactions by applying the PPI tool within CORNET 2.0 (23) to ACR4 (AT3G59420). This resulted in a network with 85 nodes that mainly lacked experimental validation (Dataset S1 and *SI Appendix*, Fig. S2). Second, we applied a TAP approach to *Arabidopsis* cell suspension cultures expressing the N- or C-terminally tagged ACR4 intracellular kinase domain (Fig. 1*A* and *SI Appendix*, Fig. S3). This analysis resulted in four putative ACR4-interacting proteins, of which two occurred in at least two biological replicates and in both assays with N- and C-terminally tagged ACR4 intracellular kinase domain and were not present in any in house background list, namely 4-HYDROXY-TETRAHYDRODIPICOLINATE REDUCTASE 1 (HTPA REDUCTASE 1/DAPB1; AT2G44040) and HTPA REDUCTASE 2/DAPB2 (AT3G59890) (Dataset S1). Based on TAP data alone, two other candidates, PROTEIN PHOSPHATASE 2A-3 (PP2A-3; AT2G42500) and PP2A-4 (AT3G58500), could not be conclusively identified as bona fide ACR4-interacting proteins as they were detected in only one technical repeat. Third, we applied a conventional high-throughput Y2H assay to screen for potential interactions with the ACR4 intracellular domain (Fig. 1*A*). This revealed four potential ACR4-interacting proteins with high confidence (Dataset S1). Finally, we screened a synthetic 15-mer peptide encompassing the Ser^{475} phosphorylation site within the intracellular juxtamembrane domain of ACR4 (Fig. 1*A*) against a 21-amino acid phage-peptide library (24, 25). When the resulting consensus-binding motifs for the phosphorylated peptide were queried against the *Arabidopsis* protein database, over 4,000 potential ACR4-interacting proteins were identified (Dataset S1). Taken together, our complementary approaches identified several putative ACR4-interacting proteins, but when we searched for overlap between the different approaches this was limited to absent (Dataset S1). This could mean that different approaches yielded different subsets of putative ACR4-interacting proteins or that we picked a large number of likely false-positives.

In Silico Quality Assessment of Putative ACR4 Interactions. To increase the confidence in the potential ACR4-interacting proteins listed in Dataset S1 and to select candidates for functional analyses, we performed in depth in silico quality assessment. Correlated gene expression is an indicator of cofunctionality of genes in common pathways and processes (26), and interacting proteins are often significantly coexpressed. First, we used CORNET 2.0 (23) to globally explore coexpression of *ACR4* and genes encoding potential ACR4-interacting proteins, which showed some coexpression (Pearson correlation coefficient > 0.55) between ACR4 and some CORNET (2/85) and phage display hits (44/4402) (Dataset S1). Second, to further support potential PPIs in the root tip and during lateral root initiation, we used available cell- and tissue-specific transcript profiling datasets (5, 27). Visualization of root tip in silico expression patterns for TAP (3/4) and Y2H candidates (2/4) through the BAR *Arabidopsis* eFP Browser (28) revealed distinct expression patterns that, at least partially, overlapped with the *ACR4* expression domain (*SI Appendix*, Fig. S2). In addition, some of the CORNET (8/85) and PHAGE DISPLAY candidates (360/4402) were—similar to *ACR4*—also transcriptionally differentially regulated in a transcriptome study of pericycle cells undergoing lateral root initiation (5) (Dataset S1). Based on the above observations, we generated a priority list for CORNET, TAP, Y2H, and PHAGE DISPLAY hits, narrowing down the number of candidates from 4,495 to 525 (Dataset S1). Next, to globally assess interactions between ACR4 and potential interacting proteins, we used the PPI tool within CORNET 2.0 (23). Indeed, several of the CORNET, Y2H, TAP, and prioritized PHAGE DISPLAY hits are connected with ACR4 and with each other in predicted and experimentally validated protein–protein interaction networks focusing on pairwise interactions (Dataset S1). To gain insight into the molecular functions represented in this protein–protein interaction network, we determined that several statistically overrepresented Gene Ontology categories with respect to biological process (5%) and molecular function (5%) were related to phosphorylation (Dataset S1), which is in agreement with the fact that ACR4 is a receptor kinase. Taken together, through our in silico assessment we increased the confidence in a subset of potential ACR4-interacting proteins (Dataset S1). However, our dataset is not necessarily comprehensive, as, for example, WUSCHEL RELATED HOMEOBOX 5 (WOX5), CRINKLY4-RELATED (CCR) proteins, and CLAVATA1 (CLV1), which were shown to interact with ACR4 (6, 29), were not retained.

ACR4 Interacts with PP2A-3. Taking the results of Dataset S1 into account allowed us to impose additional criteria to select candidates for functional analyses. Among the candidates selected by at least two approaches and with a high score in the priority list (Dataset S1), we retrieved sequences that match PP2A-3 and/or PP2A-4, which are isoforms of catalytic PP2A C subunits and that form a subclade in the family of five *Arabidopsis* PP2A C subunits (30). In general, the PP2A heterotrimeric holoenzyme, which is a major, highly conserved eukaryotic serine/threonine phosphatase, consists of a catalytic C subunit, a type A scaffolding/regulatory subunit, and a type B regulatory subunit (31). In *Arabidopsis*, PP2A phosphatases have been implicated in various hormone-regulated, cellular, and developmental processes, including spatial control of cell division and columella organization, and in innate immunity, but little is known about their dynamic and highly regulated function (32–35). In the context of our focus on formative cell division, we selected PP2A-3 (and PP2A-4) for subsequent in-depth functional characterization. First, an overlay assay indicated that PP2A-3 can specifically interact with both the naive ACR4 intracellular domain ($ACR4^{ICD}$) (endogenously phosphorylated at a limited number of residues in *Escherichia coli* through an unknown mechanism) and fully in vitro autophosphorylated $ACR4^{ICD}$ (24) (*SI Appendix*, Fig. S3 and *Supplemental Notes*). Second, gel-filtration analyses further confirmed the interaction between the ACR4 intracellular domain ($ACR4^{ICD}$) and PP2A-3 (*SI Appendix*, Fig. S3 and *Supplemental Notes*). Subsequently, the purified recombinant MBP:$ACR4^{ICD}$ was effectively pulled down with GST:PP2A-3 in vitro (Fig. 1*B*). Moreover, in *Nicotiana benthamiana* transient expression assays, ACR4:YFP:HA was able to coimmunoprecipitate FLAG:PP2A-3 in planta (Fig. 1*C*). Taken together, these data strongly indicate that ACR4 and PP2A-3 interact with each other.

***ACR4* and *PP2A-3* Are Coexpressed.** As mentioned above, *Arabidopsis* eFP Browser data suggested that *PP2A-3* is weakly expressed in columella stem cells and in the root apical meristem (*SI Appendix*, Fig. S2). To confirm this, we analyzed seedlings expressing a *pPP2A-3::n3xGFP* fusion and assessed expression in the root tip. In five independent transformants we indeed observed *pPP2A-3::n3xGFP* expression in the root tip, but *PP2A-3* was more broadly expressed than *ACR4* (5) (*SI Appendix*, Fig. S1). In addition, we observed *PP2A-3* expression during early lateral root initiation (*SI Appendix*, Fig. S1), which also overlapped with *ACR4* expression at this stage (5) (*SI Appendix*, Fig. S1). Taken together, these results show that *ACR4* and *PP2A-3* are expressed in overlapping domains, further supporting that they can physically interact.

PP2A-3 Is Involved in Columella Stem Cell Differentiation. To test genetically if PP2A-3 plays a role in ACR4-mediated stem cell regulation, we analyzed primary root length and columella stem cell differentiation in a previously characterized *pp2a-3* mutant (34). The primary root of *pp2a-3* is slightly longer than wild type

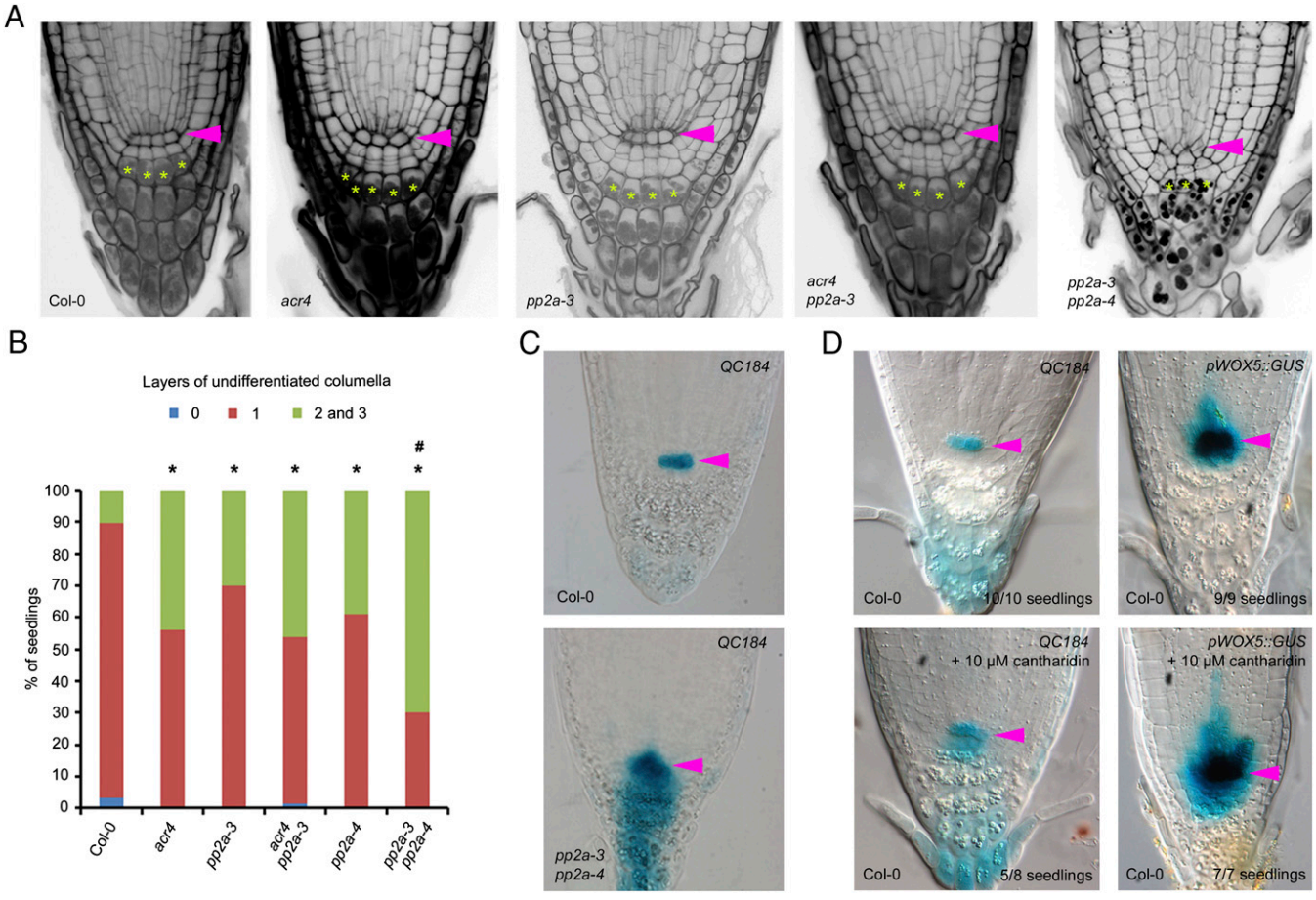


Fig. 2. PP2A-3 mediates columella stem cell divisions. (*A* and *B*) Representative images (*A*) and quantification (*B*) of columella stem cell daughter cell differentiation ($20 \leq n \geq 96$) and irregular cellular pattern in *pp2a-3 pp2a-4* (*A*, *Right*). Statistical significance (Z Test Calculator for 2 Population Proportions, $P < 0.05$) compared with Col-0 (*) or *acr4* (#) is indicated. (*C* and *D*) Expression of *QC184* and *pWOX5::GUS* in 5-d-old *pp2a-3 pp2a-4* seedlings (*C*) or in 5-d-old seedlings grown on 10 µM cantharidin (*D*). Representative pictures with number of seedlings with similar expression pattern indicated. Pink arrowhead, quiescent center. Yellow asterisk, first columella cell layer with starch granules.

(*SI Appendix*, Fig. S1). With respect to columella stem cell differentiation, we observed less differentiation in *pp2a-3* compared with wild type, which is similar to *acr4* (Fig. 2 *A* and *B*). However, because such a columella phenotype can also be explained by altered auxin distribution, levels, or response (11), the similarity between the *pp2a-3* and *acr4* mutants does not provide conclusive support for a genetic and/or physical interaction. This is especially relevant because PP2A-3 has been shown to play a role in auxin transport (36). We therefore tested to what extent *acr4* and *pp2a-3* are affected in their sensitivity to N-1-naphthylphthalamic acid (NPA) with respect to primary root length and columella differentiation. In these assays, *acr4* and *pp2a-3* appeared equally sensitive to NPA treatment as Col-0 (*SI Appendix*, Fig. S4), suggesting that there is no apparent auxin transport-mediated effect in this case. The genetic interaction between ACR4 and PP2A-3 was further supported by the *acr4 pp2a-3* double mutant, where we could not record an additive effect, arguing that both are active in the same pathway (Fig. 2 *A* and *B*). Although we cannot rule out cell-specific changes, we have excluded that the similarities in phenotype are due to a broad differential regulation of *ACR4* or *PP2A-3* expression in *pp2a-3* and *acr4* mutants, respectively (*SI Appendix*, Fig. S5). Taken together, our observations indicate a role for PP2A-3 in cellular patterning during primary root development that overlaps with ACR4 function and further suggest that this is possibly independent of an affected auxin transport capacity.

PP2A-3 and PP2A-4 Redundantly Affect Primary Root Growth. Given that PP2A-4 is closely related to PP2A-3, we explored possible redundancy with respect to primary root growth. Indeed, a double *pp2a-3 pp2a-4* mutant displayed a short primary root, further reduced columella differentiation, and severely disrupted cell organization in the root tip compared with wild type (Fig. 2 *A* and *B* and *SI Appendix*, Fig. S1) (34). However, this double-mutant phenotype appeared to be less severe than the one obtained by Ballesteros and coworkers (36), which is possibly due to the use of different T-DNA lines. Short root phenotypes associated with disrupted cell division and/or cellular patterning in the root tip are often associated with a loss of quiescent center cell identity (37, 38). To assess if the quiescent center was absent in the disrupted root tip of *pp2a-3 pp2a-4*, we analyzed the expression of the quiescent center marker *QC184* (7). Surprisingly, notwithstanding the dramatic impact on the regular cellular pattern in the root tip, *QC184* expression was not abolished and even appeared to expand into the columella (Fig. 2*C*). The latter might suggest that the stemness gradient in *pp2a-3 pp2a-4* is perturbed. Furthermore, we applied cantharidin—an inhibitor of PP2A and PP2A-related phosphatases (*SI Appendix*, *Supplemental Notes*)—to the *QC184* and *pWOX5::GUS* markers (7), demonstrating that quiescent center identity is not lost when interfering with PP2A activity (Fig. 2*D* and *SI Appendix*, Fig. S6). Interestingly, *WOX5* expression was shown to be similarly affected in the *clavata3/embryo surrounding region 40* (*cle40*) mutant, and ACR4 was identified as a target of CLE40 signaling (6, 8), further corroborating the potential connection between PP2A and ACR4. Next, evaluating sensitivity to cantharidin with respect to primary root growth revealed that *acr4* is equally sensitive to cantharidin treatment as *pp2a-3* and that both are not significantly more sensitive than the control (*SI Appendix*, Fig. S7). We furthermore established that cantharidin does not negatively affect *ACR4* expression levels and observed a similar (minor) up-regulation as in *pp2a-3 pp2a-4* (*SI Appendix*, Fig. S5). Taken together, these results further suggest that ACR4 and PP2A-3 act in the same pathway.

ACR4 Phosphorylates PP2A-3. PP2A activity and function in eukaryotic cells is regulated via posttranslational modification of PP2A subunits (39). For example, PP2A complex assembly depends on the phosphorylation status of the catalytic subunit, and phosphorylation of protein phosphatases has been shown to inactivate the enzyme (39, 40), but this has not been demonstrated in plants. To evaluate if ACR4 affects the phosphorylation status of PP2A-3, we compared the phospho-proteomes of Col-0 and *acr4* seedlings. However, although we could detect a peptide (NH_3-GAGYTFGQDISEQFNHTNNLK-COOH) for PP2A-3 (or PP2A-4) in all samples, we did not observe any (differential) phosphorylation. Because PP2A holoenzymes act in various pathways (35, 36, 41, 42) and because ACR4 acts in only a few cells, it is likely that subtle differences mediated by ACR4 could be masked. Therefore, we explored if PP2A-3 could be phosphorylated by ACR4 in vitro. Indeed, in vitro kinase assays demonstrated that purified recombinant autophosphorylated SUMO:ACR4^{ICD}, but not a mutant inactive version of ACR4^{ICD} with K540A and D641A amino acid exchanges (mACR4^{ICD}), could phosphorylate purified recombinant PP2A-3 (PP2A-3:6xHIS) (Fig. 3*A*). Subsequently, we identified the ACR4-dependent PP2A-3 phosphosites from the in vitro kinase assay using high-resolution mass spectrometry analyses. This revealed a total of nine—so far unknown—phosphorylated residues of which five are at Ser, three are at Thr, and one is at Tyr (Dataset S1 and *SI Appendix*, Fig. S8). Mapping these sites on a 3D homology model of *Arabidopsis* PP2A-3, based on the structure of the catalytic chain within the trimeric human PP2A enzyme, showed that these residues were predominantly solvent-exposed even in the trimer structure and, therefore, quite likely accessible for phosphorylation by ACR4 (Dataset S1 and *SI Appendix*, Fig. S8). Taken together, our results pinpoint PP2A-3 as a substrate for ACR4 kinase activity. Phosphorylation of the tail of the PP2A catalytic subunit plays an important role in regulating the assembly—and thus activity—of PP2A holoenzymes (39). We therefore explored PP2A activity in cellular extracts prepared from *acr4* seedlings using a PP2A phosphatase assay system (35, 43, 44). In our hands, this revealed a decrease in PP2A activity of about 19% in *acr4* compared with wild type, which was similar to that associated with the PP2A regulatory subunit mutant roots curl in npa 1 (*rcn1*) (22%) and the catalytic subunit mutant *pp2a-3* (16%) (Fig. 3*B*). Although the results did not achieve statistical significance (*P* value for *acr4* = 0.083), likely because the ACR4 impact on PP2A activity is diluted, they are reproducible and

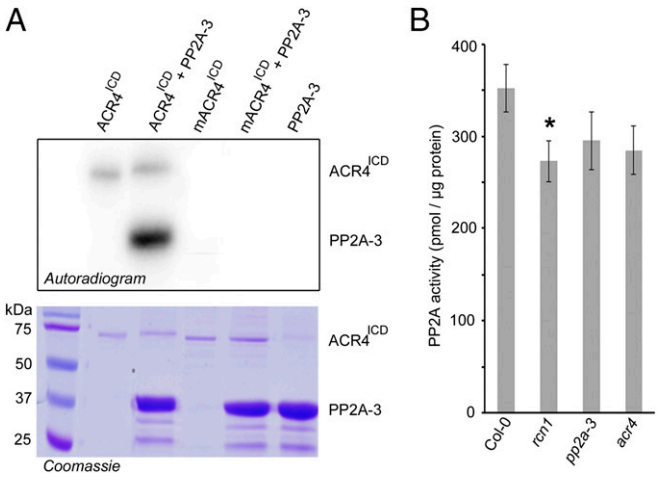


Fig. 3. PP2A-3 is phosphorylated by ACR4 kinase. (*A*) Autoradiogram for coincubated *E. coli*-expressed PP2A-3 and ACR4 kinase (ACR4^{ICD}) or mutant inactive kinase mACR4^{ICD} as indicated (*Upper*). The lanes in *A* are, from left to right, molecular weight standards, 1 µg of autophosphorylated ACR4^{ICD}, 1 µg of autophosphorylated ACR4^{ICD} incubated with 10 µg PP2A-3, 1 µg of mutant inactive kinase mACR4^{ICD}, 1 µg of mutant inactive kinase mACR4^{ICD} incubated with 10 µg PP2A-3, and 10 µg PP2A-3. Corresponding Coomassie blue-stained gel (*Lower*) was used as loading control. (*B*) Bar diagram for PP2A activity detected in whole 12-d-old seedling protein extracts as average of three biological repeats (with three technical repeats each) ± SE. Statistical significance (Student's *t* test) compared with Col-0 is indicated: **P* value < 0.05.

suggestive of ACR4 being required for some of the cellular PP2A activity.

PP2A-3 Dephosphorylates ACR4. With respect to receptor kinases, PP2A has been shown to modulate the phosphostatus of BRI1 and the coreceptor BAK1 (35, 45, 46), so we also evaluated if PP2A-3 is capable of dephosphorylating ACR4. First, using *E. coli*-expressed PP2A-3 in a phosphatase assay did not yield a convincing difference with respect to dephosphorylation of $ACR4^{ICD}$ (*SI Appendix*, Fig. S8 and *Supplemental Notes*). Therefore, to determine whether ACR4 could be a substrate of PP2A, we used—in accordance with Wu and colleagues (45)—a purified, active human PP2A to dephosphorylate the $ACR4^{ICD}$ that had been phosphorylated in vitro. This demonstrated PP2A-mediated dephosphorylation of the phosphorylated $ACR4^{ICD}$ (Fig. 4*A*) and pinpoints ACR4 as a substrate for PP2A phosphatase activity. To assess the biological importance of altering the PP2A-mediated phosphorylation status of ACR4, we analyzed ACR4:GFP in the root of the *pp2a-3 pp2a-4* double mutant. This revealed a weak GFP signal in *pp2a-3 pp2a-4*, with reduced membrane localization, compared with the control (Fig. 4*B*), which is likely not due to a change in *ACR4:GFP* expression levels (*SI Appendix*, Fig. S5). To explore this further, we investigated ACR4:GFP in the presence of the PP2A inhibitor cantharidin. This revealed a reduced membrane association of ACR4:GFP upon inhibiting PP2A activity within 5 h, whereas the membrane localization of the routinely used membrane marker FORMIN HOMOLOG 6 (FH6):GFP (47) was largely unaffected (Fig. 4 *C* and *D* and *SI Appendix*, Fig. S9). Overall, these results suggest that membrane localization of ACR4 is dependent on PP2A-3 (and potentially PP2A-4).

Conclusions

Interactions between membrane-associated proteins and soluble proteins are essential for signal transduction and for regulating plant growth and development. Here, we used various approaches to generate a prioritized list of potential ACR4-interacting proteins that are possibly involved in formative cell division, cell-to-cell communication, and root development. Taking all our interaction data together and because there is limited-to-no overlap between the different approaches, it seems that to study protein–protein interactions the use of multiple approaches is preferred as each technique seems to expose a distinct subset of potential interactors and can increase confidence in some potential interactors that would otherwise be discarded.

Starting from the prioritized, potential ACR4-interacting candidates, we identified PP2A-3 as one of the first described ACR4 substrates and showed that PP2A-3 plays an important role in the control of columella stem cell divisions and/or differentiation. Previously, it was shown that PP2A complexes associate with membranes in growing seedlings and that PP2A may interact with plasma membrane components (33, 41). Similar to the PP2A effect on BRI1 where dephosphorylated BRI1 is internalized (45, 46) and on BAK1 (35), we showed that PP2A can dephosphorylate ACR4. In this context, we also showed that PP2A activity affects the membrane localization of ACR4. The resemblance of the *acr4* and *pp2a-3* columella stem cell phenotype, together with the cell biological data, suggests that PP2A acts as a positive regulator of ACR4 function and that it is the dephosphorylated form of the ACR4 protein that is localized to the plasma membrane and is functional. On the basis of the available data, we propose a tentative model whereby, on the one hand, ACR4 phosphorylates the PP2A-3 catalytic subunit of the PP2A holoenzyme, possible facilitating complex assembly, and on the other hand, PP2A dephosphorylates ACR4, regulating its membrane localization and possibly activity (*SI Appendix*, Fig. S10). The balance between these two likely affects formative cell divisions and cell differentiation in the root, and as such ACR4

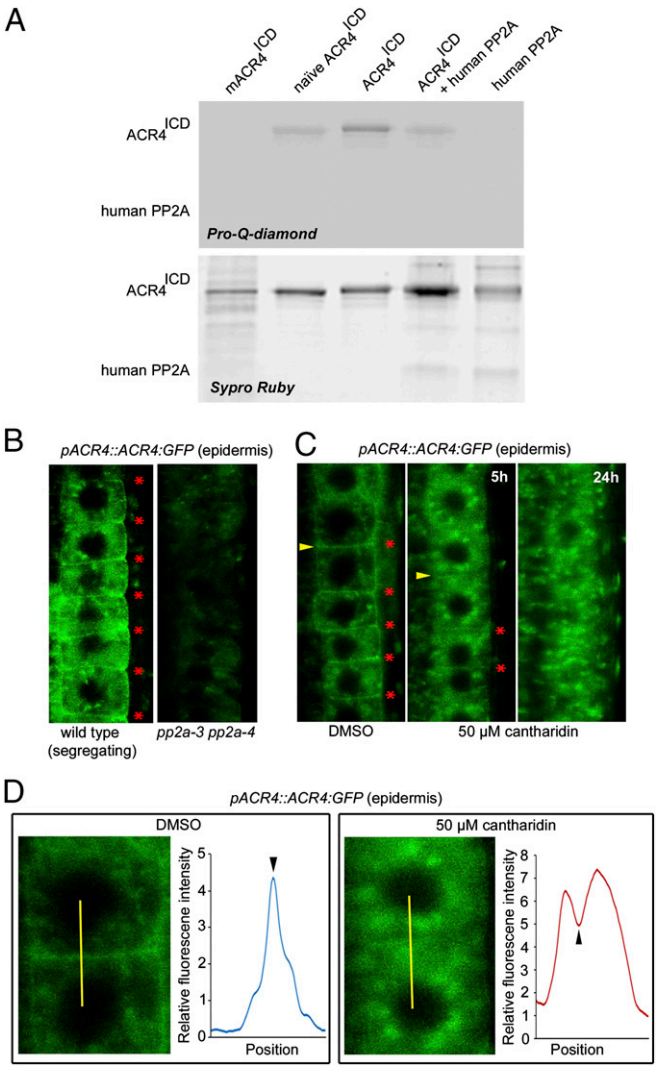


Fig. 4. PP2A-3 dephosphorylates ACR4. (*A*) Pro-Q-diamond stained gel showing the phosphorylation status of $ACR4^{ICD}$ coincubated without or with PP2A-3 as indicated (*Upper*). The same gel stained with Sypro Ruby (*Lower*) as loading control. (*B–D*) Localization of ACR4:GFP in *pp2a-3 pp2a-4* background (*B*) and following treatment with DMSO or 50 µM cantharidin for indicated hours (*C* and *D*). Red asterisk, plasma membrane with ACR4 localization; arrowhead, plasma membrane analyzed in *D*. (*D*) Detail of indicated membrane in *C* (yellow arrowhead) and quantification of GFP signal across the yellow line as smooth average graph. Black arrowhead, position of plasma membrane.

and/or PP2A appear to control their own activity. In the future, it will be important to characterize the importance of the individual ACR4 and PP2A-3 phosphosites and to evaluate these in the context of ACR4 localization and/or activity and PP2A activity and/or complex assembly, respectively. Here, it should be taken into account that, for example, in brassinosteroid signaling, PP2A type B subunits usually recruit substrates and regulate their activity (42, 48) and that membrane localization of PP2A C subunits is regulated by methylation and in turn impacts target dephosphorylation (45).

Materials and Methods

Detailed materials and methods are described in *SI Appendix, Materials and Methods*.

Columella Phenotyping. For columella phenotyping, seedlings were stained with lugol and mounted in Hoyer's solution as previously described (5).

GUS Assays. GUS assays were performed as described previously (49).

TAP. For the TAP approach, transformation of *Arabidopsis* cell suspension cultures was carried out as previously described (26, 27, 50, 51). Tandem affinity purification of protein complexes was done using the GStag (52) followed by protein precipitation and separation, according to a previously described protocol (51).

Transient Transformation. *N. benthamiana* transient transformation was performed as previously described. Protein extraction and coimmunoprecipitation were performed as previously described (53) with modifications (extraction buffer at pH 9.5).

***pACR4::ACR4:GFP* Analyses and Quantification.** To analyze membrane localization of ACR4:GFP, we processed images in ImageJ using the Plot Profile option across a selected line. Subsequently, the plot data were processed according to a moving average calculation of five values to smoothen the graph. Multiple cells ($n > 4$) in multiple seedlings ($n > 2$) were measured and showed similar results.

ACKNOWLEDGMENTS. We thank Jelle Van Leene, Remco Sprangers, Debbie Rombaut, and Dominique Eeckhout for experimental assistance and useful suggestions; Hyun-Sook Pai for the FLAG:PP2A-3 construct; Dr. Yasufumi Yamamoto for constructing the random 21-amino-acid phage-peptide library; and R. Reid Townsend and the Proteomics Core Laboratory at Washington University for mass spectrometry analysis. This work was supported by a Biotechnology and Biological Sciences Research Council (BBSRC) David Phillips Fellowship (BB_BB/H022457/1) and Marie Curie European Reintegration Grant PERG06-GA-2009-256354 (to I.D.S.); a BBSRC CASE Studentship cofunded by Bayer CropScience (to N.C.); and a BBSRC-funded position (BB/I001875/1 to M.I.). We thank the University of Nottingham School of Biosciences for studentship funding and acknowledge the University of Nottingham research committee. The VIB Bio Imaging Core acquired the Zeiss LSM780 through a Correlative Light Electron Microscopy (CLEM) grant from Minister Lieten. Work in the T.B. laboratory was financed by the Interuniversity Attraction Poles Programme IUAP P7/29 "MARS" from the Belgian Federal Science Policy Office and by a grant of the Research Foundation Flanders (FWO G027313N). E.S. is a Postdoctoral Fellow of the Research Foundation-Flanders (FWO13/PDO/144). K.Y. was supported by a grant from the Chinese Scholarship Council (CSC).

1. De Smet I, Beeckman T (2011) Asymmetric cell division in land plants and algae: The driving force for differentiation. *Nat Rev Mol Cell Biol* 12(3):177–188.
2. Scheres B (2007) Stem-cell niches: Nursery rhymes across kingdoms. *Nat Rev Mol Cell Biol* 8(5):345–354.
3. Aida M, et al. (2004) The PLETHORA genes mediate patterning of the Arabidopsis root stem cell niche. *Cell* 119(1):109–120.
4. Wildwater M, et al. (2005) The RETINOBLASTOMA-RELATED gene regulates stem cell maintenance in Arabidopsis roots. *Cell* 123(7):1337–1349.
5. De Smet I, et al. (2008) Receptor-like kinase ACR4 restricts formative cell divisions in the Arabidopsis root. *Science* 322(5901):594–597.
6. Stahl Y, et al. (2013) Moderation of Arabidopsis root stemness by CLAVATA1 and ARABIDOPSIS CRINKLY4 receptor kinase complexes. *Curr Biol* 23(5):362–371.
7. Sarkar AK, et al. (2007) Conserved factors regulate signalling in Arabidopsis thaliana shoot and root stem cell organizers. *Nature* 446(7137):811–814.
8. Stahl Y, Wink RH, Ingram GC, Simon R (2009) A signaling module controlling the stem cell niche in Arabidopsis root meristems. *Curr Biol* 19(11):909–914.
9. Zhang H, et al. (2010) ABA promotes quiescence of the quiescent centre and suppresses stem cell differentiation in the Arabidopsis primary root meristem. *Plant J* 64(5):764–774.
10. Azpeitia E, Weinstein N, Benítez M, Mendoza L, Alvarez-Buylla ER (2013) Finding missing interactions of the Arabidopsis thaliana root stem cell niche gene regulatory network. *Front Plant Sci* 4:110.
11. Ding Z, Friml J (2010) Auxin regulates distal stem cell differentiation in Arabidopsis roots. *Proc Natl Acad Sci USA* 107(26):12046–12051.
12. Kajala K, et al. (2014) Omics and modelling approaches for understanding regulation of asymmetric cell divisions in Arabidopsis and other angiosperm plants. *Ann Bot (Lond)* 113(7):1083–1105.
13. Choudhary C, Mann M (2010) Decoding signalling networks by mass spectrometry-based proteomics. *Nat Rev Mol Cell Biol* 11(6):427–439.
14. Van Damme D, et al. (2011) Arabidopsis α Aurora kinases function in formative cell division plane orientation. *Plant Cell* 23(11):4013–4024.
15. Nikonorova N, Vu LD, Czyzewicz N, Gevaert K, De Smet I (2015) A phylogenetic approach to study the origin and evolution of the CRINKLY4 family. *Front Plant Sci* 6:880.
16. Jones RB, Gordus A, Krall JA, MacBeath G (2006) A quantitative protein interaction network for the ErbB receptors using protein microarrays. *Nature* 439(7073):168–174.
17. Schulze WX, Deng L, Mann M (2005) Phosphotyrosine interactome of the ErbB-receptor kinase family. *Mol Syst Biol* 1:2005.0008.
18. Gifford ML, Dean S, Ingram GC (2003) The Arabidopsis ACR4 gene plays a role in cell layer organisation during ovule integument and sepal margin development. *Development* 130(18):4249–4258.
19. Tanaka H, et al. (2002) ACR4, a putative receptor kinase gene of Arabidopsis thaliana, that is expressed in the outer cell layers of embryos and plants, is involved in proper embryogenesis. *Plant Cell Physiol* 43(4):419–428.
20. Watanabe M, Tanaka H, Watanabe D, Machida C, Machida Y (2004) The ACR4 receptor-like kinase is required for surface formation of epidermis-related tissues in Arabidopsis thaliana. *Plant J* 39(3):298–308.
21. Bassel GW, et al. (2012) Systems analysis of plant functional, transcriptional, physical interaction, and metabolic networks. *Plant Cell* 24(10):3859–3875.
22. Jones AM, et al. (2014) Border control: A membrane-linked interactome of Arabidopsis. *Science* 344(6185):711–716.
23. De Bodt S, Hollunder J, Nelissen H, Meulemeester N, Inzé D (2012) CORNET 2.0: Integrating plant coexpression, protein-protein interactions, regulatory interactions, gene associations and functional annotations. *New Phytol* 195(3):707–720.
24. Meyer MR, Lichti CF, Townsend RR, Rao AG (2011) Identification of in vitro autophosphorylation sites and effects of phosphorylation on the Arabidopsis CRINKLY4 (ACR4) receptor-like kinase intracellular domain: Insights into conformation, oligomerization, and activity. *Biochemistry* 50(12):2170–2186.
25. Meyer MR, Shah S, Rao AG (2013) Insights into molecular interactions between the juxtamembrane and kinase subdomains of the Arabidopsis Crinkly-4 receptor-like kinase. *Arch Biochem Biophys* 535(2):101–110.
26. Wolfe CJ, Kohane IS, Butte AJ (2005) Systematic survey reveals general applicability of "guilt-by-association" within gene coexpression networks. *BMC Bioinformatics* 6:227.
27. Brady SM, et al. (2007) A high-resolution root spatiotemporal map reveals dominant expression patterns. *Science* 318(5851):801–806.
28. Winter D, et al. (2007) An "Electronic Fluorescent Pictograph" browser for exploring and analyzing large-scale biological data sets. *PLoS One* 2(8):e718.
29. Meyer MR, Shah S, Zhang J, Rohrs H, Rao AG (2015) Evidence for intermolecular interactions between the intracellular domains of the Arabidopsis receptor-like kinase ACR4, its homologs and the Wox5 transcription factor. *PLoS One* 10(3):e0118861.
30. Farkas I, Dombrádi V, Miskei M, Szabados L, Koncz C (2007) Arabidopsis PPP family of serine/threonine phosphatases. *Trends Plant Sci* 12(4):169–176.
31. Terol J, Bargues M, Carrasco P, Pérez-Alonso M, Paricio N (2002) Molecular characterization and evolution of the protein phosphatase 2A B′ regulatory subunit family in plants. *Plant Physiol* 129(2):808–822.
32. Uhrig RG, Labandera AM, Moorhead GB (2013) Arabidopsis PPP family of serine/threonine protein phosphatases: Many targets but few engines. *Trends Plant Sci* 18(9):505–513.
33. Blakeslee JJ, et al. (2008) Specificity of RCN1-mediated protein phosphatase 2A regulation in meristem organization and stress response in roots. *Plant Physiol* 146(2):539–553.
34. Spinner L, et al. (2013) A protein phosphatase 2A complex spatially controls plant cell division. *Nat Commun* 4:1863.
35. Segonzac C, et al. (2014) Negative control of BAK1 by protein phosphatase 2A during plant innate immunity. *EMBO J* 33(18):2069–2079.
36. Ballesteros I, et al. (2013) Specialized functions of the PP2A subfamily II catalytic subunits PP2A-C3 and PP2A-C4 in the distribution of auxin fluxes and development in Arabidopsis. *Plant J* 73(5):862–872.
37. Sabatini S, Heidstra R, Wildwater M, Scheres B (2003) SCARECROW is involved in positioning the stem cell niche in the Arabidopsis root meristem. *Genes Dev* 17(3):354–358.
38. Ueda M, et al. (2004) The HALTED ROOT gene encoding the 26S proteasome subunit RPT2a is essential for the maintenance of Arabidopsis meristems. *Development* 131(9):2101–2111.
39. Janssens V, Longin S, Goris J (2008) PP2A holoenzyme assembly: In cauda venenum (the sting is in the tail). *Trends Biochem Sci* 33(3):113–121.
40. Janssens V, Goris J (2001) Protein phosphatase 2A: A highly regulated family of serine/threonine phosphatases implicated in cell growth and signalling. *Biochem J* 353(Pt 3):417–439.
41. Michniewicz M, et al. (2007) Antagonistic regulation of PIN phosphorylation by PP2A and PINOID directs auxin flux. *Cell* 130(6):1044–1056.
42. Tang W, et al. (2011) PP2A activates brassinosteroid-responsive gene expression and plant growth by dephosphorylating BZR1. *Nat Cell Biol* 13(2):124–131.
43. Chen J, Hu R, Zhu Y, Shen G, Zhang H (2014) Arabidopsis PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR is essential for PROTEIN PHOSPHATASE 2A holoenzyme assembly and plays important roles in hormone signaling, salt stress response, and plant development. *Plant Physiol* 166(3):1519–1534.
44. Gao HB, Chu YJ, Xue HW (2013) Phosphatidic acid (PA) binds PP2AA1 to regulate PP2A activity and PIN1 polar localization. *Mol Plant* 6(5):1692–1702.
45. Wu G, et al. (2011) Methylation of a phosphatase specifies dephosphorylation and degradation of activated brassinosteroid receptors. *Sci Signal* 4(172):ra29.
46. Di Rubbo S, Irani NG, Russinova E (2011) PP2A phosphatases: The "on-off" regulatory switches of brassinosteroid signaling. *Sci Signal* 4(172):pe25.
47. Van Damme D, Bouget FY, Van Poucke K, Inzé D, Geelen D (2004) Molecular dissection of plant cytokinesis and phragmoplast structure: A survey of GFP-tagged proteins. *Plant J* 40(3):386–398.
48. Wang R, et al. (2016) The brassinosteroid-activated BRI1 receptor kinase is switched off by dephosphorylation mediated by cytoplasm-localized PP2A B′ subunits. *Mol Plant* 9(1):148–157.
49. Beeckman T, Viane R (2000) Embedding thin plant specimens for oriented sectioning. *Biotech Histochem* 75(1):23–26.
50. Van Leene J, et al. (2007) A tandem affinity purification-based technology platform to study the cell cycle interactome in Arabidopsis thaliana. *Mol Cell Proteomics* 6(7):1226–1238.
51. Van Leene J, Witters E, Inzé D, De Jaeger G (2008) Boosting tandem affinity purification of plant protein complexes. *Trends Plant Sci* 13(10):517–520.
52. Bürckstümmer T, et al. (2006) An efficient tandem affinity purification procedure for interaction proteomics in mammalian cells. *Nat Methods* 3(12):1013–1019.
53. Holton N, Nekrasov V, Ronald PC, Zipfel C (2015) The phylogenetically-related pattern recognition receptors EFR and XA21 recruit similar immune signaling components in monocots and dicots. *PLoS Pathog* 11(1):e1004602.

Appendix 2: 277 Putative ACR4 Interacting Proteins Were Identified by ACR4 Co-Immunoprecipitation

Author Contribution:

I prepared samples for MS analysis and assisted in data analysis.

Ratio (SAMPLE vs WT)	Protein IDs	Gene names	Protein names
37907.05104	Q9LX29	ACR4	Serine/threonine-protein kinase-like protein ACR4
312.5601932	P25858;Q56WJ4;Q56WW5;Q41949;Q56ZR3;Q5E924;Q9SAJ6	GAPC1;At1g13440	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic
277.7358872	CON__Q9U6Y5		
213.0283155	P51418;A8MRF3;Q8L7K0	RPL18AB;RPL18AA	60S ribosomal protein L18a-2;60S ribosomal protein L18a-1
145.1225831	CON__P02769;CON__P02768-1		
132.2362932	Q9ZUT9;P51427	RPS5A;RPS5B	40S ribosomal protein S5-1;40S ribosomal protein S5-2
130.9601006	Q9S7N7	PSAG	Photosystem I reaction center subunit V, chloroplastic
117.652547	Q2V2R9;Q9SY97;Q8LCR7;Q43381;Q0WR83	LHCA3;T25B24.12;Lhca3*1;At1g61520	
107.1441178	Q9LT39	At3g20820	
100.7482087	P56767	psaB	Photosystem I P700 chlorophyll a apoprotein A2
96.08000124	F4IT48;P60039;Q0WM13	At2g44120;RPL7C	60S ribosomal protein L7-3
90.01509275	Q0WSA0;Q9LSA3;Q9C8F7;Q8VZ19	At1g77940;RPL30C;RPL30A;RPL30B	60S ribosomal protein L30-3;Putative 60S ribosomal protein L30-1;60S ribosomal protein L30-2
87.08372546	Q9C5M0	DTC	Mitochondrial dicarboxylate/tricarboxylate transporter DTC
80.75820673	Q0WWI1;P31414;A8MQH1	At1g15690;AVP1	Pyrophosphate-energized vacuolar membrane proton pump 1
75.23524392	Q56WU3;B9DH71;Q05758	At3g58610	Ketol-acid reductoisomerase;Ketol-acid reductoisomerase, chloroplastic
63.69196777	P29513;Q8GY15;P29514;CON__ENSEMBL:ENSBTAP00000025008	TUBB5	Tubulin beta-5 chain
55.44405683	Q9C8S5;Q8VZ87;P0CJ48;P04778;Q42007	T1P2.1;LHCB1.2;LHCB1.1;LHCB1.3	Chlorophyll a-b binding protein 3, chloroplastic;Chlorophyll a-b binding protein 2, chloroplastic;Chlorophyll a-b binding protein 1, chloroplastic
55.12200422	G1C2W2;G1C2W7;Q04613	atp4;AtMg00640	ATP synthase protein MI25
54.63634852	Q0WLB5;Q0WNJ6	CHC2;CHC1	Clathrin heavy chain 2;Clathrin heavy chain 1
53.55750455	O65686	T4L20.200	
41.89478828	O23254	SHM4 (At4g13930)	Serine hydroxymethyltransferase 4
41.77569336	Q9LP58;Q8RWJ5;Q8LB07;O80774;Q9ZV90	F28N24.2;At1g29310;At2g34250	
39.35712203	P51422;Q9C912;Q9LMK0	RPL35AD;RPL35AC;RPL35AA	60S ribosomal protein L35a-4;60S ribosomal protein L35a-3;60S ribosomal protein L35a-1
38.38344933	Q8VZH2	APM1	Aminopeptidase M1
37.86139981	Q0WS09;O64650;Q9M2F1;B3H5X2;Q8L953	At2g45710;RPS27A;RPS27B;At3g61111;RPS27D	40S ribosomal protein S27;40S ribosomal protein S27-1;40S ribosomal protein S27-2;40S ribosomal protein S27-3
36.83327482	F4JT64;Q940J8;Q9FH82	At4g19410;PAE7;PAE11	Pectin acetylesterase 7;Pectin acetylesterase 11
36.72236701	Q9LIA8;Q9LF33;Q9FM01	UGD2	UDP-glucose 6-dehydrogenase 2
35.81593831	F4KGS3;Q9LV77;Q9LFU1;F4JBH5;P49078	ASN3;ASN2;ASN1	Asparagine synthetase [glutamine-hydrolyzing] 2;Asparagine synthetase [glutamine-hydrolyzing] 3;Asparagine synthetase [glutamine-hydrolyzing] 1
35.09309456	Q9SJT9;Q94A40;Q56YZ8		Coatomer subunit alpha-2;Coatomer subunit alpha-1
32.14141557	B9DHT7;B9DHR0;Q8W585;O80860	At2g30950;FTSH8;FTSH2	ATP-dependent zinc metalloprotease FTSH 8, chloroplastic;ATP-dependent zinc metalloprotease FTSH 2, chloroplastic
32.13889938	P56792	rpl14	50S ribosomal protein L14, chloroplastic
30.56046795	Q9SEH3;Q9FPJ4	RABD2C;RABD2B	Ras-related protein RABD2c;Ras-related protein RABD2b
29.50597703	P06525;Q9SX08	ADH1	Alcohol dehydrogenase class-P
28.30442478	Q9M591;F4J0U9	CRD1	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic
27.0808526	O65201;F4KGI8;B9DG77	ACX2;At5g65110	Acyl-coenzyme A oxidase 2, peroxisomal;Acyl-coenzyme A oxidase
26.43962757	O04019;Q9SEI2	RPT5B;RPT5A	26S protease regulatory subunit 6A homolog B;26S protease regulatory subunit 6A homolog A
24.82593801	P52901;Q8H1Y0	E1 ALPHA;IAR4	Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial;Pyruvate dehydrogenase E1 component subunit alpha-2, mitochondrial
23.68886938	B9DFR9;D9IX99;A8MRW1;Q06611;Q42039;Q42035;P61837	PIP1B;Aqua;PIP1-2;PIP1-1 (AT2G45960)	Aquaporin PIP1-2;Aquaporin PIP1-1
23.43030813	Q9FE65	RPL34B	60S ribosomal protein L34-2
20.29756776	P24636;Q6LAB6	TUBB4	Tubulin beta-4 chain
19.69321701	O23029	T1G11.19	
18.43765425	CON__Q04695;CON__Q9QWL7;CON__Q9C075;CON__Q99PS0		
16.88506227	Q570B4	FDH	3-ketoacyl-CoA synthase 10
15.5523373	Q0WRP9;O81852;Q9SA18	At4g19710;AKHSDH2;AKHSDH1	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic;Aspartokinase;Homoserine dehydrogenase;Bifunctional aspartokinase/homoserine dehydrogenase 1, chloroplastic;Aspartokinase;Homoserine dehydrogenase
14.78442142	Q9ZSI0;Q94K85	T15B16.17a;T15B16.17a:T15B16.17b	
13.98485604	Q8LB10	CLPR4	ATP-dependent Clp protease proteolytic subunit-related protein 4, chloroplastic
12.58526409	C0LGN2;C0LGG9	LRR-RLK (At3g14840)	Probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840;Probable LRR receptor-like serine/threonine-protein kinase At1g53440
11.77910609	F4JPJ7;P19456;P20649;C0Z2R2;Q93ZM8;P20431;Q9M2A0;Q9SH76;F4HU00;Q53XH7;Q42556;Q9LV11;Q9SU58;B7ZEI0;Q0WMF7;Q43128;Q9SJB3;G9B9K7	HA2;AHA2;AHA1;At4g30190;AHA3	ATPase 2, plasma membrane-type;ATPase 1, plasma membrane-type;ATPase 3, plasma membrane-type
11.56752198	P52410;F4KHF4	KAS1;KAS I	3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic
10.93497178	Q42292;Q9SMX3	VDAC3	Mitochondrial outer membrane protein porin 3
10.48408017	Q9S7M0;C0Z239;Q42016	LHCB3*1;At5g54270	
10.4296884	A8MR12;Q9LT08	At5g23540;RPN11	26S proteasome non-ATPase regulatory subunit 14 homolog
10.20326892	Q0WM94;Q9FMH8	At5g43060	
9.967341387	C0Z2H6;F4HU93;Q05431	At1g07890;APX1	L-ascorbate peroxidase 1, cytosolic
9.742976761	Q9FMU6;Q9M2Z8	MPT3	Mitochondrial phosphate carrier protein 3, mitochondrial
9.641863969	F4KDU5;Q8GYH3;P49691;Q9ASS3	At5g02870;At5g02870/F9G14_180;RPL4D	60S ribosomal protein L4-2

8.696216299	CON__P13647		
8.678773082	F4JGD2;Q9XEC4	At4g04460;APA3	Aspartic proteinase A3
8.658446942	Q42586;C0Z2E7	PYRE-F	Uridine 5-monophosphate synthase;Orotate phosphoribosyltransferase;Orotidine 5-phosphate decarboxylase
7.672007169	P56765	accD	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic
7.226932527	Q39085	DIM	Delta(24)-sterol reductase
7.220235006	F4K1Z5;Q8RX28	HDA05;HDA5	Histone deacetylase 5
7.078278832	Q9LY66;F4J296	RPL1;At3g63490	50S ribosomal protein L1, chloroplastic;Ribosomal protein
6.855518913	Q06588	ACO4	1-aminocyclopropane-1-carboxylate oxidase 4
6.535487675	Q570Q7;Q9LZH9;P49692	At2g47610;RPL7AB;RPL7AA	60S ribosomal protein L7a-2;60S ribosomal protein L7a-1
6.421985688	Q9SYL9	RPL13	50S ribosomal protein L13, chloroplastic
5.618184536	Q9XF88	LHCB4.2	Chlorophyll a-b binding protein CP29.2, chloroplastic
5.347769336	Q8VYC5;B3H739;F4IAP5;Q9LM23;Q9LPP8;Q9LPP9	At1g18270	
5.340037826	Q9C5U3;Q94BQ2;Q42271	RPT6A;RPT6B	26S protease regulatory subunit 8 homolog A;26S protease regulatory subunit 8 homolog B
4.900311261	Q9ASR0;Q56YW9	TUBB3;TUBB2	Tubulin beta-3 chain;Tubulin beta-2 chain
4.688979493	Q9SZD4;Q9SL67	RPT2A;RPT2B	26S proteasome regulatory subunit 4 homolog A;26S proteasome regulatory subunit 4 homolog B
4.628014028	I1VCA3;Q41931	ACO2	1-aminocyclopropane-1-carboxylate oxidase 2
4.588101321	Q8L7F2;Q0WWB3;Q96250	At2g33040;ATPC	ATP synthase subunit gamma, mitochondrial
4.487832783	Q0WSS0;Q9FDZ9;Q43291	RPL21E;RPL21A	60S ribosomal protein L21-2;60S ribosomal protein L21-1
4.204102861	Q8LER3	XTH7	Probable xyloglucan endotransglucosylase/hydrolase protein 7
4.116413559	Q9SIB9;Q56WE8;B3H5Y0;Q42560	ACO2;At2g05710;ACO1	Aconitate hydratase 2, mitochondrial;Aconitate hydratase;Aconitate hydratase 1
4.0168659	Q9SS17;Q8LC83	RPS24A;RPS24B	40S ribosomal protein S24-1;40S ribosomal protein S24-2
3.984559656	Q9ZVS4;Q8LF70	F15K9.17	
3.975343552	P15460	AT2S4	2S seed storage protein 4;2S seed storage protein 4 small subunit;2S seed storage protein 4 large subunit
3.795357295	Q0WWE9;P28297	At3g21720;ICL	Isocitrate lyase
3.795331078	Q8LAT5;Q0WWF3;P43296;Q8H7C0;Q570C7	At4g39090;RD19A	Cysteine proteinase RD19a
3.606461774	Q8H135;P83484;P83483;Q9C5A9;Q0WM57	At5g08670	ATP synthase subunit beta;ATP synthase subunit beta-2, mitochondrial;ATP synthase subunit beta-1, mitochondrial;ATP synthase subunit beta-3, mitochondrial
3.580519143	P56766	psaA	Photosystem I P700 chlorophyll a apoprotein A1
3.468742009	Q9FWA3		6-phosphogluconate dehydrogenase, decarboxylating 3
3.40593744	P15459;P15458;C0Z2C8	AT2S3;AT2S2;At4g27150	2S seed storage protein 3;2S seed storage protein 3 small subunit;2S seed storage protein 3 large subunit;2S seed storage protein 2;2S seed storage protein 2 small subunit;2S seed storage protein 2 large subunit
3.03618572	F4J1V2;Q0V7U1;Q0WW92;P42825;Q94AW8	ATJ3;At5g22060;At3g44110;ATJ2	Chaperone protein dnaJ 2;Chaperone protein dnaJ 3
2.983030313	Q39043;F4K007	MED37F;BIP2	Mediator of RNA polymerase II transcription subunit 37f
2.981169481	Q8LPR9	TIC110	Protein TIC110, chloroplastic
2.725124406	Q9M1P5;Q6ID97;Q9LYJ3;Q9LQC8;P36397;P0DH91;C0Z3J4;O22694	T17J13.250;ARFA1F;T15N1_160;ARF2-A;ARF1;ARF2-B	ADP-ribosylation factor 2-A;ADP-ribosylation factor 1;ADP-ribosylation factor 2-B
2.565039161	P19366;Q3ZVD9	atpB	ATP synthase subunit beta, chloroplastic
2.527597982	P27521;Q9FPI3	LHCA4;At3g47470/F1P2_20	Chlorophyll a-b binding protein 4, chloroplastic
2.443252396	Q8HT12;P56761	psbD	Photosystem II D2 protein
2.379918034	Q9FZH0	RPL35AB	60S ribosomal protein L35a-2
2.317693485	Q9C9I7	F26A9.12	
2.293527755	Q0WV25;P29511;B9DGT7;B9DFF8;Q944I2;Q0WLQ5	TUBA4;TUBA6;TUBA2;TUA6	Tubulin alpha-4 chain;Tubulin alpha-6 chain;Tubulin alpha-2 chain
2.27925544	Q9FH02;B9DHL9;C0Z226;B9DHN3;Q39102	FTSH5;At5g42270;FTSH1	ATP-dependent zinc metalloprotease FTSH 5, chloroplastic;ATP-dependent zinc metalloprotease FTSH 1, chloroplastic
2.247311806	C0SVC9;Q41963	At3g26520;TIP1-2	Aquaporin TIP1-2;Aquaporin TIP1-2, N-terminally processed
2.229514665	Q9S726	RPI3	Probable ribose-5-phosphate isomerase 3, chloroplastic
2.201325849	P25696;Q56WK5;Q944M3	ENO2;At2g36530	Bifunctional enolase 2/transcriptional activator;Enolase
2.197541068	P46283		Sedoheptulose-1,7-bisphosphatase, chloroplastic
2.192904237	Q9CA67	CHLP	Geranylgeranyl diphosphate reductase, chloroplastic
2.172639478	Q38799	PDH2	Pyruvate dehydrogenase E1 component subunit beta-1, mitochondrial
2.141719874	G1JSI6;G1JSH2;B5BRD8;Q93VB8;Q8L8Y0;Q56Z50	At1g59359;At1g58380;RPS2B;RPS2A	40S ribosomal protein S2-2;40S ribosomal protein S2-1
2.119385701	B3H4B6;Q9T029;Q8GYL5;Q9SIW5	At4g39200;RPS25E;RPS25D;RPS25A	40S ribosomal protein S25-4;40S ribosomal protein S25-3;40S ribosomal protein S25-1
2.037626906	P15455;F4K8S2	CRA1	12S seed storage protein CRA1;12S seed storage protein CRA1 alpha chain;12S seed storage protein CRA1 beta chain
2.024493251	P56777;Q8HS55	psbB	Photosystem II CP47 reaction center protein
2.007586808	B9DG17;Q08682;F4J4W3;Q8H173	P40;RPSaA	40S ribosomal protein SA;40S ribosomal protein Sa-1
1.976362781	Q0WL95;Q96293;Q96292;F4J8V9;Q8LB94;B9DHA3;Q93ZL9;C0Z223;Q8RYC2	At3g18780;ACT8;ACT2	Actin-8;Actin-2
1.949688964	P83755	psbA	Photosystem II protein D1
1.939145217	Q8W4H7;Q8GTY0;Q0WL56;P0DH99;A8MSE8;F4HUA0;C0Z2H0;Q56YZ4;B9DI33;P94009;P94008;Q56ZD4;P94010;Q56Z84;P94007	A2;A4;A3;A1;At5g60390;At1g07930	Elongation factor 1-alpha 2;Elongation factor 1-alpha 4;Elongation factor 1-alpha 3;Elongation factor 1-alpha 1;Elongation factor 1-alpha
1.931667324	P56778;Q8HT11	psbC	Photosystem II CP43 reaction center protein
1.892530991	CON__P00761		
1.889796325	F4IVZ7;P10896;Q941B7;Q8H172;Q0WLM1	RCA;At2g39730	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic
1.849816575	P49209;Q8LCC2;Q9C885;Q56W98;Q9SZX9	RPL9B;T16O9.23	60S ribosomal protein L9-1
1.820826925	Q9FL43;F4K5B9	At5g07030	
1.808667216	P25856;Q570E5;Q42213;Q56Z86	GAPA1;At3g26650	Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic

1.781614205	Q9FGY1;Q0WQK4;Q0WL73;Q94KD8	BXL1;At5g49360	Beta-D-xylosidase 1
1.762753829	F4JEL5;P41376;C0Z2Q9;A8MRZ7;F4JEL4;Q9CAI7;B9DI27;Q94A52	EIF4A1;TIF4A-1;At3g13920;TIF4A-3	Eukaryotic initiation factor 4A-1;Eukaryotic initiation factor 4A-3
1.722981707	P56798	rps3	30S ribosomal protein S3, chloroplastic
1.696393761	F4HZE0;Q8L770;B7T504	At1g09130;CLPR3	ATP-dependent Clp protease proteolytic subunit;ATP-dependent Clp protease proteolytic subunit-related protein 3, chloroplastic
1.691167666	O50008;Q9SRV5;Q0WP70;Q0WNZ5;B0FUS0;B0FUR9;B0FUR3	MS1;MS2	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1;5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2
1.611751192	Q9XF90;Q9LMQ2;Q41957	Lhcb6;F7H2.16	
1.610586298	G1C2S9;F4IMB5;A7KNE3;G1C2Z0;P92549	atp1;At2g07698;ATPA	ATP synthase subunit alpha;ATP synthase subunit alpha, mitochondrial
1.603704446	Q9FN48	CAS	Calcium sensing receptor, chloroplastic
1.601336735	P17745;B9DHZ8;Q56ZD8	TUFA;At4g20360	Elongation factor Tu, chloroplastic
1.575819003	CON__P35908;CON__Q6NXH9;CON__Q7Z794;CON__Q9R0H5;CON__P19013		
1.536088838	Q9FX54;F4HQT1;C0Z2I0	GAPC2;At1g13440	Glyceraldehyde-3-phosphate dehydrogenase GAPC2, cytosolic;Glyceraldehyde-3-phosphate dehydrogenase
1.532619452	Q9XF89	LHCB5	Chlorophyll a-b binding protein CP26, chloroplastic
1.523146464	Q0WVD8;P31167;C0Z2I5;Q41970;Q42264;B9DI48;Q56ZI7	At3g08580;AAC1	ADP,ATP carrier protein 1, mitochondrial
1.516880378	P22953;F4KCE5;Q6LAE0	MED37E;HSC70-1	Probable mediator of RNA polymerase II transcription subunit 37e
1.514111995	P25851	FBP	Fructose-1,6-bisphosphatase, chloroplastic
1.497047798	P41916;Q8H156;P41917;Q42161;Q56ZT1	RAN1;RAN3;RAN2	GTP-binding nuclear protein Ran-1;GTP-binding nuclear protein Ran-3;GTP-binding nuclear protein Ran-2
1.484769371	Q9LF98;Q9SJQ9;B3H6D7;Q9LZR9;Q8W4G8;Q56Z19;Q8LET3;F4KGQ0;O65581	F8J2_100;At2g36460	Fructose-bisphosphate aldolase
1.459966867	Q5D6C5;Q5D6C4;Q5D6C3;A7XB43;O23255;F4JTV5;F4JTV4;B9DG03;A8MQP1;Q9LK36;C0Z3F3;Q0WMC0;A0A0B4ULJ4	HOG1;SAHH1;MEE58;At4g13940;SAHH2	Adenosylhomocysteinase;Adenosylhomocysteinase 1;Adenosylhomocysteinase 2
1.449512617	Q39142;Q8LCZ4;Q9C5R6	Lhb1B1;At2g34430/T31E10.23	
1.437149672	Q0WWT6;C0Z325;Q42290;Q56Z94	At3g02090	Probable mitochondrial-processing peptidase subunit beta
1.407721251	CON__P13645;CON__P02535-1;CON__Q7Z3Z0;CON__Q7Z3Y8;CON__Q148H6;CON__Q7Z3Y9;CON__Q7Z3Y7;CON__Q99456		
1.381001022	CON__Q8N1N4-2;CON__Q7RTT2		
1.369360091	P25857	GAPB	Glyceraldehyde-3-phosphate dehydrogenase GAPB, chloroplastic
1.35476198	A8MS75;Q01667;F4JE46;F4JE43	LHCA1	Chlorophyll a-b binding protein 6, chloroplastic
1.24165612	CON__P08779;CON__Q9Z2K1;CON__Q3ZAW8;CON__P19012;CON__A2A4G1;CON__P08727;CON__P19001;CON__P35900;CON__Q9D312;CON__Q8N1A0		
1.234711046	CON__P35527		
1.230383032	P56795	rpl22	50S ribosomal protein L22, chloroplastic
1.227125554	Q9SRZ6;Q56ZW5;Q9SLK0	CICDH;At1g65930;ICDH	Cytosolic isocitrate dehydrogenase [NADP];Peroxisomal isocitrate dehydrogenase [NADP]
1.213881614	P53492;Q541W9;P53496	ACT7;ACT11	Actin-7;Actin-11
1.211928504	CON__P04259		
1.206977942	CON__P02533;CON__Q6IFX2;CON__Q61782		
1.200308827	Q9XF86;Q9SYW9;Q9SHR7;Q9S7J7;Q9XF87;C0Z391	Lhcb2.3;Lhcb2.1;LHCB2.1;LHCB2.2;Lhcb2:4	
1.18042754	Q9LUT2;Q41961;Q42242	METK4	S-adenosylmethionine synthase 4
1.176805438	Q9SIP7;Q9M339;B9DHB0;Q9FJA6	RPS3A;RPS3B;At5g35530;RPS3C	40S ribosomal protein S3-1;40S ribosomal protein S3-2;40S ribosomal protein S3-3
1.158550583	Q9SJL8	METK3	S-adenosylmethionine synthase 3
1.151299546	F4I4Z2;P36428	ALATS	Alanine--tRNA ligase
1.14876272	CON__P04264;CON__Q6IFZ6		
1.129479449	Q39099;B9DI24;Q41959;Q67Z90;Q9XIW1	XTH4;At2g06850	Xyloglucan endotransglucosylase/hydrolase protein 4
1.119615752	A8MS37;B3H4B8;Q2V3V9;Q9LRR9;Q9LRS0;Q56ZN0;Q41903;Q42040;O24500;F4JFV6	At3g14420;GLO1;GLO2	Peroxisomal (S)-2-hydroxy-acid oxidase GLO1;Peroxisomal (S)-2-hydroxy-acid oxidase GLO2
1.112088458	Q0WLE7;P17094;A8MQQ1;Q8H154;P22738;B9DHK8	At1g43170;ARP1;RP1	60S ribosomal protein L3-1
1.110577831	P31265	TCTP	Translationally-controlled tumor protein homolog
1.09603225	Q9SFB1;Q9C6U3	F17A17.37;T8G24.2	
1.078104851	F4JD96;Q9SFU1;Q9FKC0;Q9SVR0	At3g07110;RPL13AA;RPL13AD	60S ribosomal protein L13a-1;60S ribosomal protein L13a-4

1.056241759	F4IWP7;A8MQA1;B9DGA4;P41127;Q6LAB9;Q9SMT4	BBC1;At3g49010;RPL13B;RPL13C	60S ribosomal protein L13;60S ribosomal protein L13-1;Putative 60S ribosomal protein L13-2
1.045381957	Q56WH1;B9DHQ0;P11139	TUBA3;TUBA5;TUBA1	Tubulin alpha-3 chain;Tubulin alpha-5 chain;Tubulin alpha-1 chain
1.034265409	Q9ASR1;Q9SGT4;Q84R07;Q8H145;Q56WX9;Q56WY3;C0Z355;Q570K2;F4JB06;F4JB05	T6H22.13;At1g56075;At1g56070	
1.02450402	Q9ZUX4		Uncharacterized protein At2g27730, mitochondrial
1.022887803	CON__Q86YZ3		
1.017287403	Q94F20;Q940Q9;Q8LEX7;C0Z328;Q56XA8;Q9SUU6;Q8LAR0;Q0WWU1;Q9LYE7;Q8LCM9;Q8H168	At5g25460	
0.970609788	Q0WW72;Q9LFH5;P50883;Q9FF52	At3g53430;RPL12B;RPL12A;RPL12C	60S ribosomal protein L12-2;60S ribosomal protein L12-1;60S ribosomal protein L12-3
0.95460052	P56757;Q8HAW5;Q3ZVE2;Q3ZVE1	atpA	ATP synthase subunit alpha, chloroplastic
0.952484682	Q67ZX8;Q9FNP8;Q0WSH0;Q9SGA6;Q9LF30	At5g61170;RPS19C;At5g15520;RPS19A;RPS19B	40S ribosomal protein S19-3;40S ribosomal protein S19-1;40S ribosomal protein S19-2
0.936458063	CON__Q5XQN5;CON__Q922U2;CON__H-INV:HIT000016045;CON__P07744;CON__Q9DCV7;CON__Q3KNV1;CON__P08729;CON__Q9H552;CON__P78386;CON__Q9NSB2;CON__Q6ISB0		
0.918253657	Q9LRX8	RPL13AB	60S ribosomal protein L13a-2
0.905741638	P60040;A8MRH4	RPL7B;At2g01250	60S ribosomal protein L7-2
0.905483762	Q94B39;Q42139;Q7DLL6	F10M6.100	
0.903763227	Q0WWL2;F4ID91;Q8LCE1;C0Z2C2;F4ID92	At1g66200;GSR2;GLN1-2	Glutamine synthetase;Glutamine synthetase cytosolic isozyme 1-2
0.896804268	P15456	CRB	12S seed storage protein CRB;12S seed storage protein CRB alpha chain;12S seed storage protein CRB beta chain
0.867668838	F4JBY2;Q8RWV0	At3g60750;TKL-1	Transketolase-1, chloroplastic
0.836272855	Q1EBW2;P46645	At5g19550;ASP2	Aspartate aminotransferase;Aspartate aminotransferase, cytoplasmic isozyme 1
0.835718469	Q03250;C0Z387;C0Z2N6;F4IHK9	RBG7;At2g21660;CCR2	Glycine-rich RNA-binding protein 7
0.834258551	Q6KGZ1;P61841	rps7;rps7-A	30S ribosomal protein S7, chloroplastic
0.82540862	Q9SYW8;Q9M320	Lhca2;F2A19.70	
0.821101792	Q9S7Y7	XYL1	Alpha-xylosidase 1
0.817815492	Q0WWU9;Q8VYF1;O23515	At4g17390;RPL15B;RPL15A	Ribosomal protein L15;60S ribosomal protein L15-2;60S ribosomal protein L15-1
0.807404812	B9DHI9;O04487;Q56ZZ4;Q56WV5;C0Z2L8;C0Z2J4;Q9FVT2	At1g09640;At1g57720	Probable elongation factor 1-gamma 1;Probable elongation factor 1-gamma 2
0.798135571	Q9SAJ4;Q8LFV7;C0Z3A6;Q56ZW1;F4I3L1;P50318;Q9LD57	T8K14.3;At1g79550	Phosphoglycerate kinase
0.773309478	P16181;Q42068;Q42128	RPS11A	40S ribosomal protein S11-1
0.764801387	P43286;Q42114;Q56ZI3;Q42277;P43287;Q9FF53	PIP2-1	Aquaporin PIP2-1;Aquaporin PIP2-1, N-terminally processed
0.760896641	Q9LZC3;Q56Z42;B0LQB5;B0LQB3;B0LQA9	MLS	Malate synthase
0.758827975	Q9SF40;Q2V3X4;Q8LA93;B9DHP1	RPL4A;At3g09630	60S ribosomal protein L4-1
0.750307579	Q96511;Q84M88	PER69	Peroxidase 69;Peroxidase
0.740932537	Q8W4D2;Q9ZPI5	At3g06860/F17A9.1;MFP2	Peroxisomal fatty acid beta-oxidation multifunctional protein MFP2;Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase;3-hydroxyacyl-CoA dehydrogenase
0.736402069	Q8RXU5;Q9SRK6	RPL37AC;RPL37AB	60S ribosomal protein L37a-2;Putative 60S ribosomal protein L37a-1
0.725263798	Q5PNZ9;P34788;Q6LAE1	PFL;RPS18A	40S ribosomal protein S18
0.686141467	A8MQR4;Q42112;P57691;O04204	At3g09200;RPP0B;RPP0C	60S acidic ribosomal protein P0-2;60S acidic ribosomal protein P0-3
0.666258353	Q9ZU52	FBA3	Probable fructose-bisphosphate aldolase 3, chloroplastic
0.650581935	F4JM86;B9DFK6;P25819;Q940G2;O64954;F4HUL6;B9DHU0;B9DG18;C0Z2I6;Q42547	CAT2;At4g35090;At4g35090/M4E13.140	Catalase;Catalase-2
0.636577083	Q9M9W1	RPL22B	60S ribosomal protein L22-2
0.63124604	Q9M9P3;F4KGY8;P57751	UGP2	Probable UTP--glucose-1-phosphate uridylyltransferase 2;UTP--glucose-1-phosphate uridylyltransferase 1
0.607805091	B9DGD1;Q43127;Q56ZK3;C0Z2E9	At5g35630;GLN2	Glutamine synthetase;Glutamine synthetase, chloroplastic/mitochondrial
0.603832754	Q42262;C0Z2V4;Q42108;Q42297;Q42008	RPS3AB	40S ribosomal protein S3a-2
0.59595573	Q8VYK6;C0Z342;F4K5C7;Q93VH9;P49204;F4IMI7	RPS4D;At5g07090;RPS4A;RPS4B;At2g17360	40S ribosomal protein S4-3;40S ribosomal protein S4;40S ribosomal protein S4-1;40S ribosomal protein S4-2
0.584184012	Q93VG5;Q56ZZ8;Q0WSK1;Q9FIF3	RPS8A	40S ribosomal protein S8-1
0.575002412	Q9CAV0;Q56ZZ2	RPS3AA;At3g04840	40S ribosomal protein S3a-1
0.556901858	Q8LBI1;F4J912;B9DHP6;Q56X31	ATL5;At3g25520	60S ribosomal protein L5-1
0.5548995	Q1H555;Q9CAX6;Q9SIH0	At3g11510;RPS14B;RPS14A	40S ribosomal protein S14-2;40S ribosomal protein S14-1
0.542542795	Q43387	PER71	Peroxidase 71
0.528083583	E0Y422;Q9ZR03	At4g03280;petC	Cytochrome b6-f complex iron-sulfur subunit;Cytochrome b6-f complex iron-sulfur subunit, chloroplastic
0.502462128	A8MS83;Q9M3C3;Q8LD46	RPL23AB;RPL23AA	60S ribosomal protein L23a-2;60S ribosomal protein L23a-1

0.499355303	Q9M888;Q8L7N0	CCT6A;CCT6B	T-complex protein 1 subunit zeta 1;T-complex protein 1 subunit zeta 2
0.496848519	Q9C525	BGLU21	Beta-glucosidase 21
0.485500111	Q42064;Q41960;Q4PSL7	RPL8C	60S ribosomal protein L8-3
0.463353378	Q93VT9;Q2HIH6;Q08770;Q6LAD9;Q93W22;C0Z3F6	RPL10A;At1g26910;RPL10B;RPL10C	60S ribosomal protein L10-1;60S ribosomal protein L10-2;60S ribosomal protein L10-3
0.455837098	P56805	rps15	30S ribosomal protein S15, chloroplastic
0.452188313	O23211;F4JQG6	C7A10.660;At4g36700	
0.450800096	Q56WE0;Q8GRU8;F4K6B6;P55737;P51818;Q0WLP0;Q8H158;O03986;P27323	At5g56010;HSP81-2;HSP90-2;HSP90-3;At5g56030;HSP90-4	Heat shock protein 90-2;Heat shock protein 90-3;Heat shock protein 90-4
0.447864184	CON__P12763		
0.428964481	Q93VI3;F4HRW5;Q0WRE5;P51413	RPL17A;At1g67430;RPL17B	60S ribosomal protein L17-1;60S ribosomal protein L17-2
0.410914689	O48549;A8MS03	RPS6A;RPS6	40S ribosomal protein S6-1
0.406971191	Q96318;F4JLA9	CRC;CRU3	12S seed storage protein CRC;12S seed storage protein CRC alpha chain;12S seed storage protein CRC beta chain
0.391386042	B9DHP0;Q9T043	At4g27090;RPL14B	60S ribosomal protein L14-2
0.379278886	P11574	VHA-B1	V-type proton ATPase subunit B1
0.374895304	A0A075M569;Q0WVH4;P10795;Q42306;Q42046;F4HRR5	rbcS;At1g67090;RBCS-1A;RBCS1A	Ribulose bisphosphate carboxylase small chain;Ribulose bisphosphate carboxylase small chain 1A, chloroplastic
0.362117072	P23321;Q9S841	PSBO1;PSBO2	Oxygen-evolving enhancer protein 1-1, chloroplastic;Oxygen-evolving enhancer protein 1-2, chloroplastic
0.353944091	B0FV99;F4I472;Q08112;Q0WSM9;Q9FY65	RPS15;RPS15A	40S ribosomal protein S15-1
0.339789014	A0A075M4Z6;A0A075M3N4;B3H5S2;P10798;P10797;F4KA76	rbcS;At5g38410;RBCS-3B;RBCS-2B	Ribulose bisphosphate carboxylase small chain;Ribulose bisphosphate carboxylase small chain 3B, chloroplastic;Ribulose bisphosphate carboxylase small chain 2B, chloroplastic
0.325614948	O03042;Q85B88;X5ICS1;A0A075M556;A0A0F7C956;G0WXW0;H9AFL0;H9AFL1;Q9MVP0;F4INE2;P93292	rbcL;RBCL	Ribulose bisphosphate carboxylase large chain
0.3228395	A8MQY4;F4K875;F4K873;P42737;Q56X90;C0Z272;P27140	CA2;BCA2;At3g01500;BCA1	Carbonic anhydrase;Beta carbonic anhydrase 2, chloroplastic;Beta carbonic anhydrase 1, chloroplastic
0.298033901	P49206;Q8LPJ7	RPS26A;RPS26B	40S ribosomal protein S26-1;40S ribosomal protein S26-2
0.272530429	B9DI38;O23049	At1g05190;RPL6	50S ribosomal protein L6, chloroplastic
0.260503762	Q9M385	RPL17	50S ribosomal protein L17, chloroplastic
0.25448235	B9DGN3;Q9SLF7;C0Z3G4;F4IGR3	At2g27710;RPP2B	60S acidic ribosomal protein P2-2
0.253203478	Q93VP3;Q42002;Q42021;Q9C505	ELF5A-2	Eukaryotic translation initiation factor 5A-2
0.245522897	Q9M885	RPS7B	40S ribosomal protein S7-2
0.225999251	P51420;Q0WRN2;Q9STR1;Q9SLL7;A8MR49	RPL31C;At4g26230;RPL31B;RPL31A	60S ribosomal protein L31-3;60S ribosomal protein L31-2;60S ribosomal protein L31-1
0.222421279	Q0WQZ1;P42795;P42794	At2g42740;RPL11A;RPL11B	60S ribosomal protein L11-1;60S ribosomal protein L11-2
0.21512093	Q9FEF8;Q94AH9	MED36B;MED36A	Probable mediator of RNA polymerase II transcription subunit 36b;Mediator of RNA polymerase II transcription subunit 36a
0.211667087	Q8RXX5;Q8W463		50S ribosomal protein L19-2, chloroplastic
0.211098428	O80439	RPS31	30S ribosomal protein S31, chloroplastic
0.206448786	Q9FPF0	DJ1A	Protein DJ-1 homolog A
0.192940767	P56791;Q41912	rpl2-A	50S ribosomal protein L2, chloroplastic
0.172205361	Q0WRA6;Q9LD28;O81826;Q9LHQ5;Q9C681	At4g27230;RAT5	Histone H2A;Histone H2A.6;Probable histone H2A.3;Probable histone H2A.2;Probable histone H2A.1
0.168070826	Q6NR90;P59259;A8MRV1	At1g07660	Histone H4
0.165231939	B9DI04;Q9LX88;P42798	RPS15AD;RPS15AA	40S ribosomal protein S15a-4;40S ribosomal protein S15a-1
0.154247808	Q8LEF5;Q9FLN4	RPL27	50S ribosomal protein L27, chloroplastic
0.153795868	Q9SR37;B0LYE9;B0LYM3;B0LYE4;B0LYG2;B0LYI5;B0LYK9;B0LYH7;B0LYF3;B0LYF6;Q9SE50;Q9LKR7	BGLU23	Beta-glucosidase 23
0.147311618	P49201;Q1H5G2;Q9SF35	RPS23B;At3g09680;RPS23A	40S ribosomal protein S23-2;40S ribosomal protein S23-1
0.128026046	O23290;F4JUQ4	RPL36AA;At4g14320	60S ribosomal protein L36a
0.125835931	Q9LYK9	RPS26C	40S ribosomal protein S26-3
0.092619834	F4IU89;Q9SIF2;Q8LPS0;Q0WMV4;O23638;Q0WMQ3	CR88;At2g04030;hsp88.1	
0.089684144	O04314;O04313;C0Z3F0	PBP1	PYK10-binding protein 1
0.089575588	P38666;Q42347	RPL24B;RPL24A	60S ribosomal protein L24-2;60S ribosomal protein L24-1
0.084758709	Q0WT91;O23629	At3g45980;H2B	Histone H2B;Histone H2B.6
0.077945252	P16180	RPS17	30S ribosomal protein S17, chloroplastic
0.077479712	Q9LIF9;Q42252	BGLU19	Beta-glucosidase 19
0.074433253	Q8W4H8	GLL23	Inactive GDSL esterase/lipase-like protein 23
0.072684421	B9DGM0;Q9SQZ1;Q9SJ36;Q9LZ17;P49205	At5g04800;RPS17C;RPS17B;RPS17D;RPS17A	40S ribosomal protein S17-3;40S ribosomal protein S17-2;40S ribosomal protein S17-4;40S ribosomal protein S17-1
0.066522873	C0SVF3;Q9LD90	At3g57150;CBF5	H/ACA ribonucleoprotein complex subunit 4
0.063407457	Q53YQ5;Q43729	At5g17820;PER57	Peroxidase;Peroxidase 57
0.051923545	O04310	JAL34	Jacalin-related lectin 34
0.046287494	Q9SS98		Oleosin 5
0.04526696	Q67Z07;P0DJ10	PER2;PER1	Peroxidase 2;Peroxidase 1
0.040792157	P29525		Oleosin 18.5 kDa
0.037021527	P0DKC6;P0DKC5	HSD1	11-beta-hydroxysteroid dehydrogenase 1B;11-beta-hydroxysteroid dehydrogenase 1A
0.030215329	Q1H5F2;P40283;Q1H5F9;Q0WS75;Q9LZT0;Q9SI96;Q0WS50;Q9LZ45;Q9ZUS0;Q9LFF6;Q9SF55;Q42152	At5g59910;At3g46030;At5g22880;At2g37470	Histone H2B;Histone H2B.11;Histone H2B.7;Histone H2B.3;Histone H2B.9;Histone H2B.4;Histone H2B.8

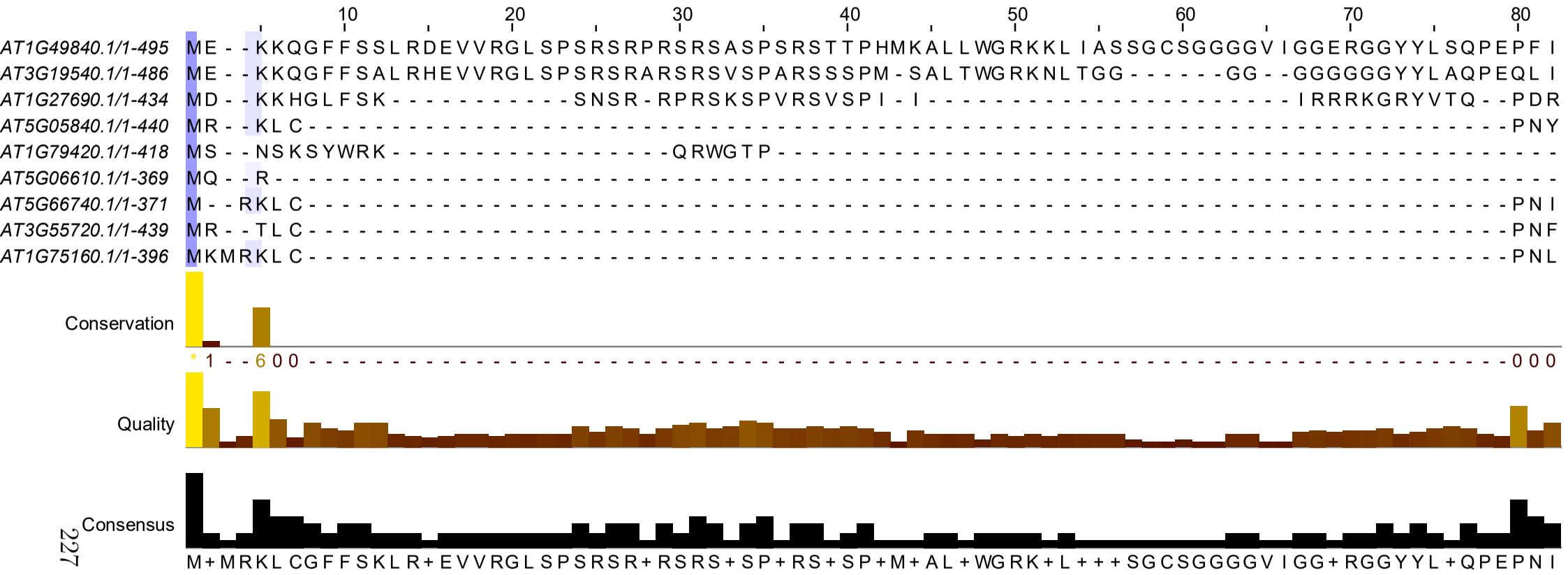
0.029145063	Q8LBJ7;P36212;P36210	RPL12C;RPL12A	50S ribosomal protein L12-3, chloroplastic;50S ribosomal protein L12-1, chloroplastic
0.028436622	B9DH43;Q9FJP3	At5g65220;RPL29	50S ribosomal protein L29, chloroplastic
0.023991901	O80837	DBP	Remorin
0.02322858	Q39165;Q56ZR4		Oleosin 21.2 kDa
0.021863382	Q9LFX8	At1g27090	
0.017857445	A8MQD7;A8MRX4;Q9LVT8;Q8LDQ7	At5g47210	
0.016627374	Q8W554;Q9LUM3;Q9C5N5;Q8LGA0	At3g14240	
0.015686342	P49211;Q9FHG2	RPL32A;RPL32B	60S ribosomal protein L32-1;60S ribosomal protein L32-2
0.012532249	O49607	SBT1.6	Subtilisin-like protease SBT1.6
0.008404012	O65351	SBT1.7	Subtilisin-like protease SBT1.7
0.007488468	Q42431	OL2	Oleosin 20.3 kDa
0.007003815	P25873	RPL15	50S ribosomal protein L15, chloroplastic
0.006789743	Q93Z83;O81494;A8MR02;Q8LEX1;Q56W20;F4IV56;F4IV58;Q6RF45;Q9SHS6;F4JZS5;O81493;O81497;F4IV59;Q9SHS5	At5g26280;F9D12.7	
0.003145819	Q9LQ31	JAL4	Jacalin-related lectin 4
0.001515703	O04311;Q8LAM1	JAL33	Jacalin-related lectin 33

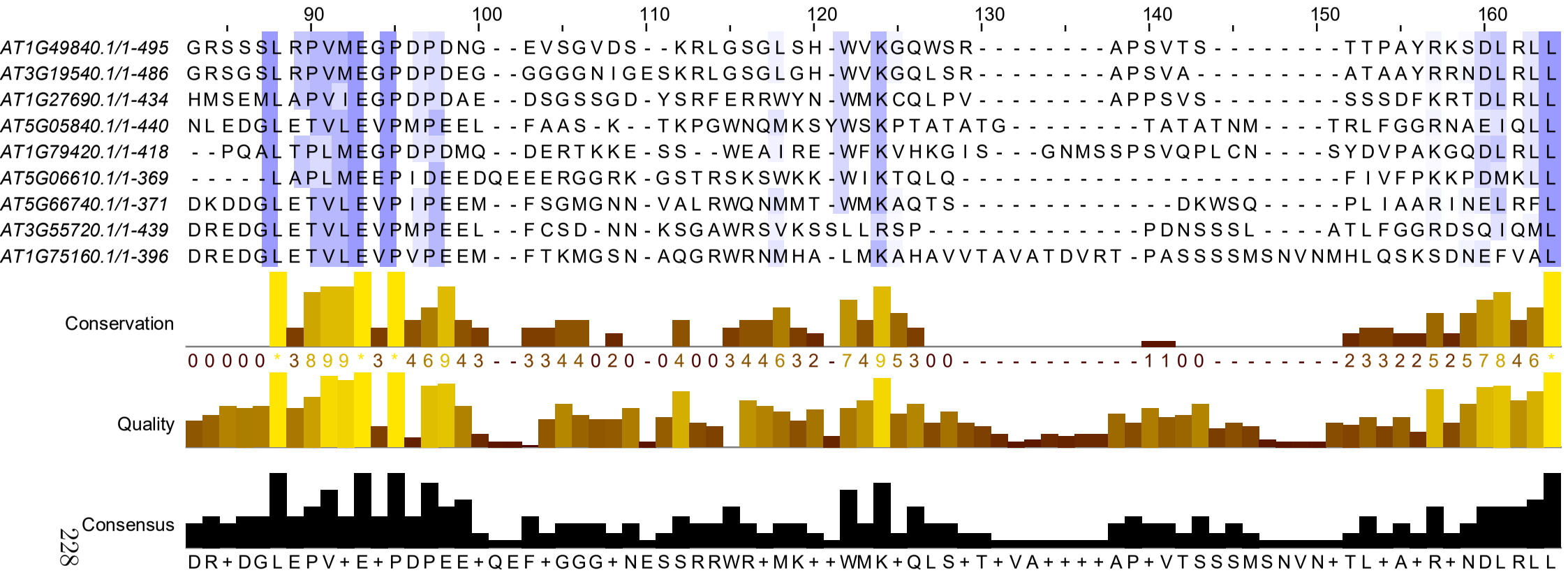
Appendix 3: List of Plant Lines and Primers Used

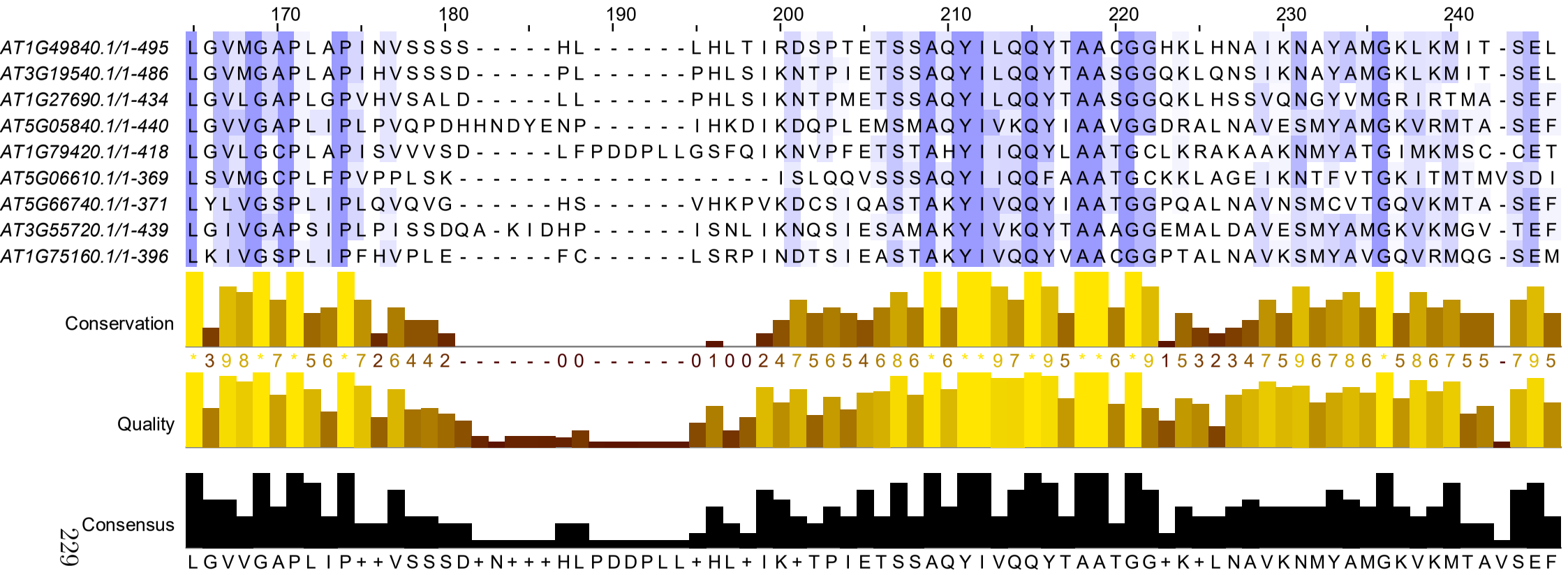
	Mutant Identification	Gene Accession	Source	Primer Name	Primer Sequence	Genotype	qPCR Primer Name	qPCR Primer Sequence
Y2H PAIP mutants	SAIL_1272_H08	At1g49840	NASC/ABRC	Unk_A_F	TCACATCATTCCCACACACAC	Hom	qUNK_F	CCTTGGCTTGGTTCTCACAC
				Unk_A_R	CAGTGGGAGAGTCTCTGATGG		qUNK_R	CACCTTCCTCTCTCCAACACA
	SAIL_222_F02	At1g49840	NASC/ABRC	Unk_B_F	ATTACCGATCGAACCCATTTC	wt	-	-
				Unk_B_R	GGAGGAAGAGACGTTAATGGG		-	-
	SALK_126340 (CI)	At5g01020	NASC/ABRC	STPK_A_F	TTTGAAGCTTCACTCCTCTGC	wt	-	-
				STPK_A_R	GATGGATCGCTCAGATCTGAG		-	-
	SALK_044339C	At5g01020	NASC/ABRC	STPK_B_F	GAGCACTTTGAGCTGTGATCC	Hom	qSTPK_F	TGACGGCCAGAAGTGATGT
				STPK_B_R	TGGGCATACGAAATAGGAGTG		qSTPK_R	GGTTCTCCAGTCTTGGGTCA
	SALK_137857 (BY)	At1g70070	NASC/ABRC	ISE2_A_F	GTTGCATCGTGCTAAGAGGAG	wt	-	-
				ISE2_A_R	TCAAGCCTCCTCAACTAGCTG		-	-
	SALK_022088C	At1g70070	NASC/ABRC	ISE2_B_F	ATGAGACGATGAACAAGGCAC	wt	-	-
				ISE2_B_R	CATTCCCCAAACTTCTCCTTC		-	-
	SALK_039754C	At2g30550	NASC/ABRC	PLAG2_A_F	AGAATTGGATCCATTGGATCC	wt	-	-
				PLAG2_A_R	TGTTATGTGTTGCCATGATGC		-	-
	SALK_003105C	At2g30550	NASC/ABRC	PLAG2_B_F	GGTTTAAGAAACGGCGAGTTC	Hom	qPLAG_F	CGAACATCAATCTCCCGAAC
				PLAG2_B_R	GCTGGAGAACTATGGATGACG		qPLAG_R	TCGTAACGGTTCCTCTCCAC
	SALK_112213C	At3g11130	NASC/ABRC	Clat_A_F	TGGTGAAAGGAAATATGCAGC	n/a	-	-
				Clat_A_R	TATATTGAAACGGAGGAAGCG		-	-
	SALK_018351C	At3g11130	NASC/ABRC	Clat_B_F	TCAATCTATTTCGCACCATCC	n/a	-	-
				Clat_B_R	CGATGAAGCTCTGTATGAGGC		-	-
ACR4 Mutants	*acr4-2*	At3g59420	EL Williams	ACR4_F	CTCAATGCTTCTTGTTGCTTC	Hom	qACR4_F	GAGCAGCAGAATGCACAAGA
				ACR4_R	CTCCTGGTCATCTCCAGT		qACR4_R	TTGCTTCCTCCCTTCATCC
	acr4-2-crr1-crr2	At3g59420-At3g09780-At2g39180	EL Williams	CRR1_F	CACACAACTCTGCCACGT	Hom	qCRR1_F	CGGTGATCAGAGAAGGCAAA
				CRR1_R	CCGTTGCTCTCTCCTCTT		qCRR1_R	GGATCCTCCCGTACACACAA
	acr4-2-crr1-crr2-crr3-crr4	At3g59420-At3g09780-At2g39180-At3g55950-at5g47850	EL Williams	CRR2_F	TGAGGCCAGACTTGACGA	Hom	qCRR2_F	TTAGCTGAGCTTGCTGTGAGG
				CRR2_R	GCAGCTTTCGGCGAAAAC		qCRR2_R	AGGCCAGACTTGACGATGAG
				CRR3_F	ACACAAATCCAATGCTCTCTC		qCRR3_F	GACGCCAGTCAACTTCAACC
				CRR3_R	TCATCTTCTTCCTCTTGTCTC		qCRR3_R	GTGACGGGAGACAAGAGGAA
				CRR4_F	CTACCTCCACCATTGACG		qCRR4_F	GGCTCATGTCGGATACTTGG
				CRR4_R	GTTTGCTTCTCCCTCTCC		qCRR4_R	AGATACGGTCTCCGTCTTTGG
LBb	-	SALK Lines		SALK_LBb	ATTTTGCCGATTTCGGAAC	-	-	-
	-	SAIL Lines		SAIL_LBb	TAGCATCTGAATTTCATAACCAATCTCGATACAC		-	-
UNK Cloning	-	At1g49840		pUNK_F	gggattaaatttgaatgataacgtgat	-	-	-
	-	At1g49840		pUNK_R	tttttatggactcttaaaaatgtaacctttc	-	-	-
	-	At1g49840		cUNK_F	ATGGAAAAGAAACAAGGTTTTTTCT	-	-	-
	-	At1g49840		cUNK_R - STOP	GACATCAATATGCCAAACAGGA	-	-	-
	-	At1g49840		cUNK_R + STOP	TCAGACATCAATATGCCAAACAG	-	-	-
	-	-		M13_F	GTAAAACGACGGCCAG	-	-	-
	-	-		M13_R	CAGGAAACAGCTATGAC	-	-	-
	-	-		35S	CACAATCCCACTATCCTTCGCAAGAC	-	-	-
	-	-		GFP	AAGTCGTGCTGCTTCATGTG	-	-	-

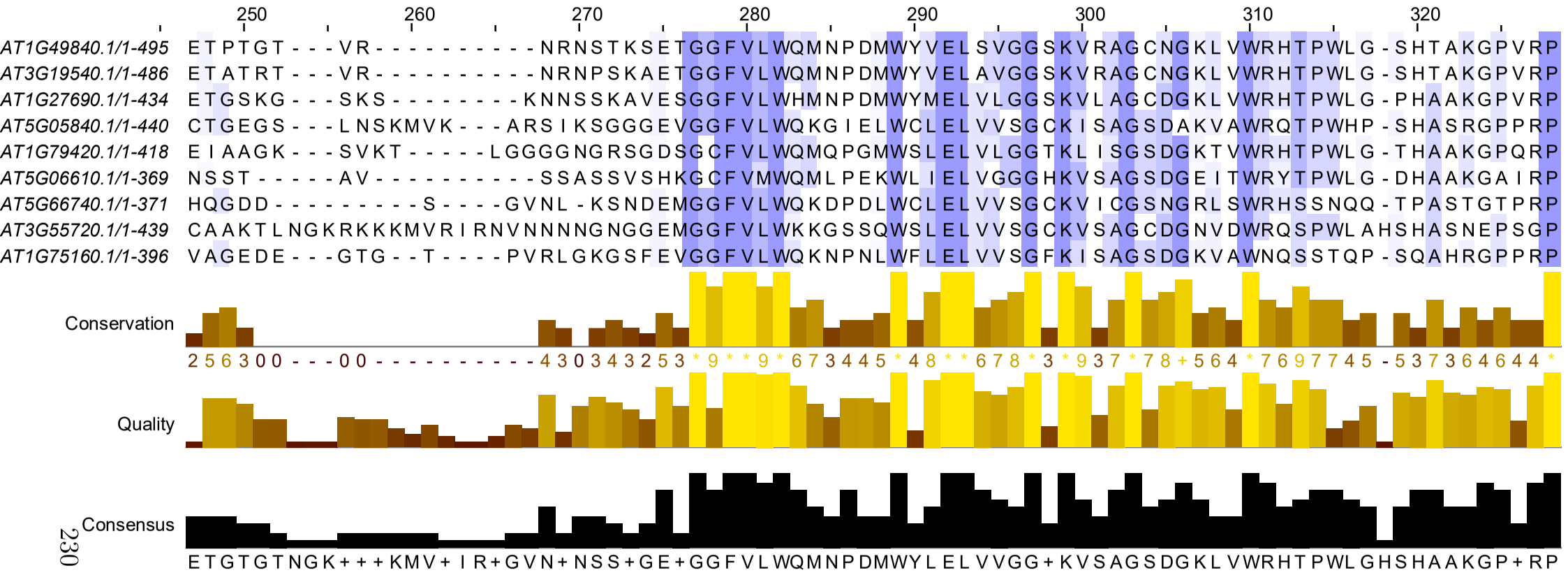
	Identification	Reference
Reporter Lines	pPIN1::PIN1:GFP	Benkova *et al.,* (2003) Local, Efflux-Dependent Auxin Gradients as a Common Module for Plant Organ Formation. *Cell;* 115(5) pp591-602
	WAVE131Y	Geldner *et al.,* (2009) Rapid, combinatorial analysis of membrane compartments in intact plants with a multicolor marker set. *Plant Journal;* 59(1) pp169-178
	pACR4::ACR4:YFP	Developed by EL Williams
	35S::ACR4:YFP	Developed by EL Williams
	pUNK::UNK:GFP	Developed by N Czyzewicz

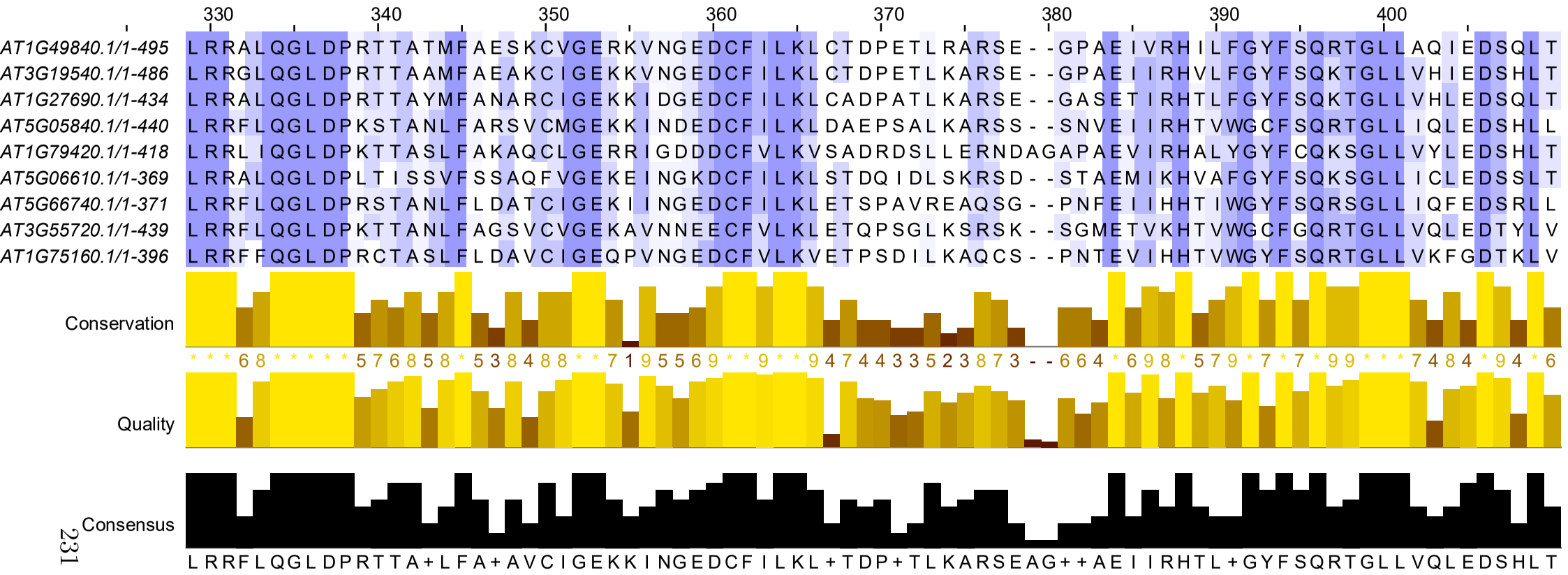
Appendix 4: Alignment of 9 UNK-like Family Members

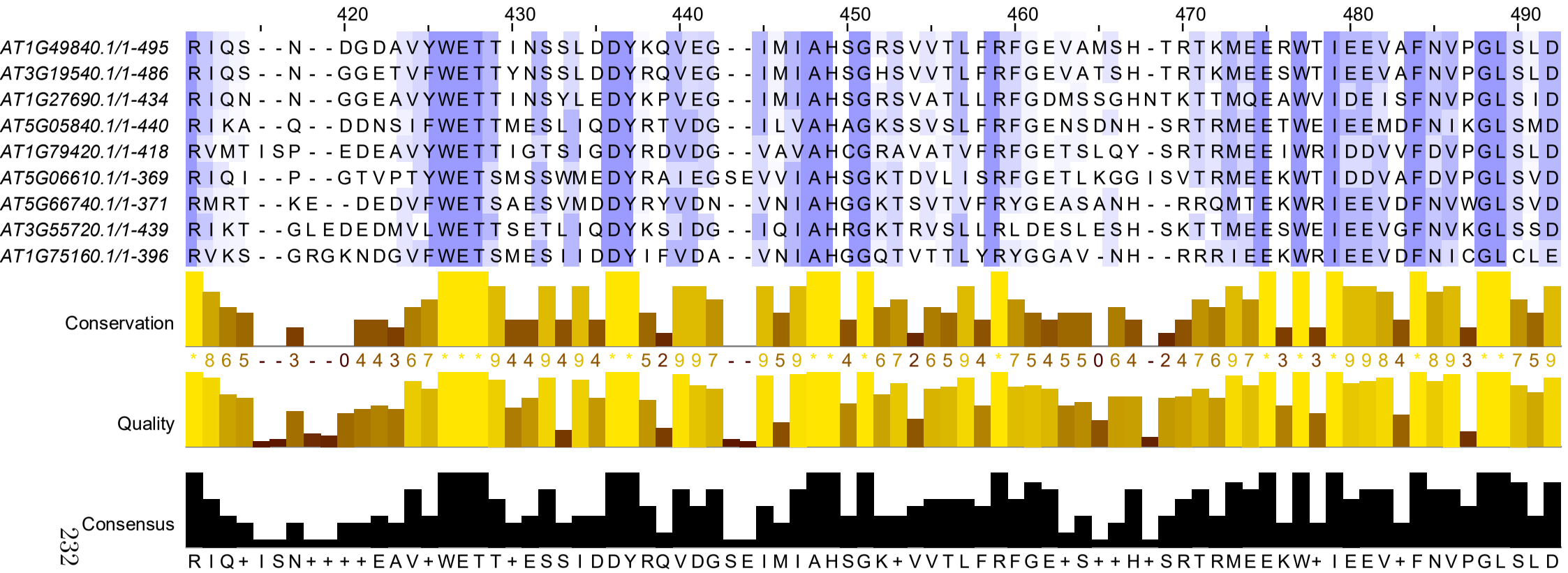

10
20
30
40
50
60
70
80
AT1G49840.1/1-495 ME--KKQGFFSSLRDEVVRGLSPSRSRPRSRSASPSRSTTPHMKALLWGRKKLIASSGCSGGGGVIGGERGGYYLSQPEPFI
AT3G19540.1/1-486 ME--KKQGFFSALRHEVVRGLSPSRSRARSRSVSPARSSSPM-SALTWGRKNLTGG------GG--GGGGGGYYLAQPEQLI
AT1G27690.1/1-434 MD--KKHGLFSK----------SNSR-RPRSKSPVRSVSPI-I----------IRRRKGRYVTQ--PDR
AT5G05840.1/1-440 MR--KLC----------PNY
AT1G79420.1/1-418 MS--NSKSYWRK----------QRWGTP----------
AT5G06610.1/1-369 MQ--R----------
AT5G66740.1/1-371 M--RKLC----------PNI
AT3G55720.1/1-439 MR--TLC----------PNF
AT1G75160.1/1-396 MKMRKLC----------PNL
Conservation
*1--600----------000
Quality
Consensus
227
M+MRKLCGFFSKLR+EVVRGLSPSRSR+RSRS+SP+RS+SP+M+AL+WGRK+L+++SGCSGGGGVIGG+RGGYYL+QPEPNI

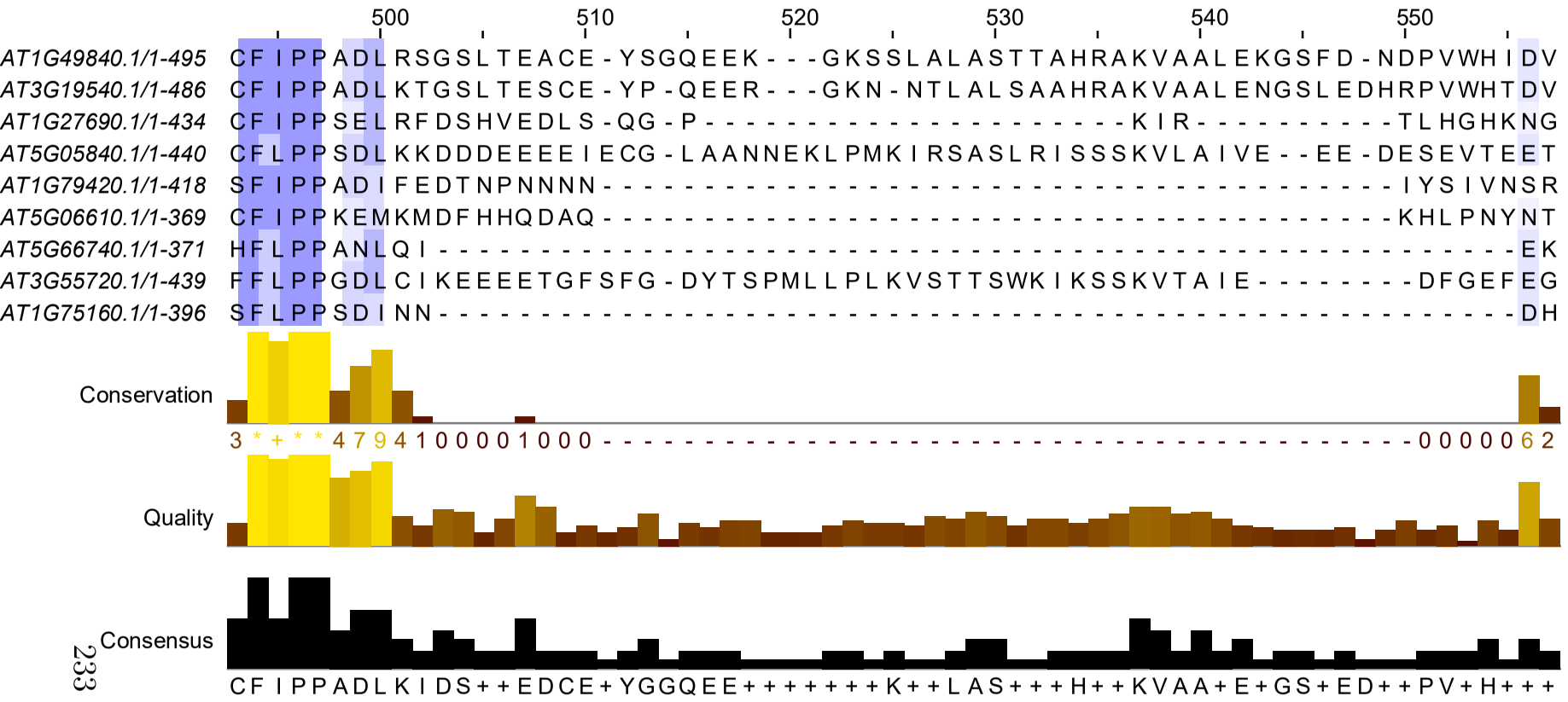

90
100
110
120
130
140
150
160
AT1G49840.1/1-495 GRSSSLRPVMEGPDPDNG--EVSGVDS--KRLGSGLSH-WVKGQWSR--------APSVTS--------TTPAYRKSDLRLL
AT3G19540.1/1-486 GRSGSLRPVMEGPDPDEG--GGGGNIGESKRLGSGLGH-WVKGQLSR--------APSVA---------ATAAYRRNDLRLL
AT1G27690.1/1-434 HMSEMLAPVIEGPDPDAE--DSGSSGD-YSRFERRWYN-WMKCQLPV--------APPSVS--------SSSDFKRTDLRLL
AT5G05840.1/1-440 NLEDGLETVLEVPMPEEL--FAAS-K--TKPGWNQMKSYWSKPTATATG--------TATATNM----TRLFGGRNAEIQLL
AT1G79420.1/1-418 --PQALTPLMEGPDPDMQ--DERTKKE-SS--WEAIRE-WFKVHKGIS---GNMSSPSVQPLCN----SYDVPAKGQDLRLL
AT5G06610.1/1-369 -----LAPLMEEPIDEEDQEEERGGRK-GSTRSKSWKK-WIKTQLQ----------FIVFPKKPDMKLL
AT5G66740.1/1-371 DKDDGLETVLEVPIPEEM--FSGMGNN-VALRWQNMMT-WMKAQTS----------DKWSQ-----PLIAARINELRFL
AT3G55720.1/1-439 DREDGLETVLEVPMPEEL--FCSD-NN-KSGAWRSVKSSLLRSP----------PDNSSSL----ATLFGGRDSQIQML
AT1G75160.1/1-396 DREDGLETVLEVPVPEEM--FTKMGSN-AQGRWRNMHA-LMKAHAVVTAVATDVRT-PASSSSMSNVNMHLQSKSDNEFVAL
Conservation
00000*3899*3*46943--33440 20-0400344632-74953 00----------1100--------2332252578 46*
Quality
Consensus
DR+DGLEPV+E+PDPEE+QEF+GGG+NESSRRWR+MK++WMK+QLS+T+VA++++AP+VTSSSMSNVN+TL+A+R+NDLRLL
228


170
180
190
200
210
220
230
240
AT1G49840.1/1-495 LGVMGAPLAPINVSSSS-----HL------LHLTIRDSPTETSSAQYILQQYTAACGGHKLHNAIKNAYAMGKLKMIT-SEL
AT3G19540.1/1-486 LGVMGAPLAPIHVSSSD-----PL------PHLSIKNTPIETSSAQYILQQYTAASGGQKLQNSIKNAYAMGKLKMIT-SEL
AT1G27690.1/1-434 LGVLGAPLGPVHVSALD-----LL------PHLSIKNTPMETSSAQYILQQYTAASGGQKLHSSVQNGYVMGRIRTMA-SEF
AT5G05840.1/1-440 LGVVGAPLIPLPVQPDHHNDYENP------IHKDIKDQPLEMSMAQYIVKQYIAAVGGDRALNAVESMYAMGKVRMTA-SEF
AT1G79420.1/1-418 LGVLGCPLAPISVVVSD-----LFPDDPLLGSFQIKNVPFETSTAHYIIQQYLAATGCLKRAKAAKNMYATGIMKMSC-CET
AT5G06610.1/1-369 LSVMGCPLFPVPPLSK-------------------ISLQQVSSSAQYIIQQFAAATGCKKLAGEIKNTFVTGKITMTMVSDI
AT5G66740.1/1-371 LYLVGSPLIPLQVQVG------HS------VHKPVKDCSIQASTAKYIVQQYIAATGGPQALNAVNSMCVTGQVKMTA-SEF
AT3G55720.1/1-439 LGIVGAPSIPLPISSDQA-KIDHP------ISNLIKNQSIESAMAKYIVKQYTAAAGGEMALDAVESMYAMGKVKMGV-TEF
AT1G75160.1/1-396 LKIVGSPLIPFHVPLE------FC------LSRPINDTSIEASTAKYIVQQYVAACGGPTALNAVKSMYAVGQVRMQG-SEM
Conservation
*398*7*56*72644 2------00------0100247565468 6*6**97*95**6*9153234759678 6*5867 55-795
Quality
Consensus
229
LGVVGAPLIP++VSSSD+N+++HLPDDPLL+HL+IK+TPIETSSAQYIVQQYTAATGG+K+LNAVKNMYAMGKVKMTAVSEF


250
260
270
280
290
300
310
320
AT1G49840.1/1-495 ETPTGT---VR----------NRNSTKSETGGFVLWQMNPDMWYVELSVGGSKVRAGCNGKLVWRHTPWLG-SHTAKGPVRP
AT3G19540.1/1-486 ETATRT---VR----------NRNPSKAETGGFVLWQMNPDMWYVELAVGGSKVRAGCNGKLVWRHTPWLG-SHTAKGPVRP
AT1G27690.1/1-434 ETGSKG---SKS--------KNNSSKAVESGGFVLWHMNPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLG-PHAAKGPVRP
AT5G05840.1/1-440 CTGEGS---LNSKMVK---ARSIKSGGGEVGGFVLWQKGIELWCLELVVSGCKISAGSDAKVAWRQTPWHP-SHASRGPPRP
AT1G79420.1/1-418 EIAAGK---SVKT-----LGGGGNGRSGDSGCFVLWQMQPGMWSLELVLGGTKLISGSSDGKTVWRHTPWLG-THAAKGPQRP
AT5G06610.1/1-369 NSST-----AV----------SSASSVSHKGCFVMWQMLPEKWLIELVGGGHKVSAGSDGEITWRYTPWLG-DHAAKGAIRP
AT5G66740.1/1-371 HQGDD----------S----GVNL-KSNDEMGGFVLWQKDPDLWCLELVVSGCKVICGSNGRLSWRHSSNQQ-TPASTGTPRP
AT3G55720.1/1-439 CAAKTLNGKRKKKMVRIRNVNNNNGNGGEMGGFVLWKKGSSQWSLELVVSGCKVSAGCDGNVDWRQSPWLAHSHASNEPSGP
AT1G75160.1/1-396 VAGEDE---GTG--T----PVRLGKGSFEVGGFVLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQP-SQAHRGPPRP
Conservation
2563 00---00----------4303432533*9**9*6734 45*48**678*3*937*78+564*7697745-5373646 44*
Quality
Consensus
230
ETGTGTNGK+++KMV+IR+GVN+NSS+GE+GGFVLWQMNPDMWYLELVVGG+KVSAGSDGKLVWRHTPWLGHSHAAKGP+RP


330
340
350
360
370
380
390
400
AT1G49840.1/1-495 L R R A L Q G L D P R T T A T M F A E S K C V G E R K V N G E D C F I L K L C T D P E T L R A R S E - - G P A E I V R H I L F G Y F S Q R T G L L A Q I E D S Q L T
AT3G19540.1/1-486 L R R G L Q G L D P R T T A A M F A E A K C I G E K K V N G E D C F I L K L C T D P E T L K A R S E - - G P A E I I R H V L F G Y F S Q K T G L L V H I E D S H L T
AT1G27690.1/1-434 L R R A L Q G L D P R T T A Y M F A N A R C I G E K K I D G E D C F I L K L C A D P A T L K A R S E - - G A S E T I R H T L F G Y F S Q K T G L L V H L E D S Q L T
AT5G05840.1/1-440 L R R F L Q G L D P K S T A N L F A R S V C M G E K K I N D E D C F I L K L D A E P S A L K A R S S - - S N V E I I R H T V W G C F S Q R T G L L I Q L E D S H L L
AT1G79420.1/1-418 L R R L I Q G L D P K T T A S L F A K A Q C L G E R R I G D D D C F V L K V S A D R D S L L E R N D A G A P A E V I R H A L Y G Y F C Q K S G L L V Y L E D S H L T
AT5G06610.1/1-369 L R R A L Q G L D P L T I S S V F S S A Q F V G E K E I N G K D C F I L K L S T D Q I D L S K R S D - - S T A E M I K H V A F G Y F S Q K S G L L I C L E D S S L T
AT5G66740.1/1-371 L R R F L Q G L D P R S T A N L F L D A T C I G E K I I N G E D C F I L K L E T S P A V R E A Q S G - - P N F E I I H H T I W G Y F S Q R S G L L I Q F E D S R L L
AT3G55720.1/1-439 L R R F L Q G L D P K T T A N L F A G S V C V G E K A V N N E E C F V L K L E T Q P S G L K S R S K - - S G M E T V K H T V W G C F G Q R T G L L V Q L E D T Y L V
AT1G75160.1/1-396 L R R F F Q G L D P R C T A S L F L D A V C I G E Q P V N G E D C F V L K V E T P S D I L K A Q C S - - P N T E V I H H T V W G Y F S Q R T G L L V K F G D T K L V
Conservation
* * * 6 8 * * * * * 5 7 6 8 5 8 * 5 3 8 4 8 8 * * 7 1 9 5 5 6 9 * * 9 * * 9 4 7 4 4 3 3 5 2 3 8 7 3 - - 6 6 4 * 6 9 8 * 5 7 9 * 7 * 7 * 9 9 * * * 7 4 8 4 * 9 4 * 6
Quality
Consensus
L R R F L Q G L D P R T T A + L F A + A V C I G E K K I N G E D C F I L K L + T D P + T L K A R S E A G + + A E I I R H T L + G Y F S Q R T G L L V Q L E D S H L T


420
430
440
450
460
470
480
490
AT1G49840.1/1-495 R I Q S - - N - - D G D A V Y W E T T I N S S L D D Y K Q V E G - - I M I A H S G R S V V T L F R F G E V A M S H - T R T K M E E R W T I E E V A F N V P G L S L D
AT3G19540.1/1-486 R I Q S - - N - - G G E T V F W E T T Y N S S L D D Y R Q V E G - - I M I A H S G H S V V T L F R F G E V A T S H - T R T K M E E S W T I E E V A F N V P G L S L D
AT1G27690.1/1-434 R I Q N - - N - - G G E A V Y W E T T I N S Y L E D Y K P V E G - - I M I A H S G R S V A T L L R F G D M S S G H N T K T T M Q E A W V I D E I S F N V P G L S I D
AT5G05840.1/1-440 R I K A - - Q - - D D N S I F W E T T M E S L I Q D Y R T V D G - - I L V A H A G K S S V S L F R F G E N S D N H - S R T R M E E T W E I E E M D F N I K G L S M D
AT1G79420.1/1-418 R V M T I S P - - E D E A V Y W E T T I G T S I G D Y R D V D G - - V A V A H C G R A V A T V F R F G E T S L Q Y - S R T R M E E I W R I D D V V F D V P G L S L D
AT5G06610.1/1-369 R I Q I - - P - - G T V P T Y W E T S M S S W M E D Y R A I E G S E V V I A H S G K T D V L I S R F G E T L K G G I S V T R M E E K W T I D D V A F D V P G L S V D
AT5G66740.1/1-371 R M R T - - K E - - D E D V F W E T S A E S V M D D Y R Y V D N - - V N I A H G G K T S V T V F R Y G E A S A N H - - R R Q M T E K W R I E E V D F N V W G L S V D
AT3G55720.1/1-439 R I K T - - G L E D E D M V L W E T T S E T L I Q D Y K S I D G - - I Q I A H R G K T R V S L L R L D E S L E S H - S K T T M E E S W E I E E V G F N V K G L S S D
AT1G75160.1/1-396 R V K S - - G R G K N D G V F W E T S M E S I I D D Y I F V D A - - V N I A H G G Q T V T T L Y R Y G G A V - N H - - R R R I E E K W R I E E V D F N I C G L C L E
Conservation
* 8 6 5 - - 3 - - 0 4 4 3 6 7 * * * 9 4 4 9 4 9 4 * * 5 2 9 9 7 - - 9 5 9 * * 4 * 6 7 2 6 5 9 4 * 7 5 4 5 5 0 6 4 - 2 4 7 6 9 7 * 3 * 3 * 9 9 8 4 * 8 9 3 * * 7 5 9
Quality
Consensus
232
R I Q + I S N + + + + E A V + W E T T + E S S I D D Y R Q V D G S E I M I A H S G K + V V T L F R F G E + S + + H + S R T R M E E K W + I E E V + F N V P G L S L D


500
510
520
530
540
550
AT1G49840.1/1-495 CFIPPADLRSGSLTEACE-YSGQEEK---GKSSLALASTTAHRAKVAALEKGSFD-NDPVWHIDV
AT3G19540.1/1-486 CFIPPADLKTGSLTESCE-YP-QEER---GKN-NTLALSAAHRAKVAALENGSLEDHRPVWHTDV
AT1G27690.1/1-434 CFIPPSELRFDSHVEDLS-QG-P----------K IR----------TLHGHKNG
AT5G05840.1/1-440 CFLPPSDLKKDDDEEEEIECG-LAANNEKLPMKIRSASLRISSSKVLAIVE--EE-DESEVTEET
AT1G79420.1/1-418 SFIPPADIFEDTNPNNNN----------IYSIVNSR
AT5G06610.1/1-369 CFIPPKEMKMDFHHQDAQ----------KHLPNYNT
AT5G66740.1/1-371 HFLPPANLQI----------EK
AT3G55720.1/1-439 FFLPPGDLCIKEEEETGFSFG-DYTSPMLLPLKVSTTSWKIKSSKVTAIE-------DFGEFEG
AT1G75160.1/1-396 SFLPPSDINN----------DH
Conservation
3*+**47941000010000----------00000062
Quality
Consensus
233
CFIPPADLKIDS++EDCE+YGGQEE+++++++K++LAS+++H++KVAA+E+GS+ED++PV+H+++

Appendix 5: Sequences and Annotations of 691 UNK Orthologues

>tr|Q9C6D0|Q9C6D0_ARATH Putative uncharacterized protein At1g49840
OS=Arabidopsis thaliana GN=F10F5.2 PE=2 SV=1
MEKKQGFFSSLRDEVVRGLSPSRSRPRSRSASPSRSTTPHMKALLWGRKKLIASSGCSGG
GGVIGGERGGYYLSQPEPFIGRSSSLRPVMEGPDPDNGEVSGVDSKRLGSGLSHWVKGQW
SRAPSVTSTTPAYRKSDLRLLLGVMGAPLAPINVSSSSHLLHLTIRDSPTETSSAQYILQ
QYTAACGGHKLHNAIKNAYAMGKLKMITSELETPTGTVRNRNSTKSETGGFVLWQMNPDM
WYVELSVGGSKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTATMFAESK
CVGERKVNGEDCFILKLCTDPETLRARSEGPAEIVRHILFGYFSQRTGLLAQIEDSQLTR
IQSNDGDAVYWETTINSSLDDYKQVEGIMIAHSGRSVVTLFRFGEVAMSHTRTKMEERWT
IEEVAFNVPGLSLDCFIPPADLRSGSLTEACEYSGQEEKGKSSLALASTTAHRAKVAALE
KGSFDNDPVWHIDV
>tr|D7KF28|D7KF28_ARALL Putative uncharacterized protein OS=Arabidopsis
lyrata subsp. lyrata GN=ARALYDRAFT_891905 PE=4 SV=1
MEKKQGFFSSLRDEVVRGLSPSRSRPRSRSASPSRSTNPHMKALLWGRKKLIASSGCSGG
GGVSGGGGGGFYLPQPEPLIGRSSSLRPVMEGPDPDNGEISGGDSKRLGSGLSHWVKGQW
SRAPSVTSTPVYRRSDLRLLLGVMGAPLAPINVSSSNHLLHLTIRDSPIETTSAQYILQQ
YTAACGGHKLHNIIKNAYAMGKLKMITSELETPTGTVRNRNSAKSETGGFVLWQMNPDMW
YVELSVGGSKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTATMFAESKC
VGERKVNGEDCFILKLCTDPETLRARSEGPAEIVRHILFGYFSQRTGLLAQIEDSQLTRI
QSNDGDAVYWETTINSSLDDYKPVEGIMIAHSGRSVVTLFRFGEVAMSHTRTKMEERWTI
EEVAFDVPGLSLDCFIPPADLRSSSLTEASEYSGQEEKGKSSIALAATTAHRAKVAALEK
GSFDNDPVWHIDV
>tr|R0ICN1|R0ICN1_9BRAS Uncharacterized protein OS=Capsella rubella
GN=CARUB_v10008984mg PE=4 SV=1
MEKKQGFFSSLKDEVVRGLSPSRSRPRSRSASPSRSSHPHMKALLWGRKKLLASSGGCSG
GGGFYLPQPEALIGRSGSLRPVMEGPDPDNGEMSGGDSKRLGSGLSHWVKGQWSRAPSVT
SAPACRKSDLRLLLGVMGAPLAPINVSSSAHLLRLTISDSPIETTSAQYILQQYTAACGG
QKLQNSIKNAYAMGKLKMITSELETPTGTVRNRNSTKSETGGFVLWQMNPDMWYVELSVG
GSKIRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTAAMFAESKCVGERKVN
GEDCFILKLCTDPETLKARSEGPAEIVRHILFGYFSQRTGLLAQIEDSQLTRIQSNDGDA
VYWETTINSSLDDYKQVEGIMIAHSGRSVVTLFRFGEVAMSHTRTKMEERWTIEEVAFDV
PGLSLDCFIPPADLRSGSLSETCEYSGQEEKGKSAIVLAASTAHRAKVAALEKGRFHENP
VWHIDV
>tr|V4MGS7|V4MGS7_EUTSA Uncharacterized protein OS=Eutrema salsugineum
GN=EUTSA_v10011429mg PE=4 SV=1
MEKKQGFFSSLRDEVVRGLSPSRSRPRSRSASPSRSNSALLWGRKKLIASSGCGGGGGGY
YLATQPEPLTGRSGSLRPVMEGPDPDDTNDGGGGGEISGDSKRLGSGLGHWVKGQLSRAP
SVASTSGYRRSDLRLLLGVLGAPLAPVHVSSSSDHLLLHLTIKDTSIEKSSAQYILQQYT
AASGGHKLQNSIKNAYAMGKLKMITSELETPTRTVRNRNPTKSEAGGFVLWQMNPDMWYV
ELSVGGSKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTATMFAESKCVG
EKKVNGEDCFILKLCTDPETLKARSEGPAEIVRHILFGYFSQRTGLLVQIEDSQLTRMQS
HGGDAVYWETTINSSLEDYKQVEGIMIAHSGRSVVTLFRFGEVAMSHTRTKMEEKWTIEE
VAFNVPGLSPDCFIPPADLRSSSLTEACEYSNQEEKGKSSIALAATAHRAKVAALEKGRF
DGNPVWHVDV
>tr|A0A087H1H1|A0A087H1H1_ARAAL Uncharacterized protein OS=Arabis alpina
GN=AALP_AA4G061900 PE=4 SV=1
MEKKQSFFSSLKDEVKRGLSPSRSRPRSRSSSPTRTNPHMKALLWARTKLISSSTGSNGV
SGANSGAYYLANQPEVLIGRSSSLRPVMEGPDLEDDNGSSSSSRSEISRDSKRIGSGLGH
WVMGQLARAPSVTTTTAAYRRSDLRLLLGVMGAPLAPIHVSSSNHLLKDNSIEASSAQYI
LQQYTAACGGQKLQNSIKNAYAMGKLKMITSELETPTRTVKNRSLTKSETGGFVLWQMNP
DMWYVELSVGGSKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTATMFAG
AKCVGEKKVNGEDCFILKLCTDPETLKARSEGPAEIVRHILFGYFSQRTGLLVQIEDSQL
TRIQSNGGGDTVYWETTINSSLDDYRQVEGIMIAHSGRSVVTLFRFGEVAMSHTRTKMEE
RWTIEEVAFNVPGLSLDCFIPPADLRSGSIAESSVYPSQDEKGKSSVALAATAHRAKVAA

LEKGRFDDNNPVWHIDV
>tr|R0G4M7|R0G4M7_9BRAS Uncharacterized protein OS=Capsella rubella
GN=CARUB_v10013565mg PE=4 SV=1
MEKKQGFFSALRDEVVRGLSPSRSRTRSRSASPARSNSPMSALTWGRKNFTGGGDVGGGG
YYLAQPEQLIGRSGSLRPVMEGPDPDEGGGAGNIGESKRLGSGLGHWVKGQLSRAPSVAA
TAAYRRNDLRLLLGVMGAPLAPIHVSSSDPLPHLSIKNTPIETSSAQYILQQYTAASGGQ
KLQNSIKNAYAMGKLKMITSELETATRTVRNRNPSKAETGGFVLWQMNPDMWYVELAVGG
SKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRGLQGLDPRTTAAMFADAKCIGEKKVNG
EDCFILKLCTDPETLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDTV
FWETTYNSSLDDYRQVEGIMIAHSGHSVVTLFRFGEVAMSHTRTKMEESWTIEEVAFNVP
GLSLDCFIPPADLKTGSLTESCDYPQEERGKNNNLALTAAHRAKVAALENGSFEDHRPVW
HTDV
>tr|D7LA02|D7LA02_ARALL Putative uncharacterized protein OS=Arabidopsis
lyrata subsp. lyrata GN=ARALYDRAFT_898334 PE=4 SV=1
MEKKQGFFSALRDEVVRGLSPSRSRARSRSVSPARSNSPMSALTWGRKNLTGGAGGGGGG
GGGYYLAQPEQLIGRSGSLRPVMEGPDPDEGGGGSTIGESKRLGSGLGHWVKGQLSRAPS
VAATAAYRRNDLRLLLGVMGAPLAPIHVSSSDPLPHLSIKNTPIETSSAQYILQQFTAAS
GGQKLQNSIKNAYAMGKLKMITSELETATRTVRNRNPSKAETGGFVLWQMNPDMWYVELA
VGGSKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKK
VNGEDCFILKLCTDPETLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGG
ETVFWETTYNSSLDDYRQVEGIMIAHSGHSVVTLFRFGEVAMSHTRTKMEESWTIEEVAF
NVPGLSLDCFIPPADLKSSSLTESCEYPQEERGKNNTLALSAAHRAKVAALENGSFEDHR
PVWHSDV
>tr|M4DCK3|M4DCK3_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra014219 PE=4 SV=1
MEMEKKQGFFSALRDEVIRSFTPSRSRPRSRSASPSRSNSHMKALLWGRKKLLASSGCSR
TAAGGYHLASQPEPLIGRSESLRPVIEGPDPDNDETQTDSKRIGSGLGHWVKGQMSRAPS
VASTRSDLRLLLGVLGAPLAPIKVSSSIRDSPIVKSLNITFRFVPETSTAQYILQQYTAA
SGGQKLQSSVKNAYANGKVKMITSELETPTRTVRNRNPTKPETGGFVLWQMNPDMWYVEL
SVGSSKVRAGCNGKLVWRHTPWLGSHTANGPVRPLRRALQGLDPRTTAAIFAESKCVGEK
KVNGEDCFILKLCTDPGTLKARSEGPAEIVRHILFGYFSQRTGLLVQFEDSQLTRIQSNS
GDAVYWETTINSSLEDYRQVEGIMIAHSGRSVVTLFRFGEVAMSHTRTKMEERWTIEEVA
FNVPGLSPDCFIPPADLRSSSLLTEACEYSDREEKGKSSIMLAAHRAKVAALEKGNLGND
HPVWQIDV
>tr|A0A0D3DJG1|A0A0D3DJG1_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MEMEKKQGFFSALRDEVIRSFTPSRSRPRSRSASPSRSNSHMKALLWGRKKLLASSGCSR
AAGGYHLASQPEPLIGRSESLRPVIEGPVPDNDETQTDSKRIGSGLGHWVKGQMSRAPSV
ASTRSDLRLPLGVLGAPLAPIKVSSSIRDSPIVETSTAHYILQQYTAASGGQKLQNSVKN
AYAYGKVKMITSELETPTRTVRNRNPTKPETGGFVLWQMNPDMWYVELSVGSSKVRAGCN
GKLVWRHTPWLGSHTANGPVRPLRRALQGLDPRTTAAIFAGSKCVGEKKVNGEDCFILKL
CTDPGTLKARSEGPAEIVRHILFGYFSQRTGLLVQIEDSQLIRIQSNSGDAVYWETTINS
SLEDYRQVEGIMIAHSGRSVVTLFRFGEVAMSHTRTKMEERWTIEEVAFNVPGLSQDCFI
PPADLRSSSLLTEACEYSDREEKGKSSIVLAAHRAKVAALEKGKLGNDHPVWHIDV
>tr|Q9LH41|Q9LH41_ARATH AT3g19540/T31J18_4 OS=Arabidopsis thaliana
GN=At3g19540 PE=2 SV=1
MEKKQGFFSALRHEVVRGLSPSRSRARSRSVSPARSSSPMSALTWGRKNLTGGGGGGGGG
GYYLAQPEQLIGRSGSLRPVMEGPDPDEGGGGGNIGESKRLGSGLGHWVKGQLSRAPSVA
ATAAYRRNDLRLLLGVMGAPLAPIHVSSSDPLPHLSIKNTPIETSSAQYILQQYTAASGG
QKLQNSIKNAYAMGKLKMITSELETATRTVRNRNPSKAETGGFVLWQMNPDMWYVELAVG
GSKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKKVN
GEDCFILKLCTDPETLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGET
VFWETTYNSSLDDYRQVEGIMIAHSGHSVVTLFRFGEVATSHTRTKMEESWTIEEVAFNV
PGLSLDCFIPPADLKTGSLTESCEYPQEERGKNNTLALSAAHRAKVAALENGSLEDHRPV

WHTDV
>tr|A0A087HAY2|A0A087HAY2_ARAAL Uncharacterized protein OS=Arabis alpina
GN=AALP_AA3G224600 PE=4 SV=1
MEKKQGFFSALRDEVVRGLSPSRSRARTRSVSPARSNTPMAALTWGKKNITGGGGYYLAQ
PEMLIGRSGSLRPVMEGPDPDEGGGGNIGESKRLGSSLGHWVKGQLSRAPSVAATASYRR
NDLRLLLGVMGAPLAPIHVSSSDPLPHLSIKNTPIETSSAQYILQQYTAASGGQKLQNSI
KNAYAMGKLKMITSELETATRTVRNRNPSKAETGGFVLWQMNPDMWYVELAVGGSKVRAG
CNGKLVWRHTPWLGSHTAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKKVNGEDCFIL
KLCTDPETLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDTVFWETTY
NSSLDDYRQVEGIMIAHSGHSVVTLFRFGEVAMSHTRTKMEESWTIEEVAFNVPGLSLDC
FIPPADLKSGSLTDSCEYTQEERGKNSAAALSAAHRAKVAALENGSFGDNRPVWHTDV
>tr|V4LBX3|V4LBX3_EUTSA Uncharacterized protein OS=Eutrema salsugineum
GN=EUTSA_v10020616mg PE=4 SV=1
MEKKQGFFSALRDEVVRGLSPSRSRARSRSVSPARSNSPMSALSWGRKNFTGGGGGGGAG
YYLAQPEQVIGRSGSLRPVMEGPDPDEGGGGGNIGESKRLGSGLGHWVKGQLSRAPSVAA
TAAYRRNDLRLLLGVMGAPLAPIHVSSADPLPHLSIKNTPIETSSAQYILQQYTAASGGQ
KLQNSFKNAYAMGKLKMITSELETATRTVRNRNPSKAETGGFVLWQMNPDMWYVELAVGG
NKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKKVNG
EDCFILKLCTDPETLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDTV
FWETTYNSSLDDYRLVEGIMIAHSGHSVVTLFRFGEVAMSHTRTKMEESWTIEEVAFNVP
GLSLDCFIPPADLKTGSLTESCEYPQEERGKSNAVALSAAHRAKVAALENGRFEDNRPVW
HADV
>tr|A0A078FQ21|A0A078FQ21_BRANA BnaA08g02370D protein OS=Brassica napus
GN=BnaA08g02370D PE=4 SV=1
MEMEKKQGFFSALRDEVIRSFTPSRSRPRSRSASPRTAAGGYHLASQPEPLIGRSESLRP
VIEGPDPDNDETQTDSKRIGSGLGHWVKGQMSRAPSVASTRSDLRLLLGVLGAPLAPIKL
SSSVRDSHIETSTAQYILQQYTAASGGQKLQSSVKNAYANGKVKMITSELETPTRTVRNR
NPTKPETGGFVLWQMNPDMWYVELSVGSSKVRAGCNGKLVWRHTPWLGSHTANGPVRPLR
RALQGLDPRTTAAIFAESKCVGEKKVNGEDCFILKLCTDPGTLKARSEGPAEIVRHILFG
YFSQRTGLLVQFEDSQLTRIQSNSGDAVYWETTINSSLEDYRQVEGIMIAHSGRSVVTLF
RFGEVAMSHTRTKMEERWTIEEVAFNVPGLSPDCFIPPADLRSSSLLTEACEYSDREEKG
KSSIMLAAHRAKVAALEKGNLGNDHPVWQIDV
>tr|A0A078H7J5|A0A078H7J5_BRANA BnaC08g02600D protein OS=Brassica napus
GN=BnaC08g02600D PE=4 SV=1
MEMEKKQGFFSALRDEVIRSFTPSRSRPRSRSASPSGCSRAAGGYHLASQPEPLIGRSES
LRPVIEGPVPDNDETQTDSKRIGSGLGHWVKGQMSRAPSVASTRSDLRLLLGVLGAPLAP
IKVSSSIRDSPIETSTAHYILQQYTAASGGQKLQNSVKNAYANGKVKMITSELETPTRTV
RNRNPTKPETGGFVLWQMNPDMWYVELSVGSSKVRAGCNGKLVWRHTPWLGSHTASGPVR
PLRRALQGLDPRTTAAIFAGSKCVGEKKVNGEDSFILKLCTDPGTLKARSEGPAEIVRHI
LFGYFSQRTGLLVQIEDSQLIRIQSNSGDAVYWETTINSSLEDYRQVEGIMIAHSGRSVV
TLFRFGEVAMSHTRTKMEERWTIEEVAFNVPGLSQDCFISPADLRSSSLLTEACEYSDRE
EKGKSSIVLAAHRAKVAALEKGKLGNDHPVWHIDV
>tr|M4FAU9|M4FAU9_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra038214 PE=4 SV=1
MEKKQGFFSALRGLSPSRSRTRSRSVSPARSSSPMTTLSWGRKNFTGSGAAGGYYVTQPE
LLIERSGSLRPVMEGPDPDEEEEGGGGGSVGDSKRLGSGLGNWVKGQLSRAPSVAATAAH
RRNDLRLLLGVMGAPLAPIHVSSSDPLPHLSIKNTPIETSSAQYILQQYTAASGGQKLKS
SIKNAYAMGKLKMITSKIQTATRTVRNRNPSKAETGGFVLWQMNPDMWYVELSVGGNKVR
AGCNGKLVWRHTPWLGSHTAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKNVNGEDCF
ILKLSTDPETLKARSEGPAEIIRHVLSGYFSQKTGLLAHIEDSHLTRIQSNGGDTVFWET
TYNSSLDDYRQVEGVMIAHSGHSVVTLFRFGEVAMSHTRTKMEESWTIEEVAFNVPGLSL
DCFIPPADLKTGSVADSCEYGQEERGKAAHRAKVAALEN
>tr|A0A0D3CIF5|A0A0D3CIF5_BRAOL Uncharacterized protein (Fragment)
OS=Brassica oleracea var. oleracea PE=4 SV=1

KLNRLSLSPGHLRGLGTKKSKLSLLRVLSSVCALKLKKKQRFRKMEKKQGFFSALRGLSP
SRSRVRSRSVSPARSSSPMKALSWGKKSSTAGGYCLSQPELSIGRSGSLRPVMEGPDPDE
EGGIGGGGNVGDSKRLGSGLGHWVKGQLSRAPSVAATAVCRRNDLRLLLGVMGAPLAPIH
VSSSDPLPHLSIKNTPIETSSAQYILQQYTAASGGQKLQSSVKNAYAMGKLKMITSELET
ASRTVRNRNPSKAESGGFVLWQMDPDMWYVELSVGGNKVRAGCNGKLVWRHTPWLGSHSA
KGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKNVNGEDCFILKLCTDPETLKARSEGPAE
IIRHVLSGYFSQKTGLLVHIEDSHLTRIQSNGGDTVFWETTYNSSLDDYRQVEGIMIAHS
GHSVVTLFRFGEEAMSHTRTKMEESWTIEEVAFNVPGLSLDCFIPPADLKTGSVTEYPQE
ERGKNNNAVVLSAAHRAKVAALENGSFEANR
>tr|M4E0Y3|M4E0Y3_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra022430 PE=4 SV=1
MEKKQGFFSALRGLSPSRSRARSRSVSPARSSSPMKALSWGKKNSSGGGYCLSQPELSIG
RSGSLRPVMEGPDPDEEGGVGGGGEGNVGDSKRLGSGLGHWVKGQLSRAPSVAATAVCRR
NDLRLLLGVMGAPLAPIHVSSSDPLPHLSIKNTPIETSSAQYILQQYTASSGGQKLQSSV
KNAYAMGKLKMITSELETASRTVTNRNPSKAESGGFVLWQMDPDMWYVELSVGGNKVRAG
CNGKLVWRHTPWLGSHSAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKNVNGEDCFIL
KLCTDPETLKARSEGPAEIIRHVLSGYFSQKTGLLVHIEDSHLTRIQSNGGDTVFWETTY
NSSLDDYRQVEGIMIAHSGHSVVTLFRFGEEAMSHTRTKMEESWTIEEVAFNVPGLSLDC
FIPPADLKTGSGTEYPQAERGKSNNAVVLSAAHRAKVAALENGSFEANR
>tr|A0A0D3ACA6|A0A0D3ACA6_BRAOL Uncharacterized protein (Fragment)
OS=Brassica oleracea var. oleracea PE=4 SV=1
IYSLFAPLRDSDETRKKKIKSFSSQAVSLCETLLLCIVKLNVTRKKKKTKVLFMEKKQGF
FSALRGLSPSRSRTRSRSVSPARSSSPMTALSWGRKNFTGGAAAANYYVTQPELLIERSG
SLRPVMEGPDLDEEEEGGGGSVGDSKRLGSGLGNWVKGQLSRAPSVAATAAHRRNDLRLL
LGVMGAPLAPIHFSSSDPLPHLSIKNTPIETSSAQYILQQYTAASGGQKLQSSIKNAYAM
GKLKMITSEIQTATRTVRNRNPSKAETGGFVLWQMNPDMWYVELSVGGNKVRAGCNGKLV
WRHTPWLGSHTAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKNVNGEDCFILKLSTDP
ETLKARSEGPAEIIRHVLSGYFSQKTGLLVHIEDSHLTRIQSNGGDTVFWETTYNSSLDD
YRQVEGVMIAHSGHSVVTLFRFGEVAMSHTRTKMEESWTIEEVAFNVPGLSLDCFIPPAD
LKTGSVADSCEYGQEERGKAAHRAKVAALEN
>tr|A0A061E039|A0A061E039_THECC Soluble secretory phospholipase A2
receptor OS=Theobroma cacao GN=TCM_007179 PE=4 SV=1
MEKKQSFFSALKEEVVRGLSPSRSRPNSPARARSPMASLLRRKKSNHNNYGGAYVAQPEP
LIVRSGSLRPVGEALAPLMEGPDPDGGEVGDSKRVGSGLGQWVKGQLSRTPSVASMSYKR
SDLRLLLGVMGAPLAPVHVSSNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNSI
RNAYAMGKLKMVASEYETATRTVKNRNGSRGAESGGFVLWQMNPDMWYVELAVGGSKVHA
GCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCFI
LKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDAVYWETT
INSYLDDYRPVEGIMIAHSGRSIVTLFRFGEVAMSHTKTKMEEAWTIEEVAFNIPGLSVD
CFIPPGDLRSGSISETCELPQDEREKGAIALAAHRAKVAALEKAQDGGADSMVWRMQV
>tr|A0A0D2PMH5|A0A0D2PMH5_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_008G021300 PE=4 SV=1
MEKKQGFFSALKQEVVRGLSPSRSRSSSPARARSPFATLLRRKKNNHNNYDGAYVAQPES
LIVRSGSLRPVGEALAPLMEGPDPDGGEVGDSKRVGSGLGQWVKGQLSRTPSVASMSYRR
SDLRLLLGVMGAPLAPVHVSSTDPLPLLSIKDTPIETSSAQYILQQYTAASGGQKLQNSI
RNAYAMGKLKMVACEYETPTTTVKNRNVSKCAESGGFVLWQMNPDMWYVELAVGGSKVHA
GCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCFI
LKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVQMEDSHLTRIQSNGGDAVYWETT
INSFLEDYRSVEGIMIAHSGRSVVTLFRFGEVAMSHTKTKMEEAWTIEEVAFNVPGLSVD
CFIPPGDLRSGSISETSELSQDERGKSAIALAAHRAKVAALQKAQDGNADSMIWRMEA
>tr|A0A078IAF5|A0A078IAF5_BRANA BnaA05g20550D protein OS=Brassica napus
GN=BnaA05g20550D PE=4 SV=1
MEKKQGFFSALRVSPARSSSPMKALSWGKKNSTGGGYCLSQPELSIGRSGSLRPVMEGPD
PDEEGGVGGGGEGNVGDSKRLGSGLGHWVKGQLSRAPSVAATAVCRRNDLRLLLGVMGAP

LAPIHVSSSDPLPHLSIKNTPIETSSAQYILQQYTASSGGQKLQSSVKNAYAMGKLKMIT
SELETASRTVRNRNPSKAESGGFVLWQMDPDMWYVELSVGGNKVRAGCNGKLVWRHTPWL
GSHSAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKNVNGEDCFILKLCTDPETLKARS
EGPAEIIRHVLSGYFSQKTGLLVHIEDSHLTRIQSNGGDTVFWETTYNSSLDDYRQVEGI
MIAHSGHSVVTLFRFGEEAMSHTRTKMEESWTIEEVAFNVPGLSLDCFIPPADLKTGSGT
EYPQEERGKSNNAVVLSAAHRAKVAALENGSFEANR
>tr|A0A078JJF3|A0A078JJF3_BRANA BnaCnng55970D protein OS=Brassica napus
GN=BnaCnng55970D PE=4 SV=1
MEKKQGFFSALRVSPARSSSPMKALSWGKKSSTAGGYCLSQPEFSIGRSGSLRPVMEGPD
PDEEGGIGGGENVGDSKRLGSGLGHWVKGQLSRAPSVAATAVCRRNDLRLLLGVMGAPLA
PIHVSSSDPLPHLSIKNTPIETSSAQYILQQYTAASGGQKLQSSVKNAYAMGKLKMITSE
IETASRTVRNRNPSKAESGGFVLWQMDPDMWYVELSVGGNKVRAGCNGKLVWRHTPWLGS
HSAKGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKNVNGEDCFILKLCTDPETLKARSEG
PAEIIRHVLSGYFSQKTGLLVHIEDSHLTRIQSNGGDTVFWETTYNSSLDDYRQVEGIMI
AHSGHSVVTLFRFGEEAMSHTRTKMEESWTIEEVAFNVPGLSLDCFIPPADLKTGSVTEY
PQEEIGKNNNAVVLSAAHRAKVAALENGSFEANR
>tr|A0A0B0MTX9|A0A0B0MTX9_GOSAR Glutamyl-tRNA (Gln) amidotransferase
subunit A OS=Gossypium arboreum GN=F383_24390 PE=4 SV=1
MEKKQGFFSALKQEVVRGLSPSRSRSSSPARARSPFATLLRRKKNNHNNYDGAYVAQPES
LILRSGSLRPVGEALAPLMEGPDPDGGEVGDSKRVGSGLGQWVKGQLSRTPSVASMSYRR
SDLRLLLGVMGAPLAPVHVSSTDPLPLLSIKDTPIETSSAQYILQQYTAASGRQKLQNSI
RNAYAMGKLKMVACEYETPTTTVKNRNVSKCAESGGFVLWQMNPDMWYVELAVGGSKVHA
GCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCFI
LKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVQMEDSHLTRIQSNGGDAVYWETT
INSFLEDYRSVEGIMIAHSGRSVVTLFRFGEVAMSHTKTKMEEAWTIEEVAFNVPGLSVD
CFIPPGDLRSGSISETSELSQDERGKSAIALAAHRAKVAALQKAQDGNADSMIWRMEA
>tr|A0A078IJR3|A0A078IJR3_BRANA BnaA01g26070D protein OS=Brassica napus
GN=BnaA01g26070D PE=4 SV=1
MEKKQGFFSALRGLSPSRSRTRKNFTGSGAAGGYYVTQPELLIERSGSLRPVMEGPDPDE
EEEGGGGGSVGDSKRLGSGLGNWVKGQLSRAPSVAATAAHRRNDLRLLLGVMGAPLAPIH
VSSSDPLPHLSIKNTPIETSSAQYILQQYTAASGGQKLKSSIKNAYAMGKLKMITSEIQT
ATRTVRNRNPSKAETGGFVLWQMNPDMWYVELSVGGNKVRAGCNGKLVWRHTPWLGSHTA
KGPVRPLRRGLQGLDPRTTAAMFAEAKCIGEKNVNGEDCFILKLSTDPETLKARSEGPAE
IIRHVLSGYFSQKTGLLVHIEDSHLTRIQSNGGDTVFWETTYNSSLDDYRQVEGVMIAHS
GHSVVTLFRFGEVAMSHTRTKMEESWTIEEVAFNVPGLSLDCFIPPADLKTGSVADSCEY
GQEERGKAAHRAKVAALEN
>tr|A5C1V9|A5C1V9_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VIT_03s0091g00410 PE=4 SV=1
MDRKQGFFAALKEEVVRGLSPARSRAKSPGRAGSPMSGLLRRRKQSHNQYVANPEPLISR
SGSLRPVVGETLTPLMEGPDPDGSEIGESKRSGLGLGHWMKGQLSRTPSVTSAAYRRSDL
RLLLGVMGAPLAPVHVSTTDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIRNA
YAMGKVKMIASEFETATRVLKNRNASKDADSGGFVLWQMNPDMWYVELAVGGSKVHAGCN
GKLVWRHTPWLGAHSAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCFILKL
CADPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDAVYWETTINS
FLEDYRPVEGIMIAHSGRSIVTLFRFGEMAMSHTKTRMEETWTIEEVAFNVPGLSVDCFI
PPADLRSGSISEACELPHEERGKSSVSLAAHRAKVAALEKTHDGGIDNVIWRMEV
>tr|B9GHV0|B9GHV0_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0001s30470g PE=4 SV=2
MEKKQGFFSALKEEVVRGLSPSRSRSNSPARTASPMSGLLRRKKHNKETSFFASQPEPVI
GRSGSLRPMVGEALSPLMEGPDPDGGEGERKRVGSGLGQWMRGQLSRAPSVTSLAYKRSD
LRLLLGVMGAPLAPVHVSTLDPLPHLSIKDTPIETSSAQYILQQYMAASGGHQVQNSIRN
AYAMGKLKMIASEFETPTRVVKNRNGARGVESGGFVLWQMNPDMWYVELAVGGSKVHAGC
NGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADAKCIGEKNINGEDCFILK
LFADPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDAVYWETTIN

SFLDDYRPVEGIMIAHSGRTVVTLYRFGEVAMSHTKTKMEEAWTIEEVAFNVPGLSVDCF
IPPADLKSGSFSEACELAQDERGKSAMALAAYRAKVAALDKSDDSCADNMIWKMEVSD
>tr|M5W5V1|M5W5V1_PRUPE Uncharacterized protein OS=Prunus persica
GN=PRUPE_ppa004459mg PE=4 SV=1
MKNKNHPTHDFLRSRKNQVRKNTLKPNQEMEKKQGFFSALKDEVVRGLSPSRSRASSPAR
SGSPMSGLLRRKKQNHHHHSHGYGGQLVAQPEPLIGRSGSLRPVMEGPDPDGGELGESKR
VGSGLGQWMRGQLSRTPSVSSVAQSNSRRSDLRLLLGVMGAPLGPLHVSSSDPLPHLSIK
DTPIETSSAQYILQQYTAASGGQKLQNSIKNAYAMGKVRMVASEFETATKVTKTRNASKC
AESGGFVLWQMNPDMWYVELAVGGSKVHAGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQ
GLDPRSTASMFTDARCIGERKINGEDCFILKLCADPQTLKARSEGPAEIIRHVLFGYFSQ
RTGLLVHMEDSHLTRIQSNGGDAIYWETTINSFLDDYRPVEGIMIAHSGRSVVTLFRFGD
MAMSHTKTRMEEAWTIEEVAFNVPGLSVDCFIPPADLRSGTISETCELPHDERGKGGGIA
IAAHRAKVAALEKEHNASVESLTWKMEI
>tr|B9RY65|B9RY65_RICCO Putative uncharacterized protein OS=Ricinus
communis GN=RCOM_0810690 PE=4 SV=1
MEKKQGFFAALKEEVVRGLSPSRSRSNSPARTASPISSFLRRKKSNSNGLHCNNLYMSQP
EVLVARSGSLRPIVGETLTPLIEGPDPDGCESESKRVVGSGLGNWMKGQLTRTPSVSSVA
YRRSDLRLLLGVLGAPLAPVHVSSIDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQ
NSIRNAYAMGKVKMIASEFETPTKVVKNRNGARGAESGGFVLWQMNPDMWYVELAVGGSK
VHAGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKIDGED
CFILKLCADPETLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDAVYW
ETTINSFLHDYKPVEGIMIAHSGRSVVTLYRFGEVAMSHTKTKMEEAWTIEEVAFNVPGL
SLDCFIPPADLRSGSISEACELPQDERGKSAMALAAHRAKVAALEKEHDSNTDNMIWKME
V
>tr|A0A0B0PJR3|A0A0B0PJR3_GOSAR Glutamyl-tRNA (Gln) amidotransferase
subunit A OS=Gossypium arboreum GN=F383_08894 PE=4 SV=1
MEKKQGFFSSLKEDVIRGLSPSRSRSNSLARTGSPMSGLLRRKKTSNQYYAGGGGYVAQP
EPLIARSGSLRPVGEALAPLMEGPDPDGVEIGDSKRVGPGIGEWVKGQLSRNPSVTASYK
RSDLRLLLGVMAAPLAPVHVNCNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNS
IRNAYAMGKLKMVACEYETATRTVKNRNGSKGAESGGFVLWQMNPDMWYVELAVGGSKVR
AGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKNVNGEDCF
ILKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWET
TIDSYLDDYRPVEGIMIAHSGRSVVTLFRFGEVAMSHTKTKMEEAWTIEEVAFNVPGLSL
DCFIPPGDLKSGSIGETCELPQDEKGKTGIVLAAQRAKLAAASNTIWQMEV
>tr|A0A068TMU3|A0A068TMU3_COFCA Uncharacterized protein OS=Coffea
canephora GN=GSCOC_T00014521001 PE=4 SV=1
MEKKQGFFSAIKEEVVRGLSPSRSRSKSPARSASPISALLRRKKTSGSTSSSGNSYVANP
EALIARSGSMRPLGETLTPLMEGPDPDGGEIGESKRVGLGQWMKGQLSRAPSVTSSGYGS
SNNNTSGGSCNRRSDLRLLLGVMGAPLAPVHVSSMDPLPHLSIKDTPIETSSAQYILQQY
TAASGGQKLQNSIRNAYAMGKLKMVASEFETATKVVKNRNAARAAESGGFVLWQMNPDMW
YVELAVGGSKVHAGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTAGMFADARC
IGEKKINGEDCFILKLCADPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRI
QSNGGDAVYWETTINSFLEDYRPVEGIMIAHSGRSVVTLFRFGEMAMSHTKTRMEEAWTI
EEVAFNVPGLSLDCFIPPADLRSGCMSEACELPQDERAKSALALAAHRAKVAALEKTHGS
NMDNVFWKVEV
>tr|A0A067F2X2|A0A067F2X2_CITSI Uncharacterized protein OS=Citrus
sinensis GN=CISIN_1g011695mg PE=4 SV=1
MEKKQGFFSALKQEVVRGLSPSRSRAASPARSMSPISSLLRRRKNQSSNHHHHQVATQEQ
LVSRSGSLRPVVGEALAPLMEGPDPDGAELGESKRVGSGLGNWVKGQLSRTPSVSAMAYR
RSDLRLLLGVMGAPLAPVHVSDNDPLPHLSIKDTPIEASSAQYILQQYTAASGGQKLQNS
IRNAYAMGKVRMVASEFETAARTVKNRNATRCAESGGFVLWQMNPDMWYVELAVGGSKVH
AGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCF
ILKLCADPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVYMEDSHLTRIQSNGGDAVYWET
TINSFLDDYRPVEGIMIAHSGRSVVTLFRFGEVAMSHSKTKMEEAWTIEEVAFNVPGLSV

DCFIPPADLRSGSISEACELANDERGKSVIALAAHRAKVAALEKSRDSSTDNMIWKTEV
>tr|V4SB82|V4SB82_9ROSI Uncharacterized protein OS=Citrus clementina
GN=CICLE_v10028343mg PE=4 SV=1
MEKKQGFFSALKQEVVRGLSPSRSRAASPARSMSPISSLLRRRKNQSSNHHHHQVATQEQ
LVSRSGSLRPVVGEALAPLMEGPDPDGAELGESKRVGSGLGNWVKGQLSRTPSVSAMAYR
RSDLRLLLGVMGAPLAPVHVSDNDPLPHLSIKDTPIEASSAQYILQQYTAASGGQKLQNS
IRNAYAMGKVRMVASEFETAARTVKNRNATRCAESGGFVLWQMNPDMWYVELAVGGSKVH
AGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCF
ILKLCADPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVYMEDSHLTRIQSNGGDAVYWET
TINSFLDDYRPVEGIMIAHSGRSVVTLFRFGEVAMSHSKTKMEEAWTIEEVAFNVPGLSV
DCFIPPADLRSGSISEACELANDERGKSVIALAAHRAKVAALEKSRDSSTDNMIWKTEV
>tr|A0A067LB46|A0A067LB46_JATCU Uncharacterized protein OS=Jatropha
curcas GN=JCGZ_16291 PE=4 SV=1
MEKKQSFFAALKEEVVRGLSPSRSRSNSPARTASPISVLLRRKKNSSNSHCNPYAAQPEL
LSMRSGSLRPAVGETLTPLIEGPDPDGGGEGESKRVGSGLGNWMKGQLTRTPSVSSLAYR
RSDLRLLLGVMGAPLAPLHVSTMDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNS
IRNAYAMGKVKMIASEFETPTRVVKNRNGSRSAESGGFVLWQMNPDMWYVELAVGGSKVH
AGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKNINGEDCF
ILKLCADPQTLQARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDAVYWET
TINSFLEDYRPVEGIMIAHSGRSVVTLYRFGEVAMSHTKTKMEEAWNIEEVAFNVPGLSL
DCFIPPADLRSASMSEACDLPQDERGKSAIALAAHRAKVAALEKQHDSSANNMIWKMEV
>tr|A0A0D2VZK7|A0A0D2VZK7_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_012G148500 PE=4 SV=1
MEKKQGFFSSLKEDVIRGLSPSRSRSNSLARTGSPMSGLLRRKKTSNQYYAGGGGYVAQP
EPLIARSGSLRPVGEALAPLMEGPDPDGVEIGDSKRVGSGIGQWVKGQLSRNPSVTASYK
RSDLRLLLGVMAAPLAPVHVNCNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNS
IRNAYAMGKLKMVACEYETATRTVKNRNGSKGAESGGFVLWQMNPDMWYVELAVGGSKVR
AGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTAGMFADARCIGEKNVNGEDCF
ILKLCTEPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWET
TIDSYLDDYRPVEGIMIAHSGRSVVTLFRFGEVAMSHTKTKMEEAWTIEEVAFNVPGLSV
DCFIPPGDLKSGSIGETCELPQDEKGKTAIVLAAQRAKLAAAGNTIWKMEV
>tr|W9RXT3|W9RXT3_9ROSA Uncharacterized protein OS=Morus notabilis
GN=L484_011503 PE=4 SV=1
MEKKQGFFSALKDEVVRGLSPSRSRGSSPARARGRSASPISGLLRRKKSGHSLAAPPEAL
IARSGSLRPLGEALAPLMEGPDPDGGDVGDSKRVGSGLGQWMRGQLSRAPSMAYRRSDLR
LLLGVMGASLAPVHVSSNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIRNAY
AMGKLRMVASEFETATKVMKNRNASRCAESGGFVLWQMNPDMWYVELAVGGSKVHAGCNG
KLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFSDARCIGEKKINGEDCFILKLC
ADPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSF
LEDYRPVEGIMIAHSGRSVVNLFRFGEMAMSHTKTKMEEAWTIEEVAFNVPGLSMDCFIP
PADLRSGVIDETCELPQDERGKGAVSIASHRAKVVALEKAHDGNMDNLIWKMEV
>tr|M1CFP3|M1CFP3_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG400025854 PE=4 SV=1
MERKQGFFSALKEEVVRGLSPGRSRTRSPARSGSPITSLLRRKKSNSSSNFAPNHEQLIS
RSGSLRPLGETLTPLMEGPDPDGGEVGDSKRVGSSIGHWMKGQLSRTPSAASTAYSKRSD
LRLLLGVMGAPLAPVHVSTSDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQSSIKN
AYAMGKLKMLASEFETPTKVVKSRNSARAAESGGFVLWQMNPDMWYVELAVGGSKVHAGC
NGKLVWRHTPWLGAHTAKGTVRPLRRALQGLDPRSTASMFANARCIGEKKINGEDCFILK
LCADPHTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGAEAVYWETTIN
SFLDDYRPVEGIMIAHSGRSVVTLFRFGEMAMSHTKTRMEETWTIEEVAFNVPGLSVDCF
IPPADLKSGSISEACELPQDERGKSAISLATHRAKVAALEKTHDSWKVEI
>tr|K4B2V2|K4B2V2_SOLLC Uncharacterized protein OS=Solanum lycopersicum
GN=Solyc01g107350.2 PE=4 SV=1
MERKQGFFSALKEEVVRGLSPGRSRARSPARSGSPITSLLRRKKSNSSSNFAPNHEQLIS

RSGSLRPLGETLTPLMEGPDPDGGEVGDSKRVGSSLGHWMKGQLSRTPSVASTAFSKRSD
LRLLLGVMGAPLAPVHVSSTDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQSSIKN
AYAMGKLKMLASEFETPTKVVKSRNSARAAESGGFVLWQMNPDMWYVELAVGGSKVHAGC
NGKLVWRHTPWLGAHTAKGTVRPLRRALQGLDPRSTASMFTNARCIGEKKINGEDCFILK
LCADPHTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGADAVYWETTIN
SFLDDYRPVEGIMIAHSGRSVVTLFRFGEMAMSHSKTRMEEAWTIEEVAFNIPGLSVDCF
IPPADLKSGSISEACELPQDERGNSAISLASHRAKVAALEKTHDSWKVEI
>tr|A0A078E4I5|A0A078E4I5_BRANA BnaC01g33310D protein OS=Brassica napus
GN=BnaC01g33310D PE=4 SV=1
MEKKQGFFSALRGLSPSRGRKNFTGGAAAANYYVTQPELLIERSGSLRPVMEGPDLDEEE
EGGGGSVGDSKRLRSGLGNWVKGQLSRAPSVAATAAHRRNDLRLLLGVMGAPLAPIHFSS
DPLPHLSIKNTPIETSSAQYILQQYTAASGGQKLQSSIKNAYAMGKLKMITSEIQTATRT
VRNRNPSKAETGGFVLWQMNPDMWYVELSVGGNKVRAGCNGKLVWRHTPWLGSHTAKGPV
RPLRRGLQGLDPRTTAAMFAEAKCIGEKNVNGEDCFILKLSTDPETLKARSEGPAEIIRH
VLSGYFSQKTGLLVHIEDSHLTRIQSNGGDTVFWETTYNSSLDDYRQVEGVMIAHSGHSV
VTLFRFGEVAMSHTRTKMEESWTIEEVAFNVPGLSLDCFIPPADLKTGSVADSCEYGQEE
RGKAAHRAKVAALEN
>tr|A0A0L9U0F0|A0A0L9U0F0_PHAAN Uncharacterized protein OS=Phaseolus
angularis GN=LR48_Vigan02g238600 PE=4 SV=1
MENKQSFFSALKDEVVRGLSPSRSRSKSPARTASPISGLLRRKKHNPDSSVARSASLRPL
GETLTPLIEGPDPDASENGDPKRIGSGLGHWMKGQLSRAPSVSYKRSDLRLLLGVMGAPL
APVHVCSTDPLPHLSIKDTPIETSSAQYILQQYLAASGGLKLQNSIRNAYAMGKVRMVAS
EFETATKVVKNRNSSRCAESGGFVLWQMNPDMWYVELVVGGSKVHAGCNGKLVWRHTPWL
GAHTAKGPVRPLRRALQGIDPRTTASMFADARCIGEKNINGEDCFILKLCTDPETLKARS
EGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSFLGDYKPVEGI
MIAHSGHSVVTLFRFGEMAMSHTKTKMEEAWTIEEVAFNVPGLSVDCFIPPADLRTGSVS
EACELPQDDRGKNSLAVHRAKVVALEKSHNCSIDNMIWKMEI
>tr|V7BDT6|V7BDT6_PHAVU Uncharacterized protein OS=Phaseolus vulgaris
GN=PHAVU_007G042600g PE=4 SV=1
MENKQSFFAALKDEVVRGLSPSRSRSKSPARTASPISALLRRKKHNPDYSVARSVSLRPL
GETLTPLIEGPDPDATENGDPKRIGSGLGHWMKGQLSRAPSVSYKRSDLRLLLGVMGAPL
APVHVCATDPLPHLSIKDTPIETSSAQYILQQYLAASGGLKLQNSIRNAYAMGKVRMVAS
EFETATKVVKNRNASRCAESGGFVLWQMNPDMWYVELVVGGSKVHAGCNGKLVWRHTPWL
GAHTAKGPVRPLRRALQGIDPRTTASMFADARCIGEKNINGEDCFILKLCTDPETLKARS
EGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSFLSDYKPVEGI
MIAHSGHSVVTLFRFGEMAMSHTKTKMEEAWTIEEVAFNVPGLSLDCFIPPADLRTGSVS
EACELPQDERGKNSLAVHRAKVVALEKSHNCSIDNMIWKMEI
>tr|I1NG05|I1NG05_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MEKKQGFFSALKDEVVRGLSPSRSRSTSPARTVSPITGLLRRKKRSPSPDSSVARSVSLR
PLGETLTPLMEGPDPDGTENGDPKRIGSGLGHWMKGQLSRAPSVSSYKRSDLRLLLGVMG
APLAPVHVSSTDPLPHLSIKDTPIETSSAQYILQQYTAASGGLKLQNSIRNAYAMGKVRM
VASEFETATRVVKNRSRCAESGGFVLWQMDPDMWYVELAVGGSKVHAGCNGKLVWRHTPW
LGAHTAKGPVRPLRRALQGIDPRTTASMFADAKCIGEKNINGEDCFILKLCTDPETLKAR
SEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSFLSDYKPVEG
IMIAHSGHSVVTLFRFGEMAMSHTKTRMEEAWTIDEVAFNVQGLSVDCFIPPADLRTASV
SEACELPQDERAKNSLAVHRAKVVALEKSHNCSIDSMIWKMEI
>tr|A0A0A0KT77|A0A0A0KT77_CUCSA Uncharacterized protein OS=Cucumis
sativus GN=Csa_4G001510 PE=4 SV=1
MEKKPSFFSALKEEVIRGLSPSRSRAKSPARTASPFSILLRRKKNQYVAHAGIPQQFIAR
SGSFRPVGEALTPLVEGPDPDGCEIGDSKRISSGLGQWMKGQLSRTPSIASSVATKRSDL
RLLLGVMGAPLAPVHVSTSDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIRNA
YAMGKLRMVAAEFETATKVMKSRNPSTRAESGGFVLWQMNPDMWYVELAVGGSKVHAGCN
GKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTIVRMFADARCIGEKKINGEDCFILKL
CADPQTLKSRSEGPAEIIRHVLFGYFSQKTGLLVYMEDSHLTRIQSNGGDAVYWETTINS

FLDDYRPVEGIMIAHSGRSVVTLFRFGEMAMSHTKTKMEEAWTIEEVAFNVPGLSMDCFI
PPADLRSCSISETSELPQDERSKSAIALAAYRAKVAALEKPDDDCMDNMTWKSDF
>tr|I1LEG8|I1LEG8_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MEKKQGFFSALKDEVVRGLSPSRSRSISPARTLSPISALLRRKKRSPSPDSSVARSASLR
PLGETLTPLMEGPDPDGTENGDPKRIGSGLGHWMKGQLSRAPSVSYKRSDLRLLLGVMGA
PLAPVHVSSTDPLPHLSIKDTPIETSSAQYILQQYTAASGGLKLQNSIRNAYAMGKVRMV
ASEFETATRVVKNRNRCAESGGFVLWQMDPDMWYVELAVGGSKVHAGCNGKLVWRHTPWL
GAHTAKGPVRPLRRALQGIDPRTTASMFADAKCIGEKNINGEDCFILKLCTDPETLKARS
EGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSFLSDYKPVEGI
MIAHSGHSVVTLFRFGEMALSHTKTRMEEAWTIDEVAFNVQGLSVDCFIPPADLRTASVS
EACELPQDERAKNSLAVHRTKVVALEKSHNCSIDSMIWKMEI
>tr|A0A072VRH6|A0A072VRH6_MEDTR Lipase OS=Medicago truncatula
GN=MTR_1g106875 PE=4 SV=1
MEKKQGFFSALKEEVVRGLSPSRTRSRSRSRSTSPARTGSPMTGLFTRKKNHPNPNLDSS
LARSGGLRPLGETLTPLIEGPDSENGDLKRIGSGLGNWMKDQLSRAPSVSYKRSDLRLLL
GVMGAPLAPFHVCSTDPLPHLSIKDTPIETSSAQYILQQYIAASGGQKLQNSIRNAYAMG
KVRMVASEFETATRVVKNRNASRCAESGGFVLWQMNPDMWYVELSVGGSKVHAGCNGKLV
WRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKNINGEDCFILKHCTDP
ETLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSFLDD
YRPVEGIMIAHSGHSVVTLFRFGEMAMSHTKTKMEEAWTIEEVAFNIPGLSLDCFIPPAD
LKTASVSEACELPQDERGKNSLGVHRTKVVALEKSHDCSIDKMIWKMEI
>tr|A0A0D2V9C5|A0A0D2V9C5_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_013G048800 PE=4 SV=1
MEKKQGFFSALKEEVIRGLSPSRSRTNSPGRARSPIAILLRRKKSGHNNYGGAYLAQPEP
LTARYGVGEALAPLMEGPDPDGGETGDSKRLGSGLGQWVMGQLSRTPSMASLSCKRSDLR
LLLGVMGAPLAPVQVCSTDPLPHLSIKDTPIETSTAQYILQQYTAASGGLKLQNSVRNAY
AMGKLKMVACEYETAAKTVKNRYGSRGAESGGFVLWQMHPDMWYVELAVGGSKVHAGCNG
KLVWRHTPWLGARTAKGPVRPLRRALQGLDPRTTASMFSDAKCIGEKTINGEDCFILKLC
TDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDTVYWETTINSY
LHDYRPVEGIMIAHSGRSVITLFRFGEAAMSHTKTRMEEAWTIEEVAFNIPGLSVDCFIP
PGDLKSGSISETYELPQDETGKSGIALSAYHAKVAALEKAQDNWLTV
>tr|A0A0B2PGY4|A0A0B2PGY4_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_021333 PE=4 SV=1
MEKKQGFFSALKDEVVRGLSPSRSRSISPARTLSPISALLRRKKRSPSPDSSVARSASLR
PLGETLTPLMEGPDPDGTEVRIGSGLGHWMKGQLSRAPSVSYKRSDLRLLLGVMGAPLAP
VHVSSTDPLPHLSIKDTPIETSSAQYILQQYTAASGGLKLQNSIRNAYAMGKVRMVASEF
ETATRVVKNRNRCAESGGFVLWQMDPDMWYVELAVGGSKVHAGCNGKLVWRHTPWLGAHT
AKGPVRPLRRALQGIDPRTTASMFADAKCIGEKNINGEDCFILKLCTDPETLKARSEGPA
EIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSFLSDYKPVEGIMIAH
SGHSVVTLFRFGEMALSHTKTRMEEAWTIDEVAFNVQGLSVDCFIPPADLRTASVSEACE
LPQDERAKNSLAVHRTKVVALEKSHNCSIDSMIWKMEI
>tr|A0A0B0PVE8|A0A0B0PVE8_GOSAR Glutamyl-tRNA (Gln) amidotransferase
subunit A OS=Gossypium arboreum GN=F383_15562 PE=4 SV=1
MEKKQGFFSALKEEVIRGLSPSRSRTNSPGRARSPIAILLRRKKSGHYNYGGAYLVQPEP
LIARYGVGEALAPLMEGPDPDGGETGDSKRLGLGLGQWVMGQLSRTPSMASLSCKRSDLR
LLLGVMGAPLAPVQVCSTDPLPHLSIKDTPIETSTAQYILQQYTAASGGLKLQNSVRNAY
AMGKLKMVACEYETAAKTVKNRYGSRGAESGGFVLWQMNPDMWYVELAVGGSKVHAGCNG
KLVWRHTPWLGARTAKGPVRPLRRALQGLDPRTTASMFSDAKCIGEKTINGEDCFILKLC
TDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDTVYWETTINSY
LHDYRPVEGIMIAHSGRSVITLFRFGEAAMSHTKTRMEEAWTIEEVAFNIPGLSVDCFIP
PGDLKSGSISETYELPQDETGKSAIALSAYHAKVAALERAQDNWLTV
>tr|B9HS91|B9HS91_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0009s09540g PE=4 SV=2
MEKKQGFFSALKEEIVGGFSPSRSRSNSPARTASSMSGLLYRKKHRKDTSSYAAQPEPLI

GKSRSSRPMVGETLSPLIEGPDPDGGVGEHKRAGSGPGLGQWMKGQLSRTPSVTSLAYKR
SDLRLLLGVMGAPLAPVHVSTLDPLPHLSIKDTPIETSSAQYILQQYMAASGGQQVQTSI
RNAYAMGKLKMIVSESETPTRVVKNRNDARGVESGGFVLWQMNPDMWYVELAVGGDKVRA
GCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKNINGEDCFI
LKVLADPQTLKARSEGPGEIIRHVLFGYFSQKTGLLVHMEDSHLTRNQSIGGDAVYWETT
INSFLDDYRPVEGIMIAHSGRSAVTLYRFGEVAMSHTKTKMEEAWTIEEVAFNVPGLSVD
CFIPPADLKPGSFSEACELPHDERGKSAVALVALRAKVAALDKSDDSCGDNMTWKTEV
>tr|A0A022RBG8|A0A022RBG8_ERYGU Uncharacterized protein OS=Erythranthe
guttata GN=MIMGU_mgv1a005888mg PE=4 SV=1
MEKRQGFFSALKEEVVRGLSPARSRAKSPGRSPSPMAGLFRRKLSSSSSDSLIPRSGSLR
PGGETLTPLMEGPDPDGDELGESKRLGSGLGQWVRGQLNRNPSVAVNENGCGSKRSDLRL
LLGVMGAPLAPVHVCTSEPFPHLSIKDTPIEASSAQYILQQYTAASGGQKVQNTIKNAYA
MGKLKMVASEFETATKVVKNRNAARAAESGGFVLWQMNHDMWYVELAVGGSKVHAGCNGK
LVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFTDSICIGEKSINGEDCFILKLAA
DPHTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDAVYWETTINSFL
DDYRPVEGIMIAHSGRSIVTLFRFGEMAMSHTKTRMEEAWTIDEVAFNVPGLSGDCFIPP
ADLRSGSVSEACELPHEERGKSVIAHRAKVAALENTGSNNTWKVES
>tr|M1BXY8|M1BXY8_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG400021537 PE=4 SV=1
MEKKQGFFSALKDEVVRGLSPAKSRGRSPSPSGSGLLRRRKGNQAPQPEVYISRSGSLRP
CVETLSPLMEGPDPNGSEVGDSKSDRWWMKGQLCRAPSVSTSGSGLQRSDLRLLLGVLGA
PLAPVHVSNNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNTMYNAYAMGKVRMM
ASDIETATKVIKNRNSSKTAESGGFVLWQMNPDMWYVELALGSSKVHAGCNGKLVWRHTP
WLGAHAAKGPVRPLRRALQGLDPRTTANMFASAKCTGEKKINGEDCFILKLCADPHTLKA
RSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQTNGGDAVYWETTINSFLDDYRPVE
GIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSEECFIPPAELRFSS
IGEACELSQGERVKTTVSAAAAAAYRAKVAALDKSRDGSNVNNIVLKMNY
>tr|A0A067KZM3|A0A067KZM3_JATCU Uncharacterized protein OS=Jatropha
curcas GN=JCGZ_16058 PE=4 SV=1
MERKQGFFSALKEEVVRGLSPARSRAKSPARSASPMSSLLRRRKGRGHYVAQPEPLIIAR
SGSLRPVEALSPLKEGPDQDDGGDSRMEGRWGHWMKGQLSRTPSVASPNACKRSDLRLLL
GVLGAPLAPVHVSSAEPLPHLSIKDTPIETSSAQYILQQYTAASGGQRVQNSIYNAYAMG
KVKMIASEFETANKVTRNKNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGKLV
WRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFTNARCIGEKKINGDDCFILKICADP
ATLKARSEGPAEIIRHVLFGYFSQKTGLLLHIEDSHLTRIQNNGGDAVYWETTINSFLDD
YRPVDGVMIAHSGRSVVTLFRFGDTAMSHTRTRMEEAWAIEEVAFNVPGLSMDCFIPPAE
LRFASISETCELPQSQRVKPAMASAAYRAKVAALDRSRDNVVSNNTMWNTDV
>tr|W1NLG2|W1NLG2_AMBTC Uncharacterized protein OS=Amborella trichopoda
GN=AMTR_s00001p00272450 PE=4 SV=1
MERKQGFFSALKEEVVRGLSPGRIRAKSPARSTSPMSGLLRRHKKSSSSSSGGVQHNQAA
VDSVLMARSGSMRPVGETLTPLMEGPDAEGCEGEGRKEGWGHWMKGQLSRTPSVSSTYNK
RSDLRLLLGVMGAPLAPVHVSTMDPLPHLSIKDTPIETSSAQYILQQYTAASGGSRLQGS
VRNAYAMGKVKMIASEFETATKVMKNRNAGKAAESGGFVLWQMMPDMWYVELAVGGSKVH
AGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFADARCIGEKQVDGEDCF
ILKLCADPQTLKARSEGPAEIIRHVLFGYFSQRTGLLVHMEDSHLTRIQSNGAGDAVYWE
TTINSFLSDYRPVEGIMIAHSGRSIVTLFRFGEMAMSHTKTRMEEVWTIEEVAFNVPGLS
IDCFIPPADIRCGSISEACELPHGERGKSMAAAAAAHRSKVAALEKRHESNVDNIIWRVE
V
>tr|A0A059AMQ1|A0A059AMQ1_EUCGR Uncharacterized protein OS=Eucalyptus
grandis GN=EUGRSUZ_I01085 PE=4 SV=1
MEKKQNFFTSLKQEVIRTLSPSRSRSGSPMSGLLRRKKGGGGGGGLASLPDQVVAWRSGS
LRPVGEALAPLMEGPDPDGGEAGDPRRSNNGSGLGQWVKGQLHRAPSVSAAACRRSDLRV
LLGVLGAPLAPVHVSSLDPLPLLSIKDTPIETSSAQYILQQYTAASGGQTLQNSVKNAYA
MGKVRMTTSEFETVSKVIKNRNSAHTGGFVLWQMDPDMWYVELAVGGSKVHAGCNGKLVW

RHTPWLGAHTAKGPVRPLRRALQGLDPRTTVSLFADARCVGEKKLNGEDCFILKLCADPQ
TLKARSEGPAEIIRHVLFGYFSQKTGLLVYLEDSHLTRIQCGGGDAVYWETTINSYLHDY
RPVEGIMIAHSGHSVVTLFRFGETAMSHTKTRMEESWTIEEVAFNVPGLSEDCFIPPADL
RSGSICDISGLHQDERGKSALALSAYRAKVAALEQADDSCTDNVIWRMEV
>tr|A0A068TZ97|A0A068TZ97_COFCA Uncharacterized protein OS=Coffea
canephora GN=GSCOC_T00034802001 PE=4 SV=1
MERKQGFFSALREEVVRGLSPGRSRRRSPSPSRSSLRRRRKGAHTVPPEAFISRSGSLRP
AVETLSPLREGPDPAGSEAGDSKSEKWGHWLCRAPSVSTAASGSGSGYQRSDLRLLLGVL
GAPLAPVHVSSNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNAIHNAYAMGKVK
MLASDIETATKVIKSRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGKLVWRH
TPWLGAHAAKGPVRPLRRALQGLDPRTTANMFANARCTGEKKINGEDCFVLKLCADPHTL
KARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSNGGDAVYWETTINSFLDDYRP
VEGIMIAHSGRSVVTLFRFGDTAMSHTKTRMEEAWTIEEVAFNVPGLSGECFIPPAELRL
GSLSEACELPQGERARTVAAAAAYRAKVVALEKSQESNVNNIVLKMDI
>tr|A5B9D3|A5B9D3_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VIT_18s0001g09450 PE=4 SV=1
MERKQGFFSALKQEVVRGLSPGRSRARCESPMSRLRRRSKKQNQVPQPDLLIGRSGNLRP
VETLSPLMEGPDPEGSECGDSRVEGGWGQWMKGQLSRAPSVSSSAYKGSDDLRLLLGVMG
APLAPVHVSSTDPLPHLSIKNTPIETSSAQYILQQYTAASGGQKLQSSIHNAYAMGKVKM
LAAEFETANKVIKTRNSSKAAEGGFVLWQMNPDMWYVELALGGSKVHAGSNGNLVWRHTP
WLGAHAAKGPVRPLRRALQGLDPRTTASMFTNARCIGEKRINGDDCFILKLCADPVTLKA
RSEGPAEIIRHVLLGYFSQKTGLLVHLEDSHLTRIQTNGGDAAYWETTINSFLDDYRPVE
GIMIAHSGRSVVTLFRFGETAMSHTKTKMEEAWSIEEVAFNVPGLSLDCFIPPAELRFGS
VSESCEFPQGERVKTAVAAAAAAAYRAKVAALEKSHESNVNKIIWKMDV
>tr|A0A059BRT4|A0A059BRT4_EUCGR Uncharacterized protein OS=Eucalyptus
grandis GN=EUGRSUZ_F02268 PE=4 SV=1
MEKKQGFFSALKDEVVRGLSPSRSRPRSRAKSPRGRSTSPMSGLFRRRKGGQVAPPELLI
SRSGSLMRPVEALSPLMEGPDPDGAECGDSRRGHWMRAPSVSSSSSSAAAAAAASKQSNL
RLLLGVLGAPLAPVHVAASDPLPHLSIKNIPIESSSAQYILQQYMAASGGQKLQNSINNA
YAMGKVRMIASEFETPNKVIKNKNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCN
GKIVWRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFTNARCIGEKMVNGEDCFILKL
CADPVTLKARSDGPAEIIRHVLFGYFSQKTGLLIHLEDSHLTRIQNNGGDAVYWETTINS
FLDDYRPVEGIMIAHSGRSVVTLFRFGETAMNHTKTRMEEAWTIEEVAFNVPGLSLDCFI
PPAEIRLSSISEACELPHGQRAKNAAANLGSNIHRARVASLDRSHGSLARSYI
>tr|A0A061FFF5|A0A061FFF5_THECC Uncharacterized protein OS=Theobroma
cacao GN=TCM_034747 PE=4 SV=1
MERKQGFFSVVRGLSPSRSRPKSPARSASPMSSLLRRRRSNNHHVSQPEPLIFRSGSFRP
AEALSPLKEGPDPDGTDGGDSRMEGRWAQWMKGQLTRAPSVSTSTCKRSDLRLLLGVLGA
PLAPVHVSTLEPLPHLSIKDTPIESSSAQYILQQYTAASGGQKLQNSIHNAYAMGRVRMI
ASEFETANKVTRNRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGKLVWRHTP
WLGAHAAKGPVRPLRRALQGLDPRTTASMFTNARCIGEKKINGEDCFILKLCADPATLKA
RSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSFLEDYRPVE
GIMIAHSGRSVVTLFRFGDTAMSHTRTRMEEAWAIEEVAFNVPGLSMDCFIPPAEIRLAS
ISEACEFSQGPRVKTTVATAPYRAKVNTLDKSS
>tr|Q2HRJ7|Q2HRJ7_MEDTR Lipase OS=Medicago truncatula GN=MTR_1g018620
PE=4 SV=1
MERKQGFFSSLKDEVVRGLSPARSRAKSPARSASPMSGLLRRRRKNQGVPPELFMTRSGS
LRPLEALSPLKEGPDGTDGEDVGNREGKWGHWMKGQLARAPSVSSSSSACKKSDLRLLLG
VLGAPLAPVHVCTTDPFPHLSIKDIPIETSSAQYILQQYIASSGGLKIQNSINNAYAMGK
VRMIASEFETANKVTRNRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGKLVW
RHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFINARCIGEKKINEEDCFILKLCADPS
TLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSFLDDY
RPVEGIMIAHSGRSVVTLFRFGETALSHTKTRMEEAWTIEEVAFNVPGLSIDCFIPPSEL
RFASISEASELPHGQRVKSAAAAAAYQAKVAQFQKSHESNTNNINWTVDV

>tr|A0A0J8BLF4|A0A0J8BLF4_BETVU Uncharacterized protein OS=Beta vulgaris subsp. vulgaris GN=BVRB_9g206310 PE=4 SV=1
MEKKQGFFSALKEEVVRGLSPGKSRAKSPARNMSPMTGLLRRRKNHHVAIPEVLIARSGS
LRPPEMLSPLREGPDQCGARDEREDTGWAHWMKRNPSVSASASSSSSSAACKRSDLRLLL
GVLGAPLAPVHVSASDPLPHLSIKDTPIETSSAQYILQQYTAASGGLKLQNSIHNAYAMG
KLKMLASDLETPNKVIKNRNSSKSAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGNLV
WRHTPWLGAHAAKGPVRPLRRALQGLDPRTTAAMFANARCIGEKKINGEDCFILKLCADP
KTLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSCLDD
YRPVEGIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSIDCFIPPAE
IRYSSVGDSCELPHGDRLKTMSATAAAYRAKVASMDRSYESNRNNMSWPIDDMHVDH
>tr|M0SU21|M0SU21_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1
MEKKQGFFSALREEVARGLTPARARGRSRSRRRGMVGGPAVPRSGSLAPLMEGPDSGEGE
GDEARKERGWGQWVKGQLSRAPSVSTSATASCRPSDLRLLLGVMAAPLAPIHVCSTDPLP
HLSIKDTPIETSSAQYILQQYTAASGGLKLLSSVRNAYAMGKVRMVATELEMATKIVRKR
NASRDAESGSFVLWQMAPDMWYVELAAGGSKVRAGCNGKLVWRHTPWLGAHAAKGPVRPL
RRALQGLDPLTTASMFANARCIGEKKVNGEDCFILKLCADPQTLRARSDGPAEVIRHVLF
GYFSQRTGLLIHIEDSHLTRIQASAGGDAAYWETSINSFIDDYRPVDGMMIAHSGHSVVT
LFRFGEVAMSHTKTRMEEAWTIEEVAFNVPGLSMDCFIPPADIKRGSISEACELPQGERG
ENTVAGNHRAKVAALEKSHDGADGNIVWRVEV
>tr|A0A0A0LNA8|A0A0A0LNA8_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_2G354900 PE=4 SV=1
MDRKQGFFSSLKDEVVRGLSPGKSRAKSPVPSTTPATTLRRRRKGAHRHSRHELLIGRSG
SLRPAEALSPLKEGPDETDADDSKMEGRWAQWMKGQLCRAPSVSCSAYKRSDLRLLLGVL
GAPLAPVHVSSSDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIQNAYAMGKVR
MVASEFETANRVIRSRNSSKDAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGRLVWRH
TPWLGAHCAKGPVRPLRRALQGLDPKTTASMFTNARCTGEKKINDEDCFILKLCADPATL
KARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSFLDDYRP
VEGIMIAHSGRSVVTLFRFGDTAMSHTKTRMEEAWTIEEVAFNVPGLSVDCFIPPAELRF
ASMSEACELPQDQIIDNAVTAQALHAKVAALDKLDDNNVVWNTDAA
>tr|V7CRS4|V7CRS4_PHAVU Uncharacterized protein OS=Phaseolus vulgaris GN=PHAVU_001G025900g PE=4 SV=1
MERKQGFFSALKDEVVRGLSPARSRAKSPARSSSPMSSLLRRRRKHHAPPPELFIARSGS
LRPTEALSPLKEGPDGTDGHDSTRGEGRWGQWMKGPLARAPSVSSSSSSSSSCKKSDLRL
LLGVLGAPLAPVHVCTTDPFPHLSIKDIPIETSSAQYILQQYIAASGGQKLQNSINNAYA
MGKVRMIASEFETANKVTRSRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGR
LVWRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFINARCIGEKKINEEDCFILKLCA
DPSTLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSFL
DDYRPVEGIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSLDCFIPP
SELRFASMSEACELPKGQRVKTAVAAAAYHAKVAQLQKSHEGNTNNINWTVDV
>tr|A0A0L9V1J6|A0A0L9V1J6_PHAAN Uncharacterized protein OS=Phaseolus angularis GN=LR48_Vigan07g266900 PE=4 SV=1
MERKQGFFSALKDEVVRGLSPARSRAKSPARSSSPMSSLLRRRRKHHAPPPELFIARSGS
LRPAEALSPLKEGPDGTDGHDSTRGEGRWGQWMKGPLARAPSVSSSSSSSSSSCKKSDLR
LLLGVLGAPLAPVHVCTTDPFPHLSIKDIPIETSSAQYILQQYIAASGGQKLQNSINNAY
AMGKVRMIASEFETANKVTRSRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNG
RLVWRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFINARCIGEKKINEEDCFILKLC
ADPSTLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSF
LDDYRPVEGIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSLDCFIP
PSELRFASMSEACELPQGQRVKTAVAAAAYHAKVAQLQKSHEGNTNNINWTVDV
>tr|I1M8S0|I1M8S0_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MERKQGFFSALKDEVVRGLSPARSRAKSPARSASPMSSLLRRRRKHHAPPPELFIARSGS
LRPAEALSPLKEGPDGTDGGQDSSRGEGRWGQWMKGPLARAPSVSSSSSSCNNKKSDLRL
LLGVLGAPLAPVHVCTTDPFPHLSIKDIPIETSSAQYILQQYIAASGGQKLQNSINNAYA

MGKVRMIASEFETANKVTRSRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGR
LVWRHTPWLGAHAAKGPVRPLRRTLQGLDPRTTASMFINTRCIGEKKINEEDCFILKLCA
DPSTLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGEAVYWETTINSFL
DDYRPVEGIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSVDCFIPP
SELRFASMSEACELPQGQRVKTAVAAAAYHAKVTQLQKSHDSHTNNINWTVDV
>tr|I1MXJ5|I1MXJ5_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MERKQGFFSALKDEVVRGLSPARSRAKSPARSASPMSSLLRRRRKHYAPPPELFIARSGS
LRPAEALSPLKEGPDGTDDGGHDSTRGEGRWGQWMKGPLARAPSVSSSSSSSCNNKKSD
LRLLLGVLGAPLAPVHVCTTDPFPHLSIKDIPIETSSAQYILQQYIAASGGQRLQNSINN
AYAMGKVRMIASEFETANKVTRSRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGC
NGRLVWRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFINARCIGEKKINEEDCFILK
LFADPSTLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGEAVYWETTIN
SFLDDYRPVEGIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSLDCF
IPPSELRFASMSEACELPQGQRVKTAVAAAAYHAKVAQLQKSHGSNTNNINWTVDV
>tr|A0A0K9RBM5|A0A0K9RBM5_SPIOL Uncharacterized protein OS=Spinacia
oleracea GN=SOVF_089300 PE=4 SV=1
MERKQGFFSALKEEVVRGLSPGKSRARSPARSGSAMTGLLRRRKGHRVAIPEVLIARSGS
LRPPEMLSPLREGPDQCGAREERDEGGWAHWMKRNPSISGSSSSSSAAACKRSDLRLLLG
VLGAPLAPVHVSASEPLPHLSIKDTPIETSSAQYILQQYTAASGGLKLQNSIHNAYAMGK
LKMLASDIETPNKVIKNRSSSKSAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGKLVW
RHTPWLGAHAAKGPVRPLRRALQGLDPRTTAAMFANARCIGEKKINGEDCFILKLCADPK
TLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTINSCLDDY
RPVEGIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSIDCFIPPAEI
RYSSVGDSCELPHGDRLKTMSATAAAYRAKVASMDRSYETNTSNMTWQMDNMHV
>tr|M5XF99|M5XF99_PRUPE Uncharacterized protein OS=Prunus persica
GN=PRUPE_ppa005287mg PE=4 SV=1
MERKQGFFSALKEEVVRGLSPGRSRAKSPARSGSPVSSLLRRRRNHHVAPPEPLMIPRSG
SVRPAEALSPLKEGPDGTDGGDSRMEGKWGHWMKGQLCRAPSVSCSAYKRSDLRLLLGVL
GAPLGPVHVSTTEPLPHLSIKDTPIESSSAQYILQQYTAASGGQKLQNSIHNAYAMGKVR
MIASEFETANRVVKNRNSSKAAESGGFVLWQMHPDMWYVELALGGSKVHAGCNGQLVWRH
TPWLGAHAAKGPVRPLRRALQGLDPRTTASMFTNSRCIGEKNINGEECFILKLSTDPLTL
KARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSFLDDYRP
VEGIMIAHSGRSVVTLFRFGETALSHTKTRMEEAWTIEEVAFNVPGLSIDCFIPPAELRF
ASMSETCELPQGQTVNNTMAAAAYRAKVASLERSHQGSVNNVMWKMDA
>tr|B9R732|B9R732_RICCO Putative uncharacterized protein OS=Ricinus
communis GN=RCOM_1588200 PE=4 SV=1
MERKQGFFSALKEEVVRGLSPARTRAKSPARSASPMSSLLRRRKGHGHGHAHHVAHPEPL
IIARSGSLRPAEALSPLKEGPDQDDGGDSRIEGRWGQWMKGQLSRTPSVASSNGCKRSDL
RLLLGVLGAPLAPVHVTTTEPLPHLSIKDTPIETSSAQYILQQFTAASGGQRVQNSIHNA
YAMGKVRMIASEFETANKVTRNRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCN
GKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPKTTASMFTNARCIGEKKINGDDCFILKI
CADPGTLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQNNGGDAVYWETTINS
FLDDYRPVDGVMIAHSGRSVVTLFRFGDTAMSHTRTRMEEAWAIEEVAFNVPGLSMDCFI
PPAELRFASISETCELPQAQRIKPPVAAATYRTKVVALDRSRDNTVSNNM
>tr|A0A0A0L3R4|A0A0A0L3R4_CUCSA Uncharacterized protein OS=Cucumis
sativus GN=Csa_4G642330 PE=4 SV=1
MERKQGFFSALKGEIVRGLSPGRSRAKSPARSASPMSGLLRRRKNHQMSQPELVIERSGS
LRPEEALSPLKEGPDGNESRESKEGKWGSWMRGQLCRAPSAVSCSAQKRSDLRLLLGVLG
APLAPVHVSSTEPQPHLAIKDIPIENSSAQYILQQYTAASGGQKLQNSVSNAYAMGKVKM
IACEFETANKVVRTRNSSKDAESGGFVLWQMKPDMWYVELALGGSKVHAGCNGKLVWRHT
PWLGAHAAKGPVRPLRRALQGLDPKTTASMFANARCIGEKSVNGEDCFILKLCTDPSTLK
ARSEGPAEIIRHTMFGYFSQKSGLLIHLEDSHLTRIQNNGSDAVYWETTINSFLDDYRPV
EGIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSIDCFIPPAELRYA
SMSEACDFSRGQGLKNAMAAAAYRAKVAALEKNPDNKVKVIWKPDI

>tr|A0A022RRM0|A0A022RRM0_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a005994mg PE=4 SV=1
MEKRQGFFTALKEEVVRGLSPSRPRASSPGRSASPMARLLRRKKAASGNHGEPPISRSSS
LRVVGETLTPLMEGPDPDGGEIGGSKRVGSGLGQWVRGQLTRNPSLAVYENGYGGNRTSD
LRLLLGVLGAPLAPAHVSSTDPLPHLSIKDTPIENSSAQYILQQYTAASGGQKVQNSIKN
AYAMGKLKMVASEFETATRVVKNRNADRAVESGSFVLWQKNPDMWYVELAVGGSKVHAGC
NGKLVWRHTPWLGPHTAKGPVRPLRRSLQGLDPRTTASMFANAICIGEKKINGEDCFILK
LSADNKTLKSRSEPPAEIIRHVLFGHFSQKSGLLVHMEDSHLTRIQSNGGDVVYWETTTN
SFLHDYKPVEGVMIAHSGRSIVTLFRFGETAMSHTRTRMEESWSIDEVAFNVPGLSVECF
IPPCDLEDCEFPREEKGKSVISVPGRRARVAVDNVVWKVEI
>tr|A0A0D2U4R9|A0A0D2U4R9_GOSRA Uncharacterized protein OS=Gossypium raimondii GN=B456_010G024300 PE=4 SV=1
MERKQGFFSVVRGLSPSRSRSKSPARSASPMSGLLRRRRNNGSHHVSQPDPLIFRSGSLR
PAEALSPLKEGPDPDGTDAGDSRMEGRWAQWMKGQLARAPSVSTSTCKRSDLRLLLGVLG
APLAPVHVSALDPFPLLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIHNAYAMGRVRM
IASEFETANKVTKNRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGKLVWRHT
PWLGAHAAKGPVRPLRRALQGLDPRTTASMFTNARCIGEKKINGEDCFILKLCADPATLK
ARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQNNGGDAVYWETTINSFLEDYRPV
EGIMIAHSGRSLVTLFRFGDTAMSHTRTRMEEAWAIEEVAFNVPGLSMDCFIPPAEIRLA
SISEACEFSQGPRVKTM
>tr|A0A0B0MG19|A0A0B0MG19_GOSAR Uncharacterized protein OS=Gossypium arboreum GN=F383_18373 PE=4 SV=1
MERKQGFFSVVRGLSPSRSRSKSPARSASPMSGLLRRRRNNVSHHVSQPDPLIFRSGSLR
PAEALSPLKEGPDPDGTDAGESRMEGRWAQWMKGQLARAPSVSTSTCKRSDLRLLLGVLG
APLAPVHVSALDPFPLLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIHNAYAMGRVRM
IASEFETANKVTKNRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNGKLVWRHT
PWLGAHAAKGPVRPLRRALQGLDPRTTASMFTNARCIGEKKINGEDCFILKLCADPATLK
ARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQNNGGDAVYWETTINSFLEDYRPV
EGIMIAHSGRSVVTLFRFGDTAMSHTRTRMEEAWAIEEVAFNVPGLSMDCFIPPAEIRLA
SISEACEFSQGPRVKTM
>tr|A0A022R7X4|A0A022R7X4_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a006034mg PE=4 SV=1
MERKQGFFSALKEEVVRGLSPARSRRGRSQSPSGSGLHRRRRGTSVGPPEMLISRSGSLR
PGAETLSPLREGPDPNGSDSGETKSDGWAHWLCRAPSVSAAAGSGYSRSDLRLLLGVLGA
PLAPVHVSNTDPLPHLSIKDTPIESSSAQYILQQYLAASGGQKLQNSIQNAYAMGKVTML
ASDIETATKVIKNKSSSKSAESGGFVLWQMNPDMWYVELALGGSKVRAGCNGKLVWRHTP
WLGAHAAKGPVRPLRRALQGLDPKTTANMFANARCTGEKKINGEDCFILKLCADPQTLKA
RSEGPAEIIRHVLFGYFSQRTGLLVHLEDSHLTRIQTNGSDAVYWETTINSFMDDYRPVE
GIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNVPGLSVECFIPPGELRFGE
ACELPQENRVKNAVAAAAYRAKVVALGKAHGGSVNSVVPI
>tr|V4V4J6|V4V4J6_9ROSI Uncharacterized protein OS=Citrus clementina GN=CICLE_v10001042mg PE=4 SV=1
MERKQGFFSALKEEVVRGLSPGRSRPKSPARSASPMSSVMRRRRGRSSHHKRVAHPEPFI
MRSGSLRPGEAALSPLKEGPDPDGTDGGDSRMEGRWAHWMRAPSVSGSACKRSDLRLLLG
VLGAPLAPVHVSAAEPLPHLSIKDTPIESSSAQYILQQYTASSGGQKLQNSIHNAYAMGR
VTMIASEFEKGNKVTRSRNSSKGAESGGFVLWQMNPDMWYVELALGDSKVHAGCNGKLVW
RHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFINARCIGEKKINGEDCFILKLCADPS
TLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSFLDDY
RPVEGIMIAHSGRSIVTLFRFGDTAMSHTRTRMEEAWAIDEVAFNVPGLSVDCFIPPAEL
RFDSVGETCEFTQGQRVRSTVGTAADRTRVASLDMSRDIGVNNITWKANG
>tr|A0A022QG72|A0A022QG72_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a005999mg PE=4 SV=1
MERKQGFFSALKDEMVRGLSPGRSRKTRSHSPSGSGLLRRRRGSSLGPPEMFVARSGRVE
ALSPLREGPDPNGSGPGDSRSDKWANWLCRAPSVSTVGQPGPAYSRSDLRLLLGVLGAPL

APVHVSNNEPLPHLSVKDTPIESSSAQYILQQYLAASGGHKLQSSIQNAYAMGKVKMLAS
DIETATKVIKSRNSAKDPELGGFVLWQMNPDMWYVELALGGSKVHAGCNGKLVWRHTPWL
GAHAAKGPVRPLRRALQGLDPRTTANMFAHARCTGEKKINGEDCFILKISTDPRTLKARS
EGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSNEGDTVYWETTINSFLDDYRPVEGI
QIAHSGRSVVTLFRFGETSMSHTKTRMEEVWNIEEVAFNVPGLSIDCFIPPAELRLGSIN
EASELPQEGGRVKNNAAAHRAKVAAALGKSRENNIAVKMNL
>tr|U5FNN9|U5FNN9_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0014s02000g PE=4 SV=1
MERKQGFFSVVRGLSPGRSRAKSPARSASPMSSLLRRRKGHGQHVAKPEPLIIPRSGSLR
PAEALSPLKEGPDQDDGGDSRMEGKWGQWMKGQLSRGGPSSVVSSSSNACNNTSKRSDLR
LLLGVLGAPLAPVHVSTAEPLPHLSIKDTPIETSSAQYILQQYTAASGGQRLQNSIHNAY
AMGKVRMIASEFETANKVTRNRNSSKAAESGGFVLWQMNPDMWYVELALGGSKVHAGCNG
KLVWRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFTNARCIGEKKINGDDCFILKIC
ADPATLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSF
LDDYRLVDGIMIAHSGRSVVTLFRFGDTAMSHTRTRMEEAWAIEEVAFNVPGLSMDCFIP
PAELRFASISETCELPRSQRVKPAVTASTHRAKVAALERSHENATNNMMWKTDV
>tr|M0SNT8|M0SNT8_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MEKKQGLFSALEEVVRGLSPARSRAKSQSPSAALLLLPRRFRPGGEALAPLMEGPDGDAP
EDGGGTRREGWGRWVRGQLSRAPSVTSSPANAAGSSSFRRSDLRLLLGVMGAPLAPMHVS
SADPLPHLSIKETPIETSSAQYILQQYTAASGGLKLQSSIRNAYAMGKVRMVASEFETAT
KVVKNRGGSARAAESGSFVLWQMAPDMWYVELAVGGSKVHAGSNGQLVWRHTPWLGVHAA
KGPVRPLRRALQGLDPLTTASMFANARCIGEKKVNGEDCFILKLCADPQTLKARSEGPAE
IIRHVLFGCFSQRTGLLVHMEDSHLTRIQSNAGGDAVYWETTINSFLDDYRPVEGIMIAH
SGRSVVTLFRFGEVAMSHTKTRMEEAWTIEEVAFNVPGLSADCFIPPADIRRGSVSETCE
LPQGERSKTSIGNRAKVAAVDKPHATAASDRIIWRVEV
>tr|A0A0C9RWX5|A0A0C9RWX5_9SPER TSA: Wollemia nobilis
Ref_Wollemi_Transcript_7749_2288 transcribed RNA sequence OS=Wollemia
nobilis PE=4 SV=1
MEKKHSFFSEVVRGLSPGKSRSNSPNSRSASPLRLLRRNKQHSQPQNDSLIARSGSLRPI
GETLAPLIEGPDPEGFDNEAKKEGWTGLQNWMRGQLTRAPSVAGYRRSDLRLLLGVLGAP
LAPVPVSSDPFPHLSIKDTPIESSSAQYILQQYIAASGGAKFQSSIRNAYAMGKVKMLAC
EYETATKVMKNKNASKAAETGGFVLWQMMPDMWYVELAVGGSKVHAGSNGKLVWRHTPWL
GAHAAKGPVRPLRRALQGLDPKTTASMFADAKCIGEKQINGEDCFILKLCADPSTLKARS
DGPAEIIRHVLFGYFSQRTGLLVLMEDSHLTRIQSTGGDAVYWETTINSFLEDYRPVDGM
MIAHSGRSLVTLFRFGETAMSHTKTRMEEVWTIEEVAFNVPGLSLDCFIPPADIMCGSVS
EACELPQEERGKSMAGSNRNKVAALEKPQEKMDNIIWRVEV
>tr|A0A0D6QVH8|A0A0D6QVH8_ARACU Uncharacterized protein OS=Araucaria
cunninghamii PE=4 SV=1
MEKKHSFFSEVVRGLSPGKSRSNSPNRSASPLRLLRRNKQHSQPQNDSLIARSGSLRPIG
ETLAPLIEGPDPEGFDNEAKKEGWTGLHNWMRGQLTRAPSVAGYRRSDLRLLLGVLGAPL
APVPVSSDPFPHLSIKDTPIESSSAQYILQQYIAASGGAKFQSSIRNAYAMGKVKMLACE
YETATKVMKNKNTSKAAETGGFVLWQMMPDMWYVELAVGGSKVHAGSNGKLVWRHTPWLG
AHAAKGPVRPLRRALQGLDPKTTASMFADAKCIGEKQINGEDCFILKLCADPSTLKARSD
GPAEIIRHVLFGYFSQRTGLLVLMEDSHLTRIQSTGGDAVYWETTINSFLDDYRPVDGMM
IAHSGRSLVTLFRFGETAMSHTKTRMEEVWTIEEVAFNVPGLSLDCFIPPADIMCGSVSE
ACELPQEERGKSMAGSNRNKVAALEKPQEKMDNIIWRVEV
>tr|A0A0E0F7A5|A0A0E0F7A5_9ORYZ Uncharacterized protein OS=Oryza
meridionalis PE=4 SV=1
MDKKQGFFSALREEVARGLSPARARRRSQAAAAAEVAAALRYAGGGGGGEMLAPLMEGPD
PESGDGGRSSSAAAAARREGWGRWVRGQLSRAPSTAGAAVVAAGGGGGGAARRNDLRLLL
GVMGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMG
KVRMVATEFETGGRVVRNRMAARAAESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLV
WRHTPWLGAHSAKGPVRPLRRALQGLDPLTTASMFAGARCIGERKVNGEDCFILKLCADP

ETLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIE
DYRPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPT
DIKSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFK
>tr|Q2QN32|Q2QN32_ORYSJ Lipase, putative, expressed OS=Oryza sativa
subsp. japonica GN=LOC_Os12g39160 PE=4 SV=1
MDKKQGFFSALREEVARGLSPARARRRSQAAAAAEVAAALRYAGGGGGGEMLAPLMEGPD
PESGDGGRSSSSAAAARREGWGRWVRGQLSRAPSTAGAAVVAAGGGGGAARRNDLRLLLG
VMGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGK
VRMVATEFETGGRVVRNRMAARATESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVW
RHTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPE
TLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIED
YRPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTD
IKSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFK
>tr|A2ZM29|A2ZM29_ORYSI Putative uncharacterized protein OS=Oryza sativa
subsp. indica GN=OsI_38888 PE=4 SV=1
MDKKQGFFSALREEVARGLSPARARRRSQAAAAAEVAAALRYAGGGGGGEMLAPLMEGPD
PESGDGGRSSSSAAAARREGWGRWVRGQLSRAPSTAGAAVVAAGGGGGAARRNDLRLLLG
VMGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGK
VRMVATEFETGGRVVRNRMAARATESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVW
RHTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPE
TLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIED
YRPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTD
IKSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFK
>tr|A0A0B2S6M8|A0A0B2S6M8_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_020048 PE=4 SV=1
MKGQLSRAPSVSSYKRSDLRLLLGVMGAPLAPVHVSSTDPLPHLSIKDTPIETSSAQYIL
QQYTAASGGLKLQNSIRNAYAMGKVRMVASEFETATRVVKNRSRCAESGGFVLWQMDPDM
WYVELAVGGSKVHAGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGIDPRTTASMFADAK
CIGEKNINGEDCFILKLCTDPETLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTR
IQSNGGDAVYWETTINSFLSDYKPVEGIMIAHSGHSVVTLFRFGEMAMSHTKTRMEEAWT
IDEVAFNVQGLSVDCFIPPADLRTASVSEACELPQDERAKNSLAVHRAKVVALEKSHNCS
IDSMIWKMEI
>tr|A0A0E0JBJ4|A0A0E0JBJ4_ORYNI Uncharacterized protein OS=Oryza nivara
PE=4 SV=1
MDKKQGFFSALREEVARGLSPARARRRSQAAAAAEVAAALRYAGGGGGGEMLAPLMEGPD
PESGDGGRSSSSAAAARREGWGRWVRGQLSRAPSTAGAAVVAAGGGGGAARRNDLRLLLG
VMGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGK
VRMVATEFETGGRVVRNRMAARATESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVW
RHTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPE
TLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIED
YRPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTD
IKSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFKTRRGVSHPA
PNHMVRDHGGGAVLSLIAILIYRSPARKKGVLSLL
>tr|A0A0E0RJ87|A0A0E0RJ87_ORYRU Uncharacterized protein OS=Oryza
rufipogon PE=4 SV=1
MDKKQGFFSALREEVARGLSPARARRRSQAAAAAEVAAALRYAGGGGGGEMLAPLMEGPD
PESGDGGRSSSSAAAARREGWGRWVRGQLSRAPSTAGAAVVAAGGGGGAARRNDLRLLLG
VMGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGK
VRMVATEFETGGRVVRNRMAARATESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVW
RHTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPE
TLRVRSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIED
YRPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTD
IKSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFKTRRGVSHPA
PNHMVRDHGGGAVLSLIAILIYRSPARKKGVLSLL

>tr|A0A059BC04|A0A059BC04_EUCGR Uncharacterized protein OS=Eucalyptus grandis GN=EUGRSUZ_G01292 PE=4 SV=1
MEGPDPEGDPKRWGGNGGSGLGQWVKGQLGRAPPVSSSSSSSPAESSSASASSGKRSDVR
MLIGVMGAPLAPVHVSVLDPLPHLSVKDTPIETSSAQYILQQYTAASGGLKLQNSIRNAY
ALGKLKMVSSEFESAMKAIKNRSSAHTGGFVLWQMNPDMWYVELAVGGSKVHAGCNGKLV
WRHTPWLGAHTAKGPVRPLRRALQGLDPRTTVSLFSDARCIGEKKLNGEDCFILKLCADP
QTLKARSEGPAEIIRHVLFGYFSQKTGLLVRIEDSHLTRIQMNGGDAAYWETTITSSLDD
YRPVEGIMIAHAGRSVVTVFRFGEMAMSHTKTRMEETWTIEEVAFNIAGLSIDCFIPPAD
LRSGPIGESCELTQDTGGKSMIPQASHRARVAALEKAHDSNVDGVIWKMEV
>tr|I1GSU0|I1GSU0_BRADI Uncharacterized protein OS=Brachypodium distachyon GN=BRADI1G22870 PE=4 SV=1
MEKERKQGFFSALKDEVVRGLSPARSRGKTPARSSSPARMLIPRRRKAPPPSEKQMRQEQ
QQQQYIPEQLIPRSGSLRPGGEALEPLIEGPDADRLAAGDFVGEDSGRRGEGFGQWVRGH
LTRTPSMASAGPGGSSGSFRHSDLRLLLGVMGAPLAPISSNLADPLPLLSIKGTPIESSS
AQYILQQYMAASGGHRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAAAIEQG
GFVLWTMAPGMWYVELAVGGSKVHAGCNGRLVWRHTPWLGAHAAKGPVRPLRRVLQGLDP
LTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKLRSEGPAEIIRHVLFGYFSQRTGL
IVHIEDSHLTRIQPHSGGDAVYWETTISSSLEDYRAVEGIVIAHAGRSAVTLFRFGEAAM
SHTKTRMEEAWSIEEVAFNVPGLSPDCFIPPADIRSGSVGEACELPPTHGGGDRAANKGG
AVHPARVAAVERSSHGHNGAVGVNVGAAAGGRGEKIVWRVQV
>tr|A0A0E0MP13|A0A0E0MP13_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1
MDKKQGFFSALREEVARGLSPARARRRSQAAAAEVAAALRYAGGGGGEMLAPLMEGPDPE
SGDGGRSSTAAARREGWGRWVRGQLARAPSTAGAAVVAAAAGGGGGGGAARRNDLRLLLG
VMGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGK
VRMVATEFETGGRVVRNRMAARAAESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVW
RHTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPE
TLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIED
YRPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTD
IKSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVTWSGALQRDFK
>tr|A0A0E0GQF6|A0A0E0GQF6_ORYNI Uncharacterized protein OS=Oryza nivara PE=4 SV=1
MERRRGGGGGGGFFAALREEVARGLSPARARGRSRSDAAELAAAMRMSGGGGGGGEMLA
PLMEGPDPESGDGEGGGGGGGGGGGGGGGRGARGRRGEGWGQWVRGQLSRTPSSVAAAA
AGAGAARNDLRLLLGVMGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGG
QKLLASVRNAYTMGKVRMVATEFETAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAV
GGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRSLRRALQGLDPLTTASMFAGARCIGERKV
NGEDCFILKLCTEPETLKARSEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGG
DAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAF
NVPGLSMDCFIPPTDIKSGSISETVELSHGEKSKVGPPPGHRAKVAALEKAVDGKVAWSG
TILEDHN
>tr|A0A0D9Y0V8|A0A0D9Y0V8_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1
MDNTTTKKQGFFSALRDEVARGLSPARSRRRSASSAAAAADVAAAMRYAGAGGEMLAPLM
EGPDPDSSDGGGGGGGGGRAVSAARREGWGRWVRGQLVRAPSTAVVAAAGTRRNDLRLLL
GVMGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMG
KVRMVATEFETGGRVVRNRMAARTAESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLV
WRHTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADP
ETLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIE
DYRPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPT
DIKSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQREFK
>tr|S8EB24|S8EB24_9LAMI Uncharacterized protein OS=Genlisea aurea GN=M569_05011 PE=4 SV=1
MRDRAGGSCAEIFAGGYMMERRQGGFFSEVVRGLSPARTRGKSPGRSVSPMSGLLRRRKV

NSDSAQVGRSGSMRPLGETLAPLIEGPDPDGDEIGEARGVGSAIGNWVMGQLTRTPSIVV
NDNGVSSRRRSDLRLLLGVMGAPLAPVHVSTSDPLPHLSIKNTPIENSSAQYILQQYTAA
SGGQRVQNSVKNAYAMGKLRMVGSEFESAAKLGKNNRTAARSAESGGFVLWQMNPDMWYV
ELAVGGSKVHAGCNGKLVWRHTPWLGAHSARGPVRPLRRALQGLDPRTTASMFGDSICIG
EKSINGEDCFILKLAADPATLKARSEGPAEIIRHVLFGYFSQKTGHLVHIEDSHLTRIQS
NGGEAVYWETTINSYLEDYRPVDGIMIAHSGRSVVTLFRFGEIAMSHSKTRMEEAWTIEE
VAFNIPGLSIDCFIPPADLRSGSSLAELPPPVSSSSSAIGRARIAALENDRSNSMDSVVW
KVEL
>tr|A0A0D2Q5N4|A0A0D2Q5N4_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_002G132800 PE=4 SV=1
MERKQESRSRAKSPARTASPMSNLLRRRRKNYSHHPEPFFFRSGGLRPAEALSPLKEGPD
PDGTDAENSRMEGRWAQWMKGQLARGGPSVSTSTCKRSDLRLLLGVLGAPLAPVHVSALD
SFSHLTIKDTPIESSSAQYILQQYTAASGGQKLQNSIHNAYAMGRVRMIASEFQTANKVT
KNRNSTKVAESGGFVLWQMNPDMWYVELALGASKVHAGCNGKLVWRHTPWLGAHATRGPV
RPLRRALQGLDPRTTASMFTNARCSGEKQINGEDCFILKLCADPATLKARSEGPAEIVRH
VLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTIDSSLEDYRLVEGIMIAHSGRSV
VTLFRFGDTAMSHTRTRMEEAWAIEEVAFNVPGLSAECFIPPDEIRLASMDEACEFSQGP
TLKTSLATAPYRPKVGKLDKSS
>tr|A0A0E0NY35|A0A0E0NY35_ORYRU Uncharacterized protein OS=Oryza
rufipogon PE=4 SV=1
MERRGGGGGGGGFFAALREEVARGLSPARARGRSRSDAAELAAAMRMSGGGGGGGEMLAP
LMEGPDPESGDGEGGGGGGGGGGGGGGGGRGARGRRGEGWGQWVRGQLSRTPSSVAAAAA
GAGAARDDPKLLLGVMGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQ
KLLASVRNAYTMGKVRMVATEFETAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAVG
GSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTTASMFAGARCIGERKVN
GEDCFILKLCTEPETLKARSEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGD
AVYWETTINSFIADYRPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFN
VPGLSMDCFIPPTDIKSGSISETVELSHGEKSKVGPPPGHRAKVAALEKAVDGKVAWSGT
ILEDHN
>tr|A0A0K9PFZ1|A0A0K9PFZ1_ZOSMR Uncharacterized protein OS=Zostera marina
GN=ZOSMA_278G00010 PE=4 SV=1
MERKQGFFSTLKEEVMRGLSPARSRTRAEGRCVSPMVGLLRRGSRRKTNNNQLHFEYSDN
QFIPRSGSLRPVGEALAPLMEGPVESDGLVEDGRKDGWGKWVKGQLSRAPSVSAVSVEGS
YRKSDLRLLLGVMGAPLAPIHVFSMDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQ
SSIRNAYAMGKVKMFASEFETATKVMKNRNSVREAESGGFVLWQMNPDMWYVELSVGGCK
VHAGCNGKLVWRHTPWLGVHSAKGPVRPLRRALQGLDPRTTASMFSNARCIGEKKINGED
CFILKLRADAQTLKSRSEGPAEIIRHVLSGYFSQRTGLLVEMEDSHLTRIQLNSGGDAVY
WDTSIKSYMEDYRSVDGIMIAHSGRSVVTLFRFGEVAMSQTKTRMEEVWSITEVAFNVPG
LSMDCFIPPADIRSCEPPPASLILK
>tr|A0A0B0PXL5|A0A0B0PXL5_GOSAR Glutamyl-tRNA (Gln) amidotransferase
subunit A OS=Gossypium arboreum GN=F383_14641 PE=4 SV=1
MEKKQGFLSALKEDIVRGLSPFRSRSNSPARPLSLMSTTLRGNKDNHHGGAHVVQLEPLR
ARSGSERPVGETLSPLMEGPEPDREKSGDPKWVGSVIGQWVKGQLCTSTNHRRSNLRLLL
GIMGAPLAPVHVSSNDPLPHLSIKDTPIETSSAHYILQQYIAATGVQKLQSSIKNAYAMG
KLKMVACEYEIATRIVKSCNVSRSAESGWFVLWQMNPAMWYVELAVSGFKVHAGCNGNLV
WRHTPWLGAHTAKGPVRPLRRALQGLDPRTTAIMFANARCIGEKNINGEDCFILKLCADP
RTLKARSEGPAEIIRHVLFGYFSQKTGLLVQMEDSHLTRVQSTGGDTVYWETTINTFLED
YHPVEGIVIAHSGHTVVTLFRFGEVAMNHTKTKMEETWTIEEVAFNIPGLSVDCFIPPSD
LSITETLEFPQDERGESAIRLRRSAERRH
>tr|I1IH44|I1IH44_BRADI Uncharacterized protein OS=Brachypodium
distachyon GN=BRADI4G03500 PE=4 SV=1
MDSSGGNRKQGFFSALRDEVARGLSPARARRRSAEAAAAAAAALRYAGGGGGEVLAPLMEG
PDPEESSGGGGGGGGDGGFGRGRKGDGWGRWVRGQLARAPSAGALAVGTGGGGGAARRSD
LRMLLGVMGAALAPVHVCAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRN

AYAMGKVRMVATECETAGRVVKNRMAARCAEPGRFVLWQMAPEMWYIELALGGSKVHAGC
NGKLVWRHTPWLGAHSAKGPVRPLRRALQGLDPLTTASMFAGARCIGERKVNGEDCFILK
LCADPETLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTI
SSFIEDYRPVEGIMIAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDC
FIPPTDIKSGSISETVELPHGGKSKVGLLTCHGVKVAALEKADDNVAWSGALQRDCK
>tr|F2D472|F2D472_HORVD Predicted protein OS=Hordeum vulgare var.
distichum PE=2 SV=1
MDKKQGFFSALRGEVARGLSPARARRRAEEAAAAKAALRYAGGGGGGEALAPLMEGPDPE
EAGAGRARRDGWGRWVRGQLARAPSSGPVASAAGAGAARRNDLRMLLGVMGAALAPVHVC
AAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGKVRMVATECETAG
RVVRNRMGARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHSAK
GPVRPLRRSLQGLDPLTTASMFAGARCIGERKVNGDDCFILKLCADPETLRARSEGLAEI
IRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHS
GRSAVTLFRFGEVAMNHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSISETVEL
PQSGKSKAGGLLPCHGAKVAALEKADDNVAWSGTLQRDCK
>tr|A0A059BKS2|A0A059BKS2_EUCGR Uncharacterized protein OS=Eucalyptus
grandis GN=EUGRSUZ_F00130 PE=4 SV=1
MERRAGFFSSLKSEVVRGLSPARSRPRAKSLSPPPPARAGSESPKSRSPSHRSRRSRRAR
RRPEAWVARHAEALSPLEEGPDPDGAEGLGARMEGRWGQWMKGQRQHSVSSSSSSSSGG
RDKGSHLRLLLGVLGAPLAPVHVNAGEPLPYLSVKDTPIETSSAHYILQQYAAASGAQKL
HSAINNAYAMGKLRMIASEFETANKGARSKNSCKAAESGRFVLWQMNPDMWYVELALGGS
KVHAGCNGKLVWRHTPWLGPHAAKGPVRPLRRALQGLDPKTTASMFAHARCVGEKKINGE
DCFVLKLCADPTTLKARCEGPTEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDPVY
WETTINSFLDDYRPVEGIMIAHSGRSVATLFRFGETARSQTKTRMEEAWTIEEVAFNVPG
LSVDCFIPPAELRFASLDKTCELPRVPWVRNVVPAARARVAAPEKSSEL
>tr|K3Z623|K3Z623_SETIT Uncharacterized protein OS=Setaria italica
GN=Si021991m.g PE=4 SV=1
MDTKKQGFFSALREEVARGLSPARARRRSASNAAEVAAALRVAGGAGEALAPLMEGPDPE
AGPGAGGGGVRREGWGRWVRGQLQLARAPAPAGADAGAARRNDLRLLLGVMGAPLAPVHV
CAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQRLLSSIRNAYAMGKVRMVATEFETG
GRVVRNRMAAQRAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHAA
KGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPEMLRARSEGLAE
IIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAH
SGRSAVTLFRFGEAAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSVSETVE
LPQGEKSKVGLLPCHRAKVAALEKADDNVAWSGALQLDCK
>tr|I1GQC7|I1GQC7_BRADI Uncharacterized protein OS=Brachypodium
distachyon GN=BRADI1G14850 PE=4 SV=1
MERRQGFFAALRQEVSRGLSPARARRRSEAAELDAALRSSAAPGGGEMLAPLMEGPDPES
GDGDGGGAGGASARKEGWGQWVRGQLARTPSSVAAAAAAGAGAARNDLRLLLGVMGAPLA
PVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLASVRNTYVMGKVRMVATE
FENAGRLVKNRNAARGAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLG
SHAAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVSGEDCFILKLCTDPETLKARTE
GLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTTNSFIEDYRPVDGI
MIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSVG
ETVELSHGEKSKFGPPPGHRAKVAALEKADDRD
>tr|A0A096T3K7|A0A096T3K7_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.56627 PE=4 SV=1
MDKERKQGFFAALKEEVVRGLSPSRSRGKSPAPPRSASPARMLIPRRRKAPAAPPPPPPE
KVLEQYLGEQLVARSGSLRPGGEALAPLIEGPDAERLAAGDPDAEDSGRREGFGHWVRGH
LTRTPSMASSAAGGGGGPGGSSGSFRRSDLRLLLGVMGAPLAPIPSKTAEPLPLLSIKGT
PIESSSAQYILHQYTAASGGYKLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGA
AAVEQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRV
LQGLDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKLRSEGPAEIIRHVLFGYF
SQRTGLMVQMEDSHLTRIQPHAGGDAVYWETTISSALEDYRAVEGVMVAHAGRSAVTLFR

FGEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGSVGEACELPSQPHGERA
RTGAAVHPSRVAAVERAGTAAGAGGRGEKKVMWRVQV
>tr|F2DM19|F2DM19_HORVD Predicted protein OS=Hordeum vulgare var.
distichum PE=2 SV=1
MERTQGFFAALKQEVARGLSPARARRRSAEAADLDAALRFSGPGAGGEMLAPLMEGPDPE
SGDGDARGAGGARREGWGRWVRGQLARTPSSVAAAAAGAGAARNDLRLLLGVMGAPLAPV
HVCAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGHKLLASVRNSYAMGKVRMVATEFE
NAGRLVKNRNAARCAEPGRFVLWQMAPEKWYIELAVGGSKVHAGCNGKLVWRHTPWLGSH
AAKGPARPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCTDPETLKARTEGL
AEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVDGIMI
AHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSVSET
VELPHGEKNKFGPPHGHRAKVAALEKTDGDELAWRGTRT
>tr|C5XD51|C5XD51_SORBI Putative uncharacterized protein Sb02g038090
OS=Sorghum bicolor GN=Sb02g038090 PE=4 SV=1
MEKERKQGFFATLKEEVVRGLSPARSRGKSPAPPRSASPARMLIPRRRKAPAAPPPPPPE
KVLQQYLGEQLVSRSGSLRPGGEALAPLIEGPDAERLAAGDPDAEDSGRREGFGHWVRGH
LTRTPSMASSAAAGGGGPGGSSGSFRRSDLRLLLGVMGAPLAPMSSKPAEPLPLLSIKGT
PIESSSAQYILHQYTAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGA
AAVEQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRV
LQGLDPLTTAGLFAEARCVGEKKVNGEDCFILKLTADPQTLKLRSEGPAEIIRHVLFGYF
SQRTGLIVHIEDSHLTRIQPHAGGDAVYWETTISSALEDYRAVEGIMIAHSGRSAVTLFR
FGEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGSVGEACELPSQSQSHGE
RAKTGAVHPSRVAAVERAHAHSANAGAGAAGRGEKIMWRVEV
>tr|B6U0X7|B6U0X7_MAIZE Putative uncharacterized protein OS=Zea mays PE=2
SV=1
MDKERKQGFFAALKEEVVRGLSPSRSRGKSPAPPRSASPARMLIPRRRKAPAAPPPPPPE
KVLEQYLGEQLVARSGSLRPGGEALAPLIEGPDAERLAAGDPDAEDSGRREGFGHWVRGH
LTRTPSMASSAAGGGGPGGSSGSFRRSDLRLLLGVMGAPLAPIPSKTAEPLPLLSIKGTP
IESSSAQYILHQYTAASGGYKLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAA
AVEQGGFVLWQMAPDMWYVELAVGGSKVHAXSNGRLVWRHTPWLGAHAAKGPVRPLRRVL
QGLDPLTTAGLFAEARCVGENKVNGEDCFILKLSADPQTLKLRSEGPAEIIRHVLFGYFS
QRTGLMVQMEDSHLTRIQPHAGGDAVYWETTISSALEDYRAVEGVMVAHSGRSAVTLFRF
GEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGSVGEACELPSQPHGERAR
TGAAVHPSRVAAVERAGTAAGAGGRGEKVMWRVQV
>tr|K3ZSC2|K3ZSC2_SETIT Uncharacterized protein OS=Setaria italica
GN=Si029502m.g PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPAPPRSASPARMLIPRRRKSAAPPQPPPEK
VLQQYLGEQLIARSGSLRPGGEALAPLIEGPDAERLAAGDPDAEDSGRREGFGNWVRGHL
TRTPSMASAAAGPGGSGASFRRSDLRLLLGVMGAPLAPIPSKLAEPLPLLSIKGTPIESS
SAQYILHQYTAASGGYKLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPTGRGAAAVEQ
GGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQGLD
PLTTAGLFAEARCVGEKKVNGEDCFILKLTADPQTLKLRSEGPAEIIRHVLFGYFSQRTG
LIVQIEDSHLTRIQPHAGGDAVYWETTISSALEDYRPVEGVMIAHSGRSAVTLFRFGEAA
MSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGSVGEACELPSQSHGERARAGAV
HPSRVAAVERAHAHYPHSANAGAAGAGGRGEKVMWRVEV
>tr|F2CVL2|F2CVL2_HORVD Predicted protein OS=Hordeum vulgare var.
distichum PE=2 SV=1
MDKERKQGFFAALKEEVVRGLSPARSRGKTPARSASPARMLIPRRRKAQPPPPDKQQQQQ
YLPEQLIPRSGSLRPGGEVLEPLIEGPDADRLAAGDFVGEDSGRREGFGHWVRGHLTRTP
SMASASAGPGGSSGSFRHSDLRLLLGVMGAPLAPISSNLADPLPLLSIKGTPIESSSAQY
ILQQYMAASGGYKMLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGTAAVEQGGFV
LWTMAPGMWYVELAVGGSKVHAGCNGRLVWRHTPWLGAHAAKGPVRPLRRVLQGLDPLTT
AGLFAEARCVGEKKVNGEDCFILKLSADPQTLKLRSEGPAEIIRHVLFGYFSQRTGLIVH
IEDSHLTRIQPHSGGDAVYWETTISSCLEDYRAVEGIVIAHAGRSAVTLFRFGEAAMSHT

KTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGSVGEACELPPHGDRAKSIAVHPARVA
AAAERAHAHGGAGAGGRGEKIVWRVEV
>tr|K4A9G8|K4A9G8_SETIT Uncharacterized protein OS=Setaria italica
GN=Si035524m.g PE=4 SV=1
MERRQGFFAALREEVARGLSPARARRKSEAADLAAAFRFAGGGGGGGEMLAPLMEGPDPE
SGDGEGCGGGGGRGARGRKEGWGHWVRGQLARAPSSVAAAAAGAGATRNDLRMLLGVMGA
PLAPVQVCTAEPLPHLSVKDTPLETSSAHYILQQYLAASGGHKLLASVRNAYTMGKVRMV
ATEHETAGRLTKNRNAGRGGEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTP
WLGAHAAKGPVRQLRRTLQGLDPLITASMFAGARCIGEKKVNGEDCFILKLSTDAETLKA
RSEGFAEMIRHVMFGYFSQRTGLLVHIEDSHLTRIQSNTGGDAIYWETTISSFMEDYRPV
DGIMIAHSGRSVVTLFRFGEVAMSHTKTRMEEVWSIEEVAFNVPGLSMDCFIPPTDIKSG
SVDETMELTNGERSRAGPPPGHRAKVAALEKAEEDKVAWGGGTILENHN
>tr|M0Z486|M0Z486_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MDKERKQGFFAALKEEVVRGLSPARSRGKTPARSASPARMLIPRRRKAQPPPPDKQQQQQ
YLPEQLIPRSGSLRPGGEVLEPLIEGPDADRLAAGDFVGEDSGRREGFGHWVRGHLTRTP
SMASASAGPGGSSGSFRHSDLRLLLGVMGAPLAPISSNLADPLPLLSIKGTPIESSSAQY
ILQQYMAASGGYKMLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGTAAVEQGGFV
LWTMAPGMWYVELAVGGSKVHAGCNGRLVWRHTPWLGAHAAKGPVRPLRRVLQGLDPLTT
AGLFAEARCVGEKKVNGEDCFILKLSADPQTLKLRSEGPAEIIRHVLFGYFSQRTGLIVH
IEDSHLTRIQPHSGGDAVYWETTISSCLEDYRAVEGIVIAHAGRSAVTLFRFGEAAMSHT
KTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGSVGEACELPPHGDRAKSIAVH
>tr|A0A0D3GT12|A0A0D3GT12_9ORYZ Uncharacterized protein OS=Oryza barthii
PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQQQPPPEKLLQ
QYFAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGGDFAGGEESARREGFGRWVRGQLA
RTPSVASSAAAAASPGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTPIE
SSSAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAASV
EQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQG
LDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQR
TGLIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRFGE
AAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAPHGERA
RHPARVAAVDRAPPHHNAGGANVGRRGDKIMWRVEV
>tr|A2YN86|A2YN86_ORYSI Putative uncharacterized protein OS=Oryza sativa
subsp. indica GN=OsI_26696 PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQQQPPPEKLLQ
QYFAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGGDFAGGEESARREGFGRWVRGQLA
RTPSVASSAAAAASPGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTPIE
SSSAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAASV
EQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQG
LDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQR
TGLIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRFGE
AAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAPHGERA
RHPARVAAVDRAPPHHNAGGANVGRRGDKIMWRVEV
>tr|A0A0E0I329|A0A0E0I329_ORYNI Uncharacterized protein OS=Oryza nivara
PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQQQPPPEKLLQ
QYFAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGGDFAGGEESARREGFGRWVRGQLA
RTPSVASSAAAAASPGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTPIE
SSSAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAASV
EQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQG
LDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQR
TGLIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRFGE
AAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAPHGERA

RHPARVAAVDRAPPHHNAGGANVGRRGDKIMWRVEV
>tr|A0A0E0QAL9|A0A0E0QAL9_ORYRU Uncharacterized protein OS=Oryza
rufipogon PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQQQPPPEKLLQ
QYFAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGGDFAGGEESARREGFGRWVRGQLA
RTPSVASSAAAAASPGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTPIE
SSSAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAASV
EQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQG
LDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQR
TGLIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRFGE
AAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAPHGERA
RHPARVAAVDRAPPHHNAGGANVGRRGDKIMWRVEV
>tr|I1QBU5|I1QBU5_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4
SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQQQPPPEKLLQ
QYFAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGGDFAGGEESARREGFGRWVRGQLA
RTPSVASSAAAAASPGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTPIE
SSSAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAASV
EQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQG
LDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQR
TGLIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRFGE
AAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAPHGERA
RHPARVAAVDRAPPHHNAGGANVGRRGDKIMWRVEV
>tr|A0A0E0AM43|A0A0E0AM43_9ORYZ Uncharacterized protein OS=Oryza
glumipatula PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQQQPPPEKLLQ
QYFAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGGDFAGGEESARREGFGRWVRGQLA
RTPSVASSAAAAASPGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTPIE
SSSAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAASV
EQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQG
LDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQR
TGLIVHIEDSHLTRIQPHSGGDAIYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRFGE
AAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAPHGERA
RHPARVAAVDRAPPHHNAGGANVGRRGDKIMWRVEV
>tr|A0A0D9X114|A0A0D9X114_9ORYZ Uncharacterized protein OS=Leersia
perrieri PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPAARSASPGRMLIPRRRKEKQPPPEKLLQQ
YFAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGGDFAGGEESTRREGFGRWVRGQLAR
TPSVASSGSGAAAAAGGGGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGT
PIESSSAQYILQQYMAASGGHRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPTGRGA
ASVEHGGFVLWQMSPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRV
LQGLDPLTTAGLFAEARCVGEKKVNGEDCFILKLSGDAQTLKQRSEGPAEIIRHVLFGYF
SQRTGLIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRAVEGIMIAHAGRSAVTLFR
FGEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGEACELPPPAAQPHG
ERPRHPARVAAVERAPSHHHNGGGGGGNVGRRGGEKIVWRVEV
>tr|A0A0E0LMW4|A0A0E0LMW4_ORYPU Uncharacterized protein OS=Oryza punctata
PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQPPPEKLLQQY
FAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGDFAGGEESARREGFGRWVRGQLARTP
SVASSAAAAAAGPGGSSDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTPIESS
SAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAASVEQ
GGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQGLD
PLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQRTG
LIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRFGEAA

MSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAPHGERARPG
AMHPARVAAVDRAPPHHNAGANVGRRGEKIMWRVEV
>tr|Q6ZLH2|Q6ZLH2_ORYSJ Lipase-like protein OS=Oryza sativa subsp.
japonica GN=OJ1174_G05.24 PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQQQPPPEKLLQ
QYFAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGGDFAGGEESARREGFGRWVRGQLA
RTPSVASSAAAAAAASPGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTP
IESSSAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAA
SVEQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVL
QGLDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFS
QRTGLIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRF
GEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAPHGE
RARHPARVAAVDRAPPHHNAGGANVGRRGDKIMWRVEV
>tr|A0A0B2SJU1|A0A0B2SJU1_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_047920 PE=4 SV=1
MERKQGFFSALKDEVVRGLSPARSEPTSSHDSTCGEGRWGQWMKGPLARAPSVSSSSSSS
SCNNKKSDLRLLLGVLGAPLAPVHVCTTDPFPHLSIKDIPIETSSAQYILQQYIAASGGQ
RLQNSINNAYAMGKVRMIASEFETANKVTRSRNSSKAAESGGFVLWQMNPDMWYVELALG
GSKVHAGCNGRLVWRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFINARCIGEKKIN
EEDCFILKLFADPSTLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGEA
VYWETTINSFLDDYRPVEGIMIAHSGRSVVTLFRFGETAMSHTKTRMEEAWTIEEVAFNV
PGLSLDCFIPPSELRFASMSEACELPQGQRVKTAVAAAAYHAKVAQLQKSHGSNTNNINW
TVDV
>tr|M0T7N0|M0T7N0_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MEKKQGFFSALREEVVRGLSPARSRSREKSTGSGRSPAAEAPALSVSFRETLAPLMEGPD
GGGSGDDDGAPTKEGWGRWVKGQLSRAPSVTSSSAGGASSSFRRSDLRLLLGVMGAPLAP
LHVSCVDPLPHLSIKNTPIETSSAQYILQQYTAASGGLKLQRSIRNAYAMGKVRMVASEF
ETATKVVKNRGGSSRTAESGGFVLWQMTPDMWYVELAVGGSKVHAGSNGKVVWRHTPWLG
AHAARGPVRPLRRALQGLDPLTTASMFADARCIGEKKVNGEDCFILKLCADPQTLKARSE
GPAEIIRHVLIQATAGGDAVYWETTINSFLDDYRPVEGIMIAHSGRSDVTLFRFGEAAMS
HTKTRMEEVWTIEEVAFNVPGLSMDCFIPPADVRCVSIGETCELAQGERGKTTTGVAHRA
KVAAVEKPQDMRDRIVWRLQV
>tr|A0A0E0EDV2|A0A0E0EDV2_9ORYZ Uncharacterized protein OS=Oryza
meridionalis PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLIPRRRKEKQQQPPPEKLLQ
QYFAEPLISRSGSLRPGGEALAPLIEGPDPERLATGGDFAGGEESARREGFGRWVRGQLA
RTPSVASSAAASAGGGPGGSGDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSIKGTP
IESSSAQYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAA
SVEQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVL
QGLDPLTTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFS
QRTGLIVHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRF
GEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAAPHG
XARQAPGARRRRGGPRASPPQCRRRQRRPPRREDHVESGSVTARLLVLLFTY
>tr|Q0DQD9|Q0DQD9_ORYSJ Os03g0606100 protein OS=Oryza sativa subsp.
japonica GN=Os03g0606100 PE=4 SV=1
MKDKEETKFINIECLTHTHYTLLEGILHSAEMQKNFIYKERLPRQEGWLQIPEDETISLF
PDVPSSQEEDLQKTILIELPSCKSYPLVKFKISIPRDSRNCQQAVWTVKEKMISGFPLLC
ERELSKQIQDYSRAASLSVHPMERRRGGGGGGGGFFAALREEVARGLSPARARGRSRSDA
AELAAAMRMSGGGGGGGEMLAPLMEGPDPESGDGEGGGGGGGGGGGGGGGRGARGRRGE
GWGQWVRGQLSRTPSSVAAAAAGAGAARNDLRLLLGVMGAPLAPVHVSAAEPLPHLSIKD
TPIETSSAQYILQQYLAASGGQKLLASVRNAYTMGKVRMVATEFETAGRLVKNRNAARCA
EPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQG
LDPLTTASMFAGARCIGERKVNGEDCFILKLCTEPETLKARSEGLAEIIRHVMFGYFSQR

TGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGE
VAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSISETVELSHGEKSKLTDFD
ECSVGDKQVEGGFGVCRTKCPLCTGSTMRSTAGQRKEPDLSRRGDEIEEGGARGDLPWRH
GSDQCFLCAWTNLEFLRSSSVKPAVILVMMAPVTAKPVRKGQQRFHSLRKNTGHGSKRLK
NILDLLLFLLLRGGLGVVGGSRGPFAFFSIRRGKKRMVVVVIASRLGLGRGAAAWRWASP
LLHVGQILVGLE
>tr|K4A945|K4A945_SETIT Uncharacterized protein OS=Setaria italica
GN=Si035401m.g PE=4 SV=1
MEKERRQGFFSALKGEVVRGLSPARSRGKSLLPRTRKTAAAAAEAPTPEELAQYAPEQFV
AHSGSLRPGGEVLAPLMEGPEVSEDDAFGEESGRRDGFGQWVRGHLARAPLMAGGGDGGS
GSFRRSDLRLLLGVMGAPLAPVSASAAEPLPHLSVKGAPIESSSAQYILQQYLAASGGAK
VLRSVRNAYAMGKVRMVASEFETATRVVKNRGSGAAASAVEQGGFVLWQMSPDMWYVELA
VGGSKVRAGCNGRLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLSTARLFAEARCVGERK
VAGEDCFILKLSADAETLRQRSEGPAEIIRHVLFGYFSQRTGLLAQLEDSHLTRIQPHAG
GDAVYWETTISSFLEDYRAVDGVAIAHAGRSAVTLFRFGETAMSHTKTRMEEAWTIQEAA
FNVPGLSTDCFIPPADIRRGSAGEPHCELPPRGGKAGAVHPARVAAAERAHPRRDAVAGD
RIHWTVEM
>tr|M0TKX1|M0TKX1_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MEKKQGFFSALEGVVRGLSPARGGGHQQQALAQVPEAPVIARSASFRPLSRAPSVTHSSS
SSSASAAANGSCSFRGSDLRLLLGVMGAPLAPIHVGTADPLPHLSIKDTPIETSSAQYIL
QQYTAASGGLKLHSSIRNAYAMGKVRMVASEFETATKVVKNRGGSTRAAESGSFVLWQMA
PDMWYVELAVGGSKVHAGSNGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTTASMFA
SARCIGEKKVNGEDCFILKLCADPQTLRARSEGPAEIIRHVLFGYFSQRTGLMVHMEDSH
LTRIQPNAGGDAVYWETTINSFLDDYRPVEGIMIAHSGRSVVTLFRFGEEAMSHTKTRME
EAWTIEEVAFNVPGLSVDCFIPPAEIRCGSIGGTCEMPQAERSRASIGNRVKVAAEKRQA
AGDNKIVWRLEVPQRKQGGDRIVHTASFCAKERE REASFFFLLQALLPFPVTLDHHHLSC
>tr|I1PDC8|I1PDC8_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4
SV=1
MRMSGGGGGGGEMLAPLMEGPDPESGDGEGGGGGGGGGGGGGGRGARGRRGEGWGQWV
RGQLSRTPSSVAAAAAGAGAARNDLRLLLGVMGAPLAPVHVSAAEPLPHLSIKDTPIETS
SAQYILQQYLAASGGQKLLASVRNAYTMGKVRMVATEFETAGRLVKNRNAARCAEPGRFV
LWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTT
ASMFAGARCIGERKVNGEDCFILKLCTEPETLKARSEGLAEIIRHVMFGYFSQRTGLLVH
IEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMSHT
KTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSISETVELSHGEKSKVGPPPGHRAKV
AALEKAVDGKVAWSGTILEDHN
>tr|Q75I37|Q75I37_ORYSJ Lipase, putative, expressed OS=Oryza sativa
subsp. japonica GN=Os03g40930 PE=4 SV=1
MRMSGGGGGGGEMLAPLMEGPDPESGDGEGGGGGGGGGGGGGGRGARGRRGEGWGQWV
RGQLSRTPSSVAAAAAGAGAARNDLRLLLGVMGAPLAPVHVSAAEPLPHLSIKDTPIETS
SAQYILQQYLAASGGQKLLASVRNAYTMGKVRMVATEFETAGRLVKNRNAARCAEPGRFV
LWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTT
ASMFAGARCIGERKVNGEDCFILKLCTEPETLKARSEGLAEIIRHVMFGYFSQRTGLLVH
IEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMSHT
KTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSISETVELSHGEKSKVGPPPGHRAKV
AALEKAVDGKVAWSGTILEDHN
>tr|C5WT66|C5WT66_SORBI Putative uncharacterized protein Sb01g014910
OS=Sorghum bicolor GN=Sb01g014910 PE=4 SV=1
MERRHGFFAALREEVARGLSPARARRKSEAADLAAAALRFAGVVGGGEMLAPLMEGPDPE
PSDGESGGACRGAARGRKEGWGHWVRGQFARAPSSAVAAAGAGALRNDLRMLLGVLGAPL
APVHVCATEPLPHLSVKDTPIETSSAQYILQQYLAASGGHKLLASLRNSYAMGKVRMVAT
EFETGGRLTKNRNAGRGGEPGRFVLWQMAPEMWYIELVVGGSKVHAGCNGKLVWRHTPWL
GAHSATGPVRPLRRSLQGLDPLMTASMFARARCIGERKVNGEDCFILKLSTDTETLKARS

EGHAEIIRHVTFGYFSQRTGLLAHIEDSHLTRIQSAAGGDAVYWETTISSFMEDYRPVDG
IMIAHSGRSAVTLFRFGEVAMSHTKTRMEEVWSIEEVAFNVPGLSMDCFIPPTDIKSGSV
GEAMELTHGERSRAGPPQGYCAKVAALEKAEEDKVAWGGGTVLESHN
>tr|C0PGR0|C0PGR0_MAIZE Uncharacterized protein OS=Zea mays
GN=LOC100383524 PE=2 SV=1
MEKERKQGFFAALKEEVVRGLSPARTRGKSPAPRSASPARMLIPRRRKAPAAPPPPPPPP
EKVLQQYLGEQLVARSGSLLRPGGEALAPLIEGPDAERLAAGDPDEEDSGHREGFGHWVR
GHLTRAPSMAAAGGPDGSFRRSDLRLLLGVMGAPLAPIPSKPAEPLPLLSIKGTTIESSS
AQYILHQYTAASGGYKLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAAAVEQG
GFVLWQMARDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQGLDP
LTTAGLFAEARCVGEKKVNGEECFILKLAADPRTLKLRSEGPAEIIRHVLFGYFSQRTGL
MVHIEDSHLTRIQPHAGGDAVYWETTTSSALEDYRAVEGVMVAHSGRSAVTLFRFGEAAM
SHTKTRMEEAWSIEEVAFNVPGLSADCFIPPADIQSGPVGEACELPSSQSRAKAVAVHPS
RVAAVDRATAAAACRGRKTTWRVEV
>tr|A0A096SK41|A0A096SK41_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.39486 PE=4 SV=1
MERRHGFFAALREEVARGLSPARARRKPDATDLAAALSFTGVAGAGEMLAPLMEGPDPEP
SDDGDGSGRRGAARGRKEGWGHWVRVQFARAPSSAVALRSDIRMLLGVMAAPLAPVRVCA
AEPLPHLSVKDTPIETSSAQYILQQYLAASGGHKLLASLRSTYAMGKVRMVATEFETAGR
LTKNRSAGRGGEPGRFVLWQMAPEMWYIELAVRGSKVHAGCNGKLVWRHTPWLGAHSAKG
PVRPLRRALQGLDPLTAASMFARARCIGERKVNGEDCFILKLSTDPEILKARSEGHAEII
RHVTFGYFSQRTGLLVHIEDSHLTRIQSAAGGDAVYWETTISSSMEDYRPVDGIVVAHSG
RSAVTLFRFGEVAMSHTKTRMEEVWSIEEVAFNVPGLSMDCFIPPTDIKSGSVGEAMELA
HGERSRAGPPPPPPGCRAKVAALGKAEEGKVAWGGGTVLENQN
>tr|C5WVN3|C5WVN3_SORBI Putative uncharacterized protein Sb01g032010
OS=Sorghum bicolor GN=Sb01g032010 PE=4 SV=1
MDKERKQGFFSALKGEVVRGLSPARSRGKSRLLPRSRKTAAAAESVAVAAAPPPEEELAQ
YAPDPLVAHSGSLRPAGEVLAPLMEGPDVADDDAFAEESGRRDGFGQWVRGHLTRAPLMS
GGGAGDGSFRRSDLRLLLGVMGAPLAPVSVSAAEPHLSVKGAPIESSSAQYILQQYLAAS
GGAKVLRSVRNAYAMGKVRMVASEFETATRVVKNRGSAAAAAVEQGGFVLWRMSPDMWYV
ELAVGGSKVRAGCNGRLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLSTAGLFAEARCVG
EKKVGDEDCFILKLSADAETLRQRSEGPAEIIRHVLFGYFSQRTGLLVHVEDSHLTRIQP
HAGGDAVYWETTISSFLEDYRAVDDGGVVIAHAGRSAVTLFRFGEMAMSHTKTRMEEAWT
IQEAAFNVPGLSTDCFIPPADIRRGGDSVGSEPCGGKAGAVHPARVVVDRVHHPRRDADK
IHWTVEM
>tr|A0A0E0KG93|A0A0E0KG93_ORYPU Uncharacterized protein OS=Oryza punctata
PE=4 SV=1
MERRSSGGFFAALREEVARGLSPARPRCGRRSDAAELAAAMRMSGGGGGEMLAPLMEGPD
PELLLGVMGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLASVRN
AYTMGKVRMVATEFETAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGC
NGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTTASMFAGAHCIGERKVNGEDCFILK
LCTEPETLKARSEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTI
NSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDC
FIPPTDIKSGSISETVELSHGEKSKVGPPPGHRAKVAALEKAVDGKVAWSGTILEDHN
>tr|A0A0D9VVJ2|A0A0D9VVJ2_9ORYZ Uncharacterized protein OS=Leersia
perrieri PE=4 SV=1
MIPVPIPFPTYHLASFALAPWLRSHSPPNGFVSTSSSSLFLSFLFFSPLLPTPLRLHPSQ
TPHFSSSSQYASLLSGLRLPHLLLHHAGRSLLLALAAIHFGIEAMEKERKQGFFAALKGE
VVRGLSPARSRGKTPAPRGASPARMLIPRSRKTPPPPPPPEQIGPEQLLVPRSGSLRPGG
GEVLAPLIEGPDMVDGDAAVREESGRRDVFGQWVRGHLSRTPSTAGSGGGGGGGSFRRSD
LRLLLGVMGAPLAPVPSSAAEALPLLSVKGTPIESSSAQYILQQYVAASGGAKLLRSARN
AYAMGKVRMVASEFETATRVVKNRGGNAGAAAASAVEQGGFVLWRMAPDMWYVELAVGGS
KVHAGCNGRLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTTAGMFAEARCVGEKKVKGE
DCFILKLSADAETLRQRSEGPAEIIRHVLFGYFSQRTGLLVHVEDSHLTRIQPHAGGDAV

YWETTISSFLDDYRPVEGGVMIAHAGRSAVTLFRFGEMAMSHTKTRMEEAWTIDEAAFNV
PGLSADCFIPPADIRCPVAGEACELPPRAKAGAVHPARVAAVHHPRVRSNAAGDGDKIVW
RVQV
>tr|K7VHR0|K7VHR0_MAIZE Uncharacterized protein OS=Zea mays
GN=LOC100502405 PE=4 SV=1
MEKESKQGFFSALKGEVVRGLSPGRSRGKSLLLPRSRKTAAAEEVAPPEKLAQYAPDPLV
THSGSLRLAGEVLAPLMEGPDVAEDDTFAEDSGRRDGFGQWVRGHLTRAPLIAGGGDGSF
RRSDLRLLLGVMGAPLAPVSVSTAEPLPLAPVKGAPIESSSAQYILQQYLAASGGAKVLR
SARNAYAMGKVRMVASEFETATRVVKNRGAAAAAAVEQGGFVLWRMSPDMWYVELAVGGS
KVRAGCNGRLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLSTAGLFAEARCVGEKKVGDE
ECFILKLSADAETLRQRSEGPAEIIRHVVFGYFSQRTGLLVQVEDSHLTRIQPHAGGDAV
YWETTISSFLEDYRAVDGVAIAHAGRSAVTLFRFGETAMSHTKTRMEEAWTIQEAAFDVP
GLSTDCFIPPADVRRDSDSVGEPCELPPRGAKAGAVHPACDAVHSRRRRDVAPADGELAT
RSTGRWRCDF
>tr|A0A0D2NHG1|A0A0D2NHG1_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_005G233600 PE=4 SV=1
MEKKQGFLSALKEDIVRGLSPSRSRSNSPARPLSLMSTTLRGNKDNHHGGAHVVKPEPLM
ARSGTVRPVGEALSPLMEGPEPDRGKSGDPKWVGSVIGQWVKGQFCTSTNHRRSNLRLLL
GIMGAPLAPIHVSSNDPLPHLSIKDTSIETSSAHYILQQYIAATGVQKLQSSIKNAYAMG
KLKMIACEYETATRIVKSCNVSRGAESGWFVLWQMNPDMWYVELAVSGCKVHAGCNGNLV
WRYTPWLGAHTAKGPVRPLRRALQGLDPRTTAIMFANARCIGEKNINGEDCFILKLCAGP
RTLKARSEGPAEIIRHVLFGYFSQKTGLLVQMEDSHLTRVQSTGGDTVYWETTINTFLED
YHPVEGIVIAHSGHTVVTLFRFGEVAMNHTKTKMEETWTIEEDERGENAIHL
>tr|S8CCR2|S8CCR2_9LAMI Uncharacterized protein OS=Genlisea aurea
GN=M569_10083 PE=4 SV=1
MRGLCRCGRVEDAYGMLAEMERRGCEADDVGVEATEKEMEHRKQGFFSTLKEDFVRGLSP
GRSRRGRSHSPSVSGHRRRRRGSSAGPPEIFVPRSGAEILSPLREGPDPNGSGLGDRKSD
RWTNWLCRAPVSVSVPRYSRSDLRLLLGVLGAPLAPVHVSHHHPLPHLCLKETTRIETSS
ALYILHQYLAASGGLKLQNSVVNAYAMGKVRMSASDIQTAAKAVAIKGKSPSGKMAESGG
FVLWQMNHDLWYVELALGGSKIHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRAIQGLDPR
TTANMFMDARCTGEKRVNGEDCFILKLCADQNTLKARSEGPAEIIRHVLFGYFSQKTGLL
VHLEDSHLTRIQNNGGDAVYWETTINSFIEDYRPVDGIMIAHSGRSVVTLFRFGETAMSH
SKTRMEEAWTIEEVAFNVQGLSMDCFIPPAELHKDRIIRSSTSSGNRSKVVDANNVVITR
VCRR
>tr|A0A0K9NXE7|A0A0K9NXE7_ZOSMR Uncharacterized protein OS=Zostera marina
GN=ZOSMA_52G00840 PE=4 SV=1
MDSVTVEKSPHSILSSIIISRLRHSFEFVCGTAVKKKKEEEKLEMEKKNTGFFTTLKKEV
IRGLSPSRSRPKRTTAKTTLPPPPPHPLRQNTTSTTNIPSILIRARHRNTVSNHHDDPPT
VASACTSTDPDGLGGRYSGGVLRNAVEVLAPLMEGPMGEDAEENRARIERKEGWGRWMKG
QLSRGTSSSSEIFNAVGLENAAHKRSDLRLLLGVMGAPLSPVGVFSLPDLLPRLSIKDTP
IECSFAQYILQQYLAATGGQKLQKSFKNAYAMGKVKMVVSGYETANKAINNCTTSSSRVA
ESGGFVLWQMNPDMWYIELSVGGNKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQG
LDPRTTAGMFGNSRCIGEKKVNGVECFVLKLTSDPQNLKARSEGPAEIIRHVMFGYFSQR
TGVLVQLEDSHLTRIQANNCGDAVYWETTINSFLDDYRPVEGMMIAHSGRSVVTLFKFGE
MAMSHSKTRMEESWCIEEVAYNVAGLSVDCFIPPADIIRSKSISSTLTGLTAPTPPSDLD
GFQKKHAPPQPPHSNRSRVAAITHQNHGNTVDNVVWRVEI
>tr|D7KBT7|D7KBT7_ARALL Putative uncharacterized protein OS=Arabidopsis
lyrata subsp. lyrata GN=ARALYDRAFT_472973 PE=4 SV=1
MDKKHGLFSKSNSRRSRSKSPVRSVSPIIIRRRKGRYVSQPDRHMSEMLAPVREGPDPDG
EDSGSSGDYSRFERRWYNWMKCQLPVAPPSVSSSSDFKRTDLRLLLGVLGAPLGPVHVSA
LDLLPHLSIKNTPMETSSAQYILQQYTAASGGQKLHSSVQNGYVMGRIRTMASEFETGSK
GSKSKNNSSKSVESGGFVLWHMNPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAK
GPVRPLRRALQGLDPRTTAYMFANARCIGEKKIDGEDCFILKLCADPATLKARSEGASET
IRHTLFGYFSQKTGLLVHLEDSQLTRIQNNGGEAVYWETTINSYLEDYKPVEGIMIAHSG

RSVATLLRFGDMSSGHNTKTTMQEAWVIDEIAFNVPGLSIDCFIPPSELRFDSHVEDLSQ
GPKIRTLHGHKNG
>tr|M0S9Z5|M0S9Z5_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MEKKQGFFSALREEVARGLSPARARARSRSESPRRSPSPVANLLLPRRWKRQPARGFPAE
LLVPASGTLAPLAEGPEGDGGDPRKEGWGRWVMGQLSRAPSVSAPSCRSSDLRLLLGVMG
APLAPVHVSLANPLPHLSIKDTPIETSTAQYILQQYTAASGGLKLLSSIRNAYAMGKVRM
VASEFETATGIIKNRNSPKDAESGGFVLWQMAPDMWYVELAVGGSKVRAGCDGNIVWRHT
PWLGAHAAKGPIRPLRRALQGIDPLTTASMFADAHQKTGLLTYMEDSHLTRIQSSTGGDA
VYWETSINSSIDDYRAVEGMMIAHSGHSVVTLFRFGEVAMSHTKTRMEEVWTIEEVAFNV
PGLSMDCFIPPADVNRGSVSEACELPQVERERGRNVMAGSHRAKVAAVERSHNVADNNIL
WRVELMEHTIYMFKHYQ
>tr|R0GPR5|R0GPR5_9BRAS Uncharacterized protein (Fragment) OS=Capsella
rubella GN=CARUB_v10012641mg PE=4 SV=1
LLPNQTFFFFIIPKNKKPNLLHLLSHTNKTLPSSPSSSSTMDKKHGGLFSKSNSRRSRSK
SPVRSVSPIIIRRRKGRYVTQPDRHMSEMLAPVIEGPDPDGEDSGSSGDYSRFERRWYNW
MKCQLPVAPPSVSSSSDFKRTDLRLLLGVLGAPLGPVHVSALDLLPHLSIKNTPMETSSA
QYILQQYTAASGGQKLHSSVQNGYVMGRIRTMASEFETGSKGSKSKNNSSKSVESGGFVL
WHMNPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAKGPVRPLRRALQGLDPRTTA
YMFANARCIGEKKIDGEDCFILKLCADPATLKARSEGASETIRHTLFGYFSQKTGLLVHL
EDSQLTRIQNNGGEAVYWETTINSYLEDYKSVEGIMIAHSGRSVATLLRFGDMSSGHNTK
TTMQEAWVIDEIAFNVPGLSMDCFIPPSELRFDSQVEDLSQGPRIKTLHGSVAPRQKNG
>tr|A0A0D3FL60|A0A0D3FL60_9ORYZ Uncharacterized protein OS=Oryza barthii
PE=4 SV=1
MERRRGGGGGGGFFAALREEVARGLLLLGVMGAPLAPVHVSAAEPLPHLSIKDTPIETS
SAQYILQQYLAASGGQKLLASVRNAYTMGKVRMVATEFETAGRLVKNRNAARCAEPGRFV
LWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTT
ASMFAGARCIGERKVNGEDCFILKLCTEPETLKARSEGLAEIIRHVMFGYFSQRTGLLFH
IEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMSHT
KTRMEEAWSIEEVVFNVPGLSMDCFIPPTDIKSGSISETVELSHGEKSKVGPPPGHRAKV
AALEKAVDGKVAWSGTILEDHN
>tr|G8A2B7|G8A2B7_MEDTR Lipase OS=Medicago truncatula GN=MTR_3g102670
PE=4 SV=1
MEKKQGLFWGLKEDLMRGMSPASSSSPMSSLLQRKKKEDVLPLELFVGGICPSTPVRPPL
EAMSPLREGPEETECSFGVSSSSDLRLLLSVLGAPLAPLHVTITEPFPHLAIKDIPIETS
SAQYILQQYIAASGGLKIQDSINNVYAMGKVRMIASEFETANKLVRTRNPTKAAQSGGFV
LWQMKPEMWYVELSLGGSKVHAGCNGKLVWRHTPWLGPHAAKGPARPLRRALQGLDPRTT
ASMFINSRCVGEKKINGEDCFILKICSDPSTLKARSEGSSEIIRHVLLGHFSQKTGLLIH
LEDSHLTRIQNNGGDAVYWETTINSFLDDYRPVEGIMIAHSGRSQVTLFKFGETAMSHTK
TRMEEAWVIEEVAFNVPGLSVDCFIPPAELRFASVSETCEFSPSQKMKSDV
>tr|F2EFR9|F2EFR9_HORVD Predicted protein OS=Hordeum vulgare var.
distichum PE=2 SV=1
MDKKQGFFSALRGEVARRNDLRMLLGVMGAALAPVHVCAAEPLPHLSIKDTPIETSSAQY
ILQQYLAASGGQKLLSSVRNSYAMGKVRMVATECETAGRVVRNRMGARCAEPGRFVLWQM
APEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHSAKGPVRPLRRSLQGLDPLTTASMF
AGARCIGERKVNGDDCFILKLCADPETLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDS
HLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMNHTKTRM
EEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSISETVELPQSGKSKAGGLLPCHGAKVAAL
EKADDNVAWSGTLQRDCK
>tr|A0A0D3BIH1|A0A0D3BIH1_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MDKKHGLFSKSHSRRSRSKSPVRAVSPIIIRRRKGRYVSQPDRHVSEMLPPVIEGPDPDG
EDSGSSGDYSRIERRWYNWMKCQLPVAPPSVSSSSGFKRTDLRLLLGVLGAPLGPVHVSA
LDLLPHLSIKNTPMETSSAQYILQQYTAASGGYKLHSSVQNGYVMGRIRTVASEFETGSK

GSKSKSNSSKAVESGGFVLWHMSPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAK
GPVRPLRRALQGLDPRTTANMFASARCIGEKKIDGEDCFILKLCADPATLKARSEGASET
IRHTLFGYFSQKTGLLVHLEDSQLTRIQNIGGEAVYWETTINSYLEDYKPVEGIVIAHSG
RSVATLLRFGDMSSGHNTKTTMQEAWVIDEIAFNVPGLSMDCFIPPSELRFDSHVEELSQ
GPKIKTLQHGSVATRHNYG
>tr|V4KVP0|V4KVP0_EUTSA Uncharacterized protein OS=Eutrema salsugineum
GN=EUTSA_v10007666mg PE=4 SV=1
MDKKHGLFSKSHSRRSRSKSPVRGVSPIIIRRRKGRYVSQPDRHMSEMLPPVIEGPDPDG
EESGNSGDYSRFERRWYNWMKCQLPVAPPSVSSSSGFKRTDLRLLLGVLGAPLGPVHVSA
LDLLPHLSIKNTPMETSSAQYILQQYTAASGGQKLHSSVQNGYVMGRIRTVASEFETGSK
GSKSKNNSSKAVESGGFVLWHMNPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAK
GPVRPLRRALQGLDPRTTANMFANARCIGEKKIDGEDCFILKLCADPATLKARSEGASET
IRHTLFGYFSQKTGLLVHLEDSQLTRIQNVGGEAVYWETTINSYLEDYKPIEGIVIAHSG
RSVATLLRFGDMSSGHNTKTTMQEAWVIDEIAFNVPGLSMDCFIPPSELRFDSHVEDSSQ
GPKIKTLQGSVATRQKNG
>tr|M1BXY9|M1BXY9_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG400021537 PE=4 SV=1
MNLQETSSAQYILQQYTAASGGQKLQNTMYNAYAMGKVRMMASDIETATKVIKNRNSSKT
AESGGFVLWQMNPDMWYVELALGSSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQ
GLDPRTTANMFASAKCTGEKKINGEDCFILKLCADPHTLKARSEGPAEIIRHVLFGYFSQ
KTGLLVHLEDSHLTRIQTNGGDAVYWETTINSFLDDYRPVEGIMIAHSGRSVVTLFRFGE
TAMSHTKTRMEEAWTIEEVAFNVPGLSEECFIPPAELRFSSIGEACELSQGERVKTTVSA
AAAAAYRAKVAALDKSRDGSNVNNIVLKMNY
>tr|Q8RWY0|Q8RWY0_ARATH Putative lipase OS=Arabidopsis thaliana
GN=At1g27690 PE=2 SV=1
MDKKHGLFSKSNSRRPRSKSPVRSVSPIIIRRRKGRYVTQPDRHMSEMLAPVIEGPDPDA
EDSGSSGDYSRFERRWYNWMKCQLPVAPPSVSSSSDFKRTDLRLLLGVLGAPLGPVHVSA
LDLLPHLSIKNTPMETSSAQYILQQYTAASGGQKLHSSVQNGYVMGRIRTMASEFETGSK
GSKSKNNSSKAVESGGFVLWHMNPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAK
GPVRPLRRALQGLDPRTTAYMFANARCIGEKKIDGEDCFILKLCADPATLKARSEGASET
IRHTLFGYFSQKTGLLVHLEDSQLTRIQNNGGEAVYWETTINSYLEDYKPVEGIMIAHSG
RSVATLLRFGDMSSGHNTKTTMQEAWVIDEISFNVPGLSIDCFIPPSELRFDSHVEDLSQ
GPKIRTLHGHKNG
>tr|A3AK99|A3AK99_ORYSJ Uncharacterized protein OS=Oryza sativa subsp.
japonica GN=OsJ_11686 PE=4 SV=1
MGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLASVRNAYTMGKV
RMVATEFETAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHAAKGPVRPLRRALQGLDPLTTASMFAGARCIGERKVNGEDCFILKLCTEPET
LKARSEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSISETVELSHGEKSKVGPPPGHRAKVAALEKAVDGKVAWSGTILEDHN
>tr|A2XJD2|A2XJD2_ORYSI Putative uncharacterized protein OS=Oryza sativa
subsp. indica GN=OsI_12556 PE=4 SV=1
MGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLASVRNAYTMGKV
RMVATEFETAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHAAKGPVRPLRRALQGLDPLTTASMFAGARCIGERKVNGEDCFILKLCTEPET
LKARSEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSISETVELSHGEKSKVGPPPGHRAKVAALEKAVDGKVAWSGTILEDHN
>tr|A0A0E0D3N6|A0A0E0D3N6_9ORYZ Uncharacterized protein OS=Oryza
meridionalis PE=4 SV=1
MGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLASVRNAYTMGKV
RMVATEFETAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHAAKGPVRPLRRALQGLDPLTTASMFAGARCIGERKVNGEDCFILKLCTEPET

LKARSEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSISETVELSHGEKSKVGPPPGHRAKVAALEKAVDGKVAWSGTILEDHN
>tr|A0A0D9ZAE5|A0A0D9ZAE5_9ORYZ Uncharacterized protein OS=Oryza
glumipatula PE=4 SV=1
MGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLASVRNAYTMGKV
RMVATEFETAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHAAKGPVRPLRRALQGLDPLTTASMFAGARCIGERKVNGEDCFILKLCTEPET
LKARSEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSISETVELSHGEKSKVGPPPGHRAKVAALEKAVDGKVAWSGTILEDHN
>tr|M4D371|M4D371_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra010924 PE=4 SV=1
MDKKHGLFSKSHSRRSRSKSPVRAVSPIIIRRRKGRYVSQPDRHVSEMLPPVIEGPDPDG
EDSGSSGDYSRLERRWYNWMKCQLPVAPPSVSSSSGFKRTDLRLLLGVLGAPLGPVHVSA
LDLLPHLSIKNTPMETSSAQYILQQYTAASGGYKLHSSVQNGYVMGRIRTVASEFETGSK
GSKSKSNSSKAVESGGFVLWHMSPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAK
GPVRPLRRALQGLDPRTTANMFASARCIGEKKIDGEDCFILKLCADPATLKARSEGASET
IRHTLFGYFSQKTGLLVHLEDSQLTRIQNIGGEAVYWETTINSYLEDYKPVEGIVIAHSG
RSVATLLRFGDMSSGHNTKTTMQEAWVIDEIAFNVPGLSMDCFIPPSELRFDSHVEELSQ
GPKIKTLQQVGGGREHSIADSQTQQKKIMVLSDFTGVGVGFGFGVGCGFGVGWGFGGMPL
NVLGVGVGGGCGVGLGLGWGFGTAFGSHYRSSRLTFQGVELEKDGKVENMSNNS
>tr|K7VD88|K7VD88_MAIZE Uncharacterized protein OS=Zea mays
GN=LOC100502405 PE=4 SV=1
MEKESKQGFFSALKGEVVRGLSPGRSRGKSLLLPRSRKTAAAEEVAPPEKLAQYAPDPLV
THSGSLRLAGEVLAPLMEGPDVAEDDTFAEDSGRRDGFGQWVRGHLTRAPLIAGGGDGSF
RRSDLRLLLGVMGAPLAPVSVSTAEPLPLAPVKGAPIVRTRLGFFSPGSPLFSRLALANA
AAFWALTPPAALDLVFMALQESSSAQYILQQYLAASGGAKVLRSARNAYAMGKVRMVASE
FETATRVVKNRGAAAAAAVEQGGFVLWRMSPDMWYVELAVGGSKVRAGCNGRLVWRHTPW
LGAHAAKGPVRPLRRALQGLDPLSTAGLFAEARCVGEKKVGDEECFILKLSADAETLRQR
SEGPAEIIRHVVFGYFSQRTGLLVQVEDSHLTRIQPHAGGDAVYWETTISSFLEDYRAVD
GVAIAHAGRSAVTLFRFGETAMSHTKTRMEEAWTIQEAAFDVPGLSTDCFIPPADVRRDS
DSVGEPCELPPRGAKAGAVHPACDAVHSRRRRDVAPADGELATRSTGRWRCDF
>tr|C5YQG5|C5YQG5_SORBI Putative uncharacterized protein Sb08g019390
OS=Sorghum bicolor GN=Sb08g019390 PE=4 SV=1
MGAPLAPVHVCAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQRLLSSIRNSYAMGKV
RMVATEFETGGRVVRNRMAAQRAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPET
LRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMIAHSGRSAVTLFRFGEAAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSISETVELPQGEKSKVGLLLCHRAKVAALEKADDNVAWSGALQLDCK
>tr|M8BB67|M8BB67_AEGTA Uncharacterized protein OS=Aegilops tauschii
GN=F775_19135 PE=4 SV=1
MGAPLAPVHVCAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGHKLLASVRNSYAMGKV
RMVATEFENAGRLVKNRNAARCAEPGRFVLWQMAPEKWYIELAVGGSKVHAGCNGKLVWR
HTPWLGSHAAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCTDPET
LKARTEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVDGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSVSETVELPHGGEKNKFGPPPGHRAKVAALEKTDGGELAWRGTHT
>tr|J3LQQ6|J3LQQ6_ORYBR Uncharacterized protein OS=Oryza brachyantha
GN=OB03G33820 PE=4 SV=1
MGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQRLLGSVRNAYTMGKV
RMVATEFEIAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHAAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCTDPET

LKGRSEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSISETVELSHGEKSKVGPPPGHRAKVAALEKAVNEKVAWSGTILEDHN
>tr|J3NEI2|J3NEI2_ORYBR Uncharacterized protein OS=Oryza brachyantha
GN=OB12G23900 PE=4 SV=1
MGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYGMGKV
RMVATEFETGGRVVRNRMAARTAESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPET
LRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSISETVELPHGEKSKAGLLPCHSAKVAALEKADDNVAWSGALQRDFK
>tr|A0A0E0BUJ1|A0A0E0BUJ1_9ORYZ Uncharacterized protein OS=Oryza
glumipatula PE=4 SV=1
MGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGKV
RMVATEFETGGRVVRNRMAARAAESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPET
LRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAIYWETTINSFIEDY
RPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTDI
KSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFK
>tr|M0UV34|M0UV34_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MGAPLAPVHVCAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGHKLLASVRNSYAMGKV
RMVATEFENAGRLVKNRNAARCAEPGRFVLWQMAPEKWYIELAVGGSKVHAGCNGKLVWR
HTPWLGSHAAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCTDPET
LKARTEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVDGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSVSETVELPHGEKNKFGPPHGHRAKVAALEKTDGDELAWRGTRT
>tr|T1N2H4|T1N2H4_TRIUA Uncharacterized protein OS=Triticum urartu PE=4
SV=1
MLKAAKVEIKKEHQVLMVKKTTSFKKKGRGKKDNFKKNSKQVAAPRKKPKSGPKPETVCF
YCKGTGHWKRNCPKYLADKKDGKVKDHDEPTNYEEVMMSPDSAKWLEAMKSEMGSMYENK
AHAQVERRNDLRMLLGVMGAALAPVHVCAAEPLPHLSIKDTPIETSSAQYILQQYLAASG
GQKLLSSVRNSYAMGKVRMVATECETAGRVVKNRMAARCAEPGRFVLWQMAPEMWYIELA
VGGSKVHAGCNGKLVWRHTPWLGAHSAKGPVRPLRRSLQGLDPLTTASMFAGARCIGERK
VNGDDCFILKLCADPETLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTG
GDAVYWETTINSFIEDYRPVEGIMIAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVA
FNVPGLSMDCFIPPTDIKSGSISETMELPQSGKSKAGGLLPCHGAK
>tr|A0A0D3HW41|A0A0D3HW41_9ORYZ Uncharacterized protein OS=Oryza barthii
PE=4 SV=1
MGAPLAPVHVAAGEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGKV
RMVATEFETGGRVVRNRMAARAAESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCADPET
LRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAIYWETTINSFIEDY
RPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTDI
KSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFKTRRGVSHPAP
NHMVRDHGGGAVLSLIAILIYRSPARKKGVLSLL
>tr|N1R122|N1R122_AEGTA Uncharacterized protein OS=Aegilops tauschii
GN=F775_18374 PE=4 SV=1
MGAALAPVHVCAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSIRNSYAMGKV
RMVATECETAGRVVRNRMAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHSAKGPVRPLRRSLQGLDPLTTASMFAGARCIGERKVNGDDCFILKLCADPET
LRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMIAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDI
KSGSISETVELPQSGKSKAGGLLPCHGAKVAALEKADDNVAWSGALQRDCK

>tr|A0A0D9VW98|A0A0D9VW98_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1
MGAPLAPVHVSAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQRLLASVRNAYTMGKV
RMVATEFETAGRLVKNRNAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWR
HTPWLGAHAAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCTEPET
LKARSEGLAEIIRHVLFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDY
RPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWNIEEVAFNVPGLSIDCFIPPTDI
KSGSISETVELSHGEKSKVKNRLKKDLEFLEPNVLCV
>tr|M0RJ83|M0RJ83_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1
MEKKQGFFSALREEVARGLSPARSRSRSESPRRGASPVADLLLPTRWKRQQPRGFPAELL
VPASGSLAPLAEGPEGEGSGPGKGGWGQWMKGRLSRAPSVSGAAASCHRSDLRLLLGVMG
APLAPVHVSPTYALPHLSIKDTPIETSSAQYILQQYTAASGGLKLLSSIRNAYAMGKVRM
VASEFETATRVIKNHSVTKDAEPGGFVLWQMAPGMWYVELAVGGSKVRAGCNGKLVWRHT
PWLGAHAAKGPVRPLRRALQGLDPLTTASMFSDAHQKTGLLTYMEDSHLTRIQSSVGGDA
VYWETSINSSIEDYRPVEGVMIAHSGRSAVNLFRFGEVAMSHTKNRMEEVWTIEEVAFNV
AGLSVDCFIPPADVKRGTVSEACELPQSERGRSSMAGSHRAKVAALDKPDGNIRWRAEK
>tr|A0A0D2W2X9|A0A0D2W2X9_GOSRA Uncharacterized protein OS=Gossypium raimondii GN=B456_013G048800 PE=4 SV=1
MEKKQGFFSALKEEVIRGLSPSRSRTNSPGRARSPIAILLRRKKSGHNNYGGAYLAQPEP
LTARYGVGEALAPLMEGPDPDGGETGDSKRLGSGLGQWVMGQLSRTPSMASLSCKRSDLR
LLLGVMGAPLAPVQVCSTDPLPHLSIKDTPIETSTAQYILQQYTAASGGLKLQNSVRNAY
AMGKLKMVACEYETAAKTVKNRYGSRGAESGGFVLWQMHPDMWYVELAVGGSKVHAGCNG
KLVWRHTPWLGARTAKGPVRPLRRALQGLDPRTTASMFSDAKCIGEKTINGEDCFILKLC
TDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGSGKLQ
>tr|M0S7N8|M0S7N8_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1
MEKKQGFFSALREEVARGLSPARARSEIARRGPSGSLAPLMEGPDPGEAEREDARRERGW
GQWVKDQLSRAPSGSAASASYRRSDLQLLLGVMAAPLAPIHVCSTDPLPHLSIKDTPIET
SSAQYILQQYTAASGGLKLLSSIRNAYAMGKVRMVATDFETATRVIKARNASRDAESGGF
VLWQMAPDMWYVELAVGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQGIDPLI
TASMFAKARQKTGLLIHIEDSHLTRIQSSAGGDAVYWETSINSFIDDYRPVEGMMIAHSG
HSVVTLFRFGEVAMSHTKTRMEESWTIEEVAFNVPGLSVDCFIPPADVKHGSIDEACELP
QGERGKNLMVGGHRAKVAALEKFGRTCLILCFERRGLCWRLIVLLDMIIWIHLLTPATSA
FVLPGAVWIVYLGPFLADR
>tr|A0A078DSE5|A0A078DSE5_BRANA BnaA08g18810D protein OS=Brassica napus GN=BnaA08g18810D PE=4 SV=1
MDKKHGLFSKSHSRRSRSKSPVRAVSPIIIRRRKGRYVSQPDRHVSEMLPPVIEGPDPDG
EDSGSSGDYSRLERRWLLLGVLGAPLGPVHVSALDLLPHLSIKNTPMETSSAQYILQQYT
AASGGYKLHSSVQNGYVMGRIRTVASEFETGSKGSKSKSNSSKAVESGGFVLWHMSPDMW
YMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAKGPVRPLRRALQGLDPRTTANMFASARC
IGEKKIDGEDCFILKLCADPATLKARSEGASETIRHTLFGYFSQKTGLLVHLEDSQLTRI
QNIGGEAVYWETTINSYLEDYKPVEGIVIAHSGRSVATLLRFGDMSSGHNTKTTMQEAWV
IDEIAFNVPGLSMDCFIPPSELRFDSHVEELSQGPKIKTLQQAGRAAAARAWETVLSPRK
IMVLSDFTGVGVGFGFGVGCGFGVGWGFGGMPLNVLGVGVGGGCGVGLGLGWGFGTAFGS
HYRSSRLTFQGVELEKDGKVENMSKNS
>tr|A0A078JQM9|A0A078JQM9_BRANA BnaCnng57140D protein OS=Brassica napus GN=BnaCnng57140D PE=4 SV=1
MDKKHGLFSKSHSRRSRSKSPVRAVSPIIIRRRKGRYVSQPDRHVSEMLPPVIEGPDPDG
EDSGSSGDYSRIERRWLLLGVLGAPLGPVHVSALDLLPHLSIKNTPMETSSAQYILQQYT
AASGGYKLHSSVQNGYVMGRIRTVASEFETGSKGSKSKSNSSKAVESGGFVLWHMSPDMW
YMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAKGPVRPLRRALQGLDPRTTANMFASARC
IGEKKIDGEDCFILKLCADPATLKARSEGASETIRHTLFGYFSQKTGLLVHLEDSQLTRI
QNIGGEAVYWETTINSYLEDYKPVEGIVIAHSGRSVATLLRFGDMSSGHNTKTTMQEAWV

IDEIAFNVPGLSMDCFIPPSELRFDSHVEELSQGPKIKTLQHGSENQSNKGGVDMTKTKK
IMVLSDFTGVGVGFGFGVGCGFGVGWGFGGMPLNVLGVGVGGGCGVGLGLGWGFGTAFGS
HYRSSRLTFQGVELEKDGKVENMSKNA
>tr|B9FY72|B9FY72_ORYSJ Uncharacterized protein OS=Oryza sativa subsp.
japonica GN=OsJ_24954 PE=4 SV=1
MGAPLAPIPSKLADPLPLLSIKGTPIESSSAQYILQQYMAASGGYRLLQSVRNAYAMGKV
RMVASEFETATRVVKNRGPSGRGAASVEQGGFVLWQMAPDMWYVELAVGGSKVHAGSNGR
LVWRHTPWLGAHAAKGPVRPLRRVLQGLDPLTTAGLFAEARCVGEKKVNGEDCFILKLSA
DPQTLKQRSEGPAEIIRHVLFGYFSQRTGLIVHIEDSHLTRIQPHSGGDAVYWETTISSA
LEDYRPVEGIMIAHAGRSAVTLFRFGEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIP
PADIRSGPVGESCELPPPAAAPHGERARHPARVAAVDRAPPHHNAGGANVGRRGDKIMWR
VEV
>tr|W5ERW1|W5ERW1_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MLFVPYDKDETSSAQYILQQYLAASGGHKLLASVRNSYAMGKVRMVATEFENAGRLVKNR
NAARCAEPGRFVLWQMAPEKWYIELAVGGSKVHAGCNGKLVWRHTPWLGSHSAKGPVRPL
RRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCTDPETLKARTEGLAEIIRHVMF
GYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVDGIMIAHSGRSAVT
LFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSVSETVELPHGGEK
NKFGPPPGHRAKVAALEKTDGGDVGEKQVDGGFRFWKFQMTSVYRKEAA
>tr|A0A0A9DTT7|A0A0A9DTT7_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MCSMQETSSAQYILQQYLAASGGQRLLSSIRNSYAMGKVRMVATEFETGGRVVRNRMVAQ
RAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRTL
QGLDPLTTASMFAGARCIGERKVNGEDCFILKLCADPETLRARSEGLAEIIRHVLFGYFS
QKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIEEYRVVEGIMVAHSGRSAVTLFRF
GELAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSVSETVELPHGEKSKTSL
LPCHRAKVAALEKADDNVAWSRALQLDCK
>tr|M0T9Q0|M0T9Q0_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MEKKQGFLPALREEEVATGPSPTRSREKGSAPEAVAPVAWKEGWGRWIRGQLSRAPSAAT
SSVAAGASSSALRSDLRLLLGVLGAPLAPVHVSSFDPLPHLSVKDTPIETSSAQYIMQQY
TAASGGLRLHRSIRNAYATGKVRMVASEFEATAKVVRTGCVSSSTTESGGFVLWQMAPDM
WYVELAVGGSKVHAGSNGKVVWRHTPWLGSHAAKGPARPLRRALQGLDPLTTASMFADAR
CIGEKTVNGEDCFVLKLSADPPTLRARSEGPAEIIRHVLIQANAGGDAVYWETTMNSSLD
DYRLVDGIMIAHSGRSTATLFRFGEKAMNHTKRRMEEAWTIDEVAFNVPGLSMDCFIPPA
DMRRGSTSEACELPRGVRGKFSSRYPQDMPEKIVCRFEVLG
>tr|M7Z8G8|M7Z8G8_TRIUA Uncharacterized protein OS=Triticum urartu
GN=TRIUR3_03908 PE=4 SV=1
MPMHASATDHTVYSDHMSLHARRRWLCCYMQPALFAYAGLTVESAQARSEKLICSTLWNI
GSSAGPEDTDIFHNFLAPNSTEATSKERDKMLPHTRRYARINVVVCMDAPACQVSIPQET
SSAQYILQQYLAASGGHRLLASVRNSYAMGKVRMVATEFENAGRLVKNRNAARCAEPGRF
VLWQMAPEKWYIELAVGGSKVHAGCNGKLVWRHTPWLGSHAAKGPVRPLRRALQGLDPLT
AASMFAGARCIGERKVNGEDCFILKLCTDPETLKARTEGLAEIIRHVMFGYFSQRTGLLV
HIEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVDGIMIAHSGRSAVTLFRFGEVAMSH
TKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSVSETVELPHGGEKSKFGPPPGHRA
KVAALEKTDGGELAWRGAHT
>tr|W5FMZ8|W5FMZ8_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MQETSSAQYILQQYLAASGGQKLLSSVRNSYAMGKVRMVATECETAGRVVRNRMAARCAE
PGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHSAKGPVRPLRRSLQGL
DPLTTASMFAGARCIGERKVNGDDCFILKLCADPETLRARSEGLAEIIRHVLFGYFSQKS
GLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEV
AMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSISETVELPQSGKSKAGGLLP

CHGAKVAALEKADDNVAWSGALQRDCK
>tr|J3MMK0|J3MMK0_ORYBR Uncharacterized protein OS=Oryza brachyantha
GN=OB07G26320 PE=4 SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKSPARSASPGRMLTPRRRKEKQPPPEKLLQQY
FAEPLISRSGSLRPGGEALAPLIEGPDPERLAAGDFAGGEESARREGFGRWVLGQLARTP
SVASSAAAGGPGGSSDSFRRSDLRLLLGVMGAPLAPIPSKLADPLPLLSVKGTPIESSSA
QYILQQYMAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAASVEQGG
FVLWQMAPDMWYVELAVGGSKVHAGSNGRLVWRHTPWLGAHAAKGPVRPLRRVLQGLDPL
TTAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQRTGLI
VHIEDSHLTRIQPHSGGDAVYWETTISSALEDYRPVEGIMVAHAGRSAVTLFRHITVYKL
LLVVPVHVNVDLAYKLTKLLYLGSFGVHLASDAEDSVAHRHHSPAGSRSPGVTDDWAGAR
TRVFEIMDDHDCTQTLTCNWISAERTSEEGKKPGSSSNWDDATESQQYLGSWWHWGAGAA
GARLSRHIIVASVAEHAAPLVTVIKFYT
>tr|A0A0D2PY89|A0A0D2PY89_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_005G233600 PE=4 SV=1
MEKKQGFLSALKEDIVRGLSPSRSRSNSPARPLSLMSTTLRGNKDNHHGGAHVVKPEPLM
ARSGTVRPVGEALSPLMEGPEPDRGKSGDPKWVGSVIGQWVKGQFCTSTNHRRSNLRLLL
GIMGAPLAPIHVSSNDPLPHLSIKDTSIETSSAHYILQQYIAATGVQKLQSSIKNAYAMG
KLKMIACEYETATRIVKSCNVSRGAESGWFVLWQMNPDMWYVELAVSGCKVHAGCNGNLV
WRYTPWLGAHTAKGPVRPLRRALQGLDPRTTAIMFANARCIGEKNINGEDCFILKLCAGP
RTLKARSEGPAEIIRHVLFGYFSQKTGLLVQMEDSHLTRVQSTGGDTVYWETTINTFLED
YHPVEG
>tr|M0TDK2|M0TDK2_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MEKKHGVLSARGRSRSESPRRMAELFLLPRRWKRLGRAADPVAPRSGSLAPLMEGPDPGE
ADAARKDRGWGQWVRGQLSRAPSISAATAAFRRTDLRLLLGVMAAPLAPVHVCSTEPLPH
LSIKDTPIETSSAQYILQQYIAASGGLKLLSSIRNAYAMGKVKMLATEFETATRVIKYRN
ATRDAEAGGFVLWQMAPDMWYIELAVGGSKVHAGCNGELVWRHAPWLGAHAAKGPVRPLR
RALQGLDPLTTASMFTNARSGLLVHLEDSHLTRIQSGAGGDAVYWETSIDSSIDDYRPVE
GTMIAHSGHSVVTLFRFGEAALSHKKTRMEEAWTIEEVAFNVPGLSMDCFIPPSDLKRGS
ISEALELPQGERGKNAVAGGHHAKVAALNKSHDDDVMWRWKSDANTI
>tr|A0A0K9NZ81|A0A0K9NZ81_ZOSMR Uncharacterized protein OS=Zostera marina
GN=ZOSMA_53G00920 PE=4 SV=1
MERKQSFFSSLKGEILRTMSPSKTARMARSLCRGDSNTFVVQSTVKSTVDGLVFGSMKSG
VLSPLREGPPESEKEKTKIWGRWMTKAGKISCVASLANSESDDLRLLLGVLGAPLVPVSV
KPVDSAPPRPVLAIDNAPIESLSAQYILQQYIAATGGSKLLSSIRNTYVMGKVKMQTSED
GKATTKLAKSLSMGKTAESGGFVLWQMNPDMWYIELSVGGTKVHVGCNGKFVWRHTPWAG
PHASKGPIRPLRRSIQGLDPRSTSNMFAKSRCTGEKNISGEGACFILKLCADPETLKSRT
EGPTEIIRHILFGYFSQKTGLLVHLEDSQLTRIQSNTGGDAVYWETTINSSLHDYRDVDG
VMIAHSGKSAITFFGFGETEVNRTGMTRLEEEWTIEEVGFNVHGLSMDCFIPIADVKFDG
SSLEGVCDIVVGYEKGKPLLPIGISGGGGNNHRAKVASIGGDVDNNSNNETAKC
>tr|D8SNS1|D8SNS1_SELML Putative uncharacterized protein (Fragment)
OS=Selaginella moellendorffii GN=SELMODRAFT_44115 PE=4 SV=1
TLAPVREGPDADADGGGGNGSLGGGGSGGGGGATKRQGSFRSWMMEQIEKTTLPLLGYKH
SDVRLLLGVLGAPLAPIAASSAHCLYARVSPRDGPIESTSAQYILHQYMAASGGSKFLAS
IHNSYAAGKIRMSLSEFETVNRVVRTKNPFRPAEAGCFVLWQMKPDMWYVELVLGGGSSK
VHAGCDGKLVWRQNPWMGPHAAKGPVRPLRRVLQGLDPLTTATIFSGAVCVGEKRLGGED
CFVLKLAADPYTLGARSDGPAEIIRHVLFGYFSQRTGLLVRIEDSHLTRIQASAGEVVYW
ETSIESTLDDYRSVDGLVIAHSGHSCVTLFRFGEVAMGHTRTRMEEDWTIEEVALNVPGL
SEDCFIPPADIR
>tr|D8SS63|D8SS63_SELML Putative uncharacterized protein (Fragment)
OS=Selaginella moellendorffii GN=SELMODRAFT_44114 PE=4 SV=1
TLAPVREGPDADADGGGGNGSLGGGGSGGGGGATKRQGSFRSWMMEQIEKTTLPLLGYKH
SDVRLLLGVLGAPLAPIAASSAHCLYARVSPRDGPIESTSAQYILHQYMAASGGSKFLAS

IHNSYAAGKIRMSLSEFETVNRVVRTKNPFRPAEAGCFVLWQMKPDMWYVELVLGGGSSK
VHAGCDGKLVWRQNPWMGPHAAKGPVRPLRRVLQGLDPLTTATIFSGAVCVGEKRLGGED
CFVLKLAADPYTLGARSDGPAEIIRHVLFGYFSQRTGLLVRIEDSHLTRIQASAGEVVYW
ETSIESTLEDYRSVDGLVIAHSGHSCVTLFRFGEVAMGHTRTRMEEDWTIEEVALNVPGL
SEDCFIPPADIR
>tr|A0A096QKT8|A0A096QKT8_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.1917 PE=4 SV=1
MTGNGRMFPVTVSCFFPKENTFAVNFGFFISAYCNRITHGVLYARAQETSSAQYILQQYL
AASGGQRLLSSIRNSYAMGKVRMVATEFEAGGRVVRNRMAAQRAEPGRFVLWQMAPEMWY
MELAVGGSKVHAGCNGKLVWRHTPWLGAHSAKGPVRPLRRALQGLDPLTAASMFAGARCI
GERKVNGEDCFILKLSADPETLRARSEGLAEIIRHVLFGYFSHKSGLLVHLEDSHLTRIQ
SATGGDAVYWETTISSSVEDYRAVDGVVVAHAGRSAVTLFRFGEAAVGLGHTKTRMEEAW
TIEEVAFDVPGLSADCFIPPTDVGPGSVSEAAELPRGERSKAAAGLVLPCHRARVAALEK
ADDGGVAWSGALQLGCK
>tr|M0RHC6|M0RHC6_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MEKEQGFFSALKEEVVRGLSPARKAHGRHSSLTLAPDAAEGWGRWVRDQLSRAPSVTYLP
SAAASASTSFRRSDLRLLLGVMGAPLAPVHVNSADLLPHLTIKDAPIEVSSAQYILQQYT
AASGGLKLQRSIHNAYAMGKLRMAASEFETATKIVKNRGSSSHSPESGGFVLWQMAPGMW
YVELAVGGSKVHAGSNGKVVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTTASMFANARC
IGEKKRTGLLVHMEDSHLTRIQANAGGDAVYWETTINSFLSDYRPVEGIMVAHSGRSDVT
LFRFDETAMSHTKTRMEEEWKIEEVVFNVPGLSMDCFIPPADISCGSVSETCELPRGDRG
KTGIAHQRKVAAVGKPQDASDKIIWRVKV
>tr|A9NUK6|A9NUK6_PICSI Putative uncharacterized protein OS=Picea
sitchensis PE=2 SV=1
MGRRSRSRRNQMLARSNRVKTLAPLMEEPTAQPYDDEDSAKKYSPWGGLRDWLRNRSVAN
TGWLMYSNGRSSAGNCPDLKLLLGVLGCPLGPIGVANDPLPHLSIKDVPIETSSAQYIVQ
QYMAATGCLKFQNSIKSSYMVGRVKMVSTEAEMATKACRNYSLKASETGCFVLWQMMPDM
WSVELVLGGSKVHAGSNGKIVWRHTPWLGSHAAKGRPRPLRRALQGLDPRTTAIMFANAR
CLGEKKIGDEDCFILKVAADPSTLHERSDGPAEIIRHVLFGYFSQKTGLLVYLEDSHLTR
IEATGIDVVYWETTIETTINNYRAVDGVMIAHSGRSVVSLFKFGECSMSHTRTRMEETWT
IDDVVFNVPGLSMDFFIPPADIIKNGSGGDACNYQSDGKPLSRKLRNGNLQQVPVGR
>tr|M7ZT93|M7ZT93_TRIUA Uncharacterized protein OS=Triticum urartu
GN=TRIUR3_21802 PE=4 SV=1
MEKERKQGFFAALKEEVESSSAQYILQQYMAASGGYKMLQSVRNAYAMGKVRMVASEFET
ATRVVKNRGPSGRGAAAVEQGGFVLWTMAPGMWYVELAVGGSKVHAGCNGRLVWRHTPWL
GAHAAKGPIFLPSSQLAMQGLDPLTTAGLFAEARCVGEKKVNGEECFILKLSADPQTLKL
RSEGPAEIIRHVLFGYFSQRTGLMVHIEDSHLTRIQPHSGGDAVYWETTISSCLEEYRAV
EGIMIAHAGRSAVTLFRFGEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSG
SVGEACELPPQHGDRAKSTAVHPARVAAAAERAHVNAGAGGRGEKIVWRVEV
>tr|A0A067H1X4|A0A067H1X4_CITSI Uncharacterized protein OS=Citrus
sinensis GN=CISIN_1g022693mg PE=4 SV=1
MGRVTMIASEFEKGNKVTRSRNSSKGAESGGFVLWQMNPDMWYVELALGDSKVHAGCNGK
LVWRHTPWLGAHAAKGPVRPLRRALQGLDPRTTASMFINARCIGEKKINGEDCFILKLCA
DPSTLKARSEGPAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQNNGGDAVYWETTINSFL
DDYRPVEGIMIAHSGRSIVTLFRFGDTAMSHTRTRMEEAWAIDEVAFNVPGLSVDCFIPP
AELRFDSVGETCEFTQGQRVRSTVGTAADRTRVASLDMSRDIGVNNITWKANG
>tr|Q9SFZ0|Q9SFZ0_ARATH T22C5.14 OS=Arabidopsis thaliana PE=4 SV=1
MDKKHGLFSKSNSRRPRSKSPVRSVSPIIIRRRKGRYVTQPDRHMSEMLAPVIEGPDPDA
EDSGSSGDYSRFERRWYNWMKCQLPVAPPSVSSSSDFKRTDLRLLLGVLGAPLGPVHVSA
LDLLPHLSIKNTPMETSSAQYILQQYTAASGGQKLHSSVQNGYVMGRIRTMASEFETGSK
GSKSKNNSSKAVESGGFVLWHMNPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAK
GPVRPLRRALQGLDPRTTAYMFANARCIGEKKIDGEDCFILKLCADPATLKARSEGASET
IRHTLFGYFSQKTGLLVHLEDSQLTRIQNNGGEAVYWETTINSYLEDYKPVEGIMIAHSG

LAILSGGGRESNLPDSPITNNKQGIIGSLWCSLTSLESVLDLGSVLVVDLALDGVLEVAV
AGWVWASGGVSGLRLGVTIVHLDLHFKASS
>tr|W5DPS7|W5DPS7_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MGKVRMVATEFENAGRLVKNRNAARCAEPGRFVLWQMAPEKWYIELAVGGSKVHAGCNGK
LVWRHTPWLGSHAAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCT
DPETLKARTEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSF
IEDYRPVDGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIP
PTDIKSGSVSETVELPHGGEKSKFGPPPGHRAKVAALEKTDGGELAWRGAHT
>tr|W5ECD5|W5ECD5_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MGKVRMVATEFENAGRLVKNRNAARCAEPGRFVLWQMAPEKWYIELAVGGSKVHAGCNGK
LVWRHTPWLGSHAAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCT
DPETLKARTEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSF
IEDYRPVDGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIP
PTDIKSGSVSETVELPHGGEKNKFGPPPGHRAKVAALEKTDGGDSVERNRSTGDFDFGNS
K
>tr|M0WTS4|M0WTS4_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MGKVRMVATECETAGRVVRNRMGARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGK
LVWRHTPWLGAHSAKGPVRPLRRSLQGLDPLTTASMFAGARCIGERKVNGDDCFILKLCA
DPETLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSF
IEDYRPVEGIMIAHSGRSAVTLFRFGEVAMNHTKTRMEEAWSIEEVAFNVPGLSMDCFIP
PTDIKSGSISETVELPQSGKSKAGGLLPCHGAKVAALEKADDNVAWSGTLQRDCK
>tr|M0UV38|M0UV38_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MGKVRMVATEFENAGRLVKNRNAARCAEPGRFVLWQMAPEKWYIELAVGGSKVHAGCNGK
LVWRHTPWLGSHAAKGPVRPLRRALQGLDPLTAASMFAGARCIGERKVNGEDCFILKLCT
DPETLKARTEGLAEIIRHVMFGYFSQRTGLLVHIEDSHLTRIQSTTGGDAVYWETTINSF
IEDYRPVDGIMIAHSGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIP
PTDIKSGSVSETVELPHGEKNKFGPPHGHRAKVAALEKTDGDELAWRGTRT
>tr|W5G4L9|W5G4L9_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MGKVRMVATECETAGRVVRNRMAARCAEPGRFVLWQMAPEMWYIELAVGGSKVHAGCNGK
LVWRHTPWLGAHSAKGPVRPLRRSLQQGLDPLTTASMFAGARCIGERKVNGDDCFILKLC
ADPETLRARSEGLAEIIRHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINS
FIEDYRPVEGIMIAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFI
PPTDIKSGSISETVELPQSGKSKAGGLLPCHGAKVAALEKADDNVAWSGALQRDCK
>tr|B9GDZ2|B9GDZ2_ORYSJ Uncharacterized protein OS=Oryza sativa subsp.
japonica GN=OsJ_36659 PE=4 SV=1
MDKKQGFFSALREEVARGLSPARARRRSQAAAAAEVAAALRAPDPESGDGGKSSFVGGGG
EEGRVGPLGCAANFSRAPLTAGAAVVAAGCCGGAARRNDLRLLLGVMGAPLGPVHVAAGE
PLPHLSIKDTPIETSSAQYILQQYLAASGGQKLLSSVRNSYAMGKVRMVATEFETGGRVV
RNRMAARATESGRFVLWQMAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHSAKGPV
RPLRRALQGLDPLTAASMFAARRLASLWHLEDLTSPGIQSTTGGDAVYWETTINSFIEDY
RPVEGIMVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTDI
KSGSISETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFK
>tr|W5BID2|W5BID2_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MEKERKQGFFAALKEEVVRGLSPARSRGKTPARSASPARMLIPRRRKAPPPPPEKQMEQQ
QYLPEQLIARSGSLRPGGEVLEPLIEGPDADRLAAGDFVGEDSGRREGFGHWVRGHLTRT
PSMASGSTGPGGSSGSFRHSDLRLLLGVMGAPLAPISSNLADPLPLLSIKGTPIESSSAQ
YILQQYMAASGGYKMLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGAAAVEQGGF
VLWTMAPGMWYVELAVGGSKVHAGCNGRLVWRHTPWLGAHAAKGPVRPLRRVLQGLDPLT

TAGLFAEARCVGEKKVNGEDCFILKLSADPQTLKLRSEGPAEIIRHVLFGYFSQRTGLIV
HIEDSHLTRIQPHS
>tr|A0A072U8X6|A0A072U8X6_MEDTR Plant/T8K14-16 protein OS=Medicago
truncatula GN=MTR_6g445110 PE=4 SV=1
MASRSARWRQSWAPQPLTPLMEGPDPEMQEEGGKKESSWETIREWFKAQKISPSGNISSQ
SFYGTIHAKTQDLRLLLGVLGCPLAPIPSDHDPALSIHHNHIKDTPFETSTAKYIIQQYL
AATGCLKQQKENKNMYATGMVKMICCETEISSGKNVKCLGTRSSENGCFVLWQMLPGMWS
LELVVGGHKIVAGSNGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKSTASLFTNAQCL
GENRIGNVDCFVLKVCADRETVIERSEGPAEVIRHILYGYFCQKSGLLIYLEDSHLTRVP
TQESDAVYWETTIGSSIGDYRDVDGILIAHQGRSIATVFRFGELSMQHSRTRMEEIWTID
DVMFNVPGLSMDHFIPPADILDNINSP
>tr|A0A022QK03|A0A022QK03_ERYGU Uncharacterized protein OS=Erythranthe
guttata GN=MIMGU_mgv1a007815mg PE=4 SV=1
MGSRSRRQLQRWCPQPLTPLMEGPDFGMEDHDCNKKETSWEVIREWFKIHRTVPVDNSFS
SSMPPSLYGPNSSSPAKMQDLRLLLGVLGCPLGPIPISDKPISHLHIKDIPLETSTAYYI
IQQYLAAAGCSKQQSLAKNMYTSGTVKLVRCETEISTGKSVRTMGSRSAENGCFVLWRMS
PGMWSLELSVGGHKVVAGSDGKIVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKSTASLFA
KAQCLGEKRIGEDDCFVLKVAADRAAVMERNEGPAEVIRHVLYGYFSQKSGLLIYMEDSH
LTRVHSEENDTVYWETTIGSSIGDYRDVDGVMIAHQGRTVATVFRFGETSMQHTRTKMEE
MWTIHDVVFNVPGLSGDSFIPPADILDTAQAVSP
>tr|A0A0A9GK08|A0A0A9GK08_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTTASM
FAGARCIGERKVNGEDCFILKLCTEPETLKARSEGLAEIIRHVMFGYFNQRTGLLVHIED
SHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTR
MEEAWTLEEVAFNVPGLSMDCFIPPTDVESGSVGEIMELSHGEKSKAVPPPGHRAKVAAL
EKAEDDKVAWGRTILKDHN
>tr|F6H9T4|F6H9T4_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VIT_19s0085g00900 PE=4 SV=1
MASRARKKQQRWCTQPLTPLMEGPDPEMQEEGTKKESSWEVIREWFRLQKGGGLGVHGSS
SFSLSLYGNIPSKTQDLRLLLGVLGCPLAPIPLATDPLHRLHIKDIPIETSSACYIIQQY
LAATGCLKQEKGMKNMYTTGTMKMICCETEISTGKSVKSLGTRSGENGCFVLWQMSPGMW
SLELVVGCNKVVAGSNGKIVWRHTPWLGTHAAKGPHRPLRRIIQGLDPKSTASLFAKAQC
LGEKRIGEDDCFVLKVAADRAAVMERNEGPAEVIRHVLYGYFSQKSGLLIYLEDSHLTRV
QAPGNDTVYWETTIGTSLWDYRDVDGVMIAHEGRTIATVFRFGEVSMQHSRTRMEELWVI
DDVVFNVPGLSFDYFIPPADIFDVDNSP
>tr|A0A0A9EDA8|A0A0A9EDA8_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MAPEMWYIELAVGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRALQGLDPLTTGSM
FAGARCIGERKVNGEDCFILKLCTEPGTLKARSEGLAEIIRHVMFGYFSQRTGLLVHIED
SHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMSHTKTR
MEEAWTIEEVAFNVPGLSMDCFIPPTDVKSGCVGETMELSHGEKSKAVPPPGHRAKVAAL
EKAEDDKVT
>tr|M0UV35|M0UV35_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MAPEKWYIELAVGGSKVHAGCNGKLVWRHTPWLGSHAAKGPVRPLRRALQGLDPLTAASM
FAGARCIGERKVNGEDCFILKLCTDPETLKARTEGLAEIIRHVMFGYFSQRTGLLVHIED
SHLTRIQSTTGGDAVYWETTINSFIEDYRPVDGIMIAHSGRSAVTLFRFGEVAMSHTKTR
MEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSVSETVELPHGEKNKFGPPHGHRAKVAAL
EKTDGDELAWRGTRT
>tr|I1KTV9|I1KTV9_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MGSRARWRQSWAPQPLTPLMEGPGPEMQEEGTKKESSWEVIREWFRTQKISPSGSFSQSS
SSFYGTIHAKTQDLRLLLGVLGCPLAPIPSAHDPTLSIHIKDTPFETSTAKYIIQQYLAA
TGCLKQQKDTKNMYATGMVKMICCETEISSGKNVKCLGTRSSENGCFVLWQMQPGMWSLE

LVVGDHKVVAGSNGKTVWRHTPWLGTHAAKGPQRPLRRLIQGLDPKTTASLFTNAQCLGE
NRIGTVDCFVLKVSADRAAVVERSEGPAEVIRHILYGYFCQKSGLLIYLEDSHLTRVPTQ
DNDTVYWETTIGSSIGDYRDVDGILIAHQGRSVATVFRFGELSMQHSRTRMEEIWTIDDV
MFNVPGLSMDHFIPPADIFDNINSP
>tr|A0A0B2QIT2|A0A0B2QIT2_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_026572 PE=4 SV=1
MGSRARWRQSWAPQPLTPLMEGPGPEMQEEGTKKESSWEVIREWFRTQKISPSGSFSQSS
SSFYGTIHAKTQDLRLLLGVLGCPLAPIPSAHDPTLSIHIKDTPFETSTAKYIIQQYLAA
TGCLKQQKDTKNMYATGMVKMICCETEISSGKNVKCLGTRSSENGCFVLWQMQPGMWSLE
LVVGDHKVVAGSNGKTVWRHTPWLGTHAAKGPQRPLRRLIQGLDPKTTASLFTNAQCLGE
NRIGTVDCFVLKVSADRAAVVERSEGPAEVIRHILYGYFCQKSGLLIYLEDSHLTRVPTQ
DNDTVYWETTIGSSIGDYRDVDGILIAHQGRSVATVFRFGELSMQHSRTRMEEIWTIDDV
MFNVPGLSMDHFIPPADIFDNINSP
>tr|A0A061FC68|A0A061FC68_THECC C-type mannose receptor 2 OS=Theobroma
cacao GN=TCM_033669 PE=4 SV=1
MGSRARRKQRWCTQTLTPLMEGPDPEMQEEGNKKESSWEVIREWFRTQKGLSASNFSMSL
YGSNSIPAKRQDLRLLLGVLGCPLAPIPLVNHPIHHIRVKDIPIETSTAHYIIQQYLAAT
GCLKQQKCAKSMYATGSVKMICCETEISSGKNVKSLGTRSGESGCFVLWQMLPGMWSLEL
VVGGNKVIAGSDGKTVWRHTSWLGTHAAKGPQRPLRRTIQGLDPKTTASLFAKAQCLGEK
RIGEDECFVLKVCADRAAVMERNEGPAEVIRHVLYGYFCQKSGLLIYLEDSHLTRVHTQE
NESVYWETTIGSSIGDYRDVDGVLIAHQGRSIATVFRFGELSMQHSRTRMEEVWRIDDVV
FNVPGLSIDSFIPPADIFDNVHSPSL
>tr|M0SB41|M0SB41_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MGAPLAPVHVSPTNSLPPLSIKDTPIETSTAQYILQQYTAATGGLKLLSSIRNSYAMGKV
TMVVSEFETASRVIKNRCSPKDAESGGFVLWQMAPDMWYVELAIGGSKVHAGCNGKLVWR
HTPWLGAHAATGSVRPLRRALQGLDPLAVVNVFADAHQKTGLLTCMEDSHLTRIQSSAGG
DAVYWETTINSRIHDYRPVEGMMIAHSGHSVVTLFRFGEVAMSHTKTRMEEAWSIEEVAF
NVPGLSMDCFIPPADVKKDGSVSEARELPPQAERGRSTMAGSHRAKVAALEKSHDVSDDN
IWWRVEV
>tr|S8BZY8|S8BZY8_9LAMI Uncharacterized protein (Fragment) OS=Genlisea
aurea GN=M569_14633 PE=4 SV=1
VLWQMNPDMWYVELSVGGSKVQAGCNGRLVWRHTPWLGAHAAKGPIRPLRRALQGLDPRT
TAAMFAGSVCTGEKAVNGEDCFVLKLAADHGTLKSRSEGPAEIIRHVMFGHFSQKTGLLV
HMEDSHLTRIQSNGGDAVYWETTISSSLDDYRRVEGTMIAHSGKSTVTLFRFGETPDSHM
KTRMEEAWTIEEVAFDIPGLSMDCFIPPADLRTGSMSEACDLP
>tr|I1MJE4|I1MJE4_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MGSKARWRQSWAPQPLTPLMEGPGPEMQEEGTKKESSWEVIREWFRTQKISPGGSFSQSS
SFYGTIHAKTQDLRLLLGVLGCPLAPIPSAHDPTLSIHIKDTPFETSTAKYIIQQYLAAT
GCLKQQKDTKNMYATGMVKMICCETEISSGKNVKCLGTRSSDNGCFVLWQMLPGMWSLEL
VVGDHKVVAGSNGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKTTASLFTNAQCLGEN
RIGTVDCFVLKVSADRAAVVERSEGPAEVIRHILYGYFCQKSGLLIYLEDSHLTRVPTQD
NDTVYWETTIGSSIGDYRDVDGVLIAHQGRSIATVFRFGELSMQHSRTRMEEIWTIDDVM
FNVPGLSMDHFIPPADIFDNINSP
>tr|A0A067F2A7|A0A067F2A7_CITSI Uncharacterized protein OS=Citrus
sinensis GN=CISIN_1g016543mg PE=4 SV=1
MSSKARRKQRWCTQTLTPLMEGPDPEMLEEGSKKESSWEVIREWFGIQKGISSGTNHNNF
SMSLEGSSIPAKRQDLRLLLGVLGCPLAPIPLVNDPILRIHIKDIPIETSSAHYIIQQYL
AATGCLKQQKRAKNMYATGTVKMVCCETEISSGKNVKSLGTRSGESGCFVLWQMLPGMWS
LELVVGGNKVIAGSDGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKITASLFAKAQCL
GEKRIGDDECFVLKVAADRAAVMERSEGPAEVIRHVLYGYFCQKSGLLIYLEDSHLTRVQ
TPENDTIYWETTIGSSIGDYSDVDGVLIAHQGRSIATVFRFGELSIQHSRTRMEEMWRID
DVVFNVPGLSMDYFIPPADIIDNEKSP

>tr|V4SEU9|V4SEU9_9ROSI Uncharacterized protein OS=Citrus clementina
GN=CICLE_v10005147mg PE=4 SV=1
MSSKARRKQRWCTQTLTPLMEGPDPEMLEEGSKKESSWEVIREWFGIQKGISSGTNHNNF
SMSLEGSSIPAKRQDLRLLLGVLGCPLAPIPLVNDPILRIHIKDIPIETSSAHYIIQQYL
AATGCLKQQKRAKNMYATGTVKMVCCETEISSGKNVKSLGTRSGESGCFVLWQMLPGMWS
LELVVGGNKVIAGSDGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKITASLFAKAQCL
GEKRIGDDECFVLKVAADRAAVMERSEGPAEVIRHVLYGYFCQKSGLLIYLEDSHLTRVQ
TPENDTIYWETTIGSSIGDYSDVDGVLIAHQGRSIATVFRFGELSIQHSRTRMEEMWRID
DVVFNVPGLSMDYFIPPADIIDNEKSP
>tr|M5WFW5|M5WFW5_PRUPE Uncharacterized protein OS=Prunus persica
GN=PRUPE_ppa006883mg PE=4 SV=1
MGSKARKKQIWCPQPLTPLMEGPDPEMQEEGGKKESSWEVIREWFRAQKGGLPNPGTNLS
TSGYGSGGTIPAKRQDLRLLLGVLGCPLAPIPQANDPIDHHLLHIKDIPFETSIAHYIIQ
QYLAATGCLKQQKCNKNMYASGSVKMVCCETEVSAGRNVKTLGTRSGESGCFVLWQMLPG
MWSLELVVGGNKVVAGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGLDPKSTASLFAKA
QCLGEKRIGEDDCFVLKVSADRAAVMERSEGPAEVIRHALYGYFCQKSGLLIYLEDSHLT
RVEAPENETVYWETTIGSSIADYRDVDGVLIAHQGRSIATVFRCGEVSMEYTRTRMEEAW
SIDDVVFNVPGLSMDYFIAPADILDSTLQSP
>tr|V7BX84|V7BX84_PHAVU Uncharacterized protein OS=Phaseolus vulgaris
GN=PHAVU_005G047500g PE=4 SV=1
MPQMGSRARWRQSWAPQPLTPLIEGPGPEMQEEGTKKESSWEVIREWFRTQKISPGGSFS
QSFYGTIHAKTQDLRLLLGVLGCPLAPIPSAHDPTLSIHIKDTPFETSTAKYIIQQYLAA
TGCLKQQKDTKNMYATGTVKMICCETEISSGKNVKCLGTRSSENGCFVLWQMLPGMWSLE
LVVGDHKVVAGSNGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKTTASLFTNAQCLGE
NRIGTVDCFVLKVSADRAAVVERSEGPAEVIRHILYGYFCQKSGLLIYLEDSHLTRVPTQ
DNDTVFWETTIGSSISDYRDVDGVLIAHQGRSIATVFRFGELSMQHSRTRMEEIWTIDDV
MFNVPGLSMDHFIPPADIFNNISSP
>tr|B9HYB8|B9HYB8_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0010s18140g PE=4 SV=1
MGSRARRKQRWSTQTLTPLLEGPDPDMQEEGNKKESSWEVIREWFRLQKGLPAGNSFSVS
LHGSIPVKGQDLRLLLGVLGCPLAPIPLVNDPIHRIHIKNTPIENSAAHYIIQQYLAATG
CLKQQKCMKNMYSTGSVKMIRCETEISSGKNVKSLGTRSGENGCFVLWQMLPGMWSLELV
VGENKVIAGSDGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKSTASLFAKAQCLGEKR
IGEDDCFVLKVAADREAVMERSEGPAEVLRHVLYGYFCQKSGLLMYLEDSHLTRVQTPEN
ETIYWETTIGSSIGDYRDVDGVLIAHQGRSIATVFRFEEVSVQHSRTRMEEVWRIDDVVF
NVPGLSMDYFIPPADIYDASP
>tr|A0A067L871|A0A067L871_JATCU Uncharacterized protein OS=Jatropha
curcas GN=JCGZ_19692 PE=4 SV=1
MGSRTRRKQRWCTQTLTPLLEGPDPDMQEEGNKKESSWEIIREWFRLQKGFSGTNNNFSS
ISPYGSFSPANKGQDLRLLLGVLGCPLAPIPLVSDPIHRIHIKDIPMENCIAHYIIQQYL
AATGCLKREKSVKNMYATGSVKMIRCETEISSGKNVKSLGTRSGENGCFVVWQMLPGMWS
LELVVGGNKVIAGSDGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKSTANLFAKAQCL
GEKRIGEDDCFVLKVAADRAAVMERSEGAAEVLRHVLYGYFCQKSGLLIYLEDSHLTRVQ
TPENDTIYWETTIGSSIGDYRDVDGTLIAHQGRSIATVFRFEEESVQHSRTRMEEIWRID
DVVFNVPGLSLDYFIPPADIFDVSP
>tr|B9HI31|B9HI31_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0008s08120g PE=4 SV=1
MGSRARWKQRWCTQTLTPLLEGPDPDMQEEGNKKESSWEIIREWFRLQRGLSAGNNFTVS
LYGSIPAKRQDLRLLLGVLGCPLAPIPLVNDPIHRIHIKNTPIENSAAHYIIQQYLASTG
CLKQQKCMKNMYSAGSVKMVRCETEISSGKNVKSLGTRSGESGCFVLWQMLPGMWSLELV
VGENKVIAGSDGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKNTANLFAKAQCLGEKR
IGEDDCFVLKVAADREAVFERSEGPAEVLRHVLYGYFCQKSGLLIYLEDSHLTRVQTPEN
ETIYWETTIGSSIGDYRDVDGVLIAHQGRSIATVFRFEELSVQHSRTRMEEVWRIDDVVF
NVPGLSMDYFIPPADIFDASP

>tr|B9SAN3|B9SAN3_RICCO Putative uncharacterized protein OS=Ricinus communis GN=RCOM_1234790 PE=4 SV=1
MGSRVRRKQRWCTQTLTPLMEGPDPDMQEDGNKKESSWEVIREWFRLQKSFSSNNYSSIS
PDGSMPANSKRQDLRLLLGVLGCPLAPIPLVTDFNFHNNFHIKGVPMENSIAHYIIQQYL
AATGSLKREKEMRNMYATGSVKMVRCETEISSGKNVKSLGTRTGENGCFVMWQMLPGMWS
LELVVGGNKVIAGSNGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKSTASLFAKAQCL
GEKQIGKEDCFVLKVAADRSAVMERSEGAAEVLRHVLYGYFCQKSGLLIYLEDSHLTRVQ
TSENDIIYWETTIGSSIDDYRDVDGVLIAHQGRSIATVFRFEEESVQHSRTKMEEIWRIG
DVVFNVPGLSLDYFIPPADIFDASP
>tr|U5D0K5|U5D0K5_AMBTC Uncharacterized protein OS=Amborella trichopoda GN=AMTR_s00032p00188960 PE=4 SV=1
MGKGLLLNSHGAYKSNWNSRKFTDLKLLLGVLGCPLAPVAVTNEPIPHISIKDTPIETSS
AHYIIQQYIAATGCSKLRTGIKNMYTTGSLTMTCSETETGGGKTGRVRNNGGSIERGCFV
LWQMKNSTNDMWSVELAVGGMKLLAGSNGKVVWRHTPWLGTHAAKGSPRPLRRVIQGLDP
RTTASMFAHAQCMGEKRAGEEDCFVLKVAADRRTVVERSEGPAEVIRHALYAYFSQRSGL
LIQVEDSHLTRVQATPSDTLYWETTISTTIGDYREVDGVLIAHSGRSTATIFRFGDDSSR
QGRSKMDEWWRIEDVVFNVPGVCVDSFIPPSDVGAGLPPS
>tr|A0A0L9UIM7|A0A0L9UIM7_PHAAN Uncharacterized protein OS=Phaseolus angularis GN=LR48_Vigan05g035400 PE=4 SV=1
MPQMGSRARWRQSWAPQPLTPLIEGPGPEMQEEGTKKESSWEVIREWFRTQKISPAGSFS
QSFYGTIHAKTQDLRLLLGVLGCPLAPIPSAHDPTLSIHIKDTPFETSTAKYIIQQYLAA
TGCLKQQKDTKNMYATGMVKMICCETEISSGKNVKCLGTRSSENGCFVLWQMLPGMWSLE
LVVGDHKVVAGSNGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKTTASLFTNAQCLGE
NRIGTVDCFVLKVSADRAAVVERSEGPAEVIRHILYGYFCQKSGLLIYLEDSHLTRVPTQ
DNDTVFWETTTGSSIGDYRDVDGVLIAHQGRSIATVFRFGELSMQHSRTRMEEIWTIDDV
MFNVPGLSMDHFIPPSDIFNNISSP
>tr|S8DTM8|S8DTM8_9LAMI Uncharacterized protein (Fragment) OS=Genlisea aurea GN=M569_08266 PE=4 SV=1
QQQQQRWSPQPLTPLMEGPDLGTEDSEGSKKESSWEVIREWFGIHRSGNEKTSCCSSPAA
AMYGPAKSQDLRLLLGVLGCPLAPIPISREPLSGVHIRDIPIEASTAYYIIQQYLAATGC
SKRGGGAKSMYAAGTVKLIRCETEISTGKSVRTIGSRSGDAGCFVLWQMSPAMWSLELAV
AGNKVVAGGDGKIVWRHTPWLGAHAAKGPQRPLRRIIQGLDPRLTASLFEKAQCLGEKQI
GGDECFVLKVAADRAAVMERNEGPAEVIRHVLYGYFSQRSGLLVYMEDSHLTRVHSAAEN
DDAVYWETTIGSSIGDYRGVDGVMIGHRGRTVATVFRFGETSAQHSRTRMEEIWKINDVV
FNVPGLSVDSFIPPAEILE
>tr|B9HHJ4|B9HHJ4_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_0008s06280g PE=4 SV=1
MRKLCPNFDREDGLETVLEVPIPEEMFASNKHSNRSWQNMKAWMRPHSERSMTTLFGGKN
TEIQLLLGVVGAPLIPLQIRCDHQLINCNIKDQPIEASMAKYIVQQYIAAVGGERALNSV
DSMYAMGKVKMEASEFCAGEGSLNSNKVLRVKNQNHGGGEMGGFVLWQKRPDLWCLELVV
SGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPKSTANLFSNSVCTGEKAI
NNEDCFVLKLEAEPSSLRARSSSNVEIIRHTLWGYFSQRTGLLVQLEDSHLLRIKASGND
SIFWETTMESTIQDYRTIDGINIAYKGRTSVSLFRFGETSESHSRTRMEEVWAIEEVDFN
IKGLSMDCFLPPSDIKKEEEGCDNVVISNNARLPFKIRSASSRINASKVVAVDDVHDSDE
NEDEDDQQ
>tr|A0A0D2UYP9|A0A0D2UYP9_GOSRA Uncharacterized protein OS=Gossypium raimondii GN=B456_009G354700 PE=4 SV=1
MGTRARRKQSWYTQTLTPLLEGPMDPEMQEEGNKKERSWEVIREWFRTQKGSSFSSSPTS
FSMSNYFYGNGSIPPARRHDLRLLLGVLGCPLAPIPLLNHPIHHIRLKDIPIETSTAHYI
IQQYLAASGCLKQRQKCGAKNMYATGRVKMICCETEISRGSGKGKNIVKSLGTRSEEMGG
CFVVWQMKPEMWSLELVVGGNKVIAGSDGKTVWRHTSWLGTHAAKGPQRPLRRIIQGLDP
KTTASLFAKAQCLGEKRIGDEDCFVLKVCADRAAVMERNEGPAEVMRHVLYGYFSQKSGL
LIYLEDSHLTRVQTQEENEGGCACAYWETTIGSCIGDYRDVDGVLIAHQGRSIATVFRFG
ELSMQHSRSRMEEFWSIDDVVFNVQGLSIDSFIPPADIFDR

>tr|A0A0B0P6K1|A0A0B0P6K1_GOSAR Uncharacterized protein OS=Gossypium arboreum GN=F383_24628 PE=4 SV=1
MGTRARRKQSWYTQTLTPLLEGPMDPEMQEEGNKKERSWEVIREWFRTQKGSSFSSSPTS
FSMSNYFYGNGSIPPARRHDLRLLLGVLGCPLAPIPLLNHPIHHIRLKDIPIETSTAHYI
IQQYLAASGCLKQRQKCGAKNMYATGSVKMICCETEISRGSGKGKNIVKSLGTRSEEMSG
CFVVWQMKPEMWSLELVVGGNKVIAGSDGKTVWRHTSWLGTHAAKGPQRPLRRIIQGLDP
KTTASLFAKAQCLGEKRIGDEDCFVLKVCADRAAVMERNEGPAEVMRHVLYGYFSQKSGL
LIYLEDSHLTRVQTQEENEGGCACAYWETTIGSSIGDYRDVDGVLIAHQGRSIATVFRFG
ELSMQHSRSRMEEFWSIDDVVFNVQGLSIDSFIPPADIFDR
>tr|W9QYT6|W9QYT6_9ROSA Uncharacterized protein OS=Morus notabilis GN=L484_019238 PE=4 SV=1
MGSKPRKKQVWCPQPLTPLMEGPDPEMQEEGSKKESSWEVIREWFRAQKGFQGSSNINSV
SSSSSSTSSSTSSSYGCNIPAKRQDLRLLLGVLGCPLAPIPQVNHPIDHHHLLHLKDIPF
ETSIAHYIIQQYLAATGCLKQQKCNKNMYASGIVKMICCETEVSTGRNVKSLGTRSGESG
CFVLWQMTPGMWSLELVVGGNKVVAGSDGKTVWRHTPWLGTHPAKGPQRPLRRLIQGLDP
KSTASLFAKAQCLGEKRIGDDNCFVLKVSADRAAVMERSEGHTEVIRHALYGYFCQKSGL
LIYLEDSHLTRVESPDNDTTADTVYWETTIGSSIGDYRDVDGVLIAHQGRSIATIFRCSE
LSMQYTRTRMEELWSIDDVVFNVPGLSVDSFLPPADILDGVH
>tr|M0T2M0|M0T2M0_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1
MRKLWPNLDREDGLDTVLEVPIPEEMFLSGDSSKSSKTLCTNVKAWVRPHVDRSPPSPIG
RGAELQLMLGVIGAPLVPLPVQAYKSTLIRDMKEDPIEVSMAKYIVQQYIAASGGEQALN
AINSMYAMGKVRMTASGLPKGNGGGHGDATDGKKAKKCGGAGEMGGFVLWQKKPDLWCLE
LMVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPRCTANLFANSVCLGE
KTINGEDCFVLRLDAEAATLRARSSSSVEIIRHTVWGYFSQRTGLLVQLEDSHLLRIKSA
VQESVYWETTMESLIEDYRPIDGVNIAHAGRTSVSLFRFGETSDGHTRTRMEETWTVEEV
DFNIWGLSMDCFLPPADLKEEKEGGDVGGVAAAATKSARPPFRVQQAVARIGISQVAAVD
VDESDSTSTEEEDGSQ
>tr|A0A0B2SWF5|A0A0B2SWF5_GLYSO Uncharacterized protein OS=Glycine soja GN=glysoja_019368 PE=4 SV=1
MGSKARWRQSWAPQPLTPLMEGPGPEMQEEGTKKESSWEVIREWFRTQKISPGGSFSQSS
SFYGTIHAKTQDLRLLLGVLGCPLAPIPSAHDPTLSIHIKDTPFETSTAKYIIQQYLAAT
GCLKQQKDTKNMYATGMVKMICCETEISSGKNVKCLGTRSSDNGCFVLWQMLPGMWSLEL
VVGDHKVVAGSNGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKTTASLFTNAQCLGEN
RIGTVDCFVLKVSAVVERSEGPAEVIRHILYGYFCQKSGLLIYLEDSHLTRVPTQDNDTV
YWETTIGSSIGDYRDVDGVLIAHQGRSIATVFRFGELSMQHSRTRFGELSMQHSRTRMEE
IWTIDDVMFNVPGLSMDHFIPPADIFDNINSP
>tr|A0A061FTG4|A0A061FTG4_THECC Emb:CAB81597.1 OS=Theobroma cacao GN=TCM_042631 PE=4 SV=1
MRKLCPNYDLPDGLDTVLEVPIPEEMFASNKSSHRSWQNMKSWMNMKPNSERPPASMTVL
FGGRNTEIQLLLGVIGAPLIPLPIKIDHDHSISKNIKDHPIEASMAKYIVKQYIAAIGGE
QALNSIDSMYAMGKVKMAASEFCAGEGSVNNRIVKVRNLRNGGGEMGGFVLWQKRPDLWC
LELVVSGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFSNSVCV
GEKTINDEDCFILKLEAEPSTLRARSSSNVEIIRHTVRGYFSQRTGLLVQLEDSHLLRIK
APGNDSIFWETTMESWIQDYKTIDGINIAHAGKTWVSLFRFGENSESHSRTRMEEAWTIE
EVDFNIKGLSMDCFLPPGDLNKEEEGYGIVSSNVRLPFKLRNGSTRVSASKIVAIDVDEC
DNSSDDEDL
>tr|D7TMI8|D7TMI8_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_13s0019g03180 PE=4 SV=1
MRKLCPNFDREDGLDTVLEVPIPEEMFPSHKSTSLSWQNVKSWMKSNPERSATSIFGGRN
TEIQLLLGVVGAPLIPLPVRCDRHPINQSIKDHPIEASMAKYIVQQYIAAAGGETALNSI
DSMYAMGKVRMVTSEFSAGEVCKNKAMKVKGVRHGGGEMGGFVLWQKRPELWCLELVVSG
CKISAGSDGVVAWRQTPWHHSHASRGPPRPLRRALQGLDPRSTANLFSNSVCIGEKTINE
EDCFILKLETETSTLRARSSRNVEIMRHTVWGYFSQRTGLLVQLADTHLLRIKSSADDSI

FWETTMESLIQDYRTIDGVNIAHAGTTAVSLFRFGENSESHSRTRMEERWTIEEVDFNIK
GLSTDCFLPPGDLKKVDEEGCDVVVGSNTKLPFKIPAASSRVSAAKVVAIDVDDSYNIDD
DDDDEL
>tr|B9HT30|B9HT30_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0010s20240g PE=4 SV=2
MRKLCPNFDREDGLDTVLEVPIPEEMFASNKHGNRSWQNMKAWMRPHNERSMTTRFGGKN
TEIQFLLGVVGAPLIPLPILCDHQFINRNIKDHPIESSMAKYIVQQYIAAVGGERALNSV
DSMYAMGKVKMVASEFCAGEGSLNNNKTLKVKNQKHGGGEMGGFVLWKKRPDLWCLELVV
SGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPKSTANLFSNSVCTGEKTI
NNEDCFVLKLEADPSSLRARSTSNVEIIRHTVWGYFSQRTGLLVQLEDSHLLRIKAPGND
SIFWETTMESSIQDYRTIDGINIAYKGRTSVSLFRFGETSESHSRTRMEEIWAIEEVDFN
IKGLSMDCFLPPSDLKKEEEVCDNVAISNSARLPFKFRSASSRICVSKVVAIDDVDDSDE
IYDEDEDRE
>tr|A0A067L8S0|A0A067L8S0_JATCU Uncharacterized protein OS=Jatropha
curcas GN=JCGZ_01346 PE=4 SV=1
MRKLCPNFDREDGLDTVLEVPIPEEMFASNKSGNRSWQNLKAWMRPNANSERSMANLFGG
RNTEIQLLLGVVGAPLVPLPICCDHQFKNRNFIDQPIEASMAKYIVQQYIAAVGGEKALN
SIDSMYAMGKVKMGASEFCAGEGSLKDSKVVKMKNLMNGSGGEMGGFVLWQKNPDLWCLE
LIVSGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPKTTANLFSNSICVGE
KTIGDEDCFILKLEAEPSLLRARSSSNVEIIRHTVWGYFSQRTGLLVQLEDSHLLRIKAS
RNESIFWETTMESKIQDYKTIDGMINIAHGGRTSVTLFRFGENSESHSRTRMEEIWNIEE
VDFNIKGLSMDCFLPPSDLKKEAEDGGYGVVSSNAKFPLKMRSASTRISASKVVALDVDD
SDTSSEDDDDDQD
>tr|A5BGB9|A5BGB9_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VITISV_019369 PE=4 SV=1
MRKLCPNFDREDGLDTVLEVPIPEEMFPSHKSTSLSWQNVKSWMKSNPERSATSIFGGRN
XEIQLLLGVVGAPLIPLXVRCDRHPINQSIKDHPIEASMAKYIVQQYIAAAGGETALNSI
DSMYAMGKVTMMASEFSAGEVCKNKAMKVKGVRHGGGEMGGFVLWQKRPELWCLELVVSG
CKISAGSDGVVAWRQTPWHHSHASRGPPRPLRRALQGLDPRSTANLFSNSVCIGEKTINE
EDCFILKLETETSTLRARSSRNVEIMRHTVWGYFSQRTGLLVQLADTHLLRIKSSADDSI
FWETTMESLIQDYRTIDGVNIAHAGTTAVSLFRFGENSESHSRTRMEERWTIEEVDFNIK
GLSXDCFLPPGDLKKVDEEGCDVVVGSNTKLPFKIPAASSRVSAAKVVAIDVDDSYNIDD
DDDDEL
>tr|A0A059A8W9|A0A059A8W9_EUCGR Uncharacterized protein OS=Eucalyptus
grandis GN=EUGRSUZ_J00255 PE=4 SV=1
MRKLCPNYEREDGLETVLEVPIPEEMFAPASKSSNRPWAHMKSWMWSSGHNKPAPALATL
LGGGRSAEVQLLLGVVGAPLVPLPISPRDHPDAPFAAHIKDHPIEASMAKYIVQQYVAAS
GGEQALGAVESMYAMGKVRMAVSELCSGEEGRAKAAVATVKSTRHGAGEVGGFVLWQKRP
ELWCLELVVSGYKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTSDLFSN
SVCIGEKAINNEDCFVLKLEAEPYTLRARSSSNVEIIRHTLWGYFSQRTGLLVQLEDSHL
LRIKSTSSESVLWETTMESLIQDYRTIDGINIAHAGRTSVSLFRFGENKESHSRTRMEEV
WAIEEVDFNIKGLSMDCFLPPADLKKEEDVCGVVPSYARVPFNVRSSSAKMSASKVVALD
IDDSYDVQGDEEL
>tr|B9SWN1|B9SWN1_RICCO Putative uncharacterized protein OS=Ricinus
communis GN=RCOM_0497920 PE=4 SV=1
MRKLCPNFDREDGLDTVLEVPIPEEMFGSNKNGNRSWQNMKAWIRPQTDKSIANLFGGKN
TEIQLLLGVVGAPLIPLPIRCDHQFINRNMKDEPIEASMAKYIVQQYIAAVGGEGALNSV
DSMYAMGKVRMAASEFCAGEGSLNNKVLKVKNMRNGGGEMGGFVLWQKRPDLWCLELVVS
GCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPKSTANLFSNSICAGEKAIN
GEDCFILKLEAETSSLRARSTSNVEMIRHTVWGYFSQRTGLLVQLEDSHLLRIKASGNDS
IFWETSMESTIHDYRTIDGINIAHGGRTSVSLFRFGENSESHSRTRMEEVWTIEEVDFNI
KGLSMDCFLPPSDLKKDGEESYVVTGNAKLPLKMRSTSTRISSSKVVAIDVDDSDNSDDE
DLDEY

>tr|A0A068VIZ1|A0A068VIZ1_COFCA Uncharacterized protein OS=Coffea canephora GN=GSCOC_T00009473001 PE=4 SV=1
MRTLCPNLDREDALETVLEVPIPEEIFASTKNRSWQNVKSWMKSHTERSPVSLFGGRNTE
IQLLLGVVGAPLVPLPICSDRYSFSKSIKNHPIETSMAKYIVQQYIAAAGGENALNSIHS
MYAMGKVKLATTEVVAGEGLSMSCNNTSNGKASKLKSTKGGPGEVGGFVLWQKRPDLWSL
ELVVSGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRSLQGLDPRSTANLFSNSICTG
EKTVYDEDCFVLKLEADPSTLRARSSSNVEIIRHSVWGYFSQRTGLLLQLEDSHLLRIKA
PGNDVLWETTMESTIQDYRTIDGVNVAHAGRTCVSLLRFGENSESRTRTRMEEVWTIEEV
DFNIKGLSIDCFLPPADLKKEDEGCGIVPSSRVSRNAKSPFKVRPNASSRVSAAAKSAAK
VAAIDEDDLETIEDEDEEL
>tr|A0A0A0L1R2|A0A0A0L1R2_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_4G280480 PE=4 SV=1
MATAVEIGNGGSSSSSSSKSRRSKQIWYSQPLTPLMEGPDPQFQDQEPNKKDSSGSNWE
FLRDWFKIQRNLTPSISQSSFTNLPNSKTQDLKLLLGVLACPLAPIPLHSNNSPPQTSYF
PPHIPLETSVPHYIIQQYLAATGCLKQQKCAKNMYATGSVKMIRCETEVSSGKSVKTVGT
RCEDTGCFVLWQMLPAMWSLELVVGGSKVVAGSDGNTVWRHTPWLGTHAAKGPQRPLRRI
IQGLDPKSTARLFEKAQCLGEKRIGEDDCFVLKVSAEREAVMERNEGPAEVIRHVLYGYF
CQKSGVLVYLEDSHLTRVQTEGDAVYWETTIGSCIGDYRDVDGVLIAHRGRSIATVFKFG
EMSTQFSRTRMEEIWSIDDVMFNVAGLSMDYFIPPADIFDSLHSHSHPHSHSHSP
>tr|A0A022R6L1|A0A022R6L1_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a025448mg PE=4 SV=1
MRTLCPNLDREDALETVLEVPVPEEMISSNKHNSWQTIRSWMLRPPLDAAAVSSVLGGRT
AEIQFLLGVIAAPLIPLPIRCDRTTVGDNIKSCPIESSMAKYIVQQYVAAAGGEHVLNSI
NSMYAVGKVKMAASEFLSGDDLSLGNNSKAGKLKNMKNGRGEIGGFVLWQKRPDLWSLEL
MVSGYKISAGSDGKVAWRQTPWQHSHASRGPPRPLRRSLQGLDPRSTANLFSNSICIGEK
TINGEDCFVLKMEAEPSTLRARSSTKVEIIRHTLWGCFSQRTGLLVQLEDSHLLRIKAPK
NDVFWETTMESSIQDYRTVEGVNIAHSGKTSVSLFRFGENSESHTRTKMEEIWSIEEVDF
NIKGLSMDCFLPPADLKREDEGSGVINVADCDDLTKNGGVPYKFMANSYRVVGGKGGSKV
VAVDEE
>tr|A0A0K9S437|A0A0K9S437_SPIOL Uncharacterized protein OS=Spinacia oleracea GN=SOVF_002250 PE=4 SV=1
MRTLCPNFDREDGLETVLEVPIPEEMFPSAKNKWPNMKSWMKPNPGRTPATLPFADRNSQ
IQLLLGVIGAPLIPLPIPSDHKVTKCIKDHPIESSMAKYIIHQYIAAMGGEHALNSIDSM
YAMGKVKMTASEFSAGENLSVNNPKADNKVVKVKGLKNGGEVGGFVLWQKKPDLWCLELV
VSGTKISAGSDGKVAWRQTPWHNSHASRGPPRPLRRSLQGLDPRMTANLFTNAICIGEKV
VNDEDCFVLKLEANPSTLEARSSSNVEIIRHTVWGYFSQRTGLLVQLEDSHLLRIKTSKS
DSIFWETTMESLIQDYQTIDGVNIAHSGKTSVSLFRYGENSENHSRTRMEEIWTIEEVDF
NIKGLSMDCFLPPSDLKKEDDGFTAVVPNSIKPTTTKTQNAAKAANTKMSTAKVAAVDDH
HTENLDGSERM
>tr|A0A0J8D217|A0A0J8D217_BETVU Uncharacterized protein OS=Beta vulgaris subsp. vulgaris GN=BVRB_2g024610 PE=4 SV=1
MRTLCPNFDREDGLETVLEVPIPEEMFPSSKNKWPNMKSWMKTNPGRAPASYPFADRNSQ
IQLLLGVIGAPLIPLPIPSDHKVNKCIKDHPIESSMAKYIIHQYIAAMGGDHALNSIDSM
YAMGKVKMMASEFSAGEGLSVHNPKSDTNKVVKVKGMRHGGEVGGFVLWSKKPDLWCLEL
VVSGTKISAGSDGKVAWRQTPWHNSHASRGPPRPLRRSLQGLDPRLTANLFTNAICIGEK
LVNDEDCFVLKLEANTSTLEARSSSNVEIIRHTVWGYFSQRTGLLVQLEDTHLLRIKTSK
SDSIFWETTMESQIQDYQTIDGVNIAHSGKTSVSLFRYGENSENHSRTRMEEVWSIEEVD
FNIKGLSMDCFLPPADLKKEDEGFAGVVPNNIKPTTKTQNIPKVVNTKVSTAKVAAVDDH
HSENLDGSERM
>tr|W9RT16|W9RT16_9ROSA Uncharacterized protein OS=Morus notabilis GN=L484_005858 PE=4 SV=1
MRKLCPNFDREDALETVLEVPIPEEMFASSNKSAVISWQNMKAWMRSSDRSQHPSNMAAV
FGGRHAEIQLLLGVVGAPLIPLPIACDHQIITRNIKDHPIEASMAKYIVKQYIAAIGGEK
ALNSIESMYAMGKVKMAASDFCSREKSLNSNKGMKMKSLRSQGEMGGFVLWQKGPELWCL

ELVVSGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFSNSVCVG
EKAINDEDCFILKLEADSSILRARSSNNVEIIRHTVWGYFSQRTGLLVQLEDSHLLRIKA
ASSENNDSIFWETTMESLIEDYRTVDGVNIAHAGRTSVSLFRFGENSQSHSRTGMEEVWA
IEEVDFNIKGLSMDCFLPPADLKKEDQETCGGLVTSTTTNARLPFKIRSASLRISASKVA
AVDLDDHENIISTSTDDDDDEHEEEEF
>tr|I1LML7|I1LML7_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MKKLCPNLDREDGLETVLEVPIPEEILTHKSGTTKAWHNMKNWMKPHAESRSNSASMAAV
FGGKNTEIQLLLGVVGAPLIPSPIASDNQPITRSIKDQHIEVSMAKYIVKQYVAAVGGER
ALNSVDSMYAMGQVKMATSEFSAGEGSVNSKKVKNLQMKGEVGGFVVWQKRPELWCLELV
VSGYKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFSNSICIGEKT
VNNEDCFILKLEAESSTLRARSNSNVEIVRHTVWGYFSQRTGLLVQLEDSHLLKLKSHES
ESIYWETNMESLIQDYRTVDGIQVAHAGKTWVSLFRFGGGPETHSRTRMEEVWQVEEVDF
NVKGLSIDCFLPPSDLKREEEENDQECGGGGVAISNNNAKLPYKIRSASFRISASKVAAV
NLDDSSCTSSESDEDL
>tr|A0A0B2Q9E1|A0A0B2Q9E1_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_017916 PE=4 SV=1
MKKLCPNLDREDGLETVLEVPIPEEILTHKSGTTKAWHNMKNWMKPHAESRSNSASMAAV
FGGKNTEIQLLLGVVGAPLIPSPIASDNQPITRSIKDQHIEVSMAKYIVKQYVAAVGGER
ALNSVDSMYAMGQVKMATSEFSAGEGSVNSKKVKNLQMKGEVGGFVVWQKRPELWCLELV
VSGYKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFSNSICIGEKT
VNNEDCFILKLEAESSTLRARSNSNVEIVRHTVWGYFSQRTGLLVQLEDSHLLKLKSHES
ESIYWETNMESLIQDYRTVDGIQVAHAGKTWVSLFRFGGGPETHSRTRMEEVWQVEEVDF
NVKGLSIDCFLPPSDLKREEEENDQECGGGGVAISNNNAKLPYKIRSASFRISASKVAAV
NLDDSSCTSSESDEDL
>tr|K4C1W6|K4C1W6_SOLLC Uncharacterized protein OS=Solanum lycopersicum
GN=Solyc05g052860.2 PE=4 SV=1
MRTLCPNLDNEDGLETVLEVPIPEEMFVNASHKNNVKSWQNMKSWIKSHSGNNNHHDNYY
YKSSAVSVIGGRNAEIQLLLGVVAAPLIPHPIKCNNHSLNKKINDHPIETSMAKYIVQQY
IAAAGGEHALNSINSMYAMGKVKMIASEFIEGDGLGLNSGKVMKIKTAKNGAGEMGGFVL
WQKRPDLWSIELVVSGCKISAGSDGKVSWRQTPWHHSHASRGPARPLRRSLQGLDPRSTA
DMFSDSICIGEKPVNGEDCFVLKFEAEPSSLKARSSSNVEIMRHTVWGYFSQRTGLLVQL
EDSHLLRLKSPKDDVFWETTMESLVQEYRTIDGVNIAHSGKTCVSLFRFGENSEGHTRTR
MEEVWTIEEVDFNIKGLSLDCFLPPSDMKKDDDQDIISDDDDINKNSRIEPKNNVIHNAN
NPKFITAIKGAAKIMAIDEDSQD
>tr|Q9FFJ4|Q9FFJ4_ARATH Emb|CAB81597.1 OS=Arabidopsis thaliana
GN=At5g05840 PE=4 SV=1
MRKLCPNYNLEDGLETVLEVPMPEELFAASKTKPGWNQMKSYWSKPTATATGTATATNMT
RLFGGRNAEIQLLLGVVGAPLIPLPVQPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYI
AAVGGDRALNAVESMYAMGKVRMTASEFCTGEGSLNSKMVKARSIKSGGGEVGGFVLWQK
GIELWCLELVVSGCKISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLF
ARSVCMGEKKINDEDCFILKLDAEPSALKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDS
HLLRIKAQDDNSIFWETTMESLIQDYRTVDGILVAHAGKSSVSLFRFGENSDNHSRTRME
ETWEIEEMDFNIKGLSMDCFLPPSDLKKDDDEEEEIECGLAANNEKLPMKIRSASLRISS
SKVLAIVEEEDESEVTEET
>tr|R0GRT3|R0GRT3_9BRAS Uncharacterized protein OS=Capsella rubella
GN=CARUB_v10002699mg PE=4 SV=1
MRKLCPNYNLEDGLETVLEVPMPEELFAASKTKPGWNQMKSYWSKPTATATGTATATNMT
RLFGGRNAEIQLLLGVVGAPLIPLPVQPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYI
AAVGGDRALNAVESMYAMGKVRMTASEFCTGEGSLNSKMVKARSIKSGGGEVGGFVLWQK
GIELWCLELVVSGCKISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLF
ARSVCMGEKKINEEDCFILKLDAEPSALKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDS
HLLRIKAQDENSIFWETTMESLIQDYRTIDGIQVAHAGRSSVSLFRFGENSDNHSRTRME
ETWEIEEMDFNIKGLSMDCFLPPSDLKKDDDEEEEVECGLAANNEKLPMKIRSASLRISS
SKILAIVEEEEDESEVTEET

>tr|V4KBR6|V4KBR6_EUTSA Uncharacterized protein OS=Eutrema salsugineum GN=EUTSA_v10018620mg PE=4 SV=1
MSNSKSYWRKQRWGTPPQTLTPLMEGPDPDMQDERAKKESSWEAIREWFKVQKSISGNMS
SPSVQPLCNSYDVVAKGQDLRLLLGVLGCPLAPISVVVVSDLLSDDPLLGSFQIKNVPFE
TSTAHYIIQQYLAATGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSG
DSGCFVLWQMQPGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQG
LDPKTTAGLFAKAQCLGERRIGDDDCFVLKVSADRDSLIERNDAGAPAEVIRHALYGYFC
QKSGLLIYLEDSHLTRVTTISPEDEAVYWETTIGSSIGDYRDVDGVAVAHCGRAVATVFR
FGETSLQYSRTRMEEIWRIDDVVFDVPGLSLDSFIPPADIFEDDNINNIHSHVNSR
>tr|M5XT29|M5XT29_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa005740mg PE=4 SV=1
MKKLCPNLDREDGLETVLEVPIPEEMFDTDNNKNNNTISWHNMKSWMKLSNTDRSQINTV
FGSKNAEVQLLLGVIGAPLIPLPIPKDHQPITRTIKDQPIEASMAKYIVKQYIAAVGGEK
ALNSVESMYAMGKVKMAASEFSTGERSLNSNNNKVKVKSLLRSTGGGGEMGGFVLWQKRP
ELWCLELVVSGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRLLQGLDPRSTANLFSN
AVCIGEKAINDEDCFILKLEADPSTLRARSSNNVEIIRHSVWGYFSQRTGLLVQLEDSHL
LKIKASSGTDSGIFWETTMESYVRDYRTVDGINIAHGGSTSVSLFRFGESSETHSRTRME
EVWEIEEVDFNIKGLSMDCFLPPGDLKKEEEEAKCGANAMVISAHSKMPFKIRSASWRIS
ASKVVAFDDDVEYDPDNSESSSDQEL
>tr|A0A0K9PMQ4|A0A0K9PMQ4_ZOSMR Uncharacterized protein OS=Zostera marina GN=ZOSMA_211G00190 PE=4 SV=1
MGSRDGERRTGRWRVQAALTPLIEGPDSEVKEEEVLKEKESSWDVIRSWFRARTIHSGGG
GGCRSSMDLKLTLGVLGCPLAPVAFPGSCESDQIPSPPPQDVPIETSSAHYIIQQYLAAT
GCSKVQSTVKNVYTTGTVRMLCHGTETSNGKNSGSRGGVENGCFVLWHMSPGMWSMELAV
AGCKIVAGCNGRIVWRHIPWVGIHAAKGPLRPLRRTVQGLNPKTTATMFTKAQCIGEKRV
GEEDCFVLKVSADGANIAERSEGHVEVMRHVLYGYFSQKSGLLMFLEDSHLTRVQPPGAD
ADTVYWETTITSSVEDYSAVDGILVAHHGHSVATVFRFGKGSANNSRTMMEEEWHIDDIV
FNVPGLSMDYFIPPAEILNNK
>tr|V4LL42|V4LL42_EUTSA Uncharacterized protein OS=Eutrema salsugineum GN=EUTSA_v10013560mg PE=4 SV=1
MRKLCPNYNLEDGLETVLEVPMPEELFSASKTKPGWNQMKSYWSKPTATHATATATNMTR
LFGGRNAEIQLLLGVVGAPLIPLPVLPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYIA
AVGGEKALNAVESMYAMGKVRMTASEFCTGEGSLNSKMVKARSIKSGGGEVGGFVLWQKG
IELWCLELVVSGCKISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLFA
RSVCMGEKKINDEDCFILKLEAEPSTLKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDSH
LLRIKAQDENSIFWETTMESLIQDYRIIDGVQVAHAGKSSVSLFRFGENSDNHSRTRMEE
TWEIEEMDFNIKGLSMDCFLPPSDLKKDDDGEEEVECGLAANNEKLPMKIRSASLRISSS
KILAIVEEEDESEVTEELHET
>tr|Q5XV51|Q5XV51_ARATH Putative uncharacterized protein OS=Arabidopsis thaliana GN=At5g05840 PE=2 SV=1
MTNVFFLISISFKFSSNPNFPQIASLSSLSLNFSLRNPFFFVFANMRKLCPNYNLEDGLE
TVLEVPMPEELFAASKTKPGWNQMKSYWSKPTATATGTATATNMTRLFGGRNAEIQLLLG
VVGAPLIPLPVQPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYIAAVGGDRALNAVESM
YAMGKVRMTASEFCTGEGSLNSKMVKARSIKSGGGEVGGFVLWQKGIELWCLELVVSGCK
ISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLFARSVCMGEKKINDED
CFILKLDAEPSALKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDSHLLRIKAQDDNSIFW
ETTMESLIQDYRTVDGILVAHAGKSSVSLFRFGENSDNHSRTRMEETWEIEEMDFNIKGL
SMDCFLPPSDLKKDDDEEEEIECGLAANNEKLPMKIRSASLRISSSKVLAIVEEEDESEV
TEET
>tr|A0A067G1B6|A0A067G1B6_CITSI Uncharacterized protein OS=Citrus sinensis GN=CISIN_1g013416mg PE=4 SV=1
MRKLCPNFDREDGLETVLEVPIPEEMFTGNKNNNNTTHRSWQNVKSWIKPHSERSTSMST
TALFGGKNTEIQLLLGVVGAPLIPLPIPSSHHDHHHPIVDKDHPIEASMAKYIVKQYVAS
VGGEKALNSIDSMYAMGKVKMAASEFCAGEGSLNDRLVKVRHLKKGVGGGEMGGFVLWQK

RPDLWCLELVVSGRKISAGSDGKLAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLF
SNSVLCVMEKTINNEDCFILKVEAEASALRARSTSNVEIIRHTVWGYFSQRTGLLVQLKD
SHLLRIKTPGNNNSIFWETTMESLIQDYRFIDGINVAHTGRTSVSLFRFGENSESHTRTK
MEEIWTIEEVDFNIEGLSMDCFLPPGDLRKEEDHGCDVITSNPKLPFKIRAASFRVSASK
VVAIDAEYSDDSTEYVDDDEEEF
>tr|V7D1D3|V7D1D3_PHAVU Uncharacterized protein OS=Phaseolus vulgaris
GN=PHAVU_001G239000g PE=4 SV=1
MKKLCPNLDREDGLETVLEVPIPEEILTHKSGTTKAWHNMKNWMKPHGESRSNSTSMSSV
FGGKNTEIQLLLGVVGAPLIPSPIASDNQPITRSIKEQHIEVSMAKYIVKQYVAAVGGER
ALNCVDSMYAMGQVKMATTEFSAGEGSVNSKKVLKVKNLQMKGEMGGFVVWQKSPELWCL
ELVVSGYKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGVDPRSTANLFSNSVCIG
EKTVNNEDCFILKLETETSTLRARSNSNVEIVRHTVWGYFSQRTGLLVQLEDSHLLKLKS
DEHESIYWETNMESLLQDYRSVDGIQIAHAGKTWVSLIRFGGGPETHSRTRMEEVWQIEE
VDFNIKGLSIDCFLPPSDLKREEENEEEAECDGGGLVASNNAKLPYKIRSASFRISASKV
AAVNMDDSCTSESDEDL
>tr|A0A0B0PXJ6|A0A0B0PXJ6_GOSAR Putative replication factor C subunit 2
OS=Gossypium arboreum GN=F383_12806 PE=4 SV=1
MRKLCPNYDLPDGLETVLEVPIPEEMFVSNKTSNHRSWQNMKSWMTLKPNTEQQRPSMVT
VFGGRNTEIQLLLGVIGAPLIPLPINHNDHFITKNIKDHPIEASMAKYIVKQYIAAVGGE
KALGCIDSMYAMGKVKMAASEFSAGEGSVNSKVVKVRNLRHGGGGEVGGFVLWQKRPELW
CLELVVSGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFTNSVC
VGEKTIDDEDCFVLKLEAEPSALRARSSSNVEIIRHTVWGCFSQRTGLLIQLEDSHLLRI
KSPGNDGVFWETTMESSIQDYRTVDAINIAHAGHTRVSLFRFGENSESHSRTRMEEVWTI
EEVDFNIKGLSTDCFLPPGDLKKEEEGFGIVPSDVRLPFKLRNDRSSRVHGSKIVAIDVD
ECDDISSSDDDDDDELF
>tr|G7JAK3|G7JAK3_MEDTR Lipase OS=Medicago truncatula GN=MTR_3g069720
PE=4 SV=2
MKKLSPNLDREDGLETVLEVPIPEEIFTHKSGTMKAWQNVKFWMKPNAAEAKAASMTAVF
GGRNSEIQLLLGVVGAPLIPSPIINSSDNYQLITPSIKDQRIEVSMAKYIMKQYVAAVGG
ERALNSVDSMYAMGQVKMATSEFSSGERGVNSNNNNKKMVKVKNVEMKGEMGGFVVWQKR
PELWCLELVVSGNKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFS
TSVCIGEKTVNKEDCFILKLEAESSALRARSNSNVEIVRHTVWGYFSQRTGLLVQLEDSH
LLKLKSSETDCVYWETNMESLIQDYRTVDGIQIAHAGKTKVSLFRFGEGPETRSRTRMEE
VWQVEEVDFNIKGLSIDCFLPPSDLKREQEETGQCGGGVVTGTNAKLPYKIRSASFRIST
SKVAAVNLDDSCTTSESDEDF
>tr|V4V9F2|V4V9F2_9ROSI Uncharacterized protein OS=Citrus clementina
GN=CICLE_v10031543mg PE=4 SV=1
MRKLCPNFDREDGLETVLEVPIPEEMFTGNKNNNNTTHRSWQNVKSWIKPHSERSSTSMS
MTALFGGKNTEIQLLLGVVGAPLIPLPIPSSHHDHHHPIVDKDHPIEASMAKYIVKQYVA
SVGGEKALNSIDSMYAMGKVKMAASEFCAGEGSLNDRLVKVRHLKKGVGGGEMGGFVLWQ
KRPDLWCLELVVSGRKISAGSDGKLAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANL
FSNSVLCVMEKTINNEDCFILKVEAEASALRARSTSNVEIIRHTVWGYFSQRTGLLVQLK
DSHLLRIKTPGNNNSIFWETTMESLIQDYRFIDGINVAHTGRTSVSLFRFGENSESHTRT
KMEEIWTIEEVDFNIEGLSMDCFLPPGDLRKEEDHGCDVITSNPKLPFKIRAASFRVSAS
KVVAIDAEYSDDSTEYVDDDEEEF
>tr|D7LZ13|D7LZ13_ARALL Putative uncharacterized protein OS=Arabidopsis
lyrata subsp. lyrata GN=ARALYDRAFT_487384 PE=4 SV=1
MRKLCPNYNLEDGLETVLEVPMPEELFAASKTKPGWNQMKSYWSKPTATATGTATATNMT
RLFGGRNAEIQLLLGVVGAPLIPLPVQPEQQNDYENPIHKDIKDQPLEMSMAQYIVKQYI
AAVGGDRALNAVESMYAMGKVRMTASEFCTGEGSLNSKMVKARSIKSGGGEVGGFVLWQK
GIELWCLELVVSGCKISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLF
ARSVCMGEKKINDEDCFILKLDAEPSALKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDS
HLLRIKAQDDNSIFWETTMESLIQDYRTVDGIQVAHAGKSSVSLFRFGENSDNHSRTRME
ETWEIEEMDFNIKGLSMDCFLPPSDLKKDDDEEEEIECGLAANNEKLPMKIRSASLRISS

SKILAIMEEEDE
>tr|M1CL40|M1CL40_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG401027132 PE=4 SV=1
MRTLCPNLDNEDGLETVLEVPIPEEMFVNSSHKNHVKSWQNMKSWIKSHSGNHHHHHHDN
YYYKSSAVSVIGGRNAEIQLLLGVVAAPLIPHPIKCNNHSLNKKINDHPIEASMAKYIVQ
QYIAAAGGEHALNSINSMYAMGKVKMMASEFIEGDGLGLNNGKVMKIKTAKNGTGEMGGF
VLWQKRPDLWSIELVVSGCKISAGSDGKVSWRQTPWHHSHASRGPARPLRRSLQGLDPRS
TADMFSDSICIGEKPVHGEDCFVLKFEADPSSLKARSSSNVEIMRHTVWGYFSQRTGLLV
QLEDSHLLRLKSPKDDVFWETTMESLIQEYRTIDGVNIAHAGKTCVSLFRFGENSEGHTR
TRMEEVWTIEEVDFNIKGLSLDCFLPPSDLKKDDDQEIISDDDDINKNSRLESKNIIHHV
NNPRFITAIKGAAKIVAIDQDSED
>tr|A0A0D2UYR4|A0A0D2UYR4_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_011G278300 PE=4 SV=1
MRKLCPNYDLPDGLETVLEVPIPEEMFVSNKTSNHRSWQNMKSWMTLKPNTEQQRPSMVT
VFGGRNTEIQLLLGVIGAPLIPLPINHNDNFITKNIKDHPIEASMAKYIVKQYIAAVGGE
KALGCIDSMYAMGKVKMAASEFSAGEGSVNSKVVKVRNLRHGGGGEVGGFVLWQKRPELW
CLELVVSGCKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFTNSVC
VGEKTIDDEDCFVLKLEAEPSALRARSSTNLEIIRHTVWGCFSQRTGLLIQLEDSHLLRI
KSPGNDGVFWETTMESSIQDYRTVDGINIAHAGHTRVSLFRFGENSESHSRTRMEEVWTI
EEVDFNIKGLSTDCFLPPGDLKKEEEGFGIVPSDVRLPFKLRNDRSSRVHGSKIVAIDVD
ECDDISSSDDDDDDELF
>tr|M4CY42|M4CY42_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra009139 PE=4 SV=1
MRKLCPNYNLEDGLETVLEVPMPEELFSASKTKPGWNQMKSFWSKPTATATATNMTRLFG
GRNAEIQLLLGVVGAPLIPLPVQPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYIAAVG
GERALNAIESMYAMGKVRMTASEFCTGEGSLNSKMVKARSIRSGGGEVGGFVLWQKGIEL
WCLELVVSGCKISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLFARSS
CMGEKKINDEDCFILKLEAEPSTLKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDSHLLR
IKAQDDNSIFWETTMESLIQDYRIIDGVQVAHAGKSSVSLFRFGENSDNHSRTRMEETWE
IEEMDFNIKGLCMDCFLPPSDLKKDDDEEEEEEEVEVECGLAANNEKLPMKIRSASLRI
SSSKVLAIVEEEDESDVTEEMEET
>tr|Q940T0|Q940T0_ARATH At1g79420/T8K14_16 OS=Arabidopsis thaliana
GN=At1g79420 PE=2 SV=1
MSNSKSYWRKQRWGTPPQALTPLMEGPDPDMQDERTKKESSWEAIREWFKVHKGISGNMS
SPSVQPLCNSYDVPAKGQDLRLLLGVLGCPLAPISVVVSDLFPDDPLLGSFQIKNVPFET
STAHYIIQQYLAATGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSGD
SGCFVLWQMQPGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGL
DPKTTASLFAKAQCLGERRIGDDDCFVLKVSADRDSLLERNDAGAPAEVIRHALYGYFCQ
KSGLLVYLEDSHLTRVMTISPEDEAVYWETTIGTSIGDYRDVDGVAVAHCGRAVATVFRF
GETSLQYSRTRMEEIWRIDDVVFDVPGLSLDSFIPPADIFEDTNPNNNNIYSIVNSR
>tr|A0A078C578|A0A078C578_ECHMU BnaA10g24720D protein OS=Echinococcus
multilocularis GN=BnaA10g24720D PE=4 SV=1
MRKLCPNYNLEDGLETVLEVPMPEELFSASKTKPGWNQMKSFWSKPTATATATNMTRLFG
GRNAEIQLLLGVVGAPLIPLPVQPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYIAAVG
GERALNAIESMYAMGKVRMTASEFCTGEGSLNSKMVKARSIRSGGGEVGGFVLWQKGIEL
WCLELVVSGCKISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLFARSS
CMGEKKINDEDCFILKLEAEPSTLKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDSHLLR
IKAQDDNSIFWETTMESLIQDYRIIDGVQVAHAGKSSVSLFRFGENSDNHSRTRMEETWE
IEEMDFNIKGLCMDCFLPPSDLKKDDDEEEKEEEEEVECGLAANNEKLPMKIRSASLRIS
SSKVLAIVDEEDESDVTEEMEET
>tr|M0RUY1|M0RUY1_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MRKLCPNLDREDGLDTVLEVPLPEEMFLSGDSSKSSKMLCINVKAWMRPHADPSPPWPVG
REAELQLPLLLGILGAPLVPFPVRSHKPTLVRGMKEAPIEVSMAKYILQQYIAASGGERA

LNAINSMYAMGKVRMMASEFPKGNGGGKRGKKCGGAVETGGFVLWQKKPDLWCLELMVSG
CKISAGSDGKVAWRQTPWHQSHASRGLPRPLRRSLQGLDPRCAANLFANSVCLGEKTINR
EDCFVLRLDAEAATLRARSSSGVQIIRHSLWGYFSQRTGLLVQLEDSHLLRIKSAQENVY
WETTMESLMEDYRPIDGVNIAHTGRTTVSSFQLGEASEGHTRTRMEETWTVEEVDFNIRG
LSKDCFLPPADLKLAGRRP
>tr|A0A0L9U8I4|A0A0L9U8I4_PHAAN Uncharacterized protein OS=Phaseolus
angularis GN=LR48_Vigan03g252700 PE=4 SV=1
MKKLCPNLDREDGLETVLEVPIPEETLTHKSGTTKAWHNMKNWMKPHAESRSNSTSMAAV
FGGKNTEIQLLLGVVGAPLIPSPIASDNQPITRSIKDQHIEVSMAKYIVKQYVAAVGGER
ALNCVDSMYAMGQVKMATTEFSAGEGNVNSKKAMKVKNLQMKGEMGGFVVWQKRPELWCL
ELVVSGYKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFGNSICIG
EKTVNNEDCFILKVESETSTLRARSNSNVEIVRHTVWGYFSQRTGLLVKLEDSHLLKLKS
HEHESIYWETNMESLLQDYRSVDGIQIAHGGKTWVSLFRFGGGPETHSRTLMEEVWQVEE
VDFNIKGLSIDCFLPPSDLKREEDNEEEAECGGGVVASNNAKLPYKIRSASFRISASKVA
AVNLDDSCTSESDEDL
>tr|I1MZ64|I1MZ64_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MKKLCPNLDREDGLETVLEVPIPEEILTHKSGTTKAWHNMKNWMKPHAESRSNSASMAAV
FGGKNTEIQLLLGVVGAPLIPSPIAPDNQPITRSIKDQHIEVSMAKYIVKQYVAAVGGER
ALNSVDSMYAMGQVKMAASEFSAGEGSVNSKKMVKVKNLQMKGEVGGFVVWQKRPELWCL
ELVVSGYKITAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFSNSICIG
EKTVNNEDCFILKLEAESSTLRARSNSNVEIVRHTVWGYFSQRTGLLVQLEDSHLLKLKS
HESESIYWETNMESLIQDYRSVDGIQVAHAGKTRVSLFRFGGGPETHSRTRMEEVWQVEE
VDFNVKGLSIDCFLPPSDLKREEEENEESCGGGVVASNNNNNAKLPYKIRSASFRISASK
VAAVNLDDSCTSSESDEDL
>tr|A0A0B2PE95|A0A0B2PE95_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_019737 PE=4 SV=1
MKKLCPNLDREDGLETVLEVPIPEEILTHKSGTTKAWHNMKNWMKPHAESRSNSASMAAV
FGGKNTEIQLLLGVVGAPLIPSPIAPDNQPITRSIKDQHIEVSMAKYIVKQYVAAVGGER
ALNSVDSMYAMGQVKMAASEFSAGEGSVNSKKMVKVKNLQMKGEVGGFVVWQKRPELWCL
ELVVSGYKITAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPRSTANLFSNSICIG
EKTVNNEDCFILKLEAESSTLRARSNSNVEIVRHTVWGYFSQRTGLLVQLEDSHLLKLKS
HESESIYWETNMESLIQDYRSVDGIQVAHAGKTRVSLFRFGGGPETHSRTRMEEVWQVEE
VDFNVKGLSIDCFLPPSDLKREEEENEESCGGGVVASNNNNNAKLPYKIRSASFRISASK
VAAVNLDDSCTSSESDEDL
>tr|A0A078DH72|A0A078DH72_BRANA BnaC06g39840D protein OS=Brassica napus
GN=BnaC06g39840D PE=4 SV=1
MSNSKSYWRKQRWGTPPQTLTPLMEGPDPDMQDERAKKESSWEAIREWFKVHKGISGNMS
SPSVQPHCNSYDVAAKGQDVRLLLGVLGCPLAPISVVGSDLLPDDPLLGSFQIKNVPFET
STAHYIIQQYLAATGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSGD
SGCFVLWQMHPGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGL
DPKTTAGLFAKAQCLGERRIGDDDCFVLKVSADRDSLIERNDAGAPAEVIRHALYGYFCQ
KSGLLIYLEDSHLTRVTTISPEDEAVYWETTIGSSIGDYRDVDGVAVAHCGRAVATVFRF
GETSLQYSRTRMEEIWRIDDVVFDVPGLSLDSFIPPADIFEDDNNISTPVCSNVNSR
>tr|A0A078DE97|A0A078DE97_BRANA BnaA07g34910D protein OS=Brassica napus
GN=BnaA07g34910D PE=4 SV=1
MSNSKSYWRKQRWGTPPQTLTPLMEGPDPDMQDERAKKESSWEAIREWFKVHKGISGNMS
SPSVQPHCNSYDVAAKGQDVRLLLGVLGCPLAPISVVGSDLLPDDPLLGSFQIKNVPFET
STAHYIIQQYLAATGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSGD
SGCFVLWQMHPGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGL
DPKTTAGLFAKAQCLGERRIGDDDCFVLKVSADRDSLIERNDAGAPAEVIRHALYGYFCQ
KSGLLIYLEDSHLTRVTTISPEDEAVYWETTIGSSIGDYRDVDGVAVAHCGRAVATVFRF
GETSLQYSRTRMEEIWRIDDVVFDVPGLSLDSFIPPADIFEDDNNISTPVYSNVNSR
>tr|A0A0D3D1U3|A0A0D3D1U3_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1

MSNSKSYWRKQRWGTPPQTLTPLMEGPDPDMQDERAKKESSWEAIREWFKVHKGISGNMS
SPSVQPHCNSYDVAAKGQDVRLLLGVLGCPLAPISVVGSDLLPDDPLLGSFQIKNVPFET
STAHYIIQQYLAATGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSGD
SGCFVLWQMHPGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGL
DPKTTAGLFAKAQCLGERRIGDDDCFVLKVSADRDSLIERNDAGAPAEVIRHALYGYFCQ
KSGLLIYLEDSHLTRVTTISPEDEAVYWETTIGSSIGDYRDVDGVAVAHCGRAVATVFRF
GETSLQYSRTRMEEIWRIDDVVFDVPGLSLDSFIPPADIFEDDNNISTPVCSNVNSR
>tr|A0A078E9V4|A0A078E9V4_BRANA BnaC09g49650D protein OS=Brassica napus
GN=BnaC09g49650D PE=4 SV=1
MRKLCPNYNLEDGLETVLEVPMPEELFSASKTKPGWNQMKSFWSKPTATATATNMTRLFG
GRNAEIQLLLGVVGAPLIPLPVQPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYIAAVG
GERALNAIESMYAMGKVRMTASEFCTGEGSLNSKMVKARSIRSGGGEVGGFVLWQKGIEL
WCLELVVSGCKISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLFARSS
CMGEKKINDEDCFILKLEAEPSTLKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDSHLLR
IKAQEDNSIFWETTMESLIQDYRIIDGVQVAHAGKSSVSLFRFGENSDNHSRTRMEETWE
IEEMDFNIKGLCMDCFLPPSDLKKDDDEEEEEEEEVEVECGLAANNEKLPMKIRSASLKI
SSSKVLAIVEEEDESDVTEEMEET
>tr|A0A0D3EHJ0|A0A0D3EHJ0_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MRKLCPNYNLEDGLETVLEVPMPEELFSASKTKPGWNQMKSFWSKPTATATATNMTRLFG
GRNAEIQLLLGVVGAPLIPLPVQPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYIAAVG
GERALNAIESMYAMGKVRMTASEFCTGEGSLNSKMVKARSIRSGGGEVGGFVLWQKGIEL
WCLELVVSGCKISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQGLDPKSTANLFARSS
CMGEKKINDEDCFILKLEAEPSTLKARSSSNVEIIRHTVWGCFSQRTGLLIQLEDSHLLR
IKAQEDNSIFWETTMESLIQDYRIIDGVQVAHAGKSSVSLFRFGENSDNHSRTRMEETWE
IEEMDFNIKGLCMDCFLPPSDLKKDDDEEEEEEEEVEVECGLAANNEKLPMKIRSASLKI
SSSKVLAIVEEEDESDVTEEMEET
>tr|M4F220|M4F220_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra035117 PE=4 SV=1
MSNSKSYWRKQRWGTPPQTLTPLMEGPDPDMQDERAKKESSWEAIREWFKVHKGISGNMS
SPSVQPHCNSYDVAAKGQDVRLLLGVLGCPLAPISVVGSDLLPDDPLLGSFQIKNVPFET
STAHYIIQQYLAATGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSGD
SGCFVLWQMHPGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGL
DPKTTAGLFAKAQCLGERRIGDDDCFVLKVSADRDSLIERNDAGAPAEVIRHALYGYFCQ
KSGLLIYLEDSHLTRVTTISPEDEAVYWETTIGSSIGDYRDVDGVAVAHCGRAVATVFRF
GETSLQYSRTRMEEIWRIDDVVFDVPGLSLDSFFPPADIFEDDNNISTPVYSNVNSR
>tr|R0IEQ5|R0IEQ5_9BRAS Uncharacterized protein OS=Capsella rubella
GN=CARUB_v10020363mg PE=4 SV=1
MSNSKSYWRKQRWGTPPQALTPLMEGPDPDMQDERTKKESSWEAIREWFKVHKGISGNMS
SPSVQPLCNSYDVPAKGQDLRLLLGVLGCPLAPISVLVSDLFPDDPLLGSFQIKNVPFET
STAHYIIQQYLAATGCLKRAKAAKNMYVTGIMKMSCCETEIAAGKSVKTLGGGGNGRSGD
SGCFVLWQMQPGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGL
DPKTTASLFAKAQCLGERRIGDDDCFVLKVSADRDSLIERNDAGAPAEVIRHALYGYFCQ
KSGLLVYLEDSHLTRVVTISPEDEAVYWETTIGTSIGDYRDVDGVAVAHCGRAVATVFRF
GETSLQYSRTRMEEIWRIDDVVFDVPGLSLDSFIPPADIFEDANNNNNPTHVYSTVNSR
>tr|A0A087HJP5|A0A087HJP5_ARAAL Uncharacterized protein OS=Arabis alpina
GN=AALP_AA2G244500 PE=4 SV=1
MSNSKSYWRKQRWGTPPQTLTPLMEGPDPDMQDERSKKESSWEAIREWFKVHKGISGNMS
SPSDQPLCNSYDVAAKGQDLRLLLGVLGCPLAPISVVVSDLLPDDPLLGSFQIKNVPFEN
STANYIIQQYLAATGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSGD
SGCFVLWQMQPGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGL
DPKTTAGLFAKAQCLGERRIGDDDCFVLKVSADRDSLIERNDAGAPAEVIRHALYGYFCQ
KSGLLVYLEDSHLTRVVTISPEDEAVYWETTIGTSIGDYRDVDGVAVAHCGRAVATVFRF
GETSLQYSRTRMEEIWRIDDVVFDVPGLSLDSFIPPADIFENDNSNNVNSR

>tr|D7KWH7|D7KWH7_ARALL Predicted protein OS=Arabidopsis lyrata subsp. lyrata GN=ARALYDRAFT_677504 PE=4 SV=1
MSNSKSYWRKQRWGTPPQALTPLMEGPDPDMQDERTKKESSWDAIREWFKVHKGISGNMS
SPSVQPLCNSYDVPAKGQDLRLLLGVLGCPLAPISVVVYDYFPMTLFLETSTAHYIIQQY
LAATGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSGDSGCFVLWQMQ
PGMWSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGLDPKTTASLFA
KAQCLGERRIGDDDCFVLKVSADRDSLLGRNDAGAPAEVIRHALYGYFCQKSGLLVYLED
SHLTRVMTISPEDEAVYWETTIGTSIGDYRDVDGVAVAHCGRAVATVFRFGETSLQYSRT
RMEEIWRIDDVVFDVPGLSLDSFIPPADIFEDANPNNNNIYSNVNSR
>tr|A0A0A0KBJ0|A0A0A0KBJ0_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_6G009410 PE=4 SV=1
MRKLCPNFDREYGLDTVLEVPIPEEMFSSNTTKTHAISWQAMKSWVKSNDKSSHATSITS
LFGGRNAEIQLLLGVVGAPLIPLPITFDQQQPINRNNNIKDNPIEASMAKYIVQQYVAAVG
GEHALNCIESMYAMGKVKMAASEFWSGEGKAAVKGKNNGKGGGGGGGGGGGGEMGGFVVW
QKRPELWCLELMLGGSKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRFLQGLDPKSTAT
LFSNSTCIGEKTINDEDCFILKLEAESSVLRARSSSSVEIIRHTVWGYFSQRTGLLVQLE
DSHLLRIKPAGSRNDNIFWETTMETLIQDYRTIDGVNIAHAGKTTVSLFRFGETAEGHSK
TKMEEYWEIEEVDFNIKGLSMDFFLPPSDLKKEEEGVGLITTSKGKFPLTMRCSGESRGF
SSRVAAIDQSEDEESEGSNESDNEDEDF
>tr|A5ASQ9|A5ASQ9_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VITISV_013340 PE=4 SV=1
MASRARKKQQRWCTQPLTPLMEGPDPEMQEEGTKKESSWEVIREWFRLQKGGGLGVHGSS
SFSLSLYGNIPSKTQDLRLLLGVLGCPLAPIPLATDPLHRLHIKDIPIETSSACYIIQQY
LAATGCLKQEKGMKNMYTTGTMKMICCETEISTGKSVKSLGTRSGENGCFVLWQMSPGMW
SLELVVGCNKVVAGSNGKIVWRHTPWLGTHAAKGPHRPLRRIIQGLDPKSTASLFAKAQC
LGEKRIGEDDCFVLKVAADRAAVMERNEGPAEVIRHRTHTSQGFKLLENDTVYWETTIGT
SLWDYRDVDGVMIAHEGRTIATVFRFGEVSMQHSRTRMEELWVIDDVVFNVPGLSFDYFI
PPADIFDVDNSP
>tr|K4BHU3|K4BHU3_SOLLC Uncharacterized protein OS=Solanum lycopersicum GN=Solyc03g078650.2 PE=4 SV=1
MRTLCPNLDREDGLETVLEVPIPEEMFASPKQRTRHNMKYHSDEKSAASVFGSRDAEIQL
LLGVVGAPLIPHPIRYQHSINTKINDHPIEASMAKYIVQQYIAAAGGEGALNSMDSMYAM
GKIKMVASEFSAGDGMGLNKGNMMKIKSTVKNGSGEMGGFVLWQKRPDLWSIELVVSGCK
ISAGSDGKVAWRQTPWHHSHASRGPARPLRRSLQGLDPKSVANLFSTSICIGEKTVNEED
CFVLKLEAEPSSLKARSSSKVEVMRHTVWGYFSQRTGLLFQLEDTHLLRIKAPGNDVFWE
TTMESLILDYRTIDGVNIAHAGRTSVSLFRFGENTEGHTRTRMEEVWTIEEVDFNIKGLS
ADCFLPPSDLMKEDEMGHDVNKKSRLGLKTPKIRSCRRSASKIMSIDEEDLEDYEADEES
>tr|M1C4J2|M1C4J2_SOLTU Uncharacterized protein OS=Solanum tuberosum GN=PGSC0003DMG400023185 PE=4 SV=1
MRTLCPNLDREDGLETVLEVPIPEEMFASPKHRTRHNMKYHTDEKSAASVFGSRDAEIQL
LLGVVGAPLIPHPIRYQHSINTKINDHPIEASMAKYIVQQYIAAAGGEGALNSIDSMYAM
GKIKMVASEFSAGDGMGLNKGNMMKIKSVKNGSGEMGGFVLWQKRPDLWSIELVVSGCKI
SAGSDGKVAWRQTPWHHSHASRGPARPLRRSLQGLDPKSVANLFSTSICIGEKTVNEEDC
FVLKLEAEPSSLKARSSSKVEVMRHTVWGYFSQRTGLLFQLEDTHLLRIKAPGNDVFWET
TMESLILDYRTIDGVNIAHAGRTSVSLFRFGENTEGHTRTRMEEVWTIEEVDFNIKGLSA
DCFLPPSDLMKEDEMGHDVNKKSRLGFKTPKIRSCRRSVSKIMSIDEEDLEDYEADEES
>tr|A0A0L9UW61|A0A0L9UW61_PHAAN Uncharacterized protein OS=Phaseolus angularis GN=LR48_Vigan07g065500 PE=4 SV=1
MKKLCPNLAREDGLQTVLEVPIPEEIFTIKSGTSRAWHNMKSWMKPNVESSTSSSLFGDQ
NTDIQLLLGVVGAPLIPLPVTSHDQPITIKSHNIEASMAKYIVKQYVAAVGGESALNWVE
SMYAVGEVRVGTTEFSGSEECVSKKKMVKVKKMQKKGEVGGFVVWQKKPELWCLELVVSG
YKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRLLQGLDPRSTANLFNNSICIGEKTVNN
EECFILKLEADSNTLQTRSSSNVEIIRHTVWGYFSQRTGLLVQLEDSHLLKLKTTANDAI
FWETNMESLIQDYKTVDGINIAHAGKTWVTLSRFGEGPESHSKTRVKEVWKIEEVDFNIK

GLSIDCFLPPSDLKKEEEKVVEDCRMAASNTKLPYKIQSASFKISVSKVAAVNVDDSSGS
ESDGDEEDM
>tr|Q9SAK6|Q9SAK6_ARATH T8K14.16 OS=Arabidopsis thaliana GN=T8K14.16 PE=4
SV=1
MEGPDPDMQDERTKKESSWEAIREWFKVHKGISGNMSSPSVQPLCNSYDVPAKGQDLRLL
LGVLGCPLAPISVVVSDLFPDDPLLGSFQIKNVPFVSITNYSLSLETSTAHYIIQQYLAA
TGCLKRAKAAKNMYATGIMKMSCCETEIAAGKSVKTLGGGGNGRSGDSGCFVLWQMQPGM
WSLELVLGGTKLISGSDGKTVWRHTPWLGTHAAKGPQRPLRRLIQGLDPKTTASLFAKAQ
CLGERRIGDDDCFVLKVSADRDSLLERNDAGAPAEVIRHALYGYFCQKSGLLVYLEDSHL
TRVMTISPEDEAVYWETTIGTSIGDYRDVDGVAVAHCGRAVATVFRFGETSLQYSRTRME
EIWRIDDVVFDVPGLSLDSFIPPADIFEDTNPNNNNIYSIVNSR
>tr|C5WQ37|C5WQ37_SORBI Putative uncharacterized protein Sb01g039970
OS=Sorghum bicolor GN=Sb01g039970 PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGGGGSRGSRFGCTAWMRSHAAERSGAGEP
CSMSRGELQLMLGVIGAPLIPLPVYHAEQSPCSVLCEQLKADPIESSSAKYIVQQYIAAS
GGEWALNKVKSMYAMGKVRMTAAELNSSDADGHGGGITGNGHRGGKKGSKGSGGEIGGFV
LWQKKPELWCLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPQLT
ASLFADSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQ
LEDSHLLQIRSSGGVGGSVFWETTMESRLGDYRAVDGVNIAHAGRTAVSLVRFGDCQDGN
TRTRMEETWNIEEVDFNIWGLSMDCFLPPSDLREGKESQDVAIGVKADARPPPIRIPAVT
VRVGPSQVAAVNMDDSDSLIARS
>tr|B4FTQ2|B4FTQ2_MAIZE Uncharacterized protein OS=Zea mays GN=umc2185
PE=2 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGSRGSTRFGCTNVKAWMRSHAADRSGAGE
PCSMTRGELQLMLGVIGAPLIPLPVYHANQSPCSVLCEQLKADPIESSSAKYIVQQYIAA
SGGEWALNKVKSMYAMGKVRMTAAELNSSDADGHGGSTGNGHHRGGKKGSKGGGGGGEIG
GFVLWQKKPELWCLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDP
QLTASLFADSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGL
LVQLEDSHLLQIRSSGGGAGGSVFWETTMESRLGDYRAVDGVNIAHAGRTAVSLVRFGDC
QDGNTRTRMEEEWNIEEVDFNIWGLSMDCFLPPSDLREGKESQDVAVVKADARPPPLRIP
AVTVRVGPSQVAAVNMDDSDSLVARS
>tr|K4A9U5|K4A9U5_SETIT Uncharacterized protein OS=Setaria italica
GN=Si035651m.g PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGGGSRGSRFGCTNAFVKAWTRSHAADRSG
AGEPCSMSRGELQLMLGVIGAPLIPLPVHHAKQSPSSVLCEQLKADPIESSSAKYIVQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDGDAHGGGGGGGSGGTGHGHRGGKKGGK
GCGGEVGGFVLWQKKPELWCLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRR
SLQGLDPQLTASLFADSVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGY
FSQRTGLLVQLEDSHLLQIRSSGGTGGSVFWETTMESRLGDYRAVDGVNIAHSGRTAVSL
VRFGDCQDGNTRTRMEEAWDIEEVDFNIWGLSMDCFLPPSDLREGKETQDVAVVKADARP
PPIRIPAVTVRVGPSQVAAVNMDDSDSLIARS
>tr|F2D0R6|F2D0R6_HORVD Predicted protein OS=Hordeum vulgare var.
distichum PE=2 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGGSRGSRFGCTSVKAWMRSHAADRSGAGE
PCSMSRGELQLMLGVIGAPLIPLPVSHAKQSPSSVLCEQLKADPIESSSAKYIVQQYIAA
SGGEWALNKVTSMYAMGKVRMTAAELNSSDADGNGRGGGRKGGSKGGGEIGGFVLWQKKP
ELWCLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPMLTASLFAE
DSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSH
LLQIKSGNGAGGSVFWETTMESRLRDYRAVDGVNIAHSGRTAVSLVRFGDTQDGNTRTRM
EEHWDIEEVDFNIWGLSMDCFLPPSDLRDAKESQDQDVAVVKAARPPPLRIPAVAVIRVG
PSQVAAVNLDETESLLARIPTPHP
>tr|Q10NJ9|Q10NJ9_ORYSJ Lipase, putative, expressed OS=Oryza sativa
subsp. japonica GN=Os03g0267500 PE=2 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSGG

AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTNMYAMGKVRMTAAELNSSDADGGGGGGGHRGGKKSSKNGGEVGGF
VLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPML
TASLFADAVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLLV
QLEDSHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHAGRTAVSLVRFGDSSDGNT
RTRMEEVWNIEEVDFNIWGLSMDCFLPPSDLKDSKEDKDVSAAVKPARPPPIRIPAVAVR
VGPSQVAAVNMDDSDSLIARS
>tr|A0A067F5W2|A0A067F5W2_CITSI Uncharacterized protein OS=Citrus
sinensis GN=CISIN_1g016543mg PE=4 SV=1
MSSKARRKQRWCTQTLTPLMEGPDPEMLEEGSKKESSWEVIREWFGIQKGISSGTNHNNF
SMSLEGSSIPAKRQDLRLLLGVLGCPLAPIPLVNDPILRIHIKDIPIETSSAHYIIQQYL
AATGCLKQQKRAKNMYATGTVKMVCCETEISSGKNVKSLGTRSGESGCFVLWQMLPGMWS
LELVVGGNKVIAGSDGKTVWRHTPWLGTHAAKGPQRPLRRIIQGLDPKITASLFAKAQCL
GEKRIGDDECFVLKVAADRAAVMERSEGPAEVIRVQTPENDTIYWETTIGSSIGDYSDVD
GVLIAHQGRSIATVFRFGELSIQHSRTRMEEMWRIDDVVFNVPGLSMDYFIPPADIIDNE
KSP
>tr|I1H738|I1H738_BRADI Uncharacterized protein OS=Brachypodium
distachyon GN=BRADI1G67010 PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGSRGSRFGCTSVKAWMRSHAADRSGAGEP
CSMSRGELQLMLGVIGAPLIPLPVSHAKQSPSSVLCEQLKGDPIESSSAKYIVQQYIAAS
GGEWALNKVKSMYAMGKVRMTAAELNSSDADGSNNGGSGHRGGKKGGKGGAGGGGEIGGF
VLWQKKPELWCLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPML
TASLFADDSVCIGERSIEGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLL
VQLEDSHLLQIKSSGHGSVFWETTMESRLGDYRAVDGVNIAHAGRTAVSLVRFGDSQDGN
TRTRMEETWNIEEVDFNIWGLSMDCFLPPSDLREGKDGQDVAAVKPARPPPLRIPAVAVR
VGPSQVAAVNLDESDSLIAR
>tr|V7B7F0|V7B7F0_PHAVU Uncharacterized protein OS=Phaseolus vulgaris
GN=PHAVU_008G227800g PE=4 SV=1
MKKLSPNLTREDGLQTVLEVPIPEEIFTIRSGTSRAWHNMKSWMKPNVESSRSSSLFGDQ
NTDIQLLLGVVGAPLIPLPITSHNHPITIKSHNIEASMAKYIVKQYVAAVGGESALNWVE
SMYAMGEVRVGTSEFSGGEECTSKKKMVKVKKVKKKGEVGGFVVWQKKPELWCLELVVSG
YKISAGSDGKVAWRQTPWHHSHASRGPPRPLRRLLQGLDPRTTANLFNNSICIGEKTVNN
EECFILKLEADSNSLHTRSSSNVEIIRHTLWGYFSQRTGLLVQLEDSHLLKLKTTTSYAI
FWETNMESLIQDYKTVDGINIAHAGKTWVTLSRFGEGPEGHSKTRVKEVWKIEEVDFNIK
GLSIDCFLPPSDLKKEEEKVVQDCTMPASNTKLPYKIQSASFKINVSKVAAVNVDDSSGT
ESDDEKDM
>tr|J3LMC2|J3LMC2_ORYBR Uncharacterized protein OS=Oryza brachyantha
GN=OB03G21980 PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGSRGSRFGCTNVKSGVRPNASDRSGAGEP
CSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQYVAAS
GGEWALNKVTSMYAMGKVKMTAAELNSSDADGGGGGHRSGKKSGKSGGEVGGFVLWQKKP
ELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPMLTASLFAD
AVCIGERGVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSHL
LQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHAGRTAVSLVRFGDSSDGNTRTRMEEV
WNIEEVDFNIWGLSMDCFLPPSDLKESKEAQDVAAVVKPARPPPIRMPAVAVRVGPSQVA
AVNMDDSDSLIARS
>tr|A0A0D9VSB9|A0A0D9VSB9_9ORYZ Uncharacterized protein OS=Leersia
perrieri PE=4 SV=1
MEGANLGPHLPAARTTHQNRYKPTETQGRRVITQHKRNPRGGSTAAKRRRRRSELALAQE
RDRAVVSMRKLCPNLERDDALDTVLEVPIPEEMFSRGGNGGSRGSRFGCTNVKSWVRPNA
SDRSGAGEPCSMSRGELQLMLGVIGAPLIPLPVDHNKQSPCSVLCEQLKADPIESSTAKY
IIQQYIAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGHRGGKKSSKNSG
EVGGFVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQG
LDPMMTASLFADAVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQR

TGLLVQLEDSHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHAGRTAVSLVRFGDS
SDGNTRTRMEEVWNIEEVDFNIWGLSMDCFLPPSDLKESKETQDVAAAAAVKPARPPPIR
IPAVAVRVGPSQVAAVNMDDSDSLIARS
>tr|B6SWD2|B6SWD2_MAIZE Putative uncharacterized protein OS=Zea mays PE=2
SV=1
MRKVCPNLERDDALDTVLEVPIPEEMFSGSGGGGGSCGFRFGCSSVKKAWMRSHAADRSG
AGEPCSMSRGELQLMLGVIGAPLVPLPVAVVCRAKQSPCSVLCEQLKTGPIESSSAKYIV
QQYVAASGGEWALDRVKSMYAMGKVRVTAAEQLNGSDAAGGGGHCGGATGKGNRGGRRKG
RGGEVGGFVLWQKRPELWCLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRS
LQGLDPQLTASLFADSVCIGERSVDGEDCFVLKVEAEASSLRARNSGSVEIVRHTLWGYF
SQRTGLLVQLEDSHLLQIRSGGGGSIFWETTMESRLGDYRAVDGVNIAHAGRTAVSLVRF
GDCQQDGSSARTRMEETWDIEEVDFNIWGLSMDCFLPPSDLREGGKESQDVAVAKADARP
PPIRIPAVAVRVGPSQVAAVSMDDSDSLVARS
>tr|A0A0D3FGN3|A0A0D3FGN3_9ORYZ Uncharacterized protein OS=Oryza barthii
PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGSSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRGGKKSSKNGGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPM
LTASLFADAVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLL
VQLEDSHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHAGRTAVSLVRFGDSSDGN
TRTRMEEVWNIEEVDFNIWGLSMDCFLPPSDLKDSKEDKDVSAAVKPARPPPIRIPAVAV
RVGPSQVAAVNMDDSDSLIARS
>tr|I1P9U7|I1P9U7_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4
SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGSSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRGGKKSSKNGGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPM
LTASLFADAVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLL
VQLEDSHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHAGRTAVSLVRFGDSSDGN
TRTRMEEVWNIEEVDFNIWGLSMDCFLPPSDLKDSKEDKDVSAAVKPARPPPIRIPAVAV
RVGPSQVAAVNMDDSDSLIARS
>tr|A0A0E0GKE0|A0A0E0GKE0_ORYNI Uncharacterized protein OS=Oryza nivara
PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRGGKKSSKNGGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPM
LTASLFADAVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLL
VQLEDSHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHAGRTAVSLVRFGDSSDGN
TRTRMEEVWNIEEVDFNIWGLSMDCFLPPSDLKDSKEDKDVSAAVKPARPPPIRIPAVAV
RVGPSQVAAVNMDDSDSLIARS
>tr|A0A0E0CYI7|A0A0E0CYI7_9ORYZ Uncharacterized protein OS=Oryza
meridionalis PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRGGKKSSKNCGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPM
LTASLFADAVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLL
VQLEDSHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHAGRTAVSLVRFGDSSDGN
TRTRMEEVWNIEEVDFNIWGLSMDCFLPPSDLKESKEDKDVSTAVKPARPPPIRIPAVAV
RVGPSQVAAVNMDDSDSLIARS

>tr|A0A0B2PUT6|A0A0B2PUT6_GLYSO Uncharacterized protein OS=Glycine soja GN=glysoja_037538 PE=4 SV=1
MKKLCPNLTREDGLETVLEVPIPEEIFTIKSGTSRAWHNMKSWMKPNVESSRSSSLFGGQ
NTDIQLLLGVVGAPLIPLPVTSHNQPITIKSHNIEASMAKYIVKQYVAAVGGESGLNSVE
SMYAMGEVRVGSEFSEGEECVSSKKTKKVQMKEEVGGFVVWQKKPELWCLELVVSGYKIS
AGSDGKVAWRQTPWHHSHASRGPPRPLRRLLQGLDPRSTANLFNNSICVGEKTVNNEECF
ILKLEADSNSLRTRSSSNVEIIRHTVWGYFSQRTGLLVQLEDSHLIKLKSNASEAIFWET
NMESLIQDYRIVDGINIAHAGKTWVTLSRLGECPESHSTTRIKEVWQIEEVDFNIKGLSM
DCFLPPSDLKREEEKGVEECGVAASNAKLPYKIQSASFKISVSKVAAINVEDSSASESDD
ENV
>tr|C6TJ39|C6TJ39_SOYBN Uncharacterized protein OS=Glycine max PE=2 SV=1
MKKLCPNLTREDGLETVLEVPIPEEIFTIKSGTSRAWHNMKSWMKPNVESSRSSSLFGGQ
NTDIQLLLGVVGAPLIPLPVTSHNQPITIKSHNIEASMAKYIVKQYVAAVGGESGLNSVE
SMYAMGEVRVGSEFSEGEECVSSKKTKKVQMKEEVGGFVVWQKKPELWCLELVVSGYKIS
AGSDGKVAWRQTPWHHSHASRGPPRPLRRLLQGLDPRSTANLFNNSICVGEKTVNNEECF
ILKLEADSNSLRTRSSSNVEIIRHTVWGYFSQRTGLLVQLEDSHLIKLKSNASEAIFWET
NMESLIQDYRIVDGINIAHAGKTWVTLSRLGECPESHSTTRIKEVWQIEEVDFNIKGLSM
DCFLPPSDLKREEEKGVEECGVAASNAKLPYKIQSASFKISVSKVAAINVEDSSASESDD
ENV
>tr|F2EHK5|F2EHK5_HORVD Predicted protein OS=Hordeum vulgare var. distichum PE=2 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGCTSVKAWMRSHAADRSGAGEPCSMSRGE
LQLMLGVIGAPLIPLPVSHAKQSPSSVLCEQLKADPIESSSAEYIVQQYIAASGGEWALN
KVTSMYAMGKVRMTAAELNSSDADGNGRGGGRKGGSKGGGEIGGFVLWQKKPELWCLELV
VSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPMLTASLFAEDSVCIGER
SIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSHLLQIKSGN
GAGGSVFWETTMESRLRDYRAVDGVNIAHSGRTAVSLVRFGDTQDGNTRTRMEEHWDIEE
VDFNIWGLSMDCFLPPSDLRDAKESQDQDVAVVKAARPPPLRIPAVAVIRVGPSQVAAVN
LDETESLLARIPTPHP
>tr|M0XTE7|M0XTE7_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGCTSVKAWMRSHAADRSGAGEPCSMSRGE
LQLMLGVIGAPLIPLPVSHAKQSPSSVLCEQLKADPIESSSAKYIVQQYIAASGGEWALN
KVTSMYAMGKVRMTAAELNSSDADGNGRGGGRKGGSKGGGEIGGFVLWQKKPELWCLELV
VSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPMLTASLFAEDSVCIGER
SIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSHLLQIKSGN
GAGGSVFWETTMESRLRDYRAVDGVNIAHSGRTAVSLVRFGDTQDGNTRTRMEEHWDIEE
VDFNIWGLSMDCFLPPSDLRDAKESQDQDVAVVKAARPPPLRIPAVAVIRVGPSQVAAVN
LDETESLLARIPTPHP
>tr|M0XTE6|M0XTE6_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1
MCNFVDALTRRENLEKENDKQEIGQSVRAATTKLREKITGKVQIPGPSCQTHEKPVQDHR
DQDERGGAITPTKRRDLLRSPSQTNIRTRAHTLGHRIASHPRSVVRVQAEEAEEIELWES
ACVPPARPMRKLCPNLERDDALDTVLEVPIPEEMFSGGGGGSRGSRFGCTSVKAWMRSHA
ADRSGAGEPCSMSRGELQLMLGVIGAPLIPLPVSHAKQSPSSVLCEQLKADPIESSSAKY
IVQQYIAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGNGRGGGRKGGSKGGGEIGG
FVLWQKKPELWCLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPM
LTASLFAEDSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGL
LVQLEDSHLLQIKSGNGAGGSVFWETTMESRLRDYRAVDGVNIAHSGRTAVSLVRFGDTQ
DGNTRTRMEEHWDIEEVDFNIWGLSMDCFLPPSDLRDAKESQDQDVAVVKAARPPPLRIP
AVAVIRVGPSQVAAVNLDETESLLARIPTPHP
>tr|A0A0E0KBR0|A0A0E0KBR0_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSCG

AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGHRAGKKNSKNGGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPM
LTASLFADAVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLL
VQLEDSHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHAGRTAVSLVRFGDSSDGN
TRTRMEEVWNIEEVDFNIWGLSMDCFLPPSDLKESKEDKDVAATVKPARPPPIRIPAVAV
RVGPSQVAAVNMDDSDSLIARS
>tr|A0A068V0X8|A0A068V0X8_COFCA Uncharacterized protein OS=Coffea
canephora GN=GSCOC_T00038542001 PE=4 SV=1
MASCRAARRNQRWCTTQPLTPLMEGPDLEMHHHHCQSGNKKETTSSWEVIREWFRAQRSL
AADPAGGGGGGGSRSFSMSSAYPANINAAKRQDLKLLLGVLACPLGPIPLPINNNENGND
DNNNNYHSYYDIPIETSTAHYIIQQYLAATGCSSKSKHQHQQQQQKVPRNMYTAGTVKMM
CFPTEISGGGTVKTLGTRSSGEKGCFVLWQMSPGMWSLELVVGGNKVLAGSDSKIVWRHT
PWLGTHAAKGPQRPLRRIIQGLDPKSTASLFAGKARCLGEKRIGDEDCFVLKVAADRATV
MERNEGPAEVIRHVLYGYFSQKSGLLIYLEDSHLTRVLPAAGRRENGSDHPSVSGAVYWE
TTIGSSIGDYRDVDGLLIAHQGRTVATVFRFGEVSTQHCRTTMEETWAIHDVVFGVPGLS
PDSFIPPADVWDESTHYSPH
>tr|C0HHH5|C0HHH5_MAIZE Uncharacterized protein OS=Zea mays
GN=LOC100381622 PE=2 SV=1
MRKVCPNLERDDALDTVLEVPIPEEMFSGGGGGGGGSCGFRFGCTSVKAWMRSHAADRCG
AGEPCSMSRGELQLMLGVIGAPLVPLPVAVCCRAEQSPCSVLCEQLKTGPIESSSAKYIV
QQYVAASGGERALDRVKSMYAMGKVRMTAAEQLNGSDAAGGHCGGATGKGNRGGRRKGRG
GEVGGFVLWQKRPELWCLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQ
GLDPQLTASLFADSVCIGERSVDGEDCFVLKVEAEASSLRARNSGSVEIVRHTLWGYFSQ
RTGLLVQLEDSHLLQIRSGGGGGGGSIFWETTVESRLGDYRAVDGVNIAHAGRTAVSLVR
FGDCQQDGSSARTRMEETWDIEEVDFNIWGLSMDCFLPPSDLREGGKESQDVAVAVAKAD
ARPPPIRIPAVAVRVGPSQVAAVSMDDSDSLIARP
>tr|A0A0D3D6E5|A0A0D3D6E5_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MDKKHGLFSKSHSHRSRSKSPVRGVSPIIIRRRKGRYVSQTDRHVSEMLPTVIEGPDPDG
EDSGSSVDYSSSRWLRRLFPRLLLGVLGAPLGPLHVSALDLPPHLSIKNTPMETSSAQYT
AASGGYKLHSSVQNGYVMGRIRTAASEFETGSKSKNNSSKAVESGGFVLWHVRLDPRTTA
NIFASARCIGEKKMDGEDCFILKLCADPATLRARSEGASETIRHTLFGYFSQKTGLLVHL
EDSQLTRIQNIGGEAVYWETTINSYLEDYKPVEGIVIAHSGRSVATLLRFGDVSSGYNTK
TTMQEAWVIDEIAFNVPGLSMDCFIPPSELRFDSHVEDLSQGPKIKTLQQGSDR
>tr|M0SSP9|M0SSP9_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MRKLCPNFDREDALDTVLEVPIPEEMFANMGTGAARWQNMRTWLKAQAFDRAATDAPTEL
SGRSAELQLLLNVVGSPLIPCPVPIDRAFSRSIRDSSIQASTAKYIIQQYIAATGGQAAL
TSVNSMYAVGKVKMSASEFHVGDQTVAAKGSGEIGGYVLWQKNPDVWYFELIMAGCKMSA
GSDGKVAWRQSASEQSHASRGPPRPLRRSLQGLDPRSTANLFSDAVCIGEKIINGEECFI
LKLEANPATLRARSAATFDIIHHKIWGYFSQRTGLLIQLEDTHLLRMKAGRRGESIFWET
SMESVIEDYRYINSINIAHAGRTMVTLFRYGEGSVNHKRKMEESWTIEEVDFNLWGLSTE
CFLPPANLKKEQDGDDSHGG
>tr|I1M801|I1M801_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MKKLCPNLTREDGLETVLEVPIPEEIFTIKSGTSRAWHNMKSWMKPNVESSRSSSLFGGQ
NTDIQLLLGVVGAPLIPLPITSHNQPITIKSHNTEASMAKYIVKQYVAAVGGESALNSVE
SMYAMGEVRVGSEFSAGEECVSSKKMGKVKKVQMKGELGGFVVWQKKPELWCLELVVSGY
KISAGSDGKVAWRQTPFHHSHASRGPPRPLRRLLQGLDPRSTGNLFNNSICIGEKTVNNE
ECFILKLEADSNSLRTRSSSNVEIIRHTVWGYFSQRTGLLVQLEDSHLLKLKSNASDAIF
WETNMESLIQDYRTVDGINIAHGGKTWVALSRFGEGPESHSRTRIKEVWQIEEVDFNIKG
LSMDCFLPPRDLMRDEEKRVEECRVVASNSKLPYKIQSASSFKISVSKVAAVNVDDSSAS
ETDDEDV

>tr|A0A0B2QLY9|A0A0B2QLY9_GLYSO Uncharacterized protein OS=Glycine soja GN=glysoja_009191 PE=4 SV=1
MKKLCPNLTREDGLETVLEVPIPEEIFTIKSGTSRAWHNMKSWMKPNVESSRSSSLFGGQ
NTDIQLLLGVVGAPLIPLPITSHNQPITIKSHNTEASMAKYIVKQYVAAVGGESALNSVE
SMYAMGEVRVGSEFSAGEECVSSKKMGKVKKVQMKGELGGFVVWQKKPELWCLELVVSGY
KISAGSDGKVAWRQTPFHHSHASRGPPRPLRRLLQGLDPRSTGNLFNNSICIGEKTVNNE
ECFILKLEADSNSLRTRSSSNVEIIRHTVWGYFSQRTGLLVQLEDSHLLKLKSNASDAIF
WETNMESLIQDYRTVDGINIAHGGKTWVALSRFGEGPESHSRTRIKEVWQIEEVDFNIKG
LSMDCFLPPRDLMRDEEKRVEECRVVASNSKLPYKIQSASSFKISVSKVAAVNVDDSSAS
ETDDEDV
>tr|W1P953|W1P953_AMBTC Uncharacterized protein OS=Amborella trichopoda GN=AMTR_s00133p00115060 PE=4 SV=1
MMGSRRRLAPLTEGPSDQDDPLDHAPYASSYLKKKQSSSRSWMEWLKEQLPLLSHKKSNL
KILLAVLGCPLSPLPLTQRKTSAVVAQVNSSAQYIIRQFEAASGCKRAEEAVKNMYVMGK
VKMVMVQVECGANSSYTLSSSLSGSGGGVVEEGCFVIWQMAPEKWLMELDVGTHKVVAGS
DGKIAWRHTPWLPSHAAKGGVRPLRRILQGLDPFTVASTFLGADYVGEKQISDEDCFMLK
LAVDREALVERSDSAAEIIKHNLVGYMSQRSGLLVHLEDSYLTRIQPPGSQATYWETTIA
SSIGDYRAIEGIMVAHSGHSSVTITRFGDGVKVGGATTRMEEAWAIEDLVFNVPGLSVDC
FIPPAEVHKESLPDITS
>tr|A0A059BZL7|A0A059BZL7_EUCGR Uncharacterized protein OS=Eucalyptus grandis GN=EUGRSUZ_F04476 PE=4 SV=1
MNARGSSVRWRQKWRQQPLEPLMEGPDPEMQQPGQRKERSWDVIREWFRSQKAGGAAHPN
DRAAELRLLLSVLGCPLAPIPLAALPHHPLRLPCSIPIQNSMAHYILKQYLAAAGCFHPH
RRRTPVANMYAAGRVKMACCETEVSSGKSVKSGGATRPTPHHGSFVLWQMTPALWSVELA
LVAGGPANSNPHSNDDFSHYVPTVNDNKVVAGSDGKIVWRHTPWLGTHAAKGPHRPLRRL
IQGLDPESTARLFGKAQCMGERSIGEEECFVLKVAAEREAVMERSEGGAEVLRHVLHGYF
SQKSGLLIYLEDSHLVRVHRVPTSNNPSEDSELEDQERHHDEEPASPGETVYWETTIGSS
IGDYREVDGLMIAHEGKSIATVFRFVETSMQYRRTRMEEAWTIHDIDFNVPGLSLDHFIP
PSDIHIPSP
>tr|D8S4C5|D8S4C5_SELML Putative uncharacterized protein OS=Selaginella moellendorffii GN=SELMODRAFT_108027 PE=4 SV=1
MLGEALPPLLEFPDKFAAKNSNGVKGWVKEQLENHLQHLGLRGSGGIAQCSKRFRARQLL
ATLGISLGPFPVGKIPPTVSPKDSPIETSSAQYIVQQYIAATGGAKLHTSIHNSYASGRL
KMVLTEFDSIIRPGRELCESGSFVLWQMFPDRWYVELSVGGTKVRAGCDAKTVWKQSPMA
GSQSVRGPIRPLRRALHGLDHKTLASMFLNARCVGEKRTDGEDCFVLKLAADSYALTAGY
RAEVIRHVAFGYFSQRSGLLVRMEDSQLTRIQAARGAVSYWEVTVETRLGEYRAVEEGAP
VVPHAGSTVVSVFRFGEESMCHTRSRVEESWWIDEAAYNVAGLSAECFIPPCDATPAPMA
SDAGEMFAQHDGFKDQNLGSSHSLW
>tr|D8R6L9|D8R6L9_SELML Putative uncharacterized protein OS=Selaginella moellendorffii GN=SELMODRAFT_168347 PE=4 SV=1
MLGEALPPLLEFPDKFAAKNSNGVKGWVKEQLENHLQHLGLRGSGGIAQCSKRFRARQLL
ATLGISLGPFPVGKIPPTVSPKDSPIETSSAQYIVQQYIAATGGAKLHTSIHNSYASGRL
KMVLTEFDSIIRPGRELCESGSFVLWQMFPDRWYVELSVGGTKVRAGCDAKTVWKQSPLA
GSQSVRGPIRPLRRALHGLDHKTLASMFLNARCVGEKRTDGEDCFVLKLAADSYALTAGY
RAEVIRHVAFGYFSQRSGLLVRMEDSQLTRIQAARGAVSYWEVTVETRLGEYRAVEEGAP
VVPHAGSTVVSVFRFGEESMCHTRSRVEESWWIDEAAYNVAGLSAECFIPPCDATPAPMA
SDAGEMFAQHDGFKDQNLGSSHSLW
>tr|A0A022PWU8|A0A022PWU8_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a003951mg PE=4 SV=1
MRTLCPNLDREDALETVLEVPIPEEIFPSNYKHRSWQSVKSWLIKPPHMERASSPAGGGH
AMEIQFLLGVIGAPLIPIPIQSHRTLFNDRTIKGQPIESSMAKYIVQQYVAAAGGEHALN
SIDSMYAMGKVKMTSSEFGAGVVQDLNNNNKMKNMKNNINGGGELGGFVLWQKSPDLWSL
ELMVSGCKISAGSDGKVAWRQTPWQQHSNSSRGPPRPLRRSLQGLDPKSTANLFSNSICI
GEKAVNNEDCFVLKLEAGPTTLRARSSSNVDIIRHTIWGCFSQRTGLLVQLEDSHLLRIK

SSGKDDVFWETNMESLIQDYRTIEGVNIAHAGKTSVSLFRFEEGNLDACTRSRMEEIWSV
EEVDFNIKGLSMDCFLPPADLKKEANEDENAGDVDGLDLGLLLFLLGDHHGQHPVLHSRL
DLFHLGILRQPEAAEELTAAPLHPVPSVSLLLVLPAPLAADLQHSAVLHFHLHFLFLQPW
QVRLEHVRLRRLPPVYARVRHRRSLARGGGLSGHRAGKRGTLEGVPEIQREWVEDVAPAA
GEKAWNQSHILQ
>tr|M0S7P7|M0S7P7_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MRKLCPNLDREDGLDTVLEVPIPEEMFASAGTGAARWRNMRTWLEAQAFDKAAAPAQLSS
RTVELQLLLNVVSSPLIPCPVPLDHPFNLSIQIRDCSIQASTAKYIIQQYIAATGGQTAL
ASVSSMYAVGKLQMSASEFHVGNQTVAAKRKGEIGGYVLWQKNPGVWYFELIMAGSKMSA
GSDGKVAWRQSASEQSHASRGPPRPLRRSLQGLDPRSTATLFSDAVCIGEKVIDGEECFI
LKLESNPATLRARSADTFDIIHHTIWGYFSQRTGLLVQLADTHLLRMKAGRRGQSKSIFW
ETSMESAIRDYRYVDGVKIAHAGRTMVTLFRYGEGSVNHKRKMEETWTIEEVDFNLWGLS
MECFLPPADLKEEEGGD
>tr|B9H9Y5|B9H9Y5_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0006s21130g PE=4 SV=1
MSRLAPLSEEPINEDEEYSTNCSKKKGYSWKNWLKTHFYLVFNKKSDLKVLLSVLGCPLF
PVSIHSKLPINEVSSSAQYIIQHFSAATGCRKLQGEVKNLFATGKVTMAMVDELGGSPMA
GATTVAEKGCFVMWQMAPNKWLIELVVDGHKVVAGSDGNVAWRHTPWLASHAAKGGVRPL
RRALQGLDPMAISAVFSPAQYMGEKRVSGTDCFVLKLSADQADLAARSDSTAEMIKHIIF
GYFSQRSGLLVHLEDSYLTRIQSPGTYPTYWETTMATKIEDYRIVEGVMIAHGGQSSVMI
TRFGDSLKSGLSITRMEETWTIDDLAFNVPGLSMDCFIPPEEMQKDYPEENLDWRSPLHR
>tr|A0A061EYY1|A0A061EYY1_THECC Uncharacterized protein OS=Theobroma
cacao GN=TCM_025023 PE=4 SV=1
MSRLAPLSEEPINEEDSANCSKKGLSWKNWLKTHFSLVFNKKSDLKILLSVLGCPLFPVS
ILSKPPINEVSSSAQYIIQHFTAATGCRKSEGRVKNIFVTGKVTMAMVDELGATAGSVAG
AAGVAQKGCFVMWQMVPNKWLIELVLGGHKVVAGSDGNVAWRHTPWLGAHAAKGGVRPLR
RALQGLDPVAISAVFSSAQYMGEKRISGTDCFVLKLCADQVDLADRSDSTAEMIKHVIFG
YFSQRSGLLVFLEDSYLTRIQSPGTHPTYWETTMATKIEDYRIVEGVMIAHSGQSSVIIT
RFGDNLKAGLSVTRMEEIWTIDDVAFNVPGLSIDCFIPPKEVQKDFPEESLDWRSPLHQ
>tr|Q84K85|Q84K85_ORYSJ Putative uncharacterized protein OJ1364E02.14
OS=Oryza sativa subsp. japonica GN=OJ1364E02.14 PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTNMYAMGKVRMTAAELNSSDADGGGGGGGGHRGGKKSSKNGGEVGGF
VLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQDRTDRS
STRTAERHDYAFAALIGPLALAVVKGLDPMLTASLFADAVCIGERSVDGEDCFVLKVEAE
ASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSHLLQIKSSGHGSVFWETTMESHLH
DYRAVDGVNIAHAGRTAVSLVRFGDSSDGNTRTRMEEVWNIEEVDFNIWGLSMDCFLPPS
DLKDSKEDKDVSAAVKPARPPPIRIPAVAVRVGPSQVAAVNMDDSDSLIARS
>tr|M5VPR7|M5VPR7_PRUPE Uncharacterized protein OS=Prunus persica
GN=PRUPE_ppa007440mg PE=4 SV=1
MGRLAPLSEEPNINEEEEATNRSSKGILRSTQTWRNWIKTHLPSLALFNKRSDFKVLLSV
LGCPLFPVSAHPKLPLNEVSSTAQYIIQHFTAATGCRKLEGKVKNIFATGKVIMAMVDEP
GPGGASSSSTATLSEKGCFVMWQMVPNKWLIELVLGGHKVAAGSDGNVAWRHTPWLGVHA
AKGGVRPLRRALQGLDPMAIAAVFSPAQYMGEKQISGVDCFVLKLSADQTDLTERSDSTA
EMIKHVIFGYFSQRNGLLVHLEDSYLTRIQSPGAYPTYWETTMSTKIEDYRTVEGVMIAH
AGQTNVIITRFGDNLKMGAAITRLEETWTIDDLAFNVPGLSMDCFIPPKEVQKDYPKKNF
DWRSPLH
>tr|A0A072VJK1|A0A072VJK1_MEDTR Lipase OS=Medicago truncatula
GN=MTR_1g054670 PE=4 SV=1
MGRLAPLSEEPINEENERKLSKYNSKKGFQLWMNWSWIKTHFSLVFNKKSNLKMLLSVLG
CPLFPVPIHPKSPLNEVSSSAQYIIQQFTAATGCRKLEGTVKNVFATGKVTMVVVDELGS
VGSGGVNGTSEKGCFVMWQMVPDNWQIEIVVGGQKVLAGSNGTIAWRHTPWLGVHAAKGG

VRPLRRALQGLDPLAVSAVFSAAQHMGEKQINGVDCFVLKLSADQKDLIERSDNTAEMIK
HAIFGYFSQRSGLLVHLEDSYLTRIQAIGTNPTYWETTMSTKIEDYRDVDGVMIAHAGST
TVMITRFGDNLKDGPAITRLEESWTIDDVAFNVQGLSIDCFLPPQELNKDCPQQHLDWRS
SLHR
>tr|A0A0K9Q683|A0A0K9Q683_ZOSMR Uncharacterized protein OS=Zostera marina
GN=ZOSMA_104G00330 PE=4 SV=1
MRILCPNYDREDSLDTILEIPIQDDMFASNTGGGRLQTLAVWVKSQAANSNSGRNAELQL
LLNVVGSPLIPCPVPVDQGITRSIRDCSIQASTAKYIVQQYVAATGGQAALNSVNSWYAV
GKVTMSASDFHMSDESVSASSSKGRGEIGSFVLWQKTPELWYLELIVSCCKVSAGGNGKL
NWRQSAAEQSHASRGPPRPLRRALQGLDPRSTANLFGDAVCIGEKVINNEDCFILKLESN
SATLRSRGSSSFEIIHHTLWGYFSQRTGLLIKFEDSHLLRMIGKKDGSIFWETSMESMIE
DYRYIDGVNIAHSGKTLVTLFRYGQAGSANHKRKMEETWNIQEIDFNIKGLTMDHFLPPA
DLKKDSDADDQESTP
>tr|A2XEX4|A2XEX4_ORYSI Putative uncharacterized protein OS=Oryza sativa
subsp. indica GN=OsI_10890 PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRGGKKSSKNGGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQDRTDR
SSTRTAERHDYAFAALIGPLALAVVKGLDPMLTASLFADAVCIGERSVDGEDCFVLKVEA
EASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSHLLQIKSSGHGSVFWETTMESHL
HDYRAVDGVNIAHAGRTAVSLVRFGDSSDGNTRTRMEEVWNIEEVDFNIWGLSMDCFLPP
SDLKDSKEDKDVSAAVKPARPPPIRIPAVAVRVGPSQVAAVNMDDSDSLIARS
>tr|A0A0D9Z554|A0A0D9Z554_9ORYZ Uncharacterized protein OS=Oryza
glumipatula PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRGGKKSSKNGGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQDRTDR
SSTRTAERHDYAFAALIGPLALAVVKGLDPMLTASLFADAVCIGERSVDGEDCFVLKVEA
EASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSHLLQIKSSGHGSVFWETTMESHL
HDYRAVDGVNIAHAGRTAVSLVRFGDSSDGNTRTRMEEVWNIEEVDFNIWGLSMDCFLPP
SDLKDSKEDKDVSAAVKPARPPPIRIPAVAVRVGPSQVAAVNMDDSDSLIARS
>tr|I1HRW5|I1HRW5_BRADI Uncharacterized protein OS=Brachypodium
distachyon GN=BRADI2G50740 PE=4 SV=1
MRKLCPNHDRDDSLDTVLEVPIPDEMLANAPGSDKRRGANMRAWLKTQAFDRATAEGPAA
AAANAELQLFLNVVGSPLVPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQAAL
QSVQSMYAVGKVRMCASEFHLGDQTVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHKMS
AGSDGKVAWRQSAAEISHVSRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKVINGEECF
ILKLEASAATLRARSAAAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSENI
FWETSMESVISDYRCIDGINIAHGGKTAVTLFRYGEGSVNHKRKLEETWTVEEADFNVYG
LSSDHFLPPSDLKKEGDDQHAG
>tr|A0A0E0NSY4|A0A0E0NSY4_ORYRU Uncharacterized protein OS=Oryza
rufipogon PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRGGKKSSKNGGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQDRTDR
SSTRTAERHDYAFAALIGPLALAVVKGLDPMLTASLFADAVCIGERSVDGEDCFVLKVEA
EASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSHLLQIKSSGHGSVFWETTMESHL
HDYRAVDGVNIAHAGRTAVSLVRFGDSSDGNTRTRMEEVWNIEEVDFNIWGLSMDCFLPP
SDLKDSKEEAPPADKDTGGGRPRRAIAGRRRQHGRFRLAHCEVMTYIAGSVTPYESCVFT
CLIAISYLW

>tr|A0A0D9V615|A0A0D9V615_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINTPGADKRRGAGGANMRAWLKNQAFDRATVGG
PASANAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQAA
LQGLQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHKM
SAGSDGKVAWRQSAAENSHVSRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKIINGEEC
FILKLEASAATLRARSAAAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSEN
IFWETSMESVISDYRHIDGINIAHGGHTNVTLFRYGEGSVNHKRKLEETWTVEEADFNVH
GLTTDYFLPPSDLKKDADEQHAG
>tr|I1NRV9|I1NRV9_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGTDKRRGAGGANMRAWLKNQAFDRATVGG
PANATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQAA
LQGLQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHKM
SAGSDGKVAWRQSAAENSHASRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKIITGEEC
FILKLEASAATLRARSAAAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSEN
IFWETTMESTISDYRHIDGINIAHGGHTAVTLFRYGEGSVNHKRKLEETWTVEEADFNLY
GLTTDYFLPPSDLKKDIDEKRAG
>tr|V7BMB5|V7BMB5_PHAVU Uncharacterized protein OS=Phaseolus vulgaris GN=PHAVU_007G262500g PE=4 SV=1
MGRLAPLSEEPINEENEGNNNSKKCLQSWRNWNWIKTHFSLLFNKKSNLKILLSVLGCPL
FPLPVHPISPLNEVSSSAQYIIQHFRAATGCKKLEGTVKNVFTTGKVTMDVVDELGSTNG
GVNVEKGCFVMWQMVPDKWQIELVLGGQKVLAGSNGAIAWRHTPWLGVHAAKGPVRPLRR
ALQGLDPLAVSAVFCAAQYMGEKQISGIDCFVLKLSADQKDLAERSDNTAEMIKHAIFGY
FSQRSGLLVYLEDSYLTRIQAPGSHPTYWETTMSTKIEDYRVVDGVMIAHAGSSTALITR
FGDNLKAGPAITRLEESWIIDDVAFNVPGLSLDCFIPPQELQRDCSSDDDVDWKSSLLHR
>tr|A0A0E0C835|A0A0E0C835_9ORYZ Uncharacterized protein OS=Oryza meridionalis PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGTDKRRGAGGANMRAWLKNQAFDRATVGG
PANANAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQAA
LQGLQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVLWQKCPEIWYFELIMAGHKM
SAGSDGKVAWRQSAAENSHASRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKIITGEEC
FILRLEASAATLRARSAAAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSEN
IFWETTMESTISDYRHIDGINIAHGGHTAVTLFRYGEGSVNHKRKLEETWTVEEADFNLY
GLTTDYFLPPSDLKKDTDEKRAG
>tr|B9IID6|B9IID6_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_0016s06230g PE=4 SV=2
MSRLAPLSEEPINEDEEYSTNCSKKKVHSWRNWLKTHFHLVFNKRSDLKVLLSVLGCPLF
PVSIHSKSPVNEVSSSAQYIIQHFTAATGCRKLQGKVKNIFATGKVTMAMVDELGGSAMA
GVTTAAQKGCFVMWQMAPNKWLIELVVDGHKVVAGSDGNVAWRHTPWLGSHAAKGGVRPL
RRALQGLDPMAISAVFSPSQYMGEKCISGMDCFVLKLSADQADLADRSDSTAEMIKHVIF
GYFSQKNGLLVYLEDSYLTRIQSPGTYPTYWETTMATKIEDYRAVEGVMIAHGGQSSVMI
SRFGDNLKEGLSITRMEETWTIDDLAFDVPGLSMDCFIPPKEVQKDYPEENLDWRSPLQ
>tr|G7KBU0|G7KBU0_MEDTR Lipase OS=Medicago truncatula GN=MTR_5g081550 PE=4 SV=1
MKKLCPNLYHEDGLETVLEVPIPEDIFTNKSGTTWKNMKQWMKPNNESRSSRFEDPNTNI
QLLLGVVGAPLIPFPITNEYKPIITRNIKGHNIEASMAKYIVKQYVAAVGGESVLNNVES
MYAMGEVRIGTSEFVAGEGGVNSKKVMKKVKKVDMKEELGGFVLWQKRPELWCLELVVSG
YKISAGSDGKVAWRQTPWHHSHASRGPPRPLKRLLQGLDPKSTANLFNNSTCIGEKTVNN
EECFILKLEAESTSLQTRSSSNIEIIGHTVLGYFSQRTGLLVQLEDTNLIKLKSSETEFI
FWETNTESLIQDYRIVDGIQIAHCGKTWVTLSRFGEGPENHSRTSINEVWKIEEVDFNIK
GLSLDCFLPPSDLKRDEEKGVVSVSNAKLPYKIQSASFKISVSKVAAIDVDDSCVSENIQ
DM
>tr|K7K8X0|K7K8X0_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1

MMGRLAPLSEEPINEENEGYNNSNSKKCLQSWRNWNWIKTHFSLAFNKKSNLKILLSVLG
CPLFPVPVHPILPLNEVSSSAQYIIQHFRAATGCRKLEGTVKNVFTTGKVTMDVVDELGS
TSGGINLEKGCFVMWQMVPDKWQIELVLGGQKVVAGSNGAIAWRHTPWLGVHAAKGGVRP
LRRALQGLDPLAVSAVFCAAQYMGEKEISGMDCFVLKLSADQKDLVERSDNTAEMIKHAI
FGYFSQRSGLLVYLEDSYLTRIQAPGSHPTYWETTMSTKIEDYRIVDGVMIAHAGSSTAL
ITRFGDNLKAGPSITRLEESWTIDDVAFNVPGLSLDCFIPPQELQRDCSSDDELDWRSFT
LA
>tr|A0A077RVE3|A0A077RVE3_WHEAT Uncharacterized protein OS=Triticum
aestivum GN=TRAES_3BF002700040CFD_c1 PE=4 SV=1
MRKLCPNHDRDDSQLDTVLEVPIPDEMLANAPGADKRRGGGPNMRAWLKTQAFDRATAEG
PAAAAANAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQ
AALQGVQSMYAVGKVKMCASEFHLGDQTVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGH
KMSAGSDGKVAWRQSAAENSHASRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKVINGE
ECFILKLEASAMTLRARSAAAFDIIHHTVWGYFSQRTGLLIQLEDNHLLRMKSGKGARRS
ENIFWETSMESVINNYRHIDGVNIAHGGKTTVTLFRYGEGSVNHKRKLEETWTVEEADFN
VKGLTSDYFLPPSDLKKEGDDQPGG
>tr|F2EJH8|F2EJH8_HORVD Predicted protein OS=Hordeum vulgare var.
distichum PE=2 SV=1
MRKLCPNHDRDDSLDTVLEVPIPDEMLANAPGADKRRGGGASMRAWLKTQAFDRATAEGP
AAAAANAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQA
ALQGLRSMYAVGKVKMCASEFHLGDQTVTAAQGRAEVGGFVLWQKCPEVWYFEIIMAGHK
MSAGSDGKVAWRQSAAEVSHVSRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKVINGEE
CFILKLEASAATLRARSAAAFDIIHHTVWGYFSQRTGLLIQLEDNHLLRMKSGKGARRSE
NIFWETSMESVINNYRHIDGVNIAHGGKTTVTLFRYGEGSVNHKRKLEETWTVEEADFNL
YGLSSDHFLPPSDLKKEGDDQHAG
>tr|D7TI91|D7TI91_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VIT_08s0007g07110 PE=4 SV=1
MNRLAPLSEEPTNDEEEDNNNSSKKVSSWRNWLKSHFSLLFNKKSDLKILLSVLGCPLFP
ISPHAGQPNTHVSSSAEYIIQHFTAATGCRKLEGKVKNVFATGKVRMAMVDELGSSGSST
AVGPTGVSQKGCFVMWQMVPDKWLIELVVGGHKVVAGSDGNVAWRHTPWIGAHAAKGGVR
PLRRVLQGLDPLAVSAVFSSAQYMGEKRIMGVDCFVLKLSADHTDLADRSDNTAEMIKHV
IFGYFSQRSGLLVYLEDSYLTRIQSPGSRPTYWETTMATKIEDYRTVEGVMIAHGGQSSA
IITRFGDNLKVGPAITRMEETWTIDDLAFNVPGLSMDCFIPPEEVQKDYPEENLDWRSPL
HRTPTPPENEKLASPGPPPIRVSITEMAGRGVFATRRIGSGDLIHTAKPLVSHPSLSSIH
SVCYFCLRKLKPVTSSEDCNVRFCSQECEEQSKVFVAVERKADWSAYDDYCRTRGLKYPL
LVKRLACMVVSGVASADCLDILQPASLSSEMISEMGEGFSLLQSAFMKAKARDECMAFLT
EQWYINVLARFRINSFRIELAGGSYEDLHSLAAASVETEAAVGNAVYMLPSFYNHDCDPN
VHIIWIDNVNARLKALREIEAGEELRICYIDASMDHDARQTILFQGFGFRCSCLRCSSGD
>tr|K4BUQ6|K4BUQ6_SOLLC Uncharacterized protein OS=Solanum lycopersicum
GN=Solyc04g078190.2 PE=4 SV=1
MEKKQGFFSALKDEVVRGLSPAKSRGRSPSPSGSGLLRRRKGNQAPQPEVYISRSGSLRP
CVETLSPLMEGPDPNGPEVGDSKSDRWWMKGQLCRAPSVSTSGSGLQRSDLRLLLGVLGA
PLAPVHVSNNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNTMYNAYAMGKVRMM
ASDIETATKVIKNRNSSKTAESGGFVLWQMNPDMWYVELALGSSKVHAGCNGKLVWRHTP
WLGAHAAKGPVRPLRVLILELLQTCLLVQNVLEKRRSTVRIASFSNFVLIHIL
>tr|A0A067JGI3|A0A067JGI3_JATCU Uncharacterized protein OS=Jatropha
curcas GN=JCGZ_03041 PE=4 SV=1
MMSRLAPLSEEPINEEDDKSNNSSKKVQSWKNWLKTHFSLVFNKKSDLKILLSVLGCPLF
PVSVHPKLPINEVSSSAQYIIQHFTAATGCRKLEGTVKNMFATGKVAMAMVDELGGSSGL
AAGATTGDTQKGCFVMWQMVPNKWLIELVVSGHKVVAGSDGNVAWRHTPWLAAHAAKGGI
RPLRRALQGLDPMAISAVFSPAQYMGEKCISGIDCFVLKLSAELSDLADRSDSSAEMIKH
VLFGYFSQRNGLLVYLEDSYLTRIQSPGTYPTYWETTIATKIEDYRTVEGVMIAHGGQSS
VIITRFGDNLKAGLSITRMEETWTIDDFAFNVAGLSMDCFIPPKEVQKDCSEEKLDWRS

>tr|C5X6Z1|C5X6Z1_SORBI Putative uncharacterized protein Sb02g031590
OS=Sorghum bicolor GN=Sb02g031590 PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGADKRRGAGGANMRAWLKNQAFDRATVDG
AASATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIIQQYIAATGGQAA
LQGVRSMYAVGKVRMCASEFHLGDQTVTTTAAQGRAEVGGFVLWQKTPEVWFFELIMGGH
KMAAGSDGKVAWRQSAAEHSHASRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKILNNE
ECFILKLEAGAATLRARSAPAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGHRRS
ENIFWETSMESVISDYRCIDGVNIAHGGHTNVTLFRYGEGSVNHKRKLEETWTVEEADFN
VHGLTADYFLPPADLKKDVDDQNK
>tr|I1JQE8|I1JQE8_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=2
MGRLATLSEEPINDQDINYNKRNSSSGSKKWPNWNWIKTHFFHKKPDLKILLSVLACPLF
PVPLHTQPDPPPLNQLSSSAQYIIQHFTAATGCRKLEGTVKNVFATGKVEMWAVDEVGNT
GVSERGCFVIWQMLPDKWQIELAVAGHKVVAGSDGAVAWRHTPWLGTHAAKGGIRPLRRA
VQGLDPLAVSAVFSAAQYMGEKQISGIDCFVLKLSPDQKDLVDRSDNTAEMIKHVAFGYF
SQRNGLLVHLEDSYLTRIQSPGTHPTYWETTMSTKIEDYKMVDGVMIAHAGHSTVIITRF
GDNLKTGPAITRLEESWTIDDVAFNVQGLSMDCFIPPKELHKDYPQEDLDWRSPLHR
>tr|K3XSN4|K3XSN4_SETIT Uncharacterized protein OS=Setaria italica
GN=Si004934m.g PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDDMLINAPGADKRRGAGGANMRAWLKNQAFDRATVDG
HASATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIIQQYIAAMGGQAA
LQGVRSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVLWQKTPEVWFFELIMAGHKM
SAGSDGKVAWRQSAAEQSHVSRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKILNGEEC
FILKLEAGAMTLRARSAPAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSEN
IFWETSMESVISDYRYIDGINIAHGGHTAVTLFRYGEGSVNHKRKLEETWTVEEADFNVH
GLTTDYFLPPADLNKDVDDQNK
>tr|K7V4N8|K7V4N8_MAIZE Uncharacterized protein OS=Zea mays
GN=ZEAMMB73_778968 PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGADKRRGAGGANMRAWLKNQAFDRATVDG
PASATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIIQQYIAATGGQAA
LQGVRSMYAVGKVRMCASEFHLGDQTVTAAQGRAEVGGFVLWQKTPEVWFFELIMAGHKM
SAGSDGKVAWRQSAAEHSRVSRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKILNNEEC
FILKLEAGAATLRARSAPAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSEN
IFWETSMESVISDYRYIDGINIAHGGHTNVTLFRYGEGSVNHKRKLEETWTVEEADFNVH
GLTTDYFLPPADLKKDDEDHNK
>tr|B9GRZ9|B9GRZ9_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0002s26320g PE=4 SV=1
MRKLCPNYDREHALDTVLEVPIPEEMFTKMGNSSASRWQNMRALMRAQAAADKSTHLQSK
SDNEFIALLKLVGSPLIPFQVNPDQPLTRPLKDCNIEASTAKYIVQQYIAAIGGSLALNS
VKSMYAVGQVKMTASEMHQGDGSVHPGGKYEVGGFVLWQKNPDLWYLELVVSGYKVSAGS
DGKVAWNQSSSQASHANRGPPRPLRRFFQGLDPRCPANLFLEAVCVAEKAVNNEDCFVLK
LETDSNTLKAQSSSNTEIVHHTIWGYFSQRTGLLVKFEDTKLVKMKPIKGNDNVFWETSI
ESVIGDYRYIEGINIAHSGKTIATLYRYGASHNHKRKIEETWMIEEVDFNICGLSMDCFL
PPADLKREQEGGEL
>tr|Q8L9E9|Q8L9E9_ARATH Putative uncharacterized protein OS=Arabidopsis
thaliana PE=2 SV=1
MQRLAPLMEEPIDEEDQEEERGGRKGSTRSKSWKKWIKTQLQFIVFPKKPDMKLLLSVMG
CPLFPVPPLSKISLQQVSSSAQYIIQQFAAATGCKKLAGEIKNTFVTGKITMTMVSDINS
STAVSSTSSVSHKGCFVMWQMLPEKWLIELVGGGHKVSAGSDGEITWRYTPWLGDHAAKG
AIRPLRRALQGLDPLTISSVFSSAQFVGEKEINGKDCFILKLSTDQIDLSKRSDSTAEMI
KHVAFGYFSQKSGLLICLEDSSLTRIQIPGTVPTYWETSMSSWMEDYRAIEGSEVVIAHS
GKTDVLISRFGETLKGGISVTRMEEKWTIDDVAFDVPGLSVDCFIPPKEMKMDFHHQDAQ
KHLPNYNT
>tr|A0A0D2SXX1|A0A0D2SXX1_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_006G144900 PE=4 SV=1

MSRLAPLSEEPISEDDSANCSKKGLSWKNWLKTHLSLVFNKKSDLKILLSVLGCPLFPVS
ALSEPPINEVSSSAQYIIQHFTAATGCRKSEGTVKNIFVTGKVTMAMVDELGATVGSVAG
AAGVAQKGCFVMWQMVPNKWLIELVVGGHKVIAGSDGNVAWRRTPWLGAHAAKGGVRPLR
RALQGLDPMAISAVFSSAQYMGEKRISSTDCFVLKLSADQVDLADRSDSTAEMIKHVIFG
YFSQRSGLLVFIEDSYLTRIQSPGTYPTYWETTMATKIEDYRLVEGVMVAHSGQSNVIIT
RFGDNLKAGLSVTRMEETWTIDDVAFNVPGLSLDCFIPPKEVQKDFPDENLDWRSPLHR
>tr|I1NAZ2|I1NAZ2_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MGRLATLSEEPINDQDNKRSTSSSSKKWRNWNWIKTHFFHKKPDLKILLSVLACPLFPVP
PNTPSDPPLNQLSSSAQYIIQHFTAATGCRKLEGTVKNVFATGKVEMWAVDEVGNTGVSE
RGCFVIWQMLPDKWQIELAVAGHKVVAGSDGTVAWRHTPWLGAHAAKGGIRPLRRAVQGL
DPLAVSAVFSAAQYMGEKQISGIDCFVLKLSPDQKDLVDRSDNTAEMIKHVAFGYFSQRN
GLLVHLEDSYLTRIQSPGTHPTYWETTMSTKIEDYKMVDGVMIAHAGHSTVIITRFGDNL
KTGPAITRLEESWTIDDVAFNVQGLSMDCFIPPKELHKDYPQEDLDWRSPLHR
>tr|M0SIX1|M0SIX1_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MARLAPLSEEPISEEESRSTARRIHSFHNWIKSHLPMLSNKRNDLKILLSVLGCPLSPLS
VSPKQPRDVASSAQYIIQQFRATTGCSKRERTAKSMYASGRVRMEMAQEHGVSSSGSASK
GHHKGCFVVWQMVPDMWLVEFAVSGHQIAAGSDGKVAWRRTPWLGAHAARGGVRPLRRAL
QAIRQGLDPETIAAVFSPAQHIGEKHIGDEECFVLELVVDDSVLSSWSDSTAEIIKHRML
GFFSQRSGLLVRLEDSQLTRIQSPGAEAMYWETTMVSCMEDYRRVDGLMIAHSGRSVANL
LRFGLGVREHRVSTQMEERWTIDDVLFNVPGLAADCFIPPEEVRRSCFYDIAIRDH
>tr|Q9FG09|Q9FG09_ARATH Gb|AAD30234.1 OS=Arabidopsis thaliana GN=F15M7.14
PE=2 SV=1
MQRLAPLMEEPIDEEDQEEERGGRKGSTRSKSWKKWIKTQLQFIVFPKKPDMKLLLSVMG
CPLFPVPPLSKISLQQVSSSAQYIIQQFAAATGCKKLAGEIKNTFVTGKITMTMVSDINS
STAVSSASSVSHKGCFVMWQMLPEKWLIELVGGGHKVSAGSDGEITWRYTPWLGDHAAKG
AIRPLRRALQGLDPLTISSVFSSAQFVGEKEINGKDCFILKLSTDQIDLSKRSDSTAEMI
KHVAFGYFSQKSGLLICLEDSSLTRIQIPGTVPTYWETSMSSWMEDYRAIEGSEVVIAHS
GKTDVLISRFGETLKGGISVTRMEEKWTIDDVAFDVPGLSVDCFIPPKEMKMDFHHQDAQ
KHLPNYNT
>tr|A0A078J1J8|A0A078J1J8_BRANA BnaA03g55420D protein OS=Brassica napus
GN=BnaA03g55420D PE=4 SV=1
MQRLAPLMEEPMDQEEQERGGGSIRTKSWKKWIKTQLQSMIIHKKPDAKVLLSVLGCPLF
PVPPLSKMSLQQVSSSAQYIIQHFAAATGCKKLERGIKNTFVTGKITMTMMNDLSGSATV
NASPVSHKGCFVMWQMLPEKWLIELVGGGHKISAGSDGEIAWRYTPWLGDHAAKGAIRPL
RRTLQGLDPLTISSVFSSAQFVGEKEINGKDCFVLKLSTDQTDLTRRSDSTAEMIKHVAF
GYFSQKSGLLLCLEDSSLTRIQTPGSLPTYWETSMSSWMEDYRAIEGSEVVIAHSGRTDV
LISRFGETLKGGISVTRMEERWTIDDVAFDVPGLSIDCFIPPKEMKMDFPHQDGPNTFPE
LLDERQKL
>tr|A0A078CV59|A0A078CV59_BRANA BnaC03g02650D protein OS=Brassica napus
GN=BnaC03g02650D PE=4 SV=1
MQRLAPLMEEPMDQEEQERGGRSIRTKSWKKWIKTQLQSMIIHKKPDAKVLLSVLGCPLF
PVPPLSKMSLQQVSSSAQYIIQHFAAATGCKKLERGIKNTFVTGKITMTMMNDLSGSATV
NASPVSHKGCFVMWQMLPEKWLIELVGGGHKISAGSDGEIAWRYTPWLGDHAAKGAIRPL
RRTLQGLDPLTISSVFSSAQFVGEKEINGKDCFVLKLSTDQTDLTRRSDSTAEMIKHVAF
GYFSQKSGLLLCLEDSSLTRIQTPGSLPTYWETSMSSWMEDYRAIEGSEVVIAHSGRTDV
LISRFGETLKGGISVTRMEERWTIDDVAFDVPGLSIDCFIPPKEMKMDFHHQDGPNTFPE
LLDERQKL
>tr|A0A0D3B008|A0A0D3B008_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MQRLAPLMEEPMDQEEQERGGRSIRTKSWKKWIKTQLQSMIIHKKPDAKVLLSVLGCPLF
PVPPLSKMSLQQVSSSAQYIIQHFAAATGCKKLERGIKNTFVTGKITMTMMNDLSGSATV
NASPVSHKGCFVMWQMLPEKWLIELVGGGHKISAGSDGEIAWRYTPWLGDHAAKGAIRPL
RRTLQGLDPLTISSVFSSAQFVGEKEINGKDCFVLKLSTDQTDLTRRSDSTAEMIKHVAF

GYFSQKSGLLLCLEDSSLTRIQTPGSLPTYWETSMSSWMEDYRAIEGSEVVIAHSGRTDV
LISRFGETLKGGISVTRMEERWTIDDVAFDVPGLSIDCFIPPKEMKMDFHHQDGPNTFPE
LLDERQKL
>tr|C5XKV6|C5XKV6_SORBI Putative uncharacterized protein Sb03g035400
OS=Sorghum bicolor GN=Sb03g035400 PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGADKRRGAGGANMRAWLKNQAFDRATVDG
AASATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIIQQYIAATGGQAA
LQGVRSMYAVGKVRMCASEFHLGDQTVTTAAAQGRAEVGGFVLWHKTPEVWFFELIIAGH
KMSAGSDGKVAWRQSAAEHSHVSRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKILHNE
ECFILKLEAGAATLRARSAPAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGHRRS
ENIFWETSMESVISDYRYIDGINIAHGGHTNVTLFRYGEGSVNHKRKLEETWTVEEADFN
VHGLTTDYFLPPADLKKDVEDQNK
>tr|W9QKK8|W9QKK8_9ROSA Uncharacterized protein OS=Morus notabilis
GN=L484_014048 PE=4 SV=1
MGRLEPLSEEPINEEDDSANSSKKGMRQTWRNWIKTHLSLVFTKRSDLKILLSVLGCPLF
PLSLHPQHSIHEVSSSAQYIIQHFTAATGCRKLEGPVKNIFATGKVTMAMGDHDLGSAGV
SAAGAASSTVCQKGCFVMWQMVPNMWLIELVVGGHKVIAGSDGNVAWRHTPWLSAHAAKG
GVRPLRRALQATNGNILQLYVQGLDPLAVSAVFSPAQYVGEKQISGIDCFMLKLSADQTD
LAERSDSTAEMIKHVIFGYFSQRSGLLVYLEDSYLTRIQSPGTYPTYWETTMSTKIDDYR
AVEGVMIAHTGQTNVVITRFGDNLKSGPAITRMEETWTIDDVAFNVPGLSLDCFIAPNEV
QKHYPEEKLDWRSPLQC
>tr|J3L4D2|J3L4D2_ORYBR Uncharacterized protein OS=Oryza brachyantha
GN=OB01G40880 PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGSDKRRGAGGANMRAWLKNQAFDRATVGG
PANATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQAA
LQGLQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHKM
SAGSDGKVAWRQSAAENSHVSRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKIINGEEC
FILKLEASAATPRAPGAAAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSEN
IFWETSMESVISDYRHIDGINIAHGGHTTVTLFRYGEGSVNHKRKLEETWTVEEADFNLY
GLTSDYFLPPSDLKKDADEQRSG
>tr|A0A067GIF3|A0A067GIF3_CITSI Uncharacterized protein OS=Citrus
sinensis GN=CISIN_1g037618mg PE=4 SV=1
MRKLCPNIEKEDGLETVLEVPIPEEMFTSMGSNVQLRWQNLSTWMKAQTSDKWSQPVIAG
RINELRFLLYLVGSPLIPLQVQLGHSVHKPVKDCSIQASTAKYIVQQYIAATGGQAALNA
VHSMCVTGQMKITASEFHQGDIEKSVNVKSNEETGGFVLWQKDPDLWFLELVVSGCKVIC
GSNGKLTWRHSSNHQGPISKGPPRPLRRFLQGLDPRSTANLFLDASCIGEKVINNEDCFI
LKLETSPAIREAQSGPNYEIIHHTIWGYFSQRSGLLIQFEDSRLLTMKTKDGNDVFWETS
TESVMHDYRYVDGINIAHGGRTRVTVFRYGEQSANHKRDMEEKWKIEDVDLNIWGLTKDH
FMPPAGVRKQTENC
>tr|V4SPB6|V4SPB6_9ROSI Uncharacterized protein OS=Citrus clementina
GN=CICLE_v10027476mg PE=4 SV=1
MRKLCPNIEKEDGLETVLEVPIPEEMFTSMGSNVQLRWQNLSTWMKAQTSDKWSQPVIAG
RINELRFLLYLVGSPLIPLQVQLGHSVHKPVKDCSIQASTAKYIVQQYIAATGGQAALNA
VHSMCVTGQMKITASEFHQGDIEKSVNVKSNEETGGFVLWQKDPDLWFLELVVSGCKVIC
GSNGKLTWRHSSNHQGPISKGPPRPLRRFLQGLDPRSTANLFLDASCIGEKVINNEDCFI
LKLETSPAIREAQSGPNYEIIHHTIWGYFSQRSGLLIQFEDSRLLTMKTKDGNDVFWETS
TESVMHDYRYVDGINIAHGGRTRVTVFRYGEQSANHKRDMEEKWKIEDVDLNIWGLTKDH
FMPPAGVRKQTENC
>tr|A0A087G5A3|A0A087G5A3_ARAAL Uncharacterized protein OS=Arabis alpina
GN=AALP_AA8G060800 PE=4 SV=1
MQRLAPLMEEPMDQEEQEEERGRGRTTRSKSWKKWIKTQLQFMGFHKKPDMKVLLSVMGC
PLFPVPPLSKISLQQVSSSAQYIIQHFAAATGCKKLAGEIKNTFVTGKITMNMVNDPNGS
TAVGNASHVSHKGCFVMWQMLPEKWLIELVGGGHKVTAGCDGEIAWRYTPWLGDHAAKGA
LRPLRRALQGLDPLTISSVFSSAQFVGEKEINGKDCFILKLSTDQIDLSRRSDSTAEMIK

HMAFGYFSQKSGLLVCLEDSSLTRIQIPGTLPTYWETSMSSLMEDYRAIEGSEVVIAHSG
KTDVLISRFGETLKGGISVTRMEEKWTIDDVAFDVPGLSVDCFIPPKEMKMDIHHQDGQK
HFTSY
>tr|D7LZS3|D7LZS3_ARALL Putative uncharacterized protein OS=Arabidopsis
lyrata subsp. lyrata GN=ARALYDRAFT_908591 PE=4 SV=1
MQRLAPLMEEPMDEEDQEDERGGGRRSKRSKSWKKWIKTQLQFIVFPKKPDMKLLLSVMG
CPLFPVPPLSKISLQQVSSSAQYIIQQFAAATGCKKLAGEIKNTFVTGKITMTMVNDLNG
SAAVSSASSVSHKGCFVMWQMLPEKWLIELVGGGHKISAGSDGEITWRYTPWLGDHAAKG
AIRPLRRALQGLDPLTISSVFSSAQFVGEKEINGKDCFILKLSTDQIDLSRRSDSTAEMI
KHVAFGYFSQKSGLLICLEDSSLTRIQIPGTVPTYWETSMSSCMEDYRAIEGSEVVIAHS
GKTDVLISRFGETLKGGISVTRMEEKWTIDDVAFDVPGLSVDCFIPPKEMKMDFHHQDAQ
KHLPNYNR
>tr|V7BKZ1|V7BKZ1_PHAVU Uncharacterized protein OS=Phaseolus vulgaris
GN=PHAVU_007G262500g PE=4 SV=1
MGRLAPLSEEPINEENEGNNNSKKCLQSWRNWNWIKTHFSLLFNKKSNLKILLSVLGCPL
FPLPVHPISPLNEYIIQHFRAATGCKKLEGTVKNVFTTGKVTMDVVDELGSTNGGVNVEK
GCFVMWQMVPDKWQIELVLGGQKVLAGSNGAIAWRHTPWLGVHAAKGPVRPLRRALQGLD
PLAVSAVFCAAQYMGEKQISGIDCFVLKLSADQKDLAERSDNTAEMIKHAIFGYFSQRSG
LLVYLEDSYLTRIQAPGSHPTYWETTMSTKIEDYRVVDGVMIAHAGSSTALITRFGDNLK
AGPAITRLEESWIIDDVAFNVPGLSLDCFIPPQELQRDCSSDDDVDWKSSLLHR
>tr|A0A0B2QIV8|A0A0B2QIV8_GLYSO Uncharacterized protein (Fragment)
OS=Glycine soja GN=glysoja_042469 PE=4 SV=1
LQGLDPRTTASMFINTRCIGEKKINEEDCFILKLCADPSTLKARSEGPAEIIRHVLFGYF
SQKTGLLVHLEDSHLTRIQNNGGEAVYWETTINSFLDDYRPVEGIMIAHSGRSVVTLFRF
GETAMSHTKTRMEEAWTIEEVAFNVPGLSVDCFIPPSELRFASMSEACELPQGQRVKTAV
AAAAYHAKVTQLQKSHDSHTNNINWTVDV
>tr|B9R7S4|B9R7S4_RICCO Putative uncharacterized protein OS=Ricinus
communis GN=RCOM_1593960 PE=4 SV=1
MRNLCPNFDKEDALDTVLEVPIPEEMFTNMGSNGASRWANMRALMRAQSADKSSHLQAKS
DNEFIALLKLVGSPLVPFQVHPDQPVTRPMIRDCSIEASTAKYIVQQYVAATGGPVALNS
VTSMYAVGQVKMAGSEMHEGNGSVQTGGKSEVGGFVLWQKNPDLWYLELVVSGYKVSAGS
DGKVAWNQSSSQPCHANRGPPRPLRRFFQGLDPRCSANLFLDAVCIGEKTVNSEECFVLK
LETDANILKTQCSPNTEILHHTIWGYFSQRTGLLVKFEDTKLVKMKPIKGNDSVYWETSM
ESVLGDYKYIEGINIAHSGKTITTLYRYGSSINHKRKIEENWRIEEVDFNICGLSTDYFL
PPADLKRDQQEGGGGD
>tr|A0A078GPZ0|A0A078GPZ0_BRANA BnaA09g35300D protein OS=Brassica napus
GN=BnaA09g35300D PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSENNKTGAWRSVKSSLLRSPPDNNSSPATLFG
GRDAQIQMLLGIVGAPLIPLPVSSDHDVLDHPISKLIKNQSIEAAMAKYIVKQYTAAAGG
ETALAGVESMYAMGKVKMGVTEFCAAKTLIGKRKKKMLKIRNVNGNGGEVGGFVLWKKGS
SQWSLELVVSGCKVSAGCDGNVAWKQSPWLEHSQASNEPSGPLRRFLQGLDPKTTANMFA
GSVCVGEKAVNEEECFVLKLETQPSGLKSRSKRGMETVKHTVWGCFSQRTGLLVQLEDTY
LVRIKTGPEEEDVVLWETTSETMIQDYKSVDGIQIAHKGRTRVSLLRLDESLESHSKTTM
EESWEIEEVGFNVKGLSSDFFLPPGDLCAKENEESEFSFGDYTSPMMIPLKVSTDSWNLK
SSKVTAIEYFGESE
>tr|M4CNW3|M4CNW3_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra005901 PE=4 SV=1
MQRLAPLMEEPMDQEEQERGGGSIRTKSWKKWIKTQLQSMIIHKKPDAKVLLSVLGCPLF
PVPPLSKMSLQQVSSSAQYIIQHFAAATGCKKLERGIKNTFVTGKITMTMMNDLSGSATV
NASPVSHKGCFVMWQMLPEKWLIELVGGGHKISAGSDGEIAWRYTPWLGDHAAKGAIRPL
RRTLQGLDPLTISSVFSSAQFVGEKEINGKDCFVLKLSTDQTDLTRRSDSTAEMIKHVAF
GYFSQKSGLLLCLEDSSLTRIQTPGSLPTYWETSMSSWMEDYRAIEGSEVVIAHSGRTDV
LISRFVETLKGGISVTRMEERWTIDDVAFDVPGLSIDCFIPPKEMKMDFHHQDGPNTFPE
LLDERQKL

>tr|Q9M050|Q9M050_ARATH Putative uncharacterized protein F1I16_130
OS=Arabidopsis thaliana GN=F1I16_130 PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSDNNKSGAWRSVKSSLLRSPPDNSSSLATLFG
GRDSQIQMLLGIVGAPSIPLPISSDQAKIDHPISNLIKNQSIESAMAKYIVKQYTAAAGG
EMALDAVESMYAMGKVKMGVTEFCAAKTLNGKRKKKMVRIRNVNNNNGNGGEMGGFVLWK
KGSSQWSLELVVSGCKVSAGCDGNVDWRQSPWLAHSHASNEPSGPLRRFLQGLDPKTTAN
LFAGSVCVGEKAVNNEECFVLKLETQPSGLKSRSKSGMETVKHTVWGCFGQRTGLLVQLE
DTYLVRIKTGLEDEDMVLWETTSETLIQDYKSIDGIQIAHRGKTRVSLLRLDESLESHSK
TTMEESWEIEEVGFNVKGLSSDFFLPPGDLCIKEEEETGFSFGDYTSPMLLPLKVSTTSW
KIKSSKVTAIEDFGEFEG
>tr|B9HEV1|B9HEV1_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0007s12620g PE=4 SV=1
MRKLCPNIDREDGLETVLEIPIPEEMYTNMGSNAELRWQNMLTWMRAQTSDKLSQPVIAA
RINELRFLLYMVGSPLIPLQVQVGHSVHKPVKDCSIQASTAKYIVQQYIAATGGQAALNA
VHSMCVTGEVKIKASEFHEGEQTINVKGSEETGGFVLWQKDPDLWMLELLVSGCKMICGS
NGKISWRHSSNQRKPISKGPPRPLRRFLQGLDPRSTANLFIDATCIGEKLIKDEDCFILK
LETSPAIREAQSGPNYEIIHHTMWGYFSQRSGLLIQFEDSRLIGLRTKDGEDIFWETSAE
SIMDDYRYVDGVNIAHSGQTRVTVFRYGEQSANHKREMEEHWKIDEVDFNIWGLTTEQFL
PPSDLEL
>tr|A0A059ASM7|A0A059ASM7_EUCGR Uncharacterized protein OS=Eucalyptus
grandis GN=EUGRSUZ_I02458 PE=4 SV=1
MRRLCPNVDREDALETVLEVPIPEEMFTSMGSSVALRMQNMLTWMKAQTSDKWSSPVIAA
RINELRFLLYLVGSPLIPLQVQLDHPVNRPIRDGSIEASTAKYIVQQYVAATGGQQAVNA
VHSMCATGQVKISASEFHQGDESVETRSTQEAGGFVLWQKNPDLWTLELVVSGCKVSCGS
NGKLSWRHSSNQQMPVSKGPPRPLRRFLQGLDPRSTANLFLDAMCIGEKIINDEDCFILK
LETSPAVREAQSGPNFDIIHHTIWGYFSQRSGLLIQFEDSRLLRMKTTKGEDADVFWETS
TESVMEEYRYVDGVNIAHRGKTTVTVIRYGEQSANHKREIEETWKIEEVDFNVWGLSVED
FMPPAEIKQGQFIW
>tr|V4S6W2|V4S6W2_9ROSI Uncharacterized protein OS=Citrus clementina
GN=CICLE_v10013489mg PE=4 SV=1
MSRLAPLSEEPINEEEQHSNSSNGSNNTKYSSKKGLSWKHWLKNHLSLVFFINKKSDLKT
LLSVLGCPLFPVPLLPKQPLNQVCSSAQYIIQHFTAAAGCRKLEGRVKNIFATGKVTMGM
GDDFGGSAGSVAIAGAGASASLGGVSEKGCFVMWQMVPNKWLIELVVGGHKVVAGSDGNL
AWRHTPWLGSHAAKGSIRPLRRALQGLDPIAVASVFSTAQYVGEKRISDIDCFVLKLAAN
QTDLADRSDSTAEMIKHVIFGYFSQRSGLLVYLEDSYLTRIQSPGTQPTYWETTMATKIE
DYRAIEGVMIAHSGQSSVIITRFGDNLKAGLSITRMEETWTIDDLAFNVAGLSLDCFIPP
KEVQKDSYPVDENLDWRSPLRRYSRCLISRLQSLHLQKRQLCSTATHNGKPSQPSPPSIQ
VALTESAGRGVFATRRIRASDLIHTAKPIITHPTLSTLNSVCYFCLRKITSSSQYFQHHN
ARFCGEVCKDNAKAFYDVERRADWSAFNDYCRSQGLKYPLLVKRLACMIISGAESADSIY
ILQPASLSPEMILELSLTLQVLNKQWYTNVLARIRINAFRIELAGGLYEDLLSSAAASIE
SEIAVGNAIYMLPSFYNHDCDPNAHIMWIDNADARLMALRDVEEGEELRICYIDASMARD
ARQALLSQGFGFQCNCLRCSSGD
>tr|A0A087GY61|A0A087GY61_ARAAL Uncharacterized protein OS=Arabis alpina
GN=AALP_AA5G196600 PE=4 SV=1
MRTLCPNFDREEGLETVLEVPMPEELFCSDNNNNKTGAWRSVKSSLLRSPPDNNSSLATL
FGGRDSQIQMLLGIVGAPSIPLQVSSDLNVLDHPISKLIKNQSIESAMAKYIVKQYTAAA
GGETVLAGVESMYAIGKVKMGVTEFCAAKTLIGKRKKKMVRIRNVNNGNGGEIGGFVLWK
KGLSHWSLELVVSGCKVSAGCDGKVAWKQSPWLAHSHASNEPSGPLRRFLQGLDPKTTAN
LFAGSVCVGEKAVNEEECFVLKLETQPSGLKSRSKTGIETIKHTVWGCFSQRTGLLVQLE
DTYLVRIKTGPEEEDVVLWETTSETTIQDYKMVDGIQIAHRGRTRVSLLRLDESLESHSK
TTMEESWEIEEVGFNVKGLSSDFFLPPGDLRTKEDEESGFCFGDYSSPMMIPLKVSTTSW
NLKSSKVNAIEDFGEFEG
>tr|U5FNU4|U5FNU4_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0016s06230g PE=4 SV=1

MSRLAPLSEEPINEDEEYSTNCSKKKVHSWRNWLKTHFHLVFNKRSDLKVLLSVLGCPLF
PVSIHSKSPVNEVSSSAQYIIQHFTAATGCRKLQGKVKNIFATGKVTMAMVDELGGSAMA
GVTTAAQKGCFVMWQMAPNKWLIELVVDGHKVVAGSDGNVAWRHTPWLGSHAAKGGVRPL
RRALQANPMAISAVFSPSQYMGEKCISGMDCFVLKLSADQADLADRSDSTAEMIKHVIFG
YFSQKNGLLVYLEDSYLTRIQSPGTYPTYWETTMATKIEDYRAVEGVMIAHGGQSSVMIS
RFGDNLKEGLSITRMEETWTIDDLAFDVPGLSMDCFIPPKEVQKDYPEENLDWRSPLQ
>tr|R0FPN3|R0FPN3_9BRAS Uncharacterized protein OS=Capsella rubella
GN=CARUB_v10017270mg PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSDNNKSGAWHSVKSSLLRSSPDNSSSIATLFG
GRDAQIQMLLGIVGAPSIPLPVSSDHDEIDHPISKLIKNQSIESAMAKYIVKQYTAAAGG
EISLAAVESMYAMGKVKMGVTEFCAAKTLVGKKKKKMVRIRNVNNNGNGGGEMGGFVLWK
KGMSQWSLELVVSGCKVSAGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPKTTAN
MFAGSVCVGEKAVNDEECFVLQLETQPAGLKSRSKSGMETVKHTVWGCFSQRTGLLVQLE
DTYLVRIKTGPEEEDVVFWETTSETLIQDYKSVDGIQIAHRGKTRVSLLRLDESLESHSK
TTMEESWEIEEVGFNVKGLSSDFFLPPGDLHTKEEEESEFSFGDYSSPMLLPLKVSTASW
KLKSSKVTSIEDFGEFEG
>tr|R0EXG6|R0EXG6_9BRAS Uncharacterized protein OS=Capsella rubella
GN=CARUB_v10026618mg PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFSGMGNNVALRWQNMMTWMKAQTSDKWSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVTGQVKMTASEFHQGDDSGANLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICG
SNGLLSWRHSSNQQTPASTGPPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGPNFEIIHHTIWGYFSQRSGLLIQFEDSRLLRMRTKEDEDVFWETSA
ESVMDDYRYVDNVNIAHGGKTSVTVFRYGEASANHRRQMSEKWRIEEVDFNVWGLSVDHF
LPPANLQIGK
>tr|K3ZCC3|K3ZCC3_SETIT Uncharacterized protein OS=Setaria italica
GN=Si024197m.g PE=4 SV=1
MRKVCANLDREDGLDTVLEVPVPESHHEPSARGGRRRRRTVTAWVRSHMDQRHRRDGAPP
SRADVQLMLGVIGAPLVPQPVEARKAMAGKDIKEEPLEVSKAKYIVEQYVAAAGGEPALS
AATSMYAMGKVRMRTAKGQKAKTGMGVVNGGGEVAGGFVVWQKMPEMWCVEMVVAGGTKM
SAGSDGKVAWRQTPWQQAHASRGPPRPLRRCVQGLDPKSTANLFSTATWVGEKCIDDDDC
FVLRVDADPSALRARSSADVEVVRHAVWGYFSQRTGLLVRLEDSHLLRIHVHGEATETAY
WETSMESSIGDYRAVDGINVAHAGRTVVSLSRFGSGADEDDGSDAARGKRTCTCLEETWS
IEEVDFNIMGLSTECFLPPRDMIPACNSKPVEKEQRKKDAVAVPVNCAAGLDVIKSKNSD
GGVRPAAARKALVPSATGLGWFGPAKVVAVETVDAAE
>tr|A0A061DFT7|A0A061DFT7_THECC Spindle assembly abnormal protein 6
OS=Theobroma cacao GN=TCM_000420 PE=4 SV=1
MRKLCPNIDREDGLETVLEVPVPEEMFTSMGSNLQVRLANMLTWMKAQTSDKWSQPVIAG
RINELRFLLYLVGSPLIPLQVQLGHSVHKPVKDCSIQASTAKYIVQQYMAATGGQQALNA
VHSMCVTGQVKITASEFHQGDASVNVKSSEEMGGFVLWQKDPDLWCLELVVSGCKVVSGS
NGKLSWRHSSNQQTPISKGPPRPLRRFLQGLDPRSTANLFIDATCIGEKIISGEDCFILK
LETSPAIREAQSGPNYEIIHHTIWGYFSQRSGLLIQFEDSRLLMMKTKDDNDVFWETRTE
SVMDDYQYIDGVNIAHGGKTSVTVFRYGEQSANHKRQIEEKWKIEDVDFNVWGLSMDHFL
PPSGLQKD
>tr|A0A087GEQ2|A0A087GEQ2_ARAAL Uncharacterized protein OS=Arabis alpina
GN=AALP_AA8G505000 PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFTGMGNNVALRWQNMMTWMKAQTSDKWSQPLIAA
RINELRFLLYLVGAPLIPLQVQVGHSVHKPVKDCSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVTGQVKMTASEFHQGEESGAHLKCNDEMGGFVLWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQLSPTSTGPPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGPNFEIIHHTIWGYFSQRSGLLIQFEDSRLLRMRTKDDEDVFWETSA
ESVMDDYRYVDNVNIAHGGKTSVTVFRYGEASANHRRQMTEKWRIEEVDFNIWGLSVDHF
LPPANLQIGKD

>tr|W9QYG5|W9QYG5_9ROSA Uncharacterized protein OS=Morus notabilis
GN=L484_014615 PE=4 SV=1
MRKLCPNIEKEDGLETVLEVPIPEEMFKSMGNNTAMRFQNMLTWMKAQTSDKWSAPIIAG
RLNELRFLLNLVGSPLIPLQVQLGHSVHRPVKDCSIQASTAKYIVQQYVAATGGQPALNS
VQSMCVTGAVKISASEFHQSSGSSDDDDGNVDVKKSSEELGGFVLWQKNPDLWCIELVVS
GCKVICGSNGKLSWRHSANQQTPISKGPPRPLRRFLQGLDPRATANLFLDAMCIGEKIID
DEDCFILKLETNPEIRDAQSGPNYEIIHHTIWGYFSQRSGLLIQFEDSRLLRMNTNSDED
VFWETSTESVMGDYRYVDGVNIAHSGKTRVTVFRYGEQSANHKREMEETWKIDEVNFNVR
GLTADYFLPPTDHRDRDQNKQQRC
>tr|A0A059AWX0|A0A059AWX0_EUCGR Uncharacterized protein (Fragment)
OS=Eucalyptus grandis GN=EUGRSUZ_H00954 PE=4 SV=1
MRKMCPNFEREDGLDTVLEVPIPEEMFTSMGSNAVLRWQNLRALMKAQSSSSSAIDYCNK
SSSSSSSSESPQQQRLSSGSRNEFMALLKLVGSPLIPFQVQSDQALTRPLKGCTIEASTA
QYIIQQYLAATGGQGALNAVHSMYAVGQVKMAASEMRQGDGSVHATGSNEVGGFVLWQKN
PDLWFLELVVAGLKVSAGSNGKVAWNQSSSQPCHANRGPPRPLRRFFQGLDPRSTANLFL
DAVCIGEKTINGEDCFALKIEAAQNILKAQSSPNTELAHHKVWGYFSQRTGLLVHFEDTK
LVRMKSIRGNDSVFWETTMESTIEDYRNVDGINIAHGGKTSVTMFRYGAAQNHKRKIEET
WRIEEVDFNICGLSMDCFLPPADLKREQE
>tr|M5VWW3|M5VWW3_PRUPE Uncharacterized protein OS=Prunus persica
GN=PRUPE_ppa007349mg PE=4 SV=1
MRKLCPNIDKEDGLETVLEVPIPEEMFTSMGSNVQLRLQNMMAWMKAQTSDKWSAPVIAG
RLNELRFLLYLVGSPLIPLQVQLGHSIHRPVRDSSIQASTAKYIVQQYTAATGGQAALNS
VNSMCVTGEVKISASDFQQGDVSLEVKRSSAESGGFLLWQKNPDLWCLELVVSGCKVICG
SNGKLSWRHSSNQQTPISQGPPRPLRRFLQGLDPRATANLFADAMCIGEKIINDDDCFIL
KLDTSPAIREAQSGPNYEIIHHTIWGYFSQRSGLLVQFEDSRLLRMTNKADDTDVFWETS
AESVIQDYKYVDSVNIAHSGRTRVKVFRYGERSANHKREMEETWKIEEVDFNIWGLTMES
FLPPADIKKQG
>tr|A0A0L9TV70|A0A0L9TV70_PHAAN Uncharacterized protein OS=Phaseolus
angularis GN=LR48_Vigan02g021900 PE=4 SV=1
MGRLAPLSEEPINEENEANNNSKKCLQSWRNWNWIKTHFSLVFNKKSNLKILLSVLGCPL
FPLPVHPLSPLNEARPVSSSAQYIIQHFRAATGCKKLEGTVKNVFTTGKVTMDVVDDLGS
TNGGNNLEKGCFVMWQMVPDKWQIELVLGGQKVLAGSNGAIAWRHTPWLGVHAAKGGVRP
LRRALQASSSSPSSSSRSHCGLDPLAVSGVFCAAQYMGEKQISGMDCFVLKLSADQKDLV
ERSDNTAEMIKHAIFGYFSQRSGLLVFLEDSYLTRIQAPGSHPTYWETTMSTKIEDYRVV
DGVMIAHAGSSTALITRFGDNLKTGPAITRLEESWIIDDVAFNVPGLSLDCFIPPQELHT
DSSSDDDVFYANL
>tr|A0A0B2S9Z8|A0A0B2S9Z8_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_002154 PE=4 SV=1
MGRLATLSEEPINDQDNKRSTSSSSKKWRNWNWIKTHFFHKKPDLKILLSVLACPLFPVP
PNTPSDPPLNQLSSSAQYIIQHFTAATGCRKLEGTVKNVFATGKVEMWAVDEVGNTGVSE
RGCFVIWQMLPDKWQIELAVAGHKVVAGSDGTVAWRHTPWLGAHAAKGGIRPLRRAGLDP
LAVSAVFSAAQYMGEKQISGIDCFVLKLSPDQKDLVDRSDNTAEMIKHVAFGYFSQRNGL
LVHLEDSYLTRIQSPGTHPTYWETTMSTKIEDYKMVDGVMIAHAGHSTVIITRFGDNLKT
GPAITRLEESWTIDDVAFNVQGLSMDCFIPPKELHKDYPQEDLDWRSPLHR
>tr|M1CEZ4|M1CEZ4_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG400025725 PE=4 SV=1
MIRLAPLSEVPTNDEETHPSSSSSSWRNWLKTHFSLIFITKKSDLRILLSVLGCPLFPVS
SNPKIPISQVSSSAEYIIEHFTAASGCRKIQGVVKNMYVSGKVSMAIVDTSSPASTISQK
GCFVLWQMVPNKWLIELVVAAHKVVAGSDGNVAWRHTPWLGSHAAKGAIRPLRRALQGLD
PLAVAAVFSAAEYIGEKNILGIDSFVLKLSANHPDLTERSDNTAEMIKHVVFGYFSQRSG
LLVYVEDSYLTRIQSPGSPPTYWETTMGTKVEDYRPVEGVMIAHSGCSSVIITRFGDNLK
AGPAITRMEETYTIDDVAFNVPGLSIDSFIPPQGLIKGYPEENLDWRSPIDR
>tr|A0A022RIJ0|A0A022RIJ0_ERYGU Uncharacterized protein OS=Erythranthe
guttata GN=MIMGU_mgv1a008713mg PE=4 SV=1

MNNRRLATVAEEPINEENTNSSRSNKKTWRKWIRNHFPHIFMNKKSHDLKILLSVLGCPL
FPVSLHPKNPIIISQVSSSAQYIIQHFTAATGCRKLSGVVKNMYATGKVVMGLVDDPGSK
SSASTPSSSVSQKGCFVIWQMVPDRWLVELVVGGHKVVAGSDGSVAWRHTPWLGAHAAKG
GVRPLRRALQGLDPVAISTVFSTAQYMGEKHISSTDCFVLKLSAEHSDLAERSDSSAEMI
KHVTLGYFSQRSGLLVYLEDSYLTRIQTPGSRPTYWETTMSTKVEDYRSVEGMMIAHSGQ
SSVIITRFGDNMKAGAEVTRMEETYVIDDLAFNVPGLSLDYFIPPDEIQKDFPQESLDWR
SPLHR
>tr|M4CSJ3|M4CSJ3_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra007185 PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSENNKTGAWRSVKSSLLRSPPDNNSSLATLFG
GRDAQIQMLLGIVGAPLIPLPVSSDHDVLDHPISKLIKNQSIEAAMAKYIVKQYTAAAGG
ETALAGVESMYAMGKVKMGVTEFCAAKTLIGKRKKKMLKIRNVNGNGGEVGGFVLWKKGS
SQWSLELVVSGCKVSAGCDGNVAWKQSPWLEHSQASNEPSGPLRRFLQGLDPKTTANMFA
GSVCVGEKAVNEEECFVLKLETQPSGLKSRSKRGMETVKHTVWGCFSQRTGLLVQLEDTY
LVRIKTGPEEEDVVLWETTSETMIQDYKSVDGIQIAHKGRTRVSLLRLDESLESHSKTTM
EESWEIEEVGFNVKGLSSDFFLPPGDLCAKENEESEFSFGDYTSPMMIPLKVSTDSWNLK
SSKVTAIEDFGESE
>tr|K4BGJ3|K4BGJ3_SOLLC Uncharacterized protein OS=Solanum lycopersicum
GN=Solyc03g051920.2 PE=4 SV=1
MIRLAPLSEVPTNDEETHSSSSSSSSWRNWLKTHFSLIFITKKSDLRILLSVLGCPLFPV
SSNPKIPISQVSSSAEYIIEHFRAASGCRKIQGVVKNMYVSGKVSMAIVDTSSPASTISQ
KGCFVLWQMVPNKWLIELVVAAHKVVAGSDGNVAWRHTPWLGSHAAKGAIRPLRRALQGL
DPLAVAAVFSAAEYIGEKNILGIDTFVLKLSANHPDLTERSDNTAEMIKHVVFGYFSQRS
GLLVYVEDSYLTRIQSPGSPPTYWETTMGTKVEDYRPVEGVMIAHSGCSSVIITRFGDNL
KAGPAITRMEETYTIDDVAFNVPGLSIDSFIPPQGLIKGYPEENLGWRSPIDR
>tr|V4KUV0|V4KUV0_EUTSA Uncharacterized protein OS=Eutrema salsugineum
GN=EUTSA_v10004430mg PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFSGMGNNVALRWQNMMTWMKAQTSDKWSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDCSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVTGQVKMTASEFHQGDDSGASLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPASTGPPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGPNFEIIHHTIWGYFSQRSGLLIQFEDSRLLRMRTKEDDDVFWETSA
ESVMDDYRYVDNVNIAHGGKTSVTVFRYGEASANHRRQMTEKWRIEEVDFNVWGLAVDHF
LPPANLQIGK
>tr|K7LD14|K7LD14_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MGRLAPLSEEPINEENEGYNNNSNPKKCLQSWRNWNWIKTHFSLVFNKKSNLKILLSVLG
CPLFPVPVHPNILPLNEVSSSAQYIIQHFRAATGCRKLEGTVKNVFTTGKVTMDVVDELG
SAGGSVNLEKGCFVMWQMVPDKWQIELVLGGQKVVAGSNGAIAWRHTPWLGVHAAKGGVR
PLRRALQGLDPLAVSSVFCAAQYMGEKEISGMDCFVLKLSAEQKDLVERSDSKAEMIKHA
IFGYFSQRSGLLVYLGDSYLTRIQAPGSHPTYWETTMSTKIEDYRIVDGVMIAHAGSSTT
LITRFGDNLKAGPSITRLEESWTIDDVAFYVKGLSLDCFIPPQELQRDCSSDDELGWRSH
A
>tr|A0A078IV82|A0A078IV82_BRANA BnaA07g37460D protein OS=Brassica napus
GN=BnaA07g37460D PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFSGMGNNPALRCQNMMTWMKAQTSDKWSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVTGQVKMTASEFHQGDESVGNLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPASTGTPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGSNFEIIHHTIWGYFSQRSGLLIQFEDSRLLSMRTKDGDVFWETSAE
SVMDDYRYVDNVNIAHGGITSVTVFRYGEASANHRRQMTEKWRIEEVDFNVWGLSVDHFR
PPANLKIGK
>tr|D7LV81|D7LV81_ARALL Putative uncharacterized protein OS=Arabidopsis
lyrata subsp. lyrata GN=ARALYDRAFT_486006 PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSDNNKSGTWRSVKSSLLRSPPDNSSSLATLFG

GRDAQIQMLLGIVGAPSIPLPVASDHDEIDHPISNLIKNQSIESAMAKYIVKQYTAAAGG
EMALAGVESMYAIGKVKMGVTEFCAAKTLNGKRKNKMVRIRNVNNNNGNGGEMGGFVLWK
KGLSQWSLELVVSGCKVSAGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPKTTAN
LFAGSVCVGEKAVNDEECFVLKLETQPSGLKSRSKSGMETVKHTVWGCFSQRTGLLVQLE
DTYLVRIKTCLEEEDMVLWETTSETLIQDYKSVDGIQIAHRGKTRVSLLRLDESLESHSK
TTMEESWEIEEVGFNVKGLSSDFFLPPGDLHTKEEEESGFSFGDYSSPMLLPLKVSTASW
KLKSSKVTAIEDFGEFEG
>tr|I6M4G0|I6M4G0_COFCA Uncharacterized protein OS=Coffea canephora
GN=111018.11 PE=4 SV=1
MRKLCPNFDREDGLETVLEVPIPEEMFAAMGNNIALRWENMATWMKAQTSDKWSSPIIAG
RYNELSFLLFIMGSPLIPLQVQLDQSIHRPVRHASIEASTAKYIVQQYIAATGGQQALNS
VNSMCALGQVKISSSEFHQGDDSVKVRNTEEAGGFVLWQKNPDLWCLELLISGCKVISGS
NGKVSWRESSNQQRPIAKGPPRPLRRFLQGLDPRSAAILFIDAVCIGEKIINDEDCFILK
LDTNQSTLEAQSGPNYEIIHHTLWGYFSQRSGLLVKFEDSRLLTVKTSRDDGEGVFWETS
TESVIEDYKYVEGVNIAHSGRTSMTVFRYGEQSANHKRELQETWKIEEVDFNVWGLNSEF
FMPPSEFQRKK
>tr|A0A067JUC5|A0A067JUC5_JATCU Uncharacterized protein OS=Jatropha
curcas GN=JCGZ_20029 PE=4 SV=1
MKKLCANVDRDDALETVLEVPIPEEMYNSMGSNKTLRWHNMLAWMKAQTSDKWSQPVIAA
RINELRFLLYMVGSPLIPLQVQVGHSVHKPVKDCSIQASTAKYIVQQYIAATGGQAALNA
VHSMCVIGEVKISTSEFHQSDQTIKVKSGGEIGGFVLWQKDPDLWILELVVSGCKVICGS
NGKVSWRHSSNQQGPISNGPPRPLRRFLQGLDPRSTANLFIDATCIGEKIINDEDCFILK
LETSPAIREAQRGPNYEIIHHTIWGYFSQRSGLLIQFEDSRLIGMRTKDDDDVFWETSTE
SVMEDYKYVDGVNIAHSGKTRVSIFRYGEQSANHKRQMEEKWKIEDVDFNVWGLSKEHFL
PPSDHIKFGKK
>tr|I1HKS2|I1HKS2_BRADI Uncharacterized protein OS=Brachypodium
distachyon GN=BRADI2G31730 PE=4 SV=1
MRKLCPNLDREDGLDTVLEVPLPELQDTAATAFSGVRRRRRSGTVKAWMRSHAADQQHRR
REPSRADVQIMLGVMGAPLVPQPVEARKAMAAGHDIKEEPLEVSKARYVMEQYVAAAGGE
AALGAATSMYAMGNVRMSTTTSSNKGGRAAKKSVGEVSGGFVVWQKKPELWCVEMVVSGG
TKLSAGSDGKVAWRQTPWQQAHASRGPPRPIRRCVQGLDPKSTADLFSSAAWVGEESVDG
EDCFVLRVDADRSALDARSSDDVEVVRHALWGYFSQRTGLLVRLEDTHLLRVPTEISSAS
EIQNLYWETTMESSIGDYRAVDGINIAHAGRTVVSLSRFTGDAEAAGRKMRPCTTTMEET
WSIEEVDFNVAGLSRECFLPPRDLLVSSSKQQQQKKKKDNAAEAALCAKSVVKAKKALVP
AVTGLGWFGPAKVVAVDDVDAADDSKDSTRASTR
>tr|A0A0E0L078|A0A0E0L078_ORYPU Uncharacterized protein OS=Oryza punctata
PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHREAPRRRGRRGGGTVKSWVRARMEHGRRRDGTAP
SRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGEEEPLEASKARYIVEQYVAAAGGEAA
LGAATSMYAMGKVRMRTTTSKGNKDKVMGVATGGEVAGGFVVWQKKPELWCVEMVVTGGV
KMSAGSDGKVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGERCVDGD
DCFVLRVDADHAALHARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHLLRIGVAHAAAES
AYWETTMESSIGDYRAVDGINIAHAGRTVVSLSRFESADAADAVRGSKRSCTTTMEETWS
IEEVDFNVVGLSMDCFLPPRDLVLNDCSKKQQKEDAAAVKDGAGAAANVKGGSDDGGKTN
GGDIGRGVVVKKALVPAVTGLGWFGPAKVAAVDDTVDDDSATAAADDDDK
>tr|A0A0D2T1Q1|A0A0D2T1Q1_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_008G068600 PE=4 SV=1
MRKLCPNIDKEDGLETVLEVPVPEEMFTSMGNNLQARLENMLTWMKAQASDKWSQPMLAG
RINELRFLLYLVGSPLIPLQVQLGHSVHKPVKDCSIQASTAKYIVQQYIAATGGQQALNA
VHSMCVTGQVKITASEFQQGDVNVKVKSTEETGGFVLWQKDPDLWCLELIISGCKVVSGS
NGKLSWRHSSNQQTPIARGPPRPLRRFLQGLDPRSTANLFIDATCIGEKIISNEDCFILK
LETNAAIREAQSGPNYEIINHTIWGYFSQRSGLMIQFEDSRLLMMKTKDDSDVFWETRTE
SVMDDYKYTDGVNIAHSGKTSVTVFRYGEQSSNHKRQIEEKWKIEDVDFNVWGLTKDDFI
PPSDMQTS

>tr|A0A078IM54|A0A078IM54_BRANA BnaA02g34690D protein OS=Brassica napus
GN=BnaA02g34690D PE=4 SV=1
MRKLCPNVDRDDGLETVLEIPIPEELFSGMGNNVALRCQNMMTWMKAQTADKLSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVIGQVKMTASEFHQGDDSNVNLKSNDEMGGFILWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPSSTGTPRPLRRFLQGLDPRSTANMFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGPEFEIIHHTIWGYFSQRSGLLIQFEDSRLLSMRTKEGDVFWETSAE
SVMDDYRYVDDVNIAHGGKTTVTVFRYGEASANHRRQMTEKWRIEEVDFNIWGLSVDHFR
PPAFLLTGN
>tr|A0A078H1S4|A0A078H1S4_BRANA BnaC07g16580D protein OS=Brassica napus
GN=BnaC07g16580D PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFSGMGNNPALRCQNMMTWMKAQTSDKWSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVTGQVKMTASEFHQGDESVGNLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPASTGTPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGSNFEIIHHTIWGYFSQRSGLLIQFEDSRLLSMGTKDGDVFWETSAE
SVMDDYRYVDNVNIAHGGITSVTVFRYGEASANHRRQMTEKWRIEEVDFNVWGLSVDHFR
PPANLKIGK
>tr|A0A0D3D8E2|A0A0D3D8E2_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFSGMGNNPALRCQNMMTWMKAQTSDKWSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVTGQVKMTASEFHQGDESVGNLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPASTGTPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGSNFEIIHHTIWGYFSQRSGLLIQFEDSRLLSMGTKDGDVFWETSAE
SVMDDYRYVDNVNIAHGGITSVTVFRYGEASANHRRQMTEKWRIEEVDFNVWGLSVDHFR
PPANLKIGK
>tr|A0A078IL80|A0A078IL80_BRANA BnaC02g43970D protein OS=Brassica napus
GN=BnaC02g43970D PE=4 SV=1
MRKLCPNVDRDDGLETVLEIPIPEELFSGMGNNVALRCQNMMTWMKAQTSDKLSQPLIAA
RINELHFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVIGQVKMTASEFHQGDDSNVNLKSNDEMGGFILWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPSSTGTPRPLRRFLQGLDPRSTANMFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGPDFEIIHHTIWGYFSQRSGLLIQFEDSRLLSMRTKEGDVFWETSAE
SVMDDYRYVDDVNIAHGGKTTVTVFRYGEASANHRRQMTEKWRIEEVDFNIWGLSVDHFR
PPANLLTGN
>tr|A0A0D3AYU7|A0A0D3AYU7_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MRKLCPNVDRDDGLETVLEIPIPEELFSGMGNNVALRCQNMMTWMKAQTSDKLSQPLIAA
RINELHFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVIGQVKMTASEFHQGDDSNVNLKSNDEMGGFILWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPSSTGTPRPLRRFLQGLDPRSTANMFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGPDFEIIHHTIWGYFSQRSGLLIQFEDSRLLSMRTKEGDVFWETSAE
SVMDDYRYVDDVNIAHGGKTTVTVFRYGEASANHRRQMTEKWRIEEVDFNIWGLSVDHFR
PPANLLTGN
>tr|M4D6I7|M4D6I7_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra012096 PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFSGMGNNPALRCQNMMTWMKAQTSDKWSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVTGQVKMTASEFHQGDESVGNLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPASTGTPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGLNFEIIHHTIWGYFSQRSGLLIQFEDSRLLSMRTKDGDVFWETSAE
SVMDDYRYVDNVNIAHGGITSVTVFRYGEASANHRRQMTEKWRIEEVDFNVWGLSVDHFR
PPANLKIGK

>tr|G7ZW25|G7ZW25_MEDTR DUF620 family protein OS=Medicago truncatula GN=MTR_5g019880 PE=4 SV=1
MKQPAAKSSLRRLCPNIDKEDGLETVLEIPIPEEMFSNMGSNVTLRWQNMLTWMKAQTED
KLSSPTVSARLNELRFLLYLVGSPLIPLQVQLGHSVHRPVRDSSIEASTAKYIVQQYIAA
TGGQPALNVVESMCVMGQVRITASDFHHTGETIEVKKTSEESGGFVLWQKDPDLWCLELI
VSGCKVSCGSNGKVSWRHSSNQQQPIAKGAPRPLRRFLQGLDPRATANLFLDAACIGEKI
INDEECFILKLETSPAIRESQSGPNFEVIHHTIWGYFSQRSGLLVQFEDSRLLTMRTKDD
NDIFWETSLESVIDDYKYVDGINVSHSGTTRVTVSRYGEQSANHKRELEERWKLEEVDFN
IWGLTAESFLPPSNLGNT
>tr|A0A0A0LGJ4|A0A0A0LGJ4_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_3G855410 PE=4 SV=1
MFTNMGTNAALRWQNLRALMKAQSTADSLNKSSSHLSAASNNEFMALLKLVGSPLIPFQV
HLDLTFNCSLRDYSIEASTAKYIVQQYVAATGGQAALNSVNSMYAVGQVKMVGSAMQQGE
DSVQARGKCEVGGFVLWQKNPDLWYLELVVSGYKVSAGSNGKVAWNQSSSQPCHANKGPP
RPLRRFFQGLDPRYTANLFEDAVCIGEKTISKEDCFILKLETAAELLKSQSTPHVEIIHH
TIWGYFSQRTGLLVQFEDTKLVRMKAGKRNDSVFWETSIASTIEDYRYVDNINIAHGGRT
TARLHRYGETLNHRRKIEESWRIEEVDFNICGLSMDCFLPPADMKRDPSDVGEQEAGES
>tr|W9S3J3|W9S3J3_9ROSA Uncharacterized protein OS=Morus notabilis GN=L484_021186 PE=4 SV=1
MRKLCPNFDKENGLETVLEVPIPEEMFTNMGSNASLRWQNLRALMKAQSAGDKSSRLSSG
SSNEFMALLKLVGSPLIPLQVQPGDALTRPIKDGSIEASTAKYIVQQYLAATGGLAALNA
INSMYAVGQVKMMGSEMHEGDESVRTKGKSEVGGFVLWQKNPDLWYLELVVSGFKVSAGS
DGKVAWNQSSSQPSHANRGPPRPLRRFFQGLDPRCIANLFLDAICSGEKTINNEDCFVLR
LETAQNILKAQSTPQTETSRHTIWGYFSQRTGLIVQFEDTKLVRVKAVRGNNESVFWETR
IVTEIEDYRYVEGINIAHSGKTCAMLYRYGEAHNHRRRIEEIWKIEEIDFNICGLSMECF
LPPADLKRDNVPEGRSQGAGES
>tr|R0HGK1|R0HGK1_9BRAS Uncharacterized protein OS=Capsella rubella GN=CARUB_v10003657mg PE=4 SV=1
MQRLAPLMEEPMDEQEQEDQERGKRSTRSKSWKKWIKTQLQIIVFPKKPDMKLLLSVMGC
PLFPVPPLSKISLHQVSSSAQYIIQQFAAATGCKKLAGEIKNTFVTGKITMSMVSDVNSS
PAVGSSSSVSHKGCFVMWQMLPEKWLIELVGGGHKVAAGSDGEITWRYTPWLGDHAAKGA
IRPLRRALQGLDPLTISSVFSSAQFVGEKEINGKDCFILKLSTDQIDLSRRSDSTAEMIK
HVAFGYFSQKSGLLICLEDSSLTRIQIPGTVPTYWETSMSSWMEDYRAIEGSEVVIAHSG
RTDVLISRFGETLRGGISVTRMEERWTIDDVVFDVPGLSVDCFIPPKEIKMDFHQHDGPP
PIRVGLTESAGRAVFATRRIGAGDLIHTAKPVVACPSLASLDSVCYLCLKKLMGSAKFQD
RGVSYCSQECQENSKGFYDVETRADWSSFVDYCRTYNFKYPLMVKRLCCMIISGALPADC
LDILQPAALSSAMISKIEDGYGLLWNAFRKANFKDDDVAFLTKQWYTAILARIRINAFRI
DLVGGSCGEDLLSLAAASVEGEGAVGHAVYMLPSFYNHDCDPNAHIMWLQNADARLNTLR
DVEEGEELRICYIDASMGYEARQTILSQGFGFICNCLRCQSGD
>tr|F4K243|F4K243_ARATH Uncharacterized protein OS=Arabidopsis thaliana GN=At5g66740 PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFSGMGNNVALRWQNMMTWMKAQTSDKWSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDCSIQASTAKYIVQQYIAATGGPQALNA
VNSMCVTGQVKMTASEFHQGDDSGVNLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPASTGTPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGPNFEIIHHTIWGYFSQRSGLLIQFEDSRLLRMRTKEDEDVFWETSA
ESVMDDYRYVDNVNIAHGGKTSVTVFRYGEASANHRRQMTEKWRIEEVDFNVWGLSVDHF
LPPANLQIEK
>tr|I1KM42|I1KM42_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MRKLCPNFDNEDGLDTVLEVPIPEEMLSGMGSNGSNRWKNMRTLMNAQFVDKSSGLSTPS
NNEFMVLLKLVGAPLIPLQVPSDHNLTRPLKDCSIRDSSAKYIVQQYVAATGGVAALNSL
ESMYAMGQVRICGSEVRRQGDGYEESVQSRGKTEVGGFVLWQKNPDLWCLELVVSGFKVS
AGSNGKLAWNHSSSQPFHANKGPPRPLRRFFQGLDPRCTANLFLDAECVGENNINNEVCF
MLRLQTDQHILQAQSMSNTEIVMHTMLGYFSQRTGLLVKFEDTKLVKMKAVKGKESVFWE

TSIESMIDDYRYIDGINIAHGGRTIATLYRYGAAHNHKHMIEETWTIEEVDFNIVGLSMD
CFLPPSDGEREHEGAEQAVGMG
>tr|A0A0B2SFD3|A0A0B2SFD3_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_007562 PE=4 SV=1
MRKLCPNFDNEDGLDTVLEVPIPEEMLSGMGSNGSNRWKNMRTLMNAQFVDKSSGLSTPS
NNEFMVLLKLVGAPLIPLQVPSDHNLTRPLKDCSIRDSSAKYIVQQYVAATGGVAALNSL
ESMYAMGQVRICGSEVRRQGDGYEESVQSRGKTEVGGFVLWQKNPDLWCLELVVSGFKVS
AGSNGKLAWNHSSSQPFHANKGPPRPLRRFFQGLDPRCTANLFLDAECVGENNINNEVCF
MLRLQTDQHILQAQSMSNTEIVMHTMLGYFSQRTGLLVKFEDTKLVKMKAVKGKESVFWE
TSIESMIDDYRYIDGINIAHGGRTIATLYRYGAAHNHKHMIEETWTIEEVDFNIVGLSMD
CFLPPSDGEREHEGAEQAVGMG
>tr|V7CHT1|V7CHT1_PHAVU Uncharacterized protein OS=Phaseolus vulgaris
GN=PHAVU_002G028700g PE=4 SV=1
MKQAAAKSSLRRLCPNIDREDGLETVLEIPIPEEMFTPMGSNVTLRWQNMLTWMKAQTED
KLATPTVAARLNELRFLLYLVGSPLIPLQVQLGHSVHRPVRDCSIEASTAKYIVQQYIAA
TGGQPALNAVDSMCVIGQIKIVASDFHQTGESIEVKKSSEEMGGFVLWQKDPDLWCLELV
VSGCKVCCGSNGKISWRHSSNQQTPIAKGAPRPLRRFLQGLDPRATANLFLDAACIGEKI
INDEECFILKLETSPAIRDAQSGSNFEIIHHTIWGYFSQRSGLLVQFEDSRLLTMRTKED
NDIFWETSLESVIEDYKYVDGINVSHSGKTRVTVSRYGEQSANHKRELEERWKIEEVDFN
IWGLTAESFLPPSNLVKT
>tr|I1K7S6|I1K7S6_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MRKLCPNFDNEDGLDTVLEVPIPEEMLSGMGSNGSSRWQNMRTLMNARFVDKSSGLSTPS
NNEFMVLLKLVGAPLIPLQVPSDHNLTRPLKDCSIRDSTAKYIVQQYVAATGGVAALNSL
ESMYAMGQVRICGSEVRRQGDGYEESVQSRGKTEVGGFVLWQKNPDLWCLELVVSGFKVS
AGSNGKLAWNHSSSQPFHANKGPPRPLRRFFQGLDPRCTANLFLDAECVGENNINNEVCF
MLRLQTDQHILQAQSMSNTEIVMHTMLGYFSQRTGLLVKFEDTKLVKMKAVKGKETVFWE
TSIESMIDDYRYIDGINIAHGGRTIATLYRYGAAHNHKHMIEETWTIEEVDFNIVGLSMD
CFLPPSDGEREHEGAEQAVGMG
>tr|V4LYA1|V4LYA1_EUTSA Uncharacterized protein OS=Eutrema salsugineum
GN=EUTSA_v10010310mg PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSDNNNKSGAWQSVKSSLLRSPPDNSSSLATLF
GGRDAQIQMLLGIVGAPSIPLPVSSDHDLLHYPISKLIKNQSIQAAMAKYIVKQYTAAAG
GEAALSGVESMYAMGKVKMGVTDFCAAKTLNGKRKQKMVRIRNVNNGNGGEMGGFVLWKK
GSSQWSLELVVSGCKVSAGCDGNVAWKQSPWLAHSHASNNEPSGPLRRFLQGLDPKTTAN
MFAGSVCIGEKVVNDEECFVLKLETQPSGLKSSSKSGMETVKHTVWGCFSQRTGLLVQLE
DTCLVRIKTGPEEEDMVLWETTAETMIEDYKTVDGIQIAHRGRTRVSLLRLDESLESHSK
TTMEESWEIEEVGFNVKGLSSDFFLPPGDLRTKEDEQSGFNFGDYSSPMLLPLKIRKLRI
SGDRISGLNRRFTDIRPDIRFQNFQNLNKRITDNGYPSLKFSIIRIRIRNNRILNFTIRI
RIRTTRISGFYGSDRIGYRIG
>tr|B9IB68|B9IB68_POPTR Uncharacterized protein OS=Populus trichocarpa
GN=POPTR_0014s17980g PE=4 SV=1
MRKLCPNYDREDALDTVLEVPIPEEMFTKMGNNSASRWQNMRALMNAQAAADKSTHLQSK
SNTEFIALLKLVGSPLIPFQAHPDQPLTRPLKDCSIGASTAKYIVQQYIAAIGGPLALNS
VKSMYAVGQVKMAASEMHQGDDSVHAEGKSEVGGFVLWQKNPDLWYLELVVSGYKVSAGS
DGKVAWNQSSSQASHANRGPPRPLRRFFQGLDPRCTANLFLEAASITEKKVSNEDCFVIK
LETDSNTLKAQSSSNTEIVHHIIWGYFSQRTGLLVKFEDTKLVKMKPIKGNDNVFWETSM
ESVVGDYRYIEGINVAHSGKTTATLHRYGASHNHKRKIEETWMIDEVDFNICGLSMDCFL
PPADLKREQEGGEQ
>tr|A0A0A0KJ26|A0A0A0KJ26_CUCSA Uncharacterized protein OS=Cucumis
sativus GN=Csa_6G502080 PE=4 SV=1
MRRLCPNIDRDDGLETILEVPIPEEMFTSMGSNVTLRWQNMSTWMKAQTSDKWSSPIIAN
RFNELRFLLYLVGSPLIPLQVQLGHSVHRPVRDCSIEASTAKYIVQQYIAATGGPAALNS
VQSMCVTGQVKIKASDFHLSDESIEVKKSTEEIGGFVLWQKNPDLWCLELVVSGCKVICG
SNGKLSWRHSSNNQQSPISTGPPRPLRRFLQGLDPRATANLFIDAMCIGEKLINDEDCFI

LKLETSPAIREAQSGPNYEIIHHTIWGYFSQRSGLLIQFEDSRLLRMRTKSDEDVFWETS
TESVMETYRYVDGVNIAHSGKTNVTVFRYGEHSANHKREMEETWKIEEVDFNIWGLTMES
FLPPPGAAVLQLHDAS
>tr|C5YVP4|C5YVP4_SORBI Putative uncharacterized protein Sb09g010410
OS=Sorghum bicolor GN=Sb09g010410 PE=4 SV=1
MRKVCANLDREDGLDTVLEVPVPELYKEPSSSGHGRRRRRTVKAWVWSRMDQHHRRYGAL
PSQADVQLMLGVIGAPLVPQPIEARKAMAGEDIKEEPLEVSKAKYIVEQYVAASGGEPAL
SAATSMYAVGKVLMRATKGQKAKTGMGVVHGGGDIAGGFVVWQKRPEMWCVEMVVAGGTK
MSAGSDGKVAWRQTPWQQAHASRGPPRPLRRCVQGLDPKSTANLFSTATWVGEKTIDGDD
CFVLRVDADPLALRARSSADVEVVRHAVWGYFSQRTGLLDRLEDSHLLRIRMQGASSAQT
AYWETSMESSIGDYRAVNGINIAHAGRTVVSLSRFGSSANDQDDGSDTDVLGSKRTCTCM
EETWSIEEVDFNIMGLSTECFLPPRDLVPCSSKPVEKEHCAGLDHSCKKEDAVGTVPATS
AVVGSCDPAAVDVKYKNSDGGVRPLATARKALVPAGTGLSWFGTAKVVAVDTAAE
>tr|A0A0B2QLK6|A0A0B2QLK6_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_022017 PE=4 SV=1
MRKLCPNFDNEDGLDTVLEVPIPEEMLSGMGSNGSNRWQNMRTLMNARFVDKSSGLSTPS
NNEFMVLLKLVGAPLIPLQVPSDHNLTRPLKDCSIRDSTAKYIVQQYVAATGGVAALNSL
ESMYAMGQVRICGSEVRRQGDGYEESVQSRGKTEVGGFVLWQKNPDLWCLELVVSGFKVS
AGSNGKLAWNHSSSQPFHANKGPPRPLRRFFQGLDPRCTANLFLDAECVGENNINNEVCF
MLRLQTDQHILQAQSMSNTEIVMHTMLGYFSQRTGLLVKFEDTKLVKMKAVKGKETVFWE
TSIESMIDDYRYIDGINIAHGGRTIATLYRYGAAHNHKHMIEETWTIEEVDFNIVGLSMD
CFLPPSDGEREHEGAEQAVGMG
>tr|M4E2S3|M4E2S3_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra023074 PE=4 SV=1
MGNNVALRCQNMMTWMKAQTSDKWSQPLIAARINELRFLLYLVGSPLIPLQVQVGHSVHK
PVKDSSIQASTAKYIVQQYIAATGGPAALNAVNSMCVTGQVKMTASEFHQGDESVGNLKS
NDEMGGFVLWQKDPDLWCLELVVSGCKVICGSNGRLSWRHSSNQQTPASTGTPRPLRRFL
QGLDPRSTANLFLDATCIGEKIINGEDCFILKLETSPAVREAQSGLNFEIIHHTIWGYFS
QRSGLLIQFEDSRLLSMRTKDGDVFWETSAESVMDDYRYVDNVNIAHGGITSVTVFRYGE
ASANHRRQMTEKWRIEEVDFNVWGLSVDHFRPPANLKIGK
>tr|A0A0D2TN14|A0A0D2TN14_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_009G203300 PE=4 SV=1
MMLMKLCPNLDNQDGLETVLEVPIPEEMYTKMGSNAILRWQNLCNFMKAQSAFCNSSYLQ
ASSDNEFLTLLKIVGTPLVPFRVDLENYMHSNPIQDSSIEASTAKYIIQQFVAATGGHLA
LRSIRNMYAVGQVQLQGSETLQGNSSVQTRVNCEFGGFVLLQKNPDLWYLELVVSGFKVS
AGCDGKVAWNQSSSQPGHAHRGPPRPLRRFSQGLDPRCTASLFINAVCIGEQVIDNEDCF
ILMLETDSKALKAQSSSQAEIIHHTVRGYFSQRTGLLTKFEDKKLVRMKTTVGNDVFWET
SVESLIQDYKYVDGINIAHGGNTITTLYRYGKSHKHKRKIEETWTIDEVDFNICGLCTET
FLPPADLKREQE
>tr|B6SXI9|B6SXI9_MAIZE Putative uncharacterized protein OS=Zea mays PE=2
SV=1
MRKVCANPDREVGLDTVLEVPVPDQLHHDPSSSSSGHGRRRRRTLKAWVRSRMDQRHRRH
SSPPSQADVQLMLGVVGAPLVPQPVQARKAMVAGEDIKEEPLEVSKAKYIVEQYVAASGG
ERALSAATSMYAVGKVLMRTRSSSSTTKQGQRACRTGMVGVVHGGAEIAGGLVLWQKGPE
VWCVEMVVAGGTKMSAGSDGRVAWRQTPWQQAHASRGPPRPLRRCVQGLNPRSTANLFST
ATWVGEKSVDGDDCFVLRVDADPLALRARSGGDVEVVRHAVWGYFSQRTGLLSRLEDSHL
LRVRATKGSPPAETTTYWETSMDSSIGDYRAVDGINVAHAGRTVVSLSRFGGSTNDDGAG
SESAGVLGRRTCTCMEENWSIEEVDFNVVGLSAECFLPPRDMVVVPCSPKPVVDEKGQCG
RLDHSCKKDDAPAALDVRNKNGNGGAGGVHRPATARKALVTAATGLPWSGTAKVVAVETF
DTTAE
>tr|A0A0D9YFB9|A0A0D9YFB9_9ORYZ Uncharacterized protein OS=Oryza
glumipatula PE=4 SV=1
MATRLLLLLLLLLGMSLKGSEGAWCVCRPDVAEAALQKALDYACGHGADCAPVTPSGSCY
SPNNVAAHCSYAANSYFQRNSQAKGATCDFGGAATLSSTDPSSGTCKYPATARDKHRNRH

GGCRHRHRYKHEHEHEHFFPGLCNCSHGSGGCARGCSLLGEIGVDARRGVAVVGVRAMRK
LCPNLDRDDSLDTVLEVPIPDEMLINAPGTDKRRGAGGANMRAWLKNQAFDRATVGGPAN
ATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQASLQG
LQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHKMSAG
SDGKVAWRQSAAENSHASRGPPRPLRRSLQVDRTLLAAAPPLPSLSTSFDITMQGLDPRS
IANLFSDAVCIGEKIITGEECFILKLEASAATLRARSAAAFDIIHHTVWGYFSQRTGLLI
QLEDSHLLRMKSGKGARRSENIFWETTMESTISDYRHIDGINIAHGGHTAVTLFRYGEGS
VNHKRKLEETWTVEEADFNLYGLTTDYFLPPSDLKKDIDEKRAG
>tr|A0A0D2RWC3|A0A0D2RWC3_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_006G144900 PE=4 SV=1
MVASKCPLASHHESIQKEKKVSSSAQYIIQHFTAATGCRKSEGTVKNIFVTGKVTMAMVD
ELGATVGSVAGAAGVAQKGCFVMWQMVPNKWLIELVVGGHKVIAGSDGNVAWRRTPWLGA
HAAKGGVRPLRRALQGLDPMAISAVFSSAQYMGEKRISSTDCFVLKLSADQVDLADRSDS
TAEMIKHVIFGYFSQRSGLLVFIEDSYLTRIQSPGTYPTYWETTMATKIEDYRLVEGVMV
AHSGQSNVIITRFGDNLKAGLSVTRMEETWTIDDVAFNVPGLSLDCFIPPKEVQKDFPDE
NLDWRSPLHR
>tr|A0A096RVF1|A0A096RVF1_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.24093 PE=4 SV=1
MKSRVALEPLAEEPGCGEEDAARRRSGLHAALHRWARLLSGGVAGDDARPAADLRVLLSV
LACPLSPVPLLPRLPRHVASSAQYIIEQFRATTGCGKLEDGAVKSMYASGRVRLSMLQEP
GGGGGGGRGHEGSFVLWQLAPSMWLVEMSVAGQSVAAGSDGRVAWRRTPWLGAHAARGGS
RPLRRALQGLDPVTIASIFSTAEHAGEKEVDGEDCFVLRLDVGPSVLSSWSDGTAEVIRH
GLTGFFSQRSGLLARLEDSQLTRIQSPGAAAMYWETTIASAVSDYRAVDGGVAVAHAGTS
TAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRSYGAAIAGG
K
>tr|C5WWU7|C5WWU7_SORBI Putative uncharacterized protein Sb01g046050
OS=Sorghum bicolor GN=Sb01g046050 PE=4 SV=1
MRSRVALEPLAEEPGGGEEEAARRRTGLHAALHRWARLLSGGAAGDDARPAADLRVLLSV
LACPLSPVPVLPRLPRHVASSAQYIIEQFRATTGCGKLEDGAVKSMYASGRVRLSMLQDP
SGGGSGVIGSGGGRGHEGSFVLWQLAPSMWLVEMSVAGQSVAAGSDGRVAWRRTPWLGAH
AARGGSRPLRRALQGLDPVTIASIFSTAEHAGEKEVDGEDCFVLRLDVGPSVLSSWSDGT
AEVIRHGLTGFFSQRSGLLARLEDSQLTRIQSPGAAAMYWETTIASTVSDYRAVDGGVAV
AHAGTSTAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRSYG
AAIAGGK
>tr|D7SPG2|D7SPG2_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VIT_04s0023g01510 PE=4 SV=1
MRKLCPNFDRDDGLETVLEVPIPEEMFNSMGSNLALRCHNMLTWMKAQTAEKWSSPIIAG
RFNELSFLLYIVGSPLIPLQVRLDNSVHRPIRDSSIEASTAKYIVQQYIAATGGQPALSS
VNSMCAIGQVRISASEFYQSDLHVKVGTTEEIGGFVLWQKNPDMWWLELVVSGCKVISGS
NGKLSWRQCSNQQSPISKGAPRPLRRFLQGLDPRSTANLFIDAVCIGEKIINNEDCFILK
LETSRAVREAQSSPKFEIIHHTIWGYFSQRSGLLMQFEDSRLLRMNTEGDDGVFWETSSE
SVIEDYRYVDGVNIAHSGKTVVTVFRYGSHSASHKREMEETWRIEEVDFNIWGLSNDFFL
PPP
>tr|A5B8N4|A5B8N4_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VITISV_016191 PE=4 SV=1
MRKLCPNFDRDDGLETVLEVPIPEEMFNSMGSNLALRCHNMLTWMKAQTAXKWSSPIIAG
RFNELSFLLYIVGSPLIPLQVRLDNSVHRPIRDSSIEASTAKYIVQQYIAATGGQPALSS
VNSMCAIGQVRISASEFYQSDLHVKVGTTEEIGGFVLWQKNPDMWWLELVVSGCKVISGS
NGKLSWRQCSNQQSPISKGAPRPLRRFLQGLDPRSTANLFIDAVCIGEKIINNEDCFILK
LETSRAVREAQSSPKFEIIHHTIWGYFSQRSGLLMQFEDSRLLRMNTEGDDGVFWETSSE
SVIEDYRYVDGVNIAHSGKTVVTVFRYGSHSASHKREMEETWRIEEVDFNIWGLSNDFFL
PPP
>tr|K7W4C3|K7W4C3_MAIZE Uncharacterized protein OS=Zea mays
GN=ZEAMMB73_778968 PE=4 SV=1

MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGADKRRGAGGANMRAWLKNQAFDRATVDG
PASATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIIQQYIAATGGQAA
LQGVRSMYAVGKVRMCASEFHLGDQTVTAAQGRAEVGGFVLWQKTPEVWFFELIMAGHKM
SAGSDGKVAWRQSAAEHSRVSRGPPRPLRRSLQVTESAEAHVRARIAFSQRRLPSCSFGY
LQGLDPRSIANLFSDAVCIGEKILNNEECFILKLEAGAATLRARSAPAFDIIHHTVWGYF
SQRTGLLIQLEDSHLLRMKSGKGARRSENIFWETSMESVISDYRYIDGINIAHGGHTNVT
LFRYGEGSVNHKRKLEETWTVEEADFNVHGLTTDYFLPPADLKKDDEDHNK
>tr|B4FQD6|B4FQD6_MAIZE Uncharacterized protein OS=Zea mays GN=Zm.103516
PE=2 SV=1
MRKVCANPDREVGLDTVLEVPVPDQLHHDPSSSSSGHGRRRRRTLKAWVRSRMDQRHRRH
SSPPSQADVQLMLGVVGAPLVPQPVQARKAMVAGEDIKEEPLEVSKAKYIVEQYVAASGG
ERALSAATSMYAVGKVLMRTRSSSTTTKQGQKARRTGMVGVVHGGAEIAGGLVLWQKGPE
VWCVEMVVAGGTKMSAGSDGRVAWRQTPWQQAHASRGPPRPLRRCVQGLNPRSTANLFST
ATWVGEKSVDGDDCFVLRVDADPLALRARSGDDVEVVRHAVWGYFSQRTGLLSRLEDSHL
LRVRATKGSPLAQTTTYWETSMDSSIGDYRAVDGINVAHAGRTVVSLSRFGGSTNDDSAG
SESAGVLGRRTCTCMEENWSIEEVDFNVVGLSAECFLPPRDMVVVPCSPKPVDDEKGQCG
RLDHSCKKDDAPAALDVRNKNGNGGAGGVHRPATARKALVTAATGLPWSGTAKVVAVETF
DTTAE
>tr|A0A0D3DTG2|A0A0D3DTG2_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSENNKTGAWRSVKSSLLRSPPDNNSSLATLFG
GRDAQIQMLLGIVGAPLIPLPVSSDHDVLDHPISKLIKNQSIEAAMAKYIVKQYTAAAGG
ETALAGVESMYAMGKVKMGVTEFCAAKTLIGKRKKKMLKIRNVNNVNGGEVGGFVLWKKG
SSQWSLELVVSGCKVSAGCDGNVAWKQSPWLEHSQASNECSGPLRRFLQGLDPKTTANMF
SGSVCVGEKGVNEEECFVLKLETQPSELKSRSKRGMETVKHTVWGCFSQRTGLLVQLEDT
YLVRIKTGPEEEDVVLWETTSETMIQDYKSVDGIQIAHKGRTRVSLLRLDESLESHSKTT
MEESWEIEEVGFNVKGLSSDFFLPPGDLCTKENEESGFSFGDYTSPMMIPLKVSTDSWNL
KSSKVTAIEDFGDSE
>tr|Q0DJM6|Q0DJM6_ORYSJ Os05g0252100 protein OS=Oryza sativa subsp.
japonica GN=Os05g0252100 PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHRQAPRRRGRRGGGGTVKSWVRARMEHGRRRDGAA
PSRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGGEGEEPLDLEASKARYIVEQYVAAA
GGEAALGAATSMYAMGKVRMRTTTTSKANKGKVMGVAAGGEVAGGFVVWQKKPDLWCVEM
VVAGGVKMSAGSDGKVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGE
RCVDGDDCFVLRVDADHAALRARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHLLRIGLA
HAAAESAYWETTMESSIGDYRAVDGINIAHAGRTAVSLSRFESADDAAAAARGSNKRSWG
TTTMEETWSIEEVDFNVVGLSMDCFLPPRDLVLNDCSKQQQKEDAAAAVVVKDAAAAVDV
KDAAGAAANAKGGSDDGKTNGGDVGRGVVVKKALVPAVTGLGWFGPAKVVAVDDTVDDGV
AAAADDDK
>tr|A2Y2F9|A2Y2F9_ORYSI Putative uncharacterized protein OS=Oryza sativa
subsp. indica GN=OsI_19188 PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHRQAPRRRGRRGGGGTVKSWVRARMEHGRRRDGAA
PSRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGGEGEEPLDLEASKARYIVEQYVAAA
GGEAALGAATSMYAMGKVRMRTTTTSKANKGKVMGVAAGGEVAGGFVVWQKKPDLWCVEM
VVAGGVKMSAGSDGKVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGE
RCVDGDDCFVLRVDADHAALRARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHLLRIGLA
HAAAESAYWETTMESSIGDYRAVDGINIAHAGRTAVSLSRFESADDAAAAARGSNKRSWG
TTTMEETWSIEEVDFNVVGLSMDCFLPPRDLVLNDCSKQQQKEDAAAAVVVKDAAAAVDV
KDAAGAAANAKGGSDDGKTNGGDVGRGVVVKKALVPAVTGLGWFGPAKVVAVDDTVDDGV
AAAADDDK
>tr|A0A0E0PJL6|A0A0E0PJL6_ORYRU Uncharacterized protein OS=Oryza
rufipogon PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHRQAPRRRGRRGGGGTVKSWVRARMEHGRRRDGAA
PSRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGGEGEEPLDLEASKARYIVEQYVAAA

GGEAALGAATSMYAMGKVRMRTTTTSKANKGKVMGVAAGGEVAGGFVVWQKKPDLWCVEM
VVAGGVKMSAGSDGKVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGE
RCVDGDDCFVLRVDADHAALRARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHLLRIGLA
HAAAESAYWETTMESSIGDYRAVDGINIAHAGRTAVSLSRFESADDAAAAARGSNKRSWG
TTTMEETWSIEEVDFNVVGLSMDCFLPPRDLVLNDCSKQQQKEDAAAAVVVKDAAAAVDV
KDAAGAAANAKGGSDDGKTNGGDVGRGVVVKKALVPAVTGLGWFGPAKVVAVDDTVDDGV
AAAADDDK
>tr|A0A059DHV9|A0A059DHV9_EUCGR Uncharacterized protein (Fragment)
OS=Eucalyptus grandis GN=EUGRSUZ_A025051 PE=4 SV=1
VSSSAQYIVQHFTAATGCRKLDGHVKNVFVTGKVTMAMTEEVGPSGAAAGATAAMASSVS
QQKGCFVMWQMLPDKWLIELVLGDQKVVAGSNGSVAWRHTPWLGAHTAKGSVRPLRRALQ
GLDPVTIAAVFSTSEYMGEKKIGDVDCFVLKLSADQADLSDRSDSTAETIKHVAFGYFSQ
KNGLLVYLEDSYLTRIQSPGTRPMYWETSMATQIRDYREVDGVMIAHSGQSSAIITRFGD
GRLRAGPEITRLEETWIIDDFAFNVPGLSVDSFIPPKDVRKDHFPLDDDWKSALD
>tr|V4LAC4|V4LAC4_EUTSA Uncharacterized protein OS=Eutrema salsugineum
GN=EUTSA_v10012901mg PE=4 SV=1
MQRLAPLMEEPMDQEEQEEERGRRSTRSKSWKKWIKTQLQFMVFQKKPDMKVLLSVLGCP
LFPVPPLSKISLQQVSSSAQYIIQHFAAATGCKKLGGEIKNTFVTGKITMTMVNDLNGST
SVGTASSVSHKGCFVMWQMLPEKWLIELVGGGHKVAAGSDGEIAWRYTPWLGDHAAKGAI
RPLRRALQGLDPLTISSVFSSAQFVGEKEINGKDCFVLKLSTDQIDLSRRSDSTAEMIKH
VAFGYFSQKSGLLVCLEDSSLTRIQIPGTVPTYWETSMSSWMEDYRAIEGSEVVIAHSGK
TDVLISRFGETLKGGISVTRMEERWTIDDVAFDVPGLSVDCFIPPKEMKMEFYHQDEELL
TLNSKKIWVSAVRRAHACTGPPPIRVGLTESAGRAVFATRRIGSGDLIHTAKPVLASPSL
LSLDSVCYLCLKKLMGSAKFHDCGVSYCSQECQENAKGFYDVETRADWSSFVDYCRTQNF
KYPLMVKRLSCMIISGALSADSLDILQPAALTSEMISKIEDGYGLLWNAFRKANFKDEDV
AFLTKQWYTAVLARIRINAFRIDLVGGSCGEDLLSLAAASVEGEGAVGHAVYMLPSFYNH
DCDPNAHILWLQNADARLMTLRDVEEGEELRICYIDASMGYEARQTLLSQGFGFCCNCLR
CQSGD
>tr|F6H1H9|F6H1H9_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VIT_18s0001g12320 PE=4 SV=1
MRKLCPNFDKENGLETVLEVPIPEEMFKSMGSNVALRWQNMRAFMKGQCIDKASRLSDGC
GPEFRLLLKLVGSPLIPVQVPLEYGATFPIKDCSIEASTAKYIVQQYIAATGGWAALNAV
HSMYAVGQVRMISSDMSEGEERVDPKGNGEVGGFVLWQKNPDLWYLELVVSGCKVSAGSD
GKVAWGQTSSQASHANRGPPRPLRRFFQGLDPRFTANLFLDAVCIGEKTINNEDCFILKM
ETSASVLKGQSTPKTEIVHHTVWGYFSMRTGLLIQFEDTKLVRMKAVKGEESVFWETSLE
SVIEDYRYVDGINIAHGGKTTATLYRYGEASNHKRRIEETWGIEEIDFNICGLTMESFLP
PADLKIYQDGGK
>tr|A9XLF9|A9XLF9_SOLBU Uncharacterized protein OS=Solanum bulbocastanum
GN=5.POTATO.3 PE=4 SV=1
MRILCPNVDKEDGLETVLEVPIPDEMFKSMGSNAALRWQNMATWMKAQTSDKWSSPIVAA
RYNELSFLLYMVGSPLIPFQIQLGQSVNRPVKHSSIEASTAKYILQQYIAATGGQPALNA
VKSMCVIGHVKITGSDFHQGDQSVKVRKSDENGGFVLWQKNPDLWCLELLISGCKVISGS
NGKISWRQSSNQIRPISKGPPRPLRRFLQGLDPRSIANLFANAVCIGEKIINEEDCFILK
LDTNQSALEAQSGPNYEILHHTIWGYFSQRSGLMIKFEDSRLLTVKTSRDDEGVFWETST
ESVMEDYKHVEGVNVAHSGKTFVTVFRYGEHSANHKRQLEERWKIEEVDFNVGRLTTDFF
MPPSDFDKERSRV
>tr|I1H9B4|I1H9B4_BRADI Uncharacterized protein OS=Brachypodium
distachyon GN=BRADI1G73890 PE=4 SV=1
MRSRVALEPLAEEPGGGEDDAARRRRSGLHAALHRWARLLSGAGTGDDGRPAADLRVLLS
VLACPLSPVPILPRLPKHVASSAQYIIEQFRATTGCGKTAAKSMYAAGKVRLAMLQEPAG
GSSASGGGHGRHHEGSFVVWQLAPAMWLVEMAVAGHSIAAGSDGRVAWRRTPWLGAHAAR
GGSRPLRRALQGLDPVMIASIFSTAEHAGEKVVDGEDCFVLRLDVGPSTLSSWSDGTAEV
IRHALTGYFSQRSGLLARIEDSQLTRIQSSPGAPAMYWETTIASTLADYRHVEGHGGVHV
CVAHSGRSTAHLARFGVGVRAARVVTRMEEAWTIDDVAFDVPGLGPDAFIPPEEVRRSRC

YDDAARK
>tr|B7ZXI2|B7ZXI2_MAIZE Uncharacterized protein OS=Zea mays GN=umc2185
PE=2 SV=1
MYAMGKVRMTAAELNSSDADGHGGSTGNGHHRGGKKGSKGGGGGGEIGGFVLWQKKPELW
CLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQGLDPQLTASLFADSVC
IGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTGLLVQLEDSHLLQI
RSSGGGAGGSVFWETTMESRLGDYRAVDGVNIAHAGRTAVSLVRFGDCQDGNTRTRMEEE
WNIEEVDFNIWGLSMDCFLPPSDLREGKESQDVAVVKADARPPPLRIPAVTVRVGPSQVA
AVNMDDSDSLVARS
>tr|V7D048|V7D048_PHAVU Uncharacterized protein OS=Phaseolus vulgaris
GN=PHAVU_001G200500g PE=4 SV=1
MAELELDKDALLPQETGPQDPTQRPRLPSLPCLSPPQTPTPLNQLSSSAQYIIQHFTAAT
GCRNLHATVRNIFATGKVEMWVVDDVGNTGVSERGCFVIWQMLPDKWQIELVVAAQKVVA
GSDGTVAWRHTPWVGAHAAKGGVRPLRRAVQGLDPLAVSAVFCEAQYMGEKQISGMDCFV
LKLSADQKDLVERSDSTAEMIKHVAFGYFSQKNGLLVHLEDSYLTRIQSPGTHPTYWETT
MSTKIDDYRMVDGVMIAHSGHSSVMITRFGDNLKTGPAITRLEESWTIDDIAFNVQGLSM
DCFIPPKELHKDYPQEDLDWRSPLHA
>tr|A0A072VF85|A0A072VF85_MEDTR DUF620 family protein OS=Medicago
truncatula GN=MTR_1g022075 PE=4 SV=1
MRKLCPNFDKVDGLETVLEVPIPEDMWTGIGSSGSNRWQNLRALMKAQISNDKCSHLSAT
SNNEFIALLKLVGSPLIPLQVQCDHTLTRPLQDSNIEASSAKYIVQQYIAATGGVGALDS
LKSMYAVGQVRMFGSEMREGDDSIQPIGRAEVGGFVLWQKNPDLWHFELVVSGFKVSAGS
DGKMAWTQSSSKPCHANKGPPRPLRRFFQGLDPRCTANLFLDAVCVGEKTINKEDCFLLK
IETAHDILQTQNTPHTEIIRHTVWGYFSQRTGLLVKFEDTKLVRMKPTKGNDSIFWETSF
ESVIEDYRYVDGIKIAHGGKTVAMLYRYGVAHNHRRRIEETWRIEEIDFNICGLSMDCFL
PPSDIKKEHEAVEQIV
>tr|A0A0D2Q5F7|A0A0D2Q5F7_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_002G128700 PE=4 SV=1
MQKMMIRKTCPIPNLHNQDGLETVLEVPILEEMFTQLGTDAALLPWLNMRALMNDNISST
PHLQAKSDTEFLALLKIVGAPLIPFQVHLLNYTLSSPLRHCPFESSSAKYIVQQFVAASG
GHLALSSATSMCAMGRVKMKGSEMQAGYDSVQLRRNCEVGDFVLWQKNPDLWYLELVVAG
FKVSAGSDGKVAWNQSTSQPGHAHRGPPRPLRRFFQGLDPRSTASLFKEAVCVGERTINN
EDCFILRLETASNVLKEQSSAQTEIIHHTIWGYFSQRSGLLMKFEDRKLVMMKPPNRKDR
VFWETTVESVVQDYKQIDGIKVAHSGNTMTTLYRYGKSHNHKRKIEETWRIDEVDFNICG
LSDETFLPPPDLKRELQ
>tr|I1PTT4|I1PTT4_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4
SV=1
MRKVCPNLDREDGLDTVLEVPVPELHREAPRRRGRRGGGGTVKSWVRARMEHGRRRDGAA
PSRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGGEGEEPLDLEASKARYIVEQYVAAA
GGEAALGAATSMYAMGKVRMRTTTTSKANKGKVMGVAAGGEVAGGFVVWQKKPELWCVEM
VVAGGVKMSAGSDGKVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGE
RCVDGDDCFVLRVDADHAVLRARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHLLRIGLA
HAAAESAYWETTMESSIGDYRAVDGINIAHAGRTAVSLSRFESADDAAAAARGSNKRSWG
TTTMEETWSIEEVDFNVVGLSMDCFLPPRDLVLNDCSKQQQKEDAAAAVVVKDAAGAAAN
AKGGSDDGKTNGGDVGRGVVVKKALVPAVTGLGWFGPAKVVAVDDTVDDGVAAAADDDK
>tr|M1A2I1|M1A2I1_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG400005161 PE=4 SV=1
MRKLCPNLDKEDGLDTVLEVPLPEEMFSKTGGCSAAIRWKNMLNLMRADKLPDRSKAVAS
GNNDQFMFLLKIVGSALIPFQVQLDHAISLPVRDGCIKASSAKYIVQQYLAASGGQAALN
SINSMYAVGQLQMAMSDIQQSGNQMNSKRTCEDGGFVLWQKNPDLWFLEFVVSDCKVSAG
SNGTVAWSHSSTNSNASKGPPRPLRRFFQGLDPRSTANLFLNAVCIGEKKIKDEGCFILK
LETSKDMLKAQSTANTEVVHHTIWGYFSQRLGVLIQFEDTKLVRLKSAKDNNDSIFWETS
MESTLKDYRYIEGINIAHSGRTAATIYRYGKNIDYRAKVEETWKIEEIDFNISGLSMDCF
LPPADVNKENEQEWDSRASLAENRTVC

>tr|Q0DUU3|Q0DUU3_ORYSJ Os03g0167400 protein OS=Oryza sativa subsp. japonica GN=Os03g0167400 PE=4 SV=1
MRSRVALETLAEEPGGGEEEAARRKSSGLQAALHRVARRLLSGAGEDARPAADLRVLLSV
LACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCGKIEGAVKSMYAAGRVRLAMLQDPA
GGGAGGGGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHAA
RGGSRPLRRALQGLDPVTIAAIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTAE
VIRHGLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVHV
AHSGRSTAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFYD
AMAAGK
>tr|B8AP97|B8AP97_ORYSI Putative uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI_10166 PE=4 SV=1
MRSRVALETLAEEPGGGEEEAARRKSSGLQAALHRVARRLLSGAGEDARPAADLRVLLSV
LACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCGKIEGAVKSMYAAGRVRLAMLQDPA
GGGAGGGGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHAA
RGGSRPLRRALQGLDPVTIAAIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTAE
VIRHGLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVHV
AHSGRSTAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFYD
AMAAGK
>tr|I1P7Y2|I1P7Y2_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1
MRSRAALETLAEEPGGGEEEAARRKSSGLQAALHRVARRLLSGAGEDARPAADLRVLLSV
LACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCAKIEGAVKSMYAAGRVRLAMLQDPA
GGGGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHAARGGS
RPLRRALQGLDPVTIAAIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTAEVIRH
GLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVHVAHSG
RSTAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFYDAMAA
GK
>tr|A0A068UIT1|A0A068UIT1_COFCA Uncharacterized protein OS=Coffea canephora GN=GSCOC_T00024821001 PE=4 SV=1
MRKLCPNLDKEDGLDTVLEVPIPEEMFTKMGSTAAHRWQNMRNLMKAQRLDKQSAYTTAA
SRNDHFTLLLKLVGSAFIPFQAQLDHAIILPIKDGSIEASTAKYIVQQYLAATGGHAVLN
SINSMYAVGQVSMVTSDEPENCQNANAKPKRGCEVGGFVLWQKNPDLWYLELVVSGCNVS
AGSDGKVAWSQSSSTSTASKGPPRPLRRFFQGLDPRSTANLFLKAVCIGEKRINDEDCFA
LKLETNLDILKAQSTPNTEIVHHTIWGYFNQRTGLLVKFEDTKLVRMKAAKGDDNVFYET
SMESFLEDYRYVEGINIAHNGRTNATIYRYGSKLNRKWKIEETWRIEEIDFNICGLSLDC
FLPPAEVKKEMEQEEQGMG
>tr|M1B753|M1B753_SOLTU Uncharacterized protein OS=Solanum tuberosum GN=PGSC0003DMG400014908 PE=4 SV=1
MRILCPNVDKEDGLETVLEVPIPDEMFKSMGSNAALRWQNMATWMKAQTSDKWSSPIVAA
RYNELSFLLYMVGSPLIPFQIQLGQSVNRPVKHSSIEASTAKYILQQYIAATGGQPALNA
VNSMCVIGHVKITGSDFHQGDQSVKVRKSDENGGFVLWQKNPDLWCLELLISGCKVISGS
NGKISWRQSSNQIRPISKGPPRPLRRFLQGLDPRSIANLFANAVCIGEKIINEEDCFILK
LDTNQSALEAQSGPNYEILHHTIWGYFSQRSGLMIKFEDSRLLTVKTSRDDEGVFWETST
ESVMEDYKHVEGVNVAHSGKTFVTVFRYGEQSANHKRQLEERWKIEEVDFNVGRLTTDFF
MPPSDFDKERARV
>tr|A0A0E0DNW8|A0A0E0DNW8_9ORYZ Uncharacterized protein OS=Oryza meridionalis PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHREAPRRRGRRGGGGTVKSWVRARMEHGRRRDGAA
PSRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGGEGEEPLDLEASKARYIVEQYVAAA
GGEAALGAATSMYAMGKVRMRTTTTSKGNKGKVMGVAASGEVAGGFVVWQKKPELWCVEM
VVAGGVKMSAGSDGKVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGE
RCVDGDDCFVLRVDADHAALRARSSGDVEVVQHAVLGYFSQRTGLLVRLEDSHLLRIGLA
HAAAAESAYWETTMESSIGDYRAVDGINIAHAGRTAVSLSRFESADDADAAARGSNKRSW
GTTTMEETWSIEEVDFNVVGLSMDCFLPPRDLVLNDCSKQQQKEDAAADVVVKDAAGAAA

NAKGGSDDGKTNGGDVGRGVVVKKALVPAVTGLGWFGPAKVVAVDDTVDDGVAAAADDDK
>tr|A0A0L9U9W3|A0A0L9U9W3_PHAAN Uncharacterized protein OS=Phaseolus angularis GN=LR48_Vigan03g291000 PE=4 SV=1
MGRLATLSEEPINEQEKRSRSCKKWRNWNWIKTHFFHKKPDLKILLSVLACPLFPVPPHS
KPHAPLNQLSSSAQYIIQHFTAATGCRNLPTTVTNVFATGKVEMWVVDDVGNTGVSERGC
FVIWQMLPDKWQIELVAATQKVVAGSDGTVAWRHTPWIGAHAAKGGVRPLRRAVQASSIG
LDPLAVSAVFCAAQYMGEKEISGMDCFVLKLSADQKDLVDRSDNTAEMIKHVAFGYFSQK
NGLLVHLEDSYLTRIQSPGTHPTYWETTMSTKIDDYRMVDGVMIAHAGHSTVIITRFGDN
LKTGPAITRLEESWTIDDVAFNVQGLSMDCFIPPKELNKDYPQEHLDWRSPLHT
>tr|A0A0E0CVQ4|A0A0E0CVQ4_9ORYZ Uncharacterized protein OS=Oryza meridionalis PE=4 SV=1
MRSRAALETLAEEPGGGEEEAARRKSSGLQAALHRVARLLSGAGEDARPAADLRVLLSVL
ACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCAKIEGAVKSMYAAGRVRLAMLQDPGA
AGGGGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHAARGG
SRPLRRALQGLDPVTIAAIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTAEVIR
HGLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGGVSVAH
SGRSTAHLARFGVGVRAARVVTRMEESWTIDDVVFNVPGLGPDAFIPPEEVRRSRFYDAM
AAGK
>tr|K4BVA1|K4BVA1_SOLLC Uncharacterized protein OS=Solanum lycopersicum GN=Solyc04g080220.2 PE=4 SV=1
MRKLSPNLDKEDGLDTVLEVPLPEEMFSKTDGSSAAIRWKKMLNLIRADKLPNRSKAVSS
GNNDQFMFLLKIVGSALIPFQVQLDHAINLPVRDGCIKASSAKYIVQQYLAASGGQAALN
SINSMYAVGQLQMAMSDIQQSGNQMNSKRTCEDGGFVLWQKNPDLWFLEFVVSDCKVSAG
SNGTVAWSHSSTNSNASKGPPRPLRRFFQGLDPRSTANLFLNAVCIGEKKIKDEGCFMLK
LETSKDMLKAQSTANTEVVHHTIWGYFSQRSGVLIQFEDTKLVRLKSAKDNNDSTFWETS
MESTLKDYRYIEGINIAHCGRTAATIYRYGKNLDYRAKVEETWKIEEIDFNISGLSMDCF
LPPADVINKENEQEWDSRASLAENRTV
>tr|M5Y396|M5Y396_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa019389mg PE=4 SV=1
MRKLCPNLDKEDGLDTVLEVPIPEEMFNSMGSNAMLRWANLRSFMKAQSHVDRSSNGKSH
FSSRSNNEFMALLKLVGSPLIPLQVHCDNALTRPIKDCSIEASTAKYIVQQYVAATGGLA
VLNSVKSMYAVGEMKMVGSEMRQGDDSVHVPTKGNSEVGGFVLWQKNPDLWYLELVVSGF
KVSAGSDGKVAWNQSGSQPCHANKGPPRPLRRFFQGLDPRSIANLFLDAVCIGEKTINKE
ESFILKLETPTEILQSQSTPQTEIVHHTIWGYFSQRTGLLIQFDDTKLVKMKSRYDNVFW
ETTMETVIGDYRYVDGINIAHGGKTSALLYRYGHAFNQKRRIEETWKIEEVDFNICGLSM
ECFLPPADLKREDGGDQ
>tr|F2D3A0|F2D3A0_HORVD Predicted protein OS=Hordeum vulgare var. distichum PE=2 SV=1
MRARVALEPLAEEPGAEDESGARRRSGLQATLHRWARILSGGAAGDDARPAADLRVLLSV
LACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCGKLEGTAKSMYAAGKVRLAMLQEPA
GAGGGGGHDNGGAGRCHEGSFVVWQLAPGMWIVEMAVAGHSVAAGSDGRVAWRRTPWLGA
HAARGGSRPLRRALQGLDPVMIASIFSTAEHAGEKQVDGEDCFVLRLDVGPSTLSSWSDG
TAEVIRHGLTGFFSQRSGLLARLEDSQLTRIQSPGAAAMYWETTIASTMADYRAVDGGVT
VAHAGRSTAHLARFGVGVRAARVVTRMEESWTIDDVAFDVPGLGPDAFIPPEEVRRSRFY
DAMAAGGK
>tr|A0A0E0JP24|A0A0E0JP24_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGTDKRRGAGGANMRAWLKNQAFDRATVGG
PGAGWFLTRSSPSSCQASTAKYIMQQYIAATGGQAALQGLQSMYAVGKVRMCASEFHLGD
QNVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHKMSAGSDGKVAWRQSAAENSHTSRGP
PRPLRRSLQGLDPRSIANLFSDAVCIGEKIITGEECFILKLEANAATLRARSAAAFDIIH
HTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSENIFWETTMESTISDYRHIDGINIAH
GGHTAVTLFRYGEGSVNHKRKLEETWTVEEADFNLYGLTTDYFLPPSDLKKDTDEKRAG

>tr|A0A0D9ZW97|A0A0D9ZW97_9ORYZ Uncharacterized protein OS=Oryza glumipatula PE=4 SV=1
MNHLAMRKVCPNLDREDGLDTVLEVPVPELHREAPRRRGRRGGGGGAVKSWVRARMEHGR
RRDGAAPSRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGGEGEEPLDLEASKARYIVE
QYVAAAGGEAALGAASSMYAMGKVRMRTTTTSKGNKGKVMGVAAGGEVAGGFVVWQKKPE
LWCVEMVVAGGVKMSAGSDGKVTWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSS
AAWVGERCVDGDDCFVLRVDADHAALRARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHL
LRIGLAHAAAESAYWETTMESSIGDYRAVDGINIAHAGRTAVSLSRFENADAAAARGNNK
RSCTTTMEETWSIEEVDFNVVGLSMDCFLPPRDLVLNDCSKQQQKEDAAAAVVVKDAAGA
ASNAKGGSDDGKTNGGDVGRGVVVKKALVPAVTGLGWFGPAKVVAVDDTVDDGVAAAADD
DKTRELSISVLAASINCT
>tr|A0A0D9WEE0|A0A0D9WEE0_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1
MRKVCPNLEREDALDTVLEVPVPELHRDAPSRRRRGAGGGKVKSWVRSRMVRRNGVAAPP
PSRAEVQLMLGVSGAPLVPQPVVARKAMAAGRRVEEEEEETNSKARYIVEQYVAAAGGEA
AIGAATSMYAMGKVRMRTTMNKGKVMGVATGGEVSGGFVVWQKKPELWCVEMVVAGGVKM
SAGSDSKVAWRQTPWQEAHASRGPPRPLRRCVQGLDPKSTADLFSTAAWVGERRVDDDDD
CFVLRVDADRAALRARSTGDVEVVRHAVLGYFSQRTGLLVRLEDTHLLRIGESAYWETTM
DSTVGDYRAVDGINIAHAGRTVVSLSRFDSADDADARRGRRAYATTTMEETWSIEEVDFN
VLGLSMDCFLPPRDLLLNDCNKKTQQKQKEDAVGDHAGKDAGKAVARKAIVPAMTGLGWF
GPAKVVAVDDTVDDDK
>tr|K4A8A8|K4A8A8_SETIT Uncharacterized protein OS=Setaria italica GN=Si035114m.g PE=4 SV=1
MSCNPALACASAIRGRRGPAEHINEIPLSPEQKGKPRPVHVGLARARLGRYSTAIDNKQG
RKPPFLNSASCTSLHQHPFVHSHASNGLLGTQGFSQWNGWVLDLLADLALEGTRSTWLGL
GGKQAGGGRLRQPPSSLSCHGHATNNNATTSAKATRRQAGASERDTESEMRSRVALEPLA
EEPGGGEEDAARRRSGLHAALHRWARLLSGGAAGDDARPAADLRVLLSVLACPLSPVPLL
PRLPRHVASSAQYIIEQFRATTGCGKLEDGAIKSMYASGRVRLSMLQDPSSGGGGGGRAH
EGSFVLWQLAPSMWLVEMSVAGQSVAAGSDGRVAWRRTPWLGAHAARGGSRPLRRALQGL
DPVTIASIFSTAEHAGEKQVDGEDCFVMRLDVGPSVLSSWSDGTAEVIRHGLTGFFSQRS
GLLARLEDSQLTRIQSPGAPAMYWETTIASAVSDYRAVDGGVAVAHAGTSTAHLARFGVG
VRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRSYGAAIAAGK
>tr|Q9FYX1|Q9FYX1_SOLLC BAC19.5 OS=Solanum lycopersicum GN=Solyc02g085490.1 PE=4 SV=1
MRILCPNVDKEDGLETVLEVPIPDEMFKSMGSNAALRWQNMATWMKAQTSDKWSSPIVAA
RYNELSFLLYMVGSPLIPFQIQLGQSVNRPVKHSSIEASTAKYILQQYIAATGGQPALNA
VNSMCVIGHVKISGSDFHQGDQSVKVRKSDENGGFVLWQKNPDLWCLELLISGCKVISGS
NGKISWRQSSNQIRPISKGPPRPLRRFLQGLDPRSISNLFANAVCIGEKIINEEDCFILK
LDTNQAALEAQSGPNYEILHHTIWGYFSQRSGLMIKFEDSRLLTVKTSRDDEGVFWETST
ESVMEDYKHVEGVNVAHSGKTFVTVFRYGEHSANHKRQLEERWKIEEVDFNVGRLTTDFF
MPPSDFDKERSRV
>tr|A0A0E0HBH9|A0A0E0HBH9_ORYNI Uncharacterized protein OS=Oryza nivara PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHREAPRRRGRRGGGGTVKSWVRARMEHGRRRDGAA
PSRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGGEGEEPLDLEASKARYIVEHYVAAV
GGEAALGSATSMYAMGKVRMRTTTTSKANKGKVMGVAAGGEVAGGFVVWQKKPELWCVEM
VVAGGVKMSAGSDGKVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGE
RCVDGDDCFVLRVDADHAALRARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHLLRIGLA
HAAAESAYWETTMESSIGDYRAVDGINIAHAGRTAVSLSRFESADDAAAAARGSNKRSWG
TTTMEETWSIEEVDFNVVGLSMDCFLPPRDLVLNDCSKQQQKEDAAAAVVVKDAAAAVVV
KDAAGAAANAKGGSDDGKTNGGDVGRGVVVKKALVPAVTGLGWFGPAKVVAVDDTVDDGV
AAAADDDK
>tr|A0A0D3EUC4|A0A0D3EUC4_9ORYZ Uncharacterized protein OS=Oryza barthii PE=4 SV=1

MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGTDKRRGAGGANMRAWLKNQAFDRATVGG
PANATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIVSHRSPARVARARVHACTAAA
STAKYIMQQYIAATGGQAALQGLQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVL
WQKCPEVWYFELIMAGHKMSAGSDGKVAWRQSAAENSHASRGPPRPLRRSLQVDRTLLAA
APPLPSLSTSFDITMQGLDPRSIANLFSDAVCIGEKIITGEECFILKLEASAATLRARSA
AAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSENIFWETTMESTISDYRHI
DGINIAHGGHTAVTLFRYGEGSVNHKRKLEETWTVEEADFNLYGLTTDYFLPPSDLKKDI
DEKRAG
>tr|A0A0E0FTJ3|A0A0E0FTJ3_ORYNI Uncharacterized protein OS=Oryza nivara
PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGTDKRRGAGGANMRAWLKNQAFDRATVGG
PANATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIVSHRSPARVARARVHACTAAA
STAKYIMQQYIAATGGQAALQGLQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVL
WQKCPEVWYFELIMAGHKMSAGSDGKVAWRQSAAENSHASRGPPRPLRRSLQVDRTLLAA
APPLPSLSTSFDITMQGLDPRSIANLFSDAVCIGEKIITGEECFILKLEASAATLRARSA
AAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSENIFWETTMESTISDYRHI
DGINIAHGGHTAVTLFRYGEGSVNHKRKLEETWTVEEADFNLYGLTTDYFLPPSDLKKDI
DEKRAG
>tr|A0A0E0N2U8|A0A0E0N2U8_ORYRU Uncharacterized protein OS=Oryza
rufipogon PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGTDKRRGAGGANMRAWLKNQAFDRATVGG
PANATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIVSHRSPARVARARVHACSAAA
STAKYIMQQYIAATGGQAALQGLQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVL
WQKCPEVWYFELIMAGHKMSAGSDGKVAWRQSAAENSHASRGPPRPLRRSLQVDRTLLAA
APPLPSLSTSFDITMQGLDPRSIANLFSDAVCIGEKIITGEECFILKLEASAATLRARSA
AAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGARRSENIFWETTMESTISDYRHI
DGINIAHGGHTAVTLFRYGEGSVNHKRKLEETWTVEEADFNLYGLTTDYFLPPSDLKKDI
DEKRAG
>tr|A0A0E0NQ69|A0A0E0NQ69_ORYRU Uncharacterized protein OS=Oryza
rufipogon PE=4 SV=1
MAGACKGCRVAFTPFRHHAFEALKAACRFTSLGSSLVAPRSYHTNTKQSKAKRDASEDFD
FDPPPTRFPLASLQRCPFPSPALHTRTAAPPSHCRPGPAPSGAHPSLAGSGDREMRSRVA
LETLAEEPGGGEEEAARRKSSGLQAALHRVARRLLSGAGEDARPAADLRVLLSVLACPLS
PVPILPRLPRHVASSAQYIIEQFRATTGCGKIEGAVKSMYAAGRVQLAMLQDPAGGGAGG
GGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHAARGGSRP
LRRALQGLDPVTIAAIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTAEVIRHGL
TGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVHVAHSGRS
TAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFYDAMAAGK
>tr|A0A0E0BAE5|A0A0E0BAE5_9ORYZ Uncharacterized protein OS=Oryza
glumipatula PE=4 SV=1
MAPQLATLAEEPGGGEEAARARRKTGLHAALHRWARARIPLRFLSGGGGGGGVGGGGGGG
RPSPDLRVLLSVLACPLSPVPVLPRHPRNVASSAQYILEQFRATTGCAKIEGAAKSMYAA
GRVRMAMTPEPGGGIGIGGGGGGGHEGCFVVWQLVPDMWLVEMAVAGHAVAAGCDGRVAW
RRTPWLGAHAARGGGARPLRRALQGLDPVTIASVFSAAEHVGEKAVDGEDCFALRLDVAP
SVLSAWGDGAAEVIRHGMTGYFSQRSGLLARLDDSQLTRIQTPGAPAMYWETTVSSRLGD
YRAADGAVVAHAGTSVAHLARFGADVGAARAVTRMEEAWTIDDVAFNVAGLCPESFIAPE
EVRSGGGGGSSSRRYDGGGGAIAKKK
>tr|A0A067KU22|A0A067KU22_JATCU Uncharacterized protein OS=Jatropha
curcas GN=JCGZ_04413 PE=4 SV=1
MRKLCPNLDKEDGLETVLEVPVPEEMFASMGSNGASRWANMRALMKAQSADKSSHLQAKS
DNEFIALLKLVGSPLIPIQIHTDQSVTRPITDGSIEALTAKYIVQQYVAAAGGTVVLNSL
TSMCAVGQVRMAGSEMQEGDDSLQTGGNSEVGGFVIWQKNPDLWYLELVVAGYKVSAGSD
GKVAWNQSSSQPCHANRGPPRPLRRFFQGLNPRCIANLFLEAVCIGEKKIINEDCFVLKL
ETDAKILKSQSSSNTEILHHTIWGYFSQRTGFLVKFEDTKLVKMKPLKGNDSVFWETSME

SVIDDYRCIEGINIAHGGKTVTTLYRYGESQNHKRKIEETWRIEEVDFNISGLYRDYFLP
PADLVRELEGGEQ
>tr|A0A0A0LBR2|A0A0A0LBR2_CUCSA Uncharacterized protein OS=Cucumis
sativus GN=Csa_3G797570 PE=4 SV=1
MNRLAPLSEEPIDEHDARTRTRNRNRTTAGAGGGGRSWRNWIRTHFSILSSAKKSDGLNV
LLSVLGCPLFPVSLQPNSAVSITNQVSSSSQYIIEHFAAATGCRKLRGRVKNIFATGKIT
MGMAEEVSSGVGGGGGGGPTGGVTQKGCFVMWQMIPNKWLIELSVGGHSIVAGSDGNVA
WRHTPWLGSHAAKGAVRPLRRAFQGLDPLAISEVFSPAQYMGEKQIMAIDCFVLKLSADQ
TDLADRSDNTAEMIKHAIYGYFCQRRGLLVYLEDSSLTRIQSPGSHPMYWETTMSTKIDD
YRTIDGVMIAHSGETDVIITRFGDDLKTGPMITRLQEIWSIDDVAFNVPGLSMDSFIPPK
QVQKN
>tr|A0A0D9Z2J5|A0A0D9Z2J5_9ORYZ Uncharacterized protein OS=Oryza
glumipatula PE=4 SV=1
MAGACKGCRVAFTPFRHHAFEALKAACRRWLLPNGILSCKQTQHACIKSDYQKFYKNNSR
FPWKFSKISAFPKEYYFGGFTSLGSSLVAPRSYHTNTKQSKAKRDASEDFDFDPPPTRFP
LASLQRCPFPSPALHTRTAAPPSHCLPGPAPSGAHPSLAGSGDREMRSRVALETLAEEPG
GGEEEAARRKSSGLQAALHRVARRLLSGAGEDARPAADLRVLLSVLACPLSPVPILPRLP
RHVASSAQYIIEQFRATTGCAKIEGAVKSMYAAGRVRLAMLQDPAGGGAGGGGGGGRGHE
GSFVMWQLAPSMWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHAARGGSRPLRRALQGLD
PVTIAVIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTAEVIRHGLTGFFSQRSG
LLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVHVAHSGRSTAHLARFGV
GVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFYDAMAAGK
>tr|A0A0E0GHA9|A0A0E0GHA9_ORYNI Uncharacterized protein OS=Oryza nivara
PE=4 SV=1
MAGACKGCRVAFTPFRHHAFEALKAACRRWLLPNGILSCKQTQHACIKSDYQKFYKNNSR
FPWKFSKISAFPKEYYFGGFTSLGSSLVAPRSYHTNTKQSKAKRDASEDFDFDPPPTRFP
LASLQRCPFPSPALHTRTAAPPSHCRPGPAPSGAHPSLALELGERERERFLEGSGDREM
RSRVALETLAEEPGGGEEEAARRKSSGLQAALHRVARRLLSGAGEDARPAADLRVLLSVL
ACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCGKIEGAVKSMYAAGRVRLAMLQDPAG
GGAGGGGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHAAR
GGSRPLRRALQGLDPVTIAAIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTAEV
IRHGLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVHVA
HSGRSTAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFYDA
MAAGK
>tr|A0A0L9UQF6|A0A0L9UQF6_PHAAN Uncharacterized protein OS=Phaseolus
angularis GN=LR48_Vigan06g043600 PE=4 SV=1
MKQAAAKSSLRRLCPNIDREDGLVTVLEIPIPEEMFTPMGSNVTLRWQNMLTWMKAQTED
KLSTPTVSARLNELRFLLYLVGSPLIPLQVQLGHSVRRPVRDCSIEASTAKYIVQQYIAA
TGGQPALNAVDSMCVLGQIKIVASDFHQTCETVEVKKTSEEMGGFVLLQKDPDLWCLEIL
VSGCKVSCGSNGKVSWRHSSNQQTPISRGAPRPLRRFLQGLDPRATANLFLDAACIGEKI
INDEECFILKLETSPAIRDAQSGPNFEIIHHTIWGYFSQRSGLLVQFEDSRLLTMRTKED
NDIFWETSLESVIEDYRYVDGINVSHSGKTRVTVSRYGEQSANHKRELEERWKIEEVDFN
VWGLNAESFLPPSNLGKT
>tr|A0A022RIX9|A0A022RIX9_ERYGU Uncharacterized protein OS=Erythranthe
guttata GN=MIMGU_mgv1a008139mg PE=4 SV=1
MNTHGQAKTKQKNVMRKMCPNFDREDSLETVLEVPIPEEMFAGLGNSVALRWQNMATWMK
AQTSDKWSSPIIAGRYNEMSFLLYIVGSPLLPFQVQVDRSIHRAVKHSSIEASTAKYIVT
QYIAATGGQPALNAVNSMCVIGHVKITGSEFHQGDDSVKVRSNEEAGGFVLWQKNPDLWC
LELLISGCKVISGSNGKLSWRQSSNQQRPISKGPPRPLRRFLQGLDPRATSNLFIDAVCI
GEKIINDEDCFILKLDTSQSTLEAQSGPKYEIIHHTVWGYFSQRSGLLVKFEDSRLLSVK
TSKEDGDVFWETSTESVIEDYKYVDGVNIAHSGKTFFTVFRYGEQSANHKRELEESWKIE
EVDFNVWGLKPEFFMPPTEFKQK
>tr|I1LHQ4|I1LHQ4_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=2
MKQPAAKSSLRRLCPNINKEDGLETVLEIPIPEEMFSTMGNNVALRWQNMLTWMKAQTED

KLATPTVASRLNELRFLLYLVGCPLIPLQVQLGHSVHRPVRDCSIEASTAKYIVQQYIAA
TGGQPALNAVDSMCVTGQIKISASDFYHTGQSIEVKKTSEEMGGFVLWQKDPDLWCLEVV
LSGCKVCCGSNGKVSWRHSSNQQTPVQRGAPRPLRRFLQGLDPRATANLFLDAACIGEKI
INDEECFILKLETSPAIRDAQSGPNFEIIHHTIWGYFSQRSGLLVQFEDCRLHSMRTKDD
NDIFWQTSLESVIEDYKYVDGINVSHSGKTRVTVSRYGEQSANHKKELEERWKIEEVDFN
IWGLNAESFLPPSNLEKT
>tr|A0A0E0M7L2|A0A0E0M7L2_ORYPU Uncharacterized protein OS=Oryza punctata
PE=4 SV=1
MAPQLATLAEEPGGGEEAAARARRKTGLHAALHRWARARIPLRFLSGGGGGGGDGGGGGG
RPSAELRVLLSVLACPLSPVPVLPRHPRNVASSAQYILEQFRATTGCAKIEGAVKSMYAA
GRVRMAMAPEPGSGGGGGGHEGCFVVWQLVPDMWLVEMAVAGHAVAAGCDGSVAWRRTPW
LGAHAARGGGARPLRRALQGLDPVTIASVFSAAEHVGEKLVDGEDCFALRLDVVPSVLST
WSDGAAEVIRHGMTGYFSQRSGLLARLDDSQLTRIQTPGAPAMYWETTISSRVDDYRAVD
GGAVVAHAGTSVAHLARFGADVGAARVVTRMEEAWTIDDVAFNVAGLCPESFIAPEEVRS
GSGSSSSSRYDGGGGAIAKK
>tr|A0A0B2QS97|A0A0B2QS97_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_037712 PE=4 SV=1
MPSLPRPSPHDPPPLNQLSSSAQYIIQHFTAATGCRKLEGTVKNVFATGKVEMWAVDEVG
NTGVSERGCFVIWQMLPDKWQIELAVAGHKVVAGSDGAVAWRHTPWLGTHAAKGGIRPLR
RAVQARMRNEEWRGMRTEKGGLDPLAVSAVFSAAQYMGEKQISGIDCFVLKLSPDQKDLV
DRSDNTAEMIKHVAFGYFSQRNGLLVHLEDSYLTRIQSPGTHPTYWETTMSTKIEDYKMV
DGVMIAHAGHSTVIITRFGDNLKTGPAITRLEESWTIDDVAFNVQGLSMDCFIPPKELHK
DYPQEDLDWRSPLHR
>tr|Q5YJQ8|Q5YJQ8_HYAOR Putative uncharacterized protein (Fragment)
OS=Hyacinthus orientalis PE=2 SV=1
KLQIFNTATEGLSQETMSARYIVHQYLAATGCVKLRQSKKSMYATGSVKMVYSESEGAAG
RMKRNGGGGDNGVFVLWQMSPGMWLVELVVAGYKVVAGCNGKIVWRHLPWLGMNAARGPQ
RPLRRIIQGLDPKSTASMFANAQCLGEKRVVGDDCFVLKVSADRAAVAERSDGNAEVIRH
ALYGYFSQRSGLLAYIEDSHLTRVQTPGSDASYWETTIGSTVGDYREVDGVLIAHQGRSV
ATVFSVRRGLGP
>tr|I1J8V0|I1J8V0_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MKQPAAKSSLRRLCPNIGKEDGLETVLEIPIPEEMFSSMGSNVNLRWQNMLAWMKAQTED
KLSTPTVASRLNELRFLLYLVGSPVIPLQVQLGHSVHRPVRDCSIEASTAKYIVQQYIAA
TGGQPALNAVDSMCVTGQIKISASDFHLNHTNETIEVKKTSEEMGGFVLWQKDPDLWCLE
LLVSGCKVCCGSNGKVSWRHSSNQQTPVSRNAPRPLRRFLQGLDPRATANLFLDAACIGE
KIINDEECFILKLETSPAIRDAQSGPNFEIIHHTIWGYFSQRSGLLVQFEDSRLHTTRTK
DDNDIFWQTSLESVIEDYKYVDGINVSHSGKTRVTVSRYGEQSANHKRELEERWKIEEVD
FNIWGLNAESFLAP
>tr|A0A0B2RV39|A0A0B2RV39_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_003237 PE=4 SV=1
MKQPAAKSSLRRLCPNIGKEDGLETVLEIPIPEEMFSSMGSNVNLRWQNMLAWMKAQTED
KLSTPTVASRLNELRFLLYLVGSPVIPLQVQLGHSVHRPVRDCSIEASTAKYIVQQYIAA
TGGQPALNAVDSMCVTGQIKISASDFHLNHTNETIEVKKTSEEMGGFVLWQKDPDLWCLE
LLVSGCKVCCGSNGKVSWRHSSNQQTPVSRNAPRPLRRFLQGLDPRATANLFLDAACIGE
KIINDEECFILKLETSPAIRDAQSGPNFEIIHHTIWGYFSQRSGLLVQFEDSRLHTTRTK
DDNDIFWQTSLESVIEDYKYVDGINVSHSGKTRVTVSRYGEQSANHKRELEERWKIEEVD
FNIWGLNAESFLAP
>tr|A0A078HIT5|A0A078HIT5_BRANA BnaA02g17150D protein OS=Brassica napus
GN=BnaCnng08130D PE=4 SV=1
MKMRKLCPNLDNEDGLETVLEVPVPEEMFTKMGSNATGRWRNMHALMKAHAVVTAVAADM
RTPASSSSMSNVNMHLQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINDTSIEASTA
KYIVQQYVAACGGPAVLNAVKSMYAVGQVRMQGSEMVAGEDEGTTTTPVRLGKGNFEVGG
FVLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPR
CTASLFLDAVCIGEQTVNNEDCFVLKVETPADILKAQCSPNTEVIHHTVWGYFSQRTGLL

VKFGDTKLVRVKSARGKSDGVFWETSMESIIDDYKYVDSVNIAHGGRTLTTLYRYGGAVN
HRRRIEEKWTIEEVDFNICGLCLESFLPPSDMNNDH
>tr|D7KSL0|D7KSL0_ARALL Putative uncharacterized protein OS=Arabidopsis
lyrata subsp. lyrata GN=ARALYDRAFT_895383 PE=4 SV=1
MKMRKLCPNLDREDGLETVLEVPVPEEMFTKMGSNAAGRWRNMHALMKAHAVVTAVATDV
KTPASSSSMSNVNMHLQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINDTSIEASTA
KYIVQQYVAACGGPAALNAVKSMYAVGQVRMQGSEMVAGEDQGTGTPVRLGKGSFEVGGF
VLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPRC
TASLFLDAVCIGEQSVNGEDCFVLKLETPSDILKAQCSPNTEVIHHTVWGYFSQRTGLLV
KFGDTKLVRVKSGRGKSDGVFWETSMESIIDDYIFVDAVNIAHGGQTVTTLYRYGGAVNH
RRRIEEKWRIEEVDFNICGLCLESFLPPSDINNDH
>tr|M4DE06|M4DE06_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra014725 PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSENNKTGSWRSVKTSFLRSSPDNNSSLSTLFG
GHDAQIQMLLGIVGAPLIPLPFSSDHDVLDHPMPKLIKNQSIEAAMAKYIVKQYTAASGG
DLALDRVESMYAMGKVKMGVTEFCAAKPLIGKRKKKMVRIKNLNNGNGGEMGGFVLWKKG
SRQWSLELVVSGCKVSAGCDGNVDWKQSPWLAHSNEPSGPLRRFLQGLDPKTTANMFAGS
VCVGEKVVNDEECFVLKLETQTSGLKSRSKNGMETVKHTVWGCFSQRTGLLVQLEDTYLV
RIKIGLDEEDVVLWETTSETMIQDYKSVDGIQIAHRGKTQVSLLRLDESLESHSKTTMEE
SWEIEEVGFNVKGLSSDFFLPPGDLCTKENEESGFNFGDFSSPMMIPLKVSKDSWKLNSS
KVTAIEDFEG
>tr|V7AVF3|V7AVF3_PHAVU Uncharacterized protein OS=Phaseolus vulgaris
GN=PHAVU_009G057200g PE=4 SV=1
MRKLCPNLDKEDGLETILEVPIPDEMLSSMGTTGFNRWQNLRTLMNTQFADKSSLNNEFL
VLLKLVGAPVIPVQLSSDHALTRPLKDCSIKDSNAKYIVQQYVAATGGVSALNSLESMYA
IGRVRICGSEMRQGEFDEEAEARGKPEVGGFVLWQKNPDLWCLELVVSGYKVSAGCDGKI
AWNHTSSQPFHPNKGPPRPLRRFFQGLDPRCTANLFQEAECVGENIINNEVCFMLKLHTA
QQVLQVQSTSNTEIVMHTIVGYFSQRTGLLVKFEDTKLVKMKTMKGKEYVFWETNIQSLI
EDYRYIDGINIAHGGTTIATLNRYGAEQNHKRMIEETWTIEEVDFNIVGLSMNSFLAPSD
GEKEQHEGTEGMG
>tr|A0A0D3AQL5|A0A0D3AQL5_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MKMRKLCPNLDNEDGLETVLEVPVPEEMFTKMGSNATGRWRNMHALMKAHAVVTAVAADM
RTPASSSSMSNVNMHLQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINDTSIEASTA
KYIVQQYVAACGGPAALNAVKSMYAVGQVRMQGSEMVAGEDEGTTTTPVRLGKGNFEVGG
FVLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPR
CTASLFLDAVCIGEQTVNNEDCFVLKVETPADILKAQCSPNTEVIHHTVWGYFSQRTGLL
VKFGDTKLVRVKSARGKSDGVFWETSMESIIDDYKYVDSVNIAHGGRTLTTLYRYGGAVN
HRRRIEEKWTIEEVDFNICGLCLESFLPPSDMNNDH
>tr|Q8S7T7|Q8S7T7_ORYSJ Putative uncharacterized protein OSJNBa0091P11.2
(Fragment) OS=Oryza sativa subsp. japonica GN=OSJNBa0091P11.2 PE=4 SV=1
KLGLVWFAHGLVGWWCVQVASSAQYIIEQFRATTGCGKIEGAVKSMYAAGRVRLAMLQDP
AGGGAGGGGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHA
ARGGSRPLRRALQGLDPVTIAAIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTA
EVIRHGLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVH
VAHSGRSTAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFY
DAMAAGK
>tr|A0A072V451|A0A072V451_MEDTR DUF620 family protein OS=Medicago
truncatula GN=MTR_3g111790 PE=4 SV=1
MLLQRQAMRKLCPNFDKADGLDTVLEVPIPEEMLTNMGTTGFNRWQNLKTLMNNAQVADK
SSGLSAPSNNEFTALLKLVGAPLIPLQVQSDHTLTRPIRDCSVRDSIGKYIVQQYVAATG
GQGALNSLQNMYAMGEVRIHGSEMRHGADDNSVHSRGKAEVGGFVLWQNNPDLWCLELVV
SGFKITAGSNGKVSWNQSSSQPFQSNRGPPRPLRRFFQGLDPRCIANLFLDAECVGENEI
NNDLCFILKLQTEQHILQAQSTSNTEIVMHTILGYFSQRTGLLVKFEDTKLVRMKTVKGK

DSVIWETNIESTIDDYKCVGGINIAHGGKTISTLYRYGAAHNHKQMIEEIWSIEEVDFNI
FGLSMDCFLPPSDHEREQHDVAEHTV
>tr|A0A061FCW8|A0A061FCW8_THECC Uncharacterized protein OS=Theobroma
cacao GN=TCM_034018 PE=4 SV=1
MGETWEKEMGVSSRILKRSSEAPKHKQTKTSGAPNPVAAKACTVIGTGDHGNMVLFVGLW
CQEIDQVIQLESSNAKSKVSIRTTSGSEGKRKEEGFLSLARAPFPLSLPFCLSLPVAMMI
RKLCPNLDKKDGLETVLEVPIPEEMYTKMGSNAALRWQNMRALMKAQSAFDKSTHLQAKS
DNEFLALLKIVGAPLIPFQVHLENYTLSGPLNSKDCSIEASTAKYIVQQYVAATGGHLAL
SSMTSMYAVGQVKMQGSEMQQGDDSVHTRGNCEVGGFVLWQKNPDLWYLELVVSGFKVSA
GSDGKVAWNQSSSQPGQANRGPPRPLRRFFQGLDPRCTASLFLDAVCIGEQAINNEDCFV
LKLETAANALKVQSSAQTEIIHHTIWGYFSQRTGLLVKFEDTKLVRMKPVKGNDSAFWET
SVETVVQDYKYIDGINIAHSGKTITTLYRYGKSYNQKRKIEETWRIDEVDFNICGLSNET
FLPPADLKREQEGGEQ
>tr|M4CVD2|M4CVD2_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra008179 PE=4 SV=1
MKMRKLCPNLDNEDGLETVLEVPVPEEMFTKMGSNATGRWRNMHALMKAHAVVTAVAADM
RTPASSSSMSNVNMHLQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINDTSIEASTA
KYIVQQYVAACGGPAALNAVKSMYAVGQVRMQGSEMVAGEDEGTTTTPVRLGKGNFEVGG
FVLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPR
GTASLFLDAVCIGEQTVNNEDCFVLKVETPADILKAQCSPNTEVIHHTVWGYFSQRTGLL
VKFGDTKLVRVKSARGKSDGVFWETSMESIIDDYKYVDSVNIAHGGRTLTTLYRYGGAVN
HRRRIEEKWTIEEVDFNICGLCLESFLPPSDMNNDH
>tr|A0A0B2NXK2|A0A0B2NXK2_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_034235 PE=4 SV=1
MMGRLAPLSEEPINEENEGYNNSNSKKCLQSWRNWNWIKTHFSLAFNKKSNLKILLSVSS
SAQYIIQHFRAATGCRKLEGTVKNVFTTGKVTMDVVDELGSTSGGINLEKGCFVMWQMVP
DKWQIELVLGGQKVVAGSNGAIAWRHTPWLGVHAAKGGVRPLRRALQANFISLQGPLCSE
TELICTHNCILGLDPLAVSAVFCAAQYMGEKEISGMDCFVLKLSADQKDLVERSDNTAEM
IKHAIFGYFSQRSGLLVYLEDSYLTRIQAPGSHPTYWETTMSTKIEDYRIVDGVMIAHAG
SSTALITRFGDNLKAGPSITRLEESWTIDDVAFNVPGLSLDCFIPPQELQRDCSSDDELD
WRSFTLA
>tr|A0A0L9V9L4|A0A0L9V9L4_PHAAN Uncharacterized protein OS=Phaseolus
angularis GN=LR48_Vigan09g023600 PE=4 SV=1
MRKLCPNFDKEDGLETVLEVPIPDEMLTSMGSNGFNRWQNLRTLMNARFPDKSSLNNEFL
VLLKIVGAPLIPVQLSSDHALTRPLKDCSIQDSNAKYIVQQYVAATGGVAALNSLESMYA
IGRVRICGSEMRQGEIDEEVEARGKPEVGGFVLWQKNPDMWCLELVVSGYKVSAGCDGKV
SWNHSSSQPFHAIKAPPRPLRRIFQGLDPRCAANLFLDAECVGENIINNEVCFMLKLQTA
QQVLLAQSTSNTDIVMHTIVGYFSQRTGLLVKFEDTKLVKIRPVKGKEYVFWETRVESLI
EDYRYVDGINIAHGGTTIATLNRYGAEQNHKRMIEETWTIEEVDFNIVGLTMNCFLPPSD
GEREQHEGTEGMG
>tr|Q9FRK7|Q9FRK7_ARATH Putative uncharacterized protein F22H5.11
OS=Arabidopsis thaliana GN=F22H5.11 PE=4 SV=1
MRKLCPNLDREDGLETVLEVPVPEEMFTKMGSNAQGRWRNMHALMKAHAVVTAVATDVRT
PASSSSMSNVNMHLQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINDTSIEASTAKY
IVQQYVAACGGPTALNAVKSMYAVGQVRMQGSEMVAGEDEGTGTPVRLGKGSFEVGGFVL
WQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPRCTA
SLFLDAVCIGEQPVNGEDCFVLKVETPSDILKAQCSPNTEVIHHTVWGYFSQRTGLLVKF
GDTKLVRVKSGRGKNDGVFWETSMESIIDDYIFVDAVNIAHGGQTVTTLYRYGGAVNHRR
RIEEKWRIEEVDFNICGLCLESFLPPSDINNDH
>tr|F4HXG1|F4HXG1_ARATH Uncharacterized protein OS=Arabidopsis thaliana
GN=At1g75160 PE=4 SV=1
MKMRKLCPNLDREDGLETVLEVPVPEEMFTKMGSNAQGRWRNMHALMKAHAVVTAVATDV
RTPASSSSMSNVNMHLQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINDTSIEASTA
KYIVQQYVAACGGPTALNAVKSMYAVGQVRMQGSEMVAGEDEGTGTPVRLGKGSFEVGGF

VLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPRC
TASLFLDAVCIGEQPVNGEDCFVLKVETPSDILKAQCSPNTEVIHHTVWGYFSQRTGLLV
KFGDTKLVRVKSGRGKNDGVFWETSMESIIDDYIFVDAVNIAHGGQTVTTLYRYGGAVNH
RRRIEEKWRIEEVDFNICGLCLESFLPPSDINNDH
>tr|A0A0B2SB77|A0A0B2SB77_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_003733 PE=4 SV=1
MFSTMGNNVALRWQNMLTWMKAQTEDKLATPTVASRLNELRFLLYLVGCPLIPLQVQLGH
SVHRPVRDCSIEASTAKYIVQQYIAATGGQPALNAVDSMCVTGQIKISASDFYHTGQSIE
VKKTSEEMGGFVLWQKDPDLWCLEVVLSGCKVCCGSNGKVSWRHSSNQQTPVQRGAPRPL
RRFLQGLDPRATANLFLDAACIGEKIINDEECFILKLETSPAIRDAQSGPNFEIIHHTIW
GYFSQRSGLLVQFEDCRLHSMRTKDDNDIFWQTSLESVIEDYKYVDGINVSHSGKTRVTV
SRYGEQSANHKKELEERWKIEEVDFNIWGLNAESFLPPSNLEKT
>tr|A0A0D3G548|A0A0D3G548_9ORYZ Uncharacterized protein OS=Oryza barthii
PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHREAPRRRGRRGGGGTVKSWVRARMEHGRRRDGAA
PSRAEVQLMLGVVGAPLVPQAVEARKAMVAGRGVGGEGEEPRGPGGVQGEYVAAAGGEAA
LGAATSMYAMGKVRMRTTTTSKANKGKVMGVAAGGEVAGGFVVWQKKPELWCVEMVVAGG
VKMSAGSDGKVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGERCVDG
DDCFVLRVDADHAALRARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHLLRIGLAHAAAE
SAYWETTMESSIGDYRAVDGINIAHAGRTAVSLSRFESADDAAAAARGSNKRSWGTTTME
ETWSIEEVDFNVVGLSMDCFLPPRDLVLNDCSKQQQKEDAAAAVVVKDAAGAAANAKGGS
DDGKTNGGDVGRGVVVKKALVPAVTGLGWFGPAKVVAVDDTVDDGVAAAADDDK
>tr|V4M912|V4M912_EUTSA Uncharacterized protein OS=Eutrema salsugineum
GN=EUTSA_v10018668mg PE=4 SV=1
MKMRKLCPNLDREDGLETVLEVPVPEEMFTKMGSNATGRWRNMHALMKAHAVVTAVAADV
RTPASSSSMSNVNMHLQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINDTSIEASTA
KYIVQQYVAACGGPAALNAVKSMYAVGQVRMQGSEMVAGEDEGTTTTPVRLGKGNFEVGG
FVLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPR
CTASLFLDAVCIGEQTVNGEDCFVLKVETPADILKAQCSANTEVIHHTVWGYFSQRTGLL
VKFGDTKLVRVKSVRGKNDGVFWETSMESTIDDYMFVDSVNIAHGGRTLTTLYRYGGAVN
HRRRIEEKWRIEEVDFNICGLCLESFLPPSDMNNDHH
>tr|Q0D503|Q0D503_ORYSJ Os07g0591100 protein OS=Oryza sativa subsp.
japonica GN=Os07g0591100 PE=4 SV=1
MWFIHGCEKCRSRRRRSTSCSSTWRRRAATGCCSRCGTRTPWARCGWWRPSSRPRRASSR
TAGPAAAAPPPSSRGASSSGRWRPTCGTSSSPSAAARCTRDPTAASSGATRRGSAPTPPR
APCARSAASSRSGHLTAARSGLADPPISITLTGVFSPLLATMQGLDPLTTAGLFAEARCV
GEKKVNGEDCFILKLSADPQTLKQRSEGPAEIIRHVLFGYFSQRTGLIVHIEDSHLTRIQ
PHSGGDAVYWETTISSALEDYRPVEGIMIAHAGRSAVTLFRFGEAAMSHTKTRMEEAWSI
EEVAFNVPGLSVDCFIPPADIRSGPVGESCELPPPAAAPHGERARHPARVAAVDRAPPHH
NAGGANVGRRGDKIMWRVEV
>tr|A0A0E0IRZ6|A0A0E0IRZ6_ORYNI Uncharacterized protein OS=Oryza nivara
PE=4 SV=1
MAPQLATLAEEPGGGEEAARARRKTGLHAALHRWARARIPLRFLSGGGGGGGGVGGGGGG
GHPSPDLRVLLSVLACPLSPVPVLPRHPRNVASSAQYILEQFRATTGCGKIEGAAKSMYA
AGRVRMAMAPEPGIGIGIGIGGGGGGGHEGCFVVWQLVPDMWLVEMAVAGHAVAAGCDGR
VAWRRTPWLGAHAARGGGARPLRRALQGLDPVTIASVFSAAEHVGEKAVDGEDCFALRLD
VAPSVLSAWGDGAAEVIRHGMTGYFSQRSGLLARLDDSQLTRIQTPGAPAMYWETTVSSR
LGDYRAADGGAAVVAHAGTSVAHLARFGADVGAARAFTRMEEEWTIDDVAFNVAGLCPES
FIAPEEVRSGGGGGSSSSRRYDGGGGAIAKKK
>tr|A9XLD9|A9XLD9_CAPFR Uncharacterized protein OS=Capsicum frutescens
GN=5.PEPPER.3 PE=4 SV=1
MRILCPNVDREDGLETVLEVPIPDEMFKSMGSNAALRWQNMATWMKAQTSDKWSSPIVAA
RYNELSFLLFMIGSPLIPFQIEIGQSVTRPVKHSSIEASTAKYILQQYIAATGGQPALNA
VNSMCVVGQVKITASDFHQGDQNVKARKSEENGGFVLWQKNPDLWCLELLISGCKVISGS

NGKISWRQSSNQIRPISKGPPRPLRRFLQGLDPRSIANLFANAVCIGEKIVCDQDCFILK
LDTNQAALEAQSGPNYEILHHTIWGYFSQRSGLIIKFEDSRLLTVKTSRDDEGVFWETST
ESVMGDYKYVDGVNVAHCGKTYVTVFRYGEHSANHKRQLEEKWKIEEVDFNVGRLTTEFF
MPPSDFVNEHSRF
>tr|A0A0A9EYY7|A0A0A9EYY7_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MFAGARCIGERKVNGEDCFILKLCTEPETLKARSEGLAEIIRHVMFGYFNQRTGLLVHIE
DSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMIAHSGRSAVTLFRFGEVAMSHTKT
RMEEAWTLEEVAFNVPGLSMDCFIPPTDVESGSVGEIMELSHGEKSKAIPPPGHRAKVAA
LEKAEDDKVAWGRTILEDHN
>tr|A0A0B2PYF5|A0A0B2PYF5_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_008682 PE=4 SV=1
MRKLCPNYEKVNGLETVLEVPIPEDMWTSIGSTASNRWLNLRALLRAQINSNKTSSSSSS
SSSSSSYLVASSNNEFIDLLKLVGCPLIPLQVQSDHTLTRPLKDASSIEASSAKYIVQQY
IGAIGGMVAMDSLKSMYAVGQVRMFGSEMRQGGENIKPKGKAEVGGFVLWQKNPDLWHFE
LIVSGFKVSAGSDGKVAWNQSSSQLSQANQGPPRPLRRFFQGLDPRCTANLFIDAVCVGE
KTINNEDCFTLKLETAHNILQALNTSHTEILRHTVRGYFSQRTGLLVKFEDTKLVRMKHA
KGNDSVFWETSMESVIEDYRCVDGINIGHGGKTVAILYKYGMAHNHQRKIEETWRIEEVD
FNICGLSMDCFLPPSDLKKEQHGVV
>tr|A0A087HIK2|A0A087HIK2_ARAAL Uncharacterized protein OS=Arabis alpina
GN=AALP_AA2G193400 PE=4 SV=1
MFAKMGSNATGRWRNMHALMKAHAVVTAVADVRMPASSSSISNVNMHLQSKSDNEFVALL
KIVGSPLIPFHVPLEFCLSRPIKDTSIEASTAKYIVQQYVAACGGPAALNAVKSMYAVGQ
VRMQGSEMVAGEDEGTATPVRLGKGSFEVGGFVLWQKNPNLWFLELVVSGFKISAGSDGK
VAWNQSSTQPSQAHRGPPRPLRRFFQGLDPRCTASLFLDAVCIGEQTVNGEDCFVLKVET
PADILKAQCSPNTEVIHHTVWGFFSQRTGLLVKFGDTKLVKVKSVRGKSDGVFWETSMES
IIDDYMFVDSVNIAHSGQTVTTLYRYGGAVNHRRRIEEKWKIEEVDFNICGLCLESFLPP
SDINNDH
>tr|A0A0J8CA11|A0A0J8CA11_BETVU Uncharacterized protein OS=Beta vulgaris
subsp. vulgaris GN=BVRB_6g137530 PE=4 SV=1
MRKLCPNLDKEDALETILEVPIPEEMFNNMGNNVALRCQNMQQWMKAQTSDKWSSPVILG
RINELRFLLYHVGSPLIPLQVHIDNINRPVRDSSIQTSTAKYIVQQYIAATGGQAAISSI
QSMCVIGHAKIGATAFHLGDQAVKGKNTEETGGFVLWQKNPNLWCLEFVVSGCKVFSGNN
GKLSWRQSSNQPCVTTGSPRPLRRFLQGLDPRATANLFIDATCIGEKVINNEDCFILKLE
TSQATLDAQSGAKFEIIHHTLWGYFSQRSGLLLQFEDSRMLRLKNSVENDDGDGVFWETS
AESVIEDYRYVDGINIAHSGKTSVRVFRYGEHSANHQREIEETWKIDEVGFNIWGLDPDF
FTPPTDVQVELET
>tr|M0RGN7|M0RGN7_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MGPRSRGRNHVCSVQPLGPLMEGPDPEAHGEGAKKERYWEVIRTWLRLHMDKAMSGAHSS
TPFHARSASKRTDLRLILGVLGCPLAPIPVTIDAPTHIFCIKDSPMETCSARYIIQQYLA
ATGCLKQCMKSMYAAGTVKMVCHEPPRTGGERGCFVLWQKSPGMWSVELVVAGHKVVSGS
NGKVVWRSVPWLGTHAARGPQRPLRRLVQGLDPKSTARMFAEARSGLLTYIEDSHLARVE
APGSDAMYWETTIGSVIEDYREVDGVLVAHQGRSAATVLRFGDASARRSRIRMEEAWRIE
DVVFDVAGLSVDCFIPPKEIMAGFRGK
>tr|M0U3B9|M0U3B9_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MGPRIRRKNRVCLAQPLTPLVEGPDLDDAHGERAKKEKYWESIGTWLRLHKDKGMSGSHF
SIPFHGSGASKWTDLKLILSVLGCPLAPLPLTTEPSHHFSFKDSPIEASSARYIIQQYLA
ATGCLKHHEYMKSMYAAGRVKMVSRETDGPSGKIGARSGAGHGCFVLWQKSPGMWLVELV
VAGCKVAAGSNGKVAWRNVPWLGTDAARGPQRPLRRIIQGLDPKGTASMFTKARSGLLVY
IEDSHLTRVQAPGSDTMYWETTIGSTMGDYKEVDGVLVAHQGRSAASVFRFGDASAQSSR
IRMEEEWRIEDVVFNVAGLSADCFIPPREMLTNFHGK

>tr|F2DHZ6|F2DHZ6_HORVD Predicted protein OS=Hordeum vulgare var. distichum PE=2 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHQEAPARSRRTVKAWMRSHMHIDHQQHRRDGAAPP
RADVQIMLGVMGAPLVPQPVQPRRPMGGRGNKEEPLEQSKARYIVEQYVAAAGGEAALSA
ATSMFAMGKVRMSSSTTSKSKSKAAKKGAGEVHGGFVVWQKKPELWCVEMVVAGGTKMSA
GSDGNVAWRQTPWQQAHASRGPPRPIRRCVQGLDPKSTADLFSSAASVGEESVDGEDCFL
LRVDAEPSALHARSSADVEVIRHALWGYFSQRTGLLVRLEDSHLLRIPKPAESGGEGKAA
SASMYWETTMESIIGDYRPVDGINIAHAGRTVVSVSPFTTAAGAVEDADADADARRKRPC
TCMEETWSIEEVEFNIAGLSTECFLPPRDLLLGTSNSKEQPRHKKGQGDKATKGGRDSDG
GCGIRAAVAKKALVPVVTGLGWFGPAKVAAVDSLDAADESEDTTYAPAR
>tr|Q10R94|Q10R94_ORYSJ Lipase, putative, expressed OS=Oryza sativa subsp. japonica GN=LOC_Os03g07120 PE=4 SV=1
MAGACKGCRVAFTPFRHHAFEALKAACRRWLLPNGILSCKQTQHACIKSDYQKFYKNNSR
FPWKFSKISAFPKEYYFGGFTSLGSSLVAPRSYHTNTKQSKAKRDASEDFDFDPPPTRFP
LASLQRCPFPSPALHTRTAAPPSHCRPGPAPSGAHPSLAVASSAQYIIEQFRATTGCGKI
EGAVKSMYAAGRVRLAMLQDPAGGGAGGGGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQH
VAAGSDGRVAWRRTPWVGAHAARGGSRPLRRALQGLDPVTIAAIFSTAEHAGEKLVDGED
CFVLRLDVGPSVLSSWSDGTAEVIRHGLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYW
ETTISSSLADYRAVDGGGGVHVAHSGRSTAHLARFGVGVRAARVVTRMEESWTIDDVAFN
VPGLGPDAFIPPEEVRRSRFYDAMAAGK
>tr|B8AA38|B8AA38_ORYSI Putative uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI_03846 PE=4 SV=1
MRKLCPNLDRNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMQQYIAATGGQAALQ
GLQSMYAVGKVRMCASEFHLGDQNVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHKMSA
GSDGKVAWRQSAAENSHASRGPPRPLRRSLQVDRTLLAAAPPLPSLSTSFDITMQGLDPR
SIANLFSDAVCIGEKIITGEECFILKLEASAATLRARSAAAFDIIHHTVWGYFSQRTGLL
IQLEDSHLLRMKSGKGARRSENIFWETTMESTISDYRHIDGINIAHGGHTAVTLFRYGEG
SVNHKRKLEETWTVEEADFNLYGLTTDYFLPPSDLKKDIDEKRAG
>tr|A0A0E0EXP7|A0A0E0EXP7_9ORYZ Uncharacterized protein OS=Oryza meridionalis PE=4 SV=1
MAPQLATLAEEPGGGEEAARSRRKTGLHAALHRWARARIPLRFLSGGGGGGGVGGGGGGG
RPSPDLRVLLSVLACPLSPVPVLPRHPRNVASSAQYILEQFRATTGCAKIEGAAKSMYAA
GRVRMAMAPEPGIGIGGGGGGGGGGGGGGHEGCFVVWQLVPDMWLVEMAVAGHAVAAGCDG
RVAWRRTPWLGAHAARGGGARPLRRALQGLDPVTIASVFSAAEHVGEKAVDGEDCFALRL
DVAPSVLSAWGDGAAEVIRHGMTGYFSQRSGLLARLDDSQLTRIQTPGAPAMYWETTVSS
RLGDYRAADGGAAVVAHAGTSVAHLARFGADVGAARAVTRMEEAWTIDDVAFNVAGLCPE
SFIAPEEVRSGGGGGGSSSSXLSSNNNENTNYKKISYKTDSKTLDTETQDLTF
>tr|A0A0D3CWJ0|A0A0D3CWJ0_BRAOL Uncharacterized protein OS=Brassica oleracea var. oleracea PE=4 SV=1
MKMRKLCPNLDDEDGLETVLEVPVPEEMFTKMGSNATGRWRNMHALMKAHAVVTAVAADM
RTPASSSSMSNVNMHMQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINVPSIEASTA
KYIVQQYVAACGGPAALNAVKSMYAVGQVRMQGSGMVAGEDEGITATPVRLGKGNFEVGG
FVLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPR
CTASLFLDAVCIGEQTINGEDCFVLKVETPADILKAQCSANTEVIHHTVWGYFSQRTGLL
VKFGDTKLVRVRSARGKNDGVFWETSMESIIDDYMYVDSVNIAHSGRTLTTLYRYGGAVN
HRRRIEEKWRIEEVDFNICGLCLESFLPPSDMNNDH
>tr|W4ZX39|W4ZX39_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHQEVPARRRRTVNLKAWMRTHMHIDHQHMHRRDGV
QVMLGVMGAPLVPQPVQPRRPMGGRDSKEEPLELSKARYIVEQYVAAAGGEAALSAATSM
FAMGKVRMSSTTSKSSKATKKGMGEVHGGFVVWQKKPELWCVEMVVAGGTKMSAGSDGKV
AWRQTPWQQQAHASRGPPRPIRRCVQGLDPKSTADLFSSAASVGEEAVDGEDCFVLRVDA
EPSALHARSGADVEVIRHALWGYFSQRTGLLVRLEDSHLLRIPRPADAAYASMYWETTMA
STIGDYRPVDGINIAHAGRTVVSVSPFTRAAGAVDDADARRKRPCTCMEETWSIEELEFN

IAGLSTECFLPPRDLVFSDSKDQPRHNKEQGDKAAKGARDGDGGCGIRVAVPKKALVPVV
TGLGWFGPAKVAAVDSLDAADESKDTTYASTR
>tr|I1MXV4|I1MXV4_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MRKLCPNYEKVNGLETVLEVPIPEDMWTSIGSTASNRWLNLRALLRAQINSNKTSSSSSS
SSSSSSYLVASSNNEFIDLLKLVGCPLIPLQVQSDHTLTRPLKDASSIEASSAKYIVQQY
IGAIGGMVAMDSLKSMYAVGQVRMFGSEMRQGGENIKPKGKAEVGGFVLWQKNPDLWHFE
LIVSGFKVSAGSDGKVAWNQSSSQLSQANQGPPRPLRRFFQGLDPRCTANLFIDAVCVGE
KTINNEDCFTLKLETAHNILQALNTSHTEILRHTVRGYFSQRTGLLVKFEDTKLVRMKHA
KGNDSVFWETSMESVIEDYRCVDGINIGHGGKTVAILYKYGMAHNHQRKIEETWRIEEVD
FNICGLSMDCFLAPSDLKKEQHGVV
>tr|R0GFN9|R0GFN9_9BRAS Uncharacterized protein OS=Capsella rubella
GN=CARUB_v10022220mg PE=4 SV=1
MKMRKLCPNLDREDGLETVLEVPVPEEMFAKMGSNAAGRWRNMHTLMKAHAVVTAVAADI
RTPASSSSMSNVNMHLQSKSDNEFVALLKIVGSPLIPFHVPLEFCLNRPINDTSIEASTA
KYIVQQYVAACGGPAALNAVKSMYAVGQVRMQGSEMVAGEDEGTTTPVRLGKGCFEVGGF
VLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPRC
TASLFLDAVCIGEQSVNREDCFVLKLETPSDILKAQCSPNTEVIHHTVWGYFSQRTGLLV
KFGDTKLVRVKSGRGKSDGVFWETSMESIIDDYIFVDAVNIAHGGQTVTTLYRYGGAVNH
RRRIEEKWRIEEVDFNICGLCLESFLPPSDMMQ
>tr|M4CHT5|M4CHT5_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra003768 PE=4 SV=1
MKMRKLCPNLDDEDGLETVLEVPVPEEMFTKMGSNATGRWRNMHALMKAHAVVTAVAADM
RTPASSSSMSNVNMHMQSKSDNEFVALLKIVGSPLIPFHVPLEFCLSRPINVPSIEASTA
KYIVQQYVAACGGPAALNAVKSMYAVGQVRMQGSGMVAGEDEGITATPVRLGKGNFEVGG
FVLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPR
CTASLFLDAVCIGEQTINGEDCFVLKVETPADILKAQCSANTEVIHHTVWGYFSQRTGLL
VKFGDTKLVRVRSARGKNDGVFWETSMESIIDDYMYVDSVNIAHGGRTLTTLYRYGGAVN
HRRRIEEKWRIEEVDFNICGLCLESFLPPSDMNNDR
>tr|M0Z487|M0Z487_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MDKERKQGFFAALKEEVVRGLSPARSRGKTPARSASPARMLIPRRRKAQPPPPDKQQQQQ
YLPEQLIPRSGSLRPGGEVLEPLIEGPDADRLAAGDFVGEDSGRREGFGHWVRGHLTRTP
SMASASAGPGGSSGSFRHSDLRLLLGVMGAPLAPISSNLADPLPLLSIKGTPIESSSAQY
ILQQYMAASGGYKMLQSVRNAYAMGKVRMVASEFETATRVVKNRGPSGRGTAAVEQGGFV
LWTMAPGMWYVELAVGGSKVHAGCNGRLVWRHTPWLGAHAAKGPVRPLRRVLQVSTLPPL
FSFSPPFSPTTSQIFLPPTCKLQCRVLIR
>tr|A0A078BTN5|A0A078BTN5_ECHMU BnaA07g21860D protein OS=Echinococcus
multilocularis GN=BnaA07g21860D PE=4 SV=1
MKMRKLCPNLDDEDGLETVLEVPVPEEMFTKMGSNATGRWRNMHALMKAHAVVTAVAADM
RTPASSSSMSNIVGSPLIPFHVPLEFCLSRPINVPSIEASTAKYIVQQYVAACGGPAALN
AVKSMYAVGQVRMQGSGMVAGEDEGITATPVRLGKGNFEVGGFVLWQKNPNLWFLELVVS
GFKISAGSDGKVAWNQSSTQPSQAHRGPPRPLRRFFQGLDPRCTASLFLDAVCIGEQTIN
GEDCFVLKVETPADILKAKCSANTEVIHHTVWGYFSQRTGLLVKFGDTKLVRVRSARGKN
DGVFWETSMESIIDDYMYVDSVNIAHGGRTLTTLYRYGGAVNHRRRIEEKWRIEEVDFNI
CGLCLESFLPPSDMNNDR
>tr|A0A0K9P4K2|A0A0K9P4K2_ZOSMR Uncharacterized protein OS=Zostera marina
GN=ZOSMA_38G00460 PE=4 SV=1
MGQLAPIKEEPVDEEDGAKKMKRLSTIKKKMAWTKWQWIKTRLSLISSPKKPNNIKILLS
VLGCPLSPISTPHPSSSSSLLVPLKGISSKAQYIIQQFRGVTQMGKSLKSLYASGNVEVS
MVKTAEETEEEEDQRWMSERGRFVVWEMDPGMWLIELVVSGWKIVAGSDGNTAWRNTPWI
GTHAAPGGVRPLRRALQGLNPSTITSVFSTSQYMGEKEMDGQDCFVLLLEADQPTLLARS
DHAAKIIKHIMIGYFSQTTGLLVHLDDLQLTRIQVSASVQPIFWETTINSQIRDYKPVEH
GILVAHSGRSIVRLAKIQQGIEKQHQETTTMEEEWTIHDIAFDIPGLSSDYFIPPEEVAK

>tr|S8CDE2|S8CDE2_9LAMI Uncharacterized protein (Fragment) OS=Genlisea aurea GN=M569_09803 PE=4 SV=1
MRTLCPDLRRRDGLDTVLEVPIPEETFQSTLSPAQLHLLLGLLGAPLIPMPLPCCDPTLN
GGDHPIGKSMARYIVRQYVAASGGDHALDSIHSMYAVGKVDMEFIGGESGEVGGFVVWQK
RPNLWSFELMVSGAKISAGSDGKVVWHQTPWQDPHASRGPPRPLRRLLQGLDPRLVADVF
SDSVCTGEKRVRNEDCFVLKVEAEASTLRARSSAANYDIIRHTLWGCFSQKTGLLIQIED
SHLVRLKGNDVFWETATESFIRDYRTIEGINIPHRGRTDVSLLRFGGGGSWECEVRTRMQ
EIWVIEEVGFNIKGLSPDSFLPPAELKAEDDSD
>tr|A0A078JPG4|A0A078JPG4_BRANA BnaCnng60070D protein OS=Brassica napus GN=BnaCnng60070D PE=4 SV=1
MKKKLEASTAKYIVQQYVAACGGPAALNAVKSMYAVGQVRMQGSGMVAGEDEGITATPVR
LGKGNFEVGGFVLWQKNPNLWFLELVVSGFKISAGSDGKVAWNQSSTQPSQAHRGPPRPL
RRFFQGLDPRCTASLFLDAACIGEQTINGEDCFVLKVETPADILKAQCSANTEVIHHTVW
GYFSQRTGLLVKFGDTKLVRVRSARGKNDGVFWETSMESIIDDYMYVDSVNIAHSGRTLT
TLYRYGGAVNHRRRIEEKWRIEEVDFNICGLCLESFLPPSDMNNDH
>tr|M4ESP1|M4ESP1_BRARP Uncharacterized protein OS=Brassica rapa subsp. pekinensis GN=Bra031821 PE=4 SV=1
MRKLCPNVDRDDGLETVLEILIPEELFSGMGNNVALMCQNMMTWMKAQTADKLSQPLIAA
RINELRFLLYLVGSPLIPLQVQVGHSVHKPVKDSSIQASTAKYIVQQYIAATGGPAALNA
VNSMCVIGQVKMTASEFHQGDDSNVNLKSNDEMGGFILWQKDPDLWCLELVVSGCKVICG
SNGRLSWRHSSNQQTPSSTGTPRPLRRFLQGLDPRSTANMFLDATCIGEKIINGEDCFIL
KLETSPAVREAQSGPEFEIIHHTIWGYFSQRSGLLIQFEDSRLLSMRTKEGDVFWETSAE
SVMDDYRYVDDVNIAHGGKTTVTVFRYGEASANHRRQMTEKWRIEEVDFNIWGLSVGRPI
VVPDRTGHALLPTLYGQAMKHNTHFFVEYLALDLLMASDGSCQGVIALNMEDGTLHRFRS
AQTILATGVGLWKSRAGPSIYEARSKSYYIKETNLESSQGVSDSESGDLKEYKEHADNFM
EINYHPPPRRDSNTLTPSSSFFIRCGILRNSEGERFMERYAPTAKDLASRDVVSRSVTIE
IREGRGVDAVVPGLMAAGEAACASVHGASRLGANSLLDILVFGRACANRVAEISKPGETL
EENAGKKIIEWLNKLRHSSGSLPTSSIRLNMQLSSAPKKHWKKRKHERKAEEHMLGRISR
FDSTSSFNMHIYDLTPLSNNIMTRDGKRAHPQPNGPPRHGLKFSRVTAGWPAAGCGIEKQ
CPIPPRLVHRSLRVGPRVTIQKLNVSFDA
>tr|A0A0E0QZ06|A0A0E0QZ06_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1
MAPQLATLAEEPGGGEEAARARRKTGLHAALHRWARARIPLRFLSGGGGGGGVGGGGGGG
RPSPDLRVLLSVLACPLSPVPVLPRHPRNVASSAQYILEQFRATTGCAKIEGAAKSMYAA
GRVRMAMAPEPGGGIGIGGGGGGGHEGCFVVWQLVPDMWLVEMAVAGHAVAAGCDGRVAW
RRTPWLDAHAARGGGARPLRRALQGLDPVTIASVFSAAEHVGEKAVDGEDCFALRLDVAP
SVLSAWGDGAAEVIRHGMTGYFSQRSGLLARLDDSQLTRIQTPGAPAMYWETTVSSRLGD
YRAADGAVVAHAGTSVAHLARFGADVGAARAVTRMEEAWTIDDVAFNVAGLCPAAPPAAT
TAAAALSPRRSDVTDRMFF
>tr|V4T9P2|V4T9P2_9ROSI Uncharacterized protein OS=Citrus clementina GN=CICLE_v10003238mg PE=4 SV=1
MRKLCPNYDREDGLDTVLEVPIPEEMFNKMGSTAALRWHNLRALMKAQSQSCDRSSFLQA
KSSNEFMALLKLVGSPLISFQLQLDNPPSRFVKNASIEASTAKYIVQQYIAATGGQAALN
WVNSMYAVGEVKMLGSEMQQGDDSVSAKGNCEAGGFVLWQKNPDLWCLELVVAGFKICAG
SNGKVAWNQSSSQPNVAHRGPPRPLRRFFQGLDPRCIASLFSDAVCIAEEKIDNEDCFVL
KVEANAATLRAQNSPNTEVVHHTIWGYFSQRTGLLIKFEDTKLVRMKSAKGTDSVFWETS
MASTIEDYRYVDAINVAHCGKTVTTLYRYGGAHNHKRKIEETWKIEEVDYNICGLSVETF
LPPAEVRRGNDVGEQSVC
>tr|A0A067GXS5|A0A067GXS5_CITSI Uncharacterized protein OS=Citrus sinensis GN=CISIN_1g047077mg PE=4 SV=1
MRKLCPNYDREDGLDTVLEVPIPEEMFNKMGSTAALRWHNLRALMKAQSQSCDRSSYLQA
KSSNEFMALLKLVGSPLISFQLQLDNPPSRFVKNASIEASTAKYIVQQYIAATGGQAALN
SVNSMYAVGEVKMLGSEMQQGDDSVSAKGNCEAGGFVLWQKNPDLWCLELVVAGFKICAG
SNGKVAWNQSSSQPNVAHRGPPRPLRRFFQGLDPRCIASLFSDAVCIAEEKIDNEDCFVL

KVEANAATLRAQNSPNTEVVHHTIWGYFSQRTGLLIKFEDTKLVRMKSAKGTDSVFWETS
MASTIEDYRYVDAINVAHCGKTVTTLYRYGGAHNHKRKIEETWRIEEVDYNICGLSVETF
LPPAEVRRENDVGEQSVC
>tr|K4CD41|K4CD41_SOLLC Uncharacterized protein OS=Solanum lycopersicum
GN=Solyc07g022840.1 PE=4 SV=1
MRTLCPNFDKKNGLETVLEIPIPEEMFEKFSSNGNGALQWKNMSNLMSTQITDKYSSQHA
ALDQFMFLFKIVGSALVPFQVQFDPTVKLPLKEDSTAKYIVQQYVAACGGQAALNSVNSM
CAVGKVKMSTLDMHKSGSNNNSICHCEVGGFVLWQKNLDQWVLELVVSGCKVIAGSNGKV
AWSQSSSNSCASKGPPRPLRRFFQGLDPRSTANLFSNAICFGEKTIKDEECFILKFESSI
EMLKAQSTTNTEVVHHTIWGYFSQRTGLLVQFEDTKLVRLKTTKGDSNVFWETSMESFLE
DYRYIEGINVAHSGKTAATIFRYGKNIDYRAKIEETWFIEEIDFNIFGLSMECFLPPSDV
NKETEFEDQLISC
>tr|K7WD01|K7WD01_MAIZE Uncharacterized protein OS=Zea mays
GN=LOC100502405 PE=4 SV=1
MEKESKQGFFSALKGEVVRGLSPGRSRGKSLLLPRSRKTAAAEEVAPPEKLAQYAPDPLV
THSGSLRLAGEVLAPLMEGPDVAEDDTFAEDSGRRDGFGQWVRGHLTRAPLIAGGGDGSF
RRSDLRLLLGVMGAPLAPVSVSTAEPLPLAPVKGAPIESSSAQYILQQYLAASGGAKVLR
SARNAYAMGKVRMVASEFETATRVVKNRGAAAAAAVEQGGFVLWRMSPDMWYVELAVGGS
KVRAGCNGRLVWRHTPWLGAHAAKGPVRPLRRALQVAFPSRARLDACHWLVPTIVCVCVR
ARVYCAGSGSAVDCGAVRGGAVRGREEGGRRGVLHPEAVGGRGDAAAAERGSGGDHPARG
VRVLQPAHGPAGAGGGLAPDAHPAARRRGRRVLGDHHQLVPGGLPRGGRRGDRARGAVRR
DAVPVRRDGHEPHQDAHGGGVDHPGGRLRRAGPVHRLLHPAGRRPARLRLRGRALRAPAA
RRQGRRRAPRVRRGALAAAAGCGPGRWGAGDKIYRTVEMRFLTVGDGTDRADSYRKSSTI
TSS
>tr|M0TCI2|M0TCI2_MUSAM Uncharacterized protein OS=Musa acuminata subsp.
malaccensis PE=4 SV=1
MRKLWPNLDREDGLDTVLEVPIPEETFLSDASSRSNKTLCSNIKAWMRSHVDRSPPSPIG
RGAELQLMLGVIGAPLVPLPVQAYRSTLVRGMEKDPIEVSMAKYIVQQYIAASGGEQALN
AINSMYAVGKVRMTASEFPKGHGGGGDTASNNRKVRKGGGFDGAGEIGGFVLWQKKPHLW
CLELMVSGCKFSAGSDGKVAWRQTPWHQSHASRGPPLPLRRSLQGLDPRCTANLFARSRT
GLLLQLVDSRLLRIKYSASKGSVYWESTMESLIEDYRPIDGVNIAHAGRTKVSLFRFGET
SDGHTRTRMEETWNVEEVDFNIWGLSTDCFLPPADLKEDEEGADVGDGPVATAPPPSSVQ
PAATRIGPSQVAAVDPFMYPLTY
>tr|B9FBI7|B9FBI7_ORYSJ Uncharacterized protein OS=Oryza sativa subsp.
japonica GN=OsJ_09551 PE=4 SV=1
MRSRVALETLAEEPGGGEEEAARRKSSGLQAALHRVARRLLSGAGEDARPAADLRVLLSV
LACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCGKIEGAVKSMYAAGRVRLAMLQDPA
GGGAGGGGGGGRGHEGSFVMWQLAPSMWIVEMAVAGQHVAAGERRKGWPGAGSPWVGAQA
ARGGSRPLRRALQGFDPVTIAAIFSTAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTA
EVIRHGLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVH
VAHSGRSTAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFY
DAMAAGK
>tr|A0A022RZL1|A0A022RZL1_ERYGU Uncharacterized protein OS=Erythranthe
guttata GN=MIMGU_mgv1a007621mg PE=4 SV=1
MVNHSMRKLCPNLDKEGGLETVLEVPIPEEMFNKMGSNAVLRWHNMRNLMRAQHHHRSSA
ADKWASVTNPLSSGSSSSSGTTTNNIDQFMLLLKLVGSAFIPYRVQLDRAITKPIKDGSI
EASTAKYIVQQYLAATGGLSALNSINSMYAVGQVKMEVASDGVQQQNNEPAKRSCEAGGF
VLWQKNPDLWYLELVVSGHKISAGSDGKIAWSQSSSNSNATRGPPRPLRRFFQGLDPRST
ANLFLNTVCIGEKTIQNEDCFILKLDTCSEILKAQSTPNTEVVHHTIWGYFSQRTGLLIQ
FEDTKLIRMKTPVGDESVFYETSMESVLEDYRIVDGINIAHGGKTSASLYRYGKTLKRKW
KLEETWKIEEVDFNICGLSFDYFLPPAEAVKKGNEPYENGI
>tr|W5AB98|W5AB98_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MRKVCPNLDREDGLDTVLEVPVPELHQEVPARRRRRRTVKAWMRSHMHIDHHHMHHRDGV

QVMLGVMGAPLVPQPVQPRRPMGGRDSKEEPLELSKARYIVEQYVAAAGGEAALSAATSM
FAMGKVRMSSTTSKSSKATKKGMGEVHGGFVVWQKKPELWCVEMVMAGGTKMSAGSDGKV
AWRQTPWQQQAHASRGPPRLIRRCVQGLDPKSTADLFSSAASAGEEAVDGEDCFVLRVDA
EPSALHARSSADVEVIRHALWGYFSQRTGLLVRLEDSHLLRIPRPADAGGEGKAASASMY
WETAMASTIGDYRPLDGINIAHAGRTIVSVSPFTRAAGAVDDVDADARRKRPCTCMEETW
SIEEVEFNIAGLSTECFLPPRDLLLSDSKEQPRHNKEQGDKAAKGARDSVKAAYDSDGGC
GIRAAVPKKALVPVVTGLGWFGPAKVAAVDSLDAADESKDATYASTR
>tr|A0A0D2S3E9|A0A0D2S3E9_GOSRA Uncharacterized protein OS=Gossypium
raimondii GN=B456_006G144900 PE=4 SV=1
MAMVDELGATVGSVAGAAGVAQKGCFVMWQMVPNKWLIELVVGGHKVIAGSDGNVAWRRT
PWLGAHAAKGGVRPLRRALQGLDPMAISAVFSSAQYMGEKRISSTDCFVLKLSADQVDLA
DRSDSTAEMIKHVIFGYFSQRSGLLVFIEDSYLTRIQSPGTYPTYWETTMATKIEDYRLV
EGVMVAHSGQSNVIITRFGDNLKAGLSVTRMEETWTIDDVAFNVPGLSLDCFIPPKEVQK
DFPDENLDWRSPLHR
>tr|A0A0D3FE93|A0A0D3FE93_9ORYZ Uncharacterized protein OS=Oryza barthii
PE=4 SV=1
MSGEVCECGCVVAIVFQFLHFQNHQGRKCGLNHHPWPVLARVAESPSLPSAITHAFEALK
AACRRWLLPNGILSCKQTQTRMHKIRLSGVDQRRKATTSTEYPCFTSLGSSLVAPRSYHT
NTKQSKAKHDASEDFDFDPPPTRFPLASLQRCPFPSPALHTRTAAPPSHCRPGPAPSGAH
PSLASRAALETLAEEPGGGEEEAARRKSSGLQAALHRVARRLLSGAGEDARPAADLRVLL
SVLACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCAKIEGAVKSMYAAGRVRLAMLQD
PAGVWIVEMAVAGQHVAAGSDGRVAWRRTPWVGAHAARGGSRPLRRALQGLDPVTIAAIF
STAEHAGEKLVDGEDCFVLRLDVGPSVLSSWSDGTAEVIRHGLTGFFSQRSGLLVRLEDS
QLTRIQSPGAAAMYWETTISSSLADYRAVDGGGGVHVAHSGRSTAHLARFGVGVRAARVV
TRMEESWTIDDVAFNVPGLGPDAFIPPEEVRRSRFYDAMAAGK
>tr|A0A0D9XJM0|A0A0D9XJM0_9ORYZ Uncharacterized protein OS=Leersia
perrieri PE=4 SV=1
MAPPQLATLAEEPGGEEDAAGRGRRRRKAGIHAALHRWAKARIPLRFLSGVGGGSGGDEG
RRPSADLRVLLSVLACPLSPVPVLPLHPRNVASSAQYILEQFRATTGCGKMAEVKSMYAA
GRVRMAMTPEPGGGGGHEGCFVVWQLVPDMWLVEMAVAGHAIAAGCDGRVAWRRTPWLGA
HAARGGGARPLRRALQGLDPVTIASVFTAAEHVGEKSVDGEDCFALRLDVSPAVLAAWSD
GAAEVIRHGITGYFSHRSGLLARLDDSQLTRIQPNPGSPALYWETTLSTRLADYRPVLLD
AAGGGGVVVVAHAGTSVAHLARFGADVGTARAVTRMEEAWSIDDVAFNVAGLCPESFIAP
EEVRGRGSSRRYDVYGGGGKRK
>tr|S8DHA9|S8DHA9_9LAMI Uncharacterized protein OS=Genlisea aurea
GN=M569_12569 PE=4 SV=1
MHTCSSSSHHGQPQRNKHKNTMRKMCPNFDREDALETVLEVPIPEEMFSGLGNNVALRWQ
NMATWMKAQTPDKWSSPIIAGRYNEMSFLLYIVGSPILPFQIQVDRAIQRAVKHSSIEAS
TAKYIVQQYIAATGGQPALNAVNSMCVVGHVRISGSEFHQGDENVKVRSNHDAGGFVLWQ
KNPDLWCFELLISGCKVIAGSNGKISWRQSSNQQRPICTGPPRTPRRFLQGLDPRATANL
FIEAVCIGEKIINEEDCFILKVDTSQSTLEEQSGAKHEIIHHTIWGYFSQRSGLLVKFED
SRLLSLKTNKEDGDVFWETSMESVIEDYRYVDGVNVAHGGRTAFTVFRYGERSANHKREL
VETWKLEEVDFNVSGLKPQFFMPPPPQ
>tr|B9ET59|B9ET59_ORYSJ Uncharacterized protein OS=Oryza sativa subsp.
japonica GN=OsJ_03556 PE=4 SV=1
MRKLCPNLDRDDSLDTVLEVPIPDEMLINAPGTDKRRGAGGANMRAWLKNQAFDRATVGG
PANATAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIVSHRSPARVARARVHACSAAG
WFLTRSSPSSCVCARVWSASVDGQVHHAAVHRGDGPGRRLCRGLQSMYAVGKVRMCASEF
HLGDQNVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHKMSAGSDGKVAWRQSAAENSHA
SRGPPRPLRRSLQVDRTLLAAAPPLPSLSTSFDITMQGLDPRSIANLFSDAVCIGEKIIT
GEECFILKLEASAATLRARSAAAFDIIHHTVWGYFSQRTGLLIQLEDSHLLRMKSGKGAR
RSENIFWETTMESTISDYRHIDGINIAHGGHTAVTLFRYGEGSVNHKRKLEETWTVEEAD
FNLYGLTTDYFLPPSDLKKDIDEKRAG

>tr|A0A096RVF2|A0A096RVF2_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.24093 PE=4 SV=1
MYASGRVRLSMLQEPGGGGGGGRGHEGSFVLWQLAPSMWLVEMSVAGQSVAAGSDGRVAW
RRTPWLGAHAARGGSRPLRRALQGLDPVTIASIFSTAEHAGEKEVDGEDCFVLRLDVGPS
VLSSWSDGTAEVIRHGLTGFFSQRSGLLARLEDSQLTRIQSPGAAAMYWETTIASAVSDY
RAVDGGVAVAHAGTSTAHLARFGVGVRAARVVTRMEESWTIDDVAFNVPGLGPDAFIPPE
EVRRSRSYGAAIAGGK
>tr|M8C3I0|M8C3I0_AEGTA Uncharacterized protein OS=Aegilops tauschii
GN=F775_18690 PE=4 SV=1
MRKLCPNNDRDDSLDTVLEVPIPDEMLANAPGADKRRGGGPNMRAWLKTQAFDRATADGP
AAAAANAELQLFLNVVGSPLIPCPVPHDRAFSRSIRDSSIQASTAKYIMHQYIAATGGQA
ALQGVQSMYAVGKVKMCASEFHLGDQTVTAAQGRAEVGGFVLWQKCPEVWYFELIMAGHK
MSAGSDGKVAWRQSAAENSHASRGPPRPLRRSLQGLDPRSIANLFSDAVCIGEKVINGEE
CFILKLEASATTLRARSAAAFDIIHHTVWGYFSQRTGLLIQLEDNHLLRMKSGKGARRSE
NIFWETSMESVINNYRHIDGVNIAHGGKTTATLRGSWRRRGRWRRPTST
>tr|A0A0K9PXX8|A0A0K9PXX8_ZOSMR Uncharacterized protein OS=Zostera marina
GN=ZOSMA_154G00290 PE=4 SV=1
MRRMCPNDDSKNDGMFKLETVLEVPLPEEIFIDPPTDSGGRRWRLSKTNHRWASQPSLKI
NPPTQVRNTDLPLLLTVISTPLIPCSTVLTQTTSSFITNKQSDMEKLQAKYIMRQYIAAT
GGDKMTGSMYAMGKVSMKISEMDGVILTSEGIGRVMGGFVLWKKSPDLWCIELMICGYKI
SAGSDGNVVWRQTPWCLPHSTRGPPRSLRRSIQGIDPWLTANMFANAACIGNTMINKEEC
FILKIDSEPSGPCARRGSNVEILEHTVWGYFSHRSGLLVQLNDTHVLKNIEGGSSDIGGS
NSGSSKWITNFQSTIEDYRNIDGVYIAHSGRSSASLQMLGDSTVRTTMEENWEIVEVDFD
VRGLSMDCFLPPSDLKKPEKEDVGLFSANCSSNFSYGQFPSQQGLNHRKSSLAGFRIGSS
KSKAAAVEVKNIPKNIYINI
>tr|A0A0K9S2M1|A0A0K9S2M1_SPIOL Uncharacterized protein OS=Spinacia
oleracea GN=SOVF_000930 PE=4 SV=1
MVVKNIFATGKVSMTMLEEPSLSGSSAVVVAAGATHKGCFVMWEMLPNKWSIELVVGGHK
VLAGSDGNVAWRYTPWLGSHPAKGGVRPLRRALQGLDPMAISEAFSVAQYMGEKEMMGVD
CFVLKLSAEQNDLADRSDNTAETIKHVTFGYFSQKNGLLVYLEDSYLTRIQSPGGCPRYW
ETTMGSKIEDYRTVDGVMIAHSGQTHAIITRFGDNLKSGPTILRMEETWMIDDFAFNVQG
LSMDCFILPQDVKSNSLEEKLKQTPLFPLDR
>tr|A0A078ELS1|A0A078ELS1_BRANA BnaC04g25310D protein OS=Brassica napus
GN=BnaC04g25310D PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSENNKTGSWRSVKTSLLRSPPDNNSSLSTLFG
GRDAQIQMLLGIVGAPLIPLPVSSDHDVLDHPMPKLIKNQSIEAAMAKYIVKQYTAASGG
EVALDRVESMYAMGKVKMGVTEFCAAKTQIGKRKKKMVRIKNLNNGNGGEMGGFVLWKKG
SSQWSLELVVSGCKVSAGCDGLDPKTTANMFAGSVCVGEKVVNDEECFVLKLETQTSGLK
SRSKGGMETVKHTVWGCFSQRTGLLVKLEDTYLVRIKIGPEDEDVVLWETTSETMIQDYK
SVDGIQIAHRGKTQVSLLRLDESLESHSKTTMEESWEIEEVGFNVKGLSSDFFLPPGDLC
TKENEESGFNFGDFSSPMMIPLKVSKDSWKLKSSKVTAIEDFQG
>tr|A0A0D3BXN7|A0A0D3BXN7_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSENNKTGSWRSVKTSLLRSPPDNNSSLSTLFG
GRDAQIQMLLGIVGAPLIPLPVSSDHDVLDHPMPKLIKNQSIEAAMAKYIVKQYTAASGG
EVALDRVESMYAMGKVKMGVTEFCAAKTQIGKRKKKMVRIKNLNNGNGGEMGGFVLWKKG
SSQWSLELVVSGCKVSAGCDGLDPKTTANMFAGSVCVGEKVVNDEECFVLKLETQTSGLK
SRSKGGMETVKHTVWGCFSQRTGLLVKLEDTYLVRIKIGPEDEDVVLWETTSETMIQDYK
SVDGIQIAHRGKTQVSLLRLDESLESHSKTTMEESWEIEEVGFNVKGLSSDFFLPPGDLC
TKENEESGFNFGDFSSPMMIPLKVSKDSWKLKSSKVTAIEDFQG
>tr|A0A0K9RZP7|A0A0K9RZP7_SPIOL Uncharacterized protein OS=Spinacia
oleracea GN=SOVF_015540 PE=4 SV=1
MQQTSTAKYIVQQYIAATGGQAAISSIQSMCVIGHAKIGATVFHLGDQIVRGKNTEEVGG
FVLWQKNPDLWSLEFVVSGCKVFSGSNGKVSWRQSSNQPSVTTGSPRPLRRFLQGLDPRA

TANLFIDAICIGEKVINHEDCFILKLETSQTTLDAQSGPKYEIIHHTLWGYFSQRSGLLL
QFEDSRMLRLKNNVDNDDGDGVFWEISAESFIEDYRYVDGINIAHSGKTSVRVFRYGEHS
ANHQREIDETWKIDEVGFNIWGLDPDFFLPPRESQVEASAF
>tr|A0A0J8CHT1|A0A0J8CHT1_BETVU Uncharacterized protein OS=Beta vulgaris
subsp. vulgaris GN=BVRB_4g085350 PE=4 SV=1
MVVKNIFATGKVSMTMLEEPSLSGSPAAVVAAGATHKGCFVMWEMLPNKWSIELVVDGHK
VLAGSDGNVAWRYTPWLGSHPAKGGVRPLRRALQGLDPMAISEAFSVAQYMGEKEIMGID
CFVLKLSAEQDDLADRSDNIAETIKHVTFGYFSQKSGFLVYLEDSYLTRIQSPGACPRYW
ETTMGSKIEDYRTVEGVMIAHSGQTHAIITRFGDNLKSGTPTILRMEEAWMIDDFAFNVQ
GLSMDCFILPQDVKSNCLEEKLKQVPYFPLDR
>tr|U3MZQ7|U3MZQ7_AVIMR Receptor-like cytosolic serine/threonine-protein
kinase RBK1 (Fragment) OS=Avicennia marina var. marina PE=4 SV=1
GGFVLWQMNPDMWYVELAVGRSKVHAGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLD
PRTTAAMFAKAICIGEKNINGEDCFILKLAADHQTLKARSEGPAEIIRHVLFGYFSQKTG
LLVHMEDSHLTRIQSN
>tr|M7YT52|M7YT52_TRIUA Uncharacterized protein OS=Triticum urartu
GN=TRIUR3_20267 PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHQEVPARRRRTVNLKAWMRTHMHIDHQHMHRRDGV
QVMLGVMGAPLVPQPVQPRRPMGGRDSKEEPLELSKARYIVEQYVAAAGGEAALSAATSM
FAMGKVRMSSTTSKSSKATKKGMGEVHGGFVVWQKKPELWCVEMVVAGGTKMSAGSDGKV
AWRQTPWQQQAHASRGPPRPIRRCVQGLDPKSTADLFSSAASVGEEAVDGEDCFVLRVDA
EPSALHARSGADVEVIRHALWGYFSQRTGLLVRLEDSHLYRPVDGINIAHAGRTVVSVSP
FTRAAGAVDDADARRKRPCTCMEETWSIEEVEFNIAGLSTECFLPPRDLVLSDSKDQPRH
NKEQGDKAAKGARDGDGGCGIRAAVPKKALVPVVTGLGWFGPAKVAAVDSLDAADESKDT
TQRAARRSLLLAMRGEADEASGCDWRGAGEDGVEARKAGMGAGVEELRAAQKLEVETMAL
PVHGEK
>tr|D7MMD6|D7MMD6_ARALL Predicted protein OS=Arabidopsis lyrata subsp.
lyrata GN=ARALYDRAFT_686430 PE=4 SV=1
MCVTGQVKMTASEFHQGDESGVNLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICGSNG
RLSWRHSSNQQTPASTGTPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFILKLE
TSPAVREAQSGPNFEIIHHTIWGYFSQRSGLLIQFEDSRLLRMRTKEDDDVFWETSAESV
MDDYRYVDNVNIAHGGKTSVTVFRYGEASANHRRQMTEKWRIEEVDFNVWGLSVDHFLPP
ANLQIEK
>tr|A0A078CFZ4|A0A078CFZ4_BRANA BnaA04g03400D protein OS=Brassica napus
GN=BnaA04g03400D PE=4 SV=1
MRTLCPNFDREDGLETVLEVPMPEELFCSENNKTGSWRSVKTSFLRSSPDNNSSLSTLFG
GHDAQIQMLLGIVGAPLIPLPFSSDHDVLDHPMPKLIKNQSIEAAMAKYIVKQYTAAAGG
ETALAGVESMYAMGKVKMGVTEFCAAKTLIGKRKKKMVRIKNLNNGNGGEMGGFVLWKKG
SRQWSLELVVSGCKVSAGCDGLDPKTTANMFAGSVCVGEKVVNDEECFVLKLETQTSGLK
SRSKGGMETVKHTVWGCFSQRTGLLVKLEDTYLVRIKIGPEDEDVVLWETTSETMIQDYK
SVDGIQIAHRGKTQVSLLRLDESLESHSKTTMEESWEIEEVGFNVKGLSSDFFLPPGDLC
TKENEESGFNFGDFSSPMMIPLKVSKDSWKLNSSKVTAIEDFEG
>tr|Q9LVQ6|Q9LVQ6_ARATH Emb|CAB81597.1 OS=Arabidopsis thaliana
GN=At5g66740 PE=4 SV=1
MCVTGQVKMTASEFHQGDDSGVNLKSNDEMGGFVLWQKDPDLWCLELVVSGCKVICGSNG
RLSWRHSSNQQTPASTGTPRPLRRFLQGLDPRSTANLFLDATCIGEKIINGEDCFILKLE
TSPAVREAQSGPNFEIIHHTIWGYFSQRSGLLIQFEDSRLLRMRTKEDEDVFWETSAESV
MDDYRYVDNVNIAHGGKTSVTVFRYGEASANHRRQMTEKWRIEEVDFNVWGLSVDHFLPP
ANLQIEK
>tr|S8E369|S8E369_9LAMI Uncharacterized protein (Fragment) OS=Genlisea
aurea GN=M569_04607 PE=4 SV=1
MRKLCPNLDRKDGLETVLEVPIPEEMFNKMGSDAAVRWQNMRSLMRPKNPSALDRFAAAA
SAASSFSNYDFLLKLVGSAFIPYSVQLDQAVAKPIRDGPIESSTAKYIVKQYVAATGGLA
ALNSISSMYAVGQVKMSVVSDAIEASKRACEVGGFVLWQKNPDLWYLELVISGFKINAGS

DGKIAWNQSSSSSNPTKGPPKALRRFFQGLDPRSTANLFLNTACVGETRVEDEDCFILRT
ETDRETLKSQSTCNTEIVQHTIWGYFSQRTGLLVRFQDSKLIKMKLGEELSIYETVMESS
MEDYRCVDEIKIAHGGTTRASLCRHGTKAKKTWILEESWRIEEVDFNICGLANEHFLPPS
D
>tr|M1B3E0|M1B3E0_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG400013939 PE=4 SV=1
MCAVGQVKISTSDMHQSGINDNSKCHCEVGAFVLWQKNPDQWVLELVVSGCKVSAGSNGK
VAWSQSSSSSSASKGPPRPLRRFFQGLDPRSTANLFSNAICFGEKTIKDEECFILKLESS
IEMLKAQSMINTEVVHHTIWGYFSQRTGLLVQFEDTKLVRLKSTKGDSNVFWETSMESIL
EDYRYIEGINVVHSGKTAATIYRYGKNIDYRAKIEETWFIEEIDFNIFGLSMECFLPPAD
VNKETEFEDQAIAC
>tr|A0A0E0K989|A0A0E0K989_ORYPU Uncharacterized protein OS=Oryza punctata
PE=4 SV=1
MRSRAALEPLAEEPGGGEEEAAARRKSGLQAALHRVARLLSGAGDGARPAADLRVLLSVL
ACPLSPVPILPRLPRHVASSAQYIIEQFRATTGCAKIEGAVKSMYAAGRVRLAMLQEPAG
AVAGAGGGRGHEGSFVVWQLEPSMWIVEMAVAGQHGLDPVTIAAIFSTAEHAGEKLVDGE
ECFVLRLDVGPSVLSSWSDGTAEVIRHGLTGFFSQRSGLLVRLEDSQLTRIQSPGAAAMY
WETTISSSLADYRAVDGGGAVCVAHAGRSTAHLARFGVGVRAARVVTRMEESWTIDDVVF
NVPGLGPDAFIPPEEVRRSRFYDAMAAGKVS
>tr|N1R4Y8|N1R4Y8_AEGTA Uncharacterized protein OS=Aegilops tauschii
GN=F775_20644 PE=4 SV=1
MGAPLAPISSNLADPLPLLSIKGTPIESSSAQYILQQYMAASGGYKMLQSVRNAYAMGKG
LDPLTTAGLFAEARCVGEKKVNGEECFILKLSADPQTLKLRSEGPAEIIRHVLFGYFSQR
TGLMVHIEDSHLTRIQPHSGGDAVYWETTISSCLEDYRAVEGIMIAHAGRSAVTLFRFGE
AAMSHTKTRMEEAWSIEEKF
>tr|A3F4A7|A3F4A7_9ROSI Putative uncharacterized protein (Fragment)
OS=Trichosanthes dioica PE=2 SV=1
LRTNSSAQYILQQYTAASGGQKLQNSVGNAYAMGKVKMIACEFETANKVVRTRNSSKDAE
SGGFVLWLMKPDMWYVELALGGSKVHAGCNGKLVWRHTPWLGAHAAKGPVRPLRRSLQGL
DPKTTASMFANARCIGEKSVTQDSSITS
>tr|M7YNW3|M7YNW3_TRIUA Uncharacterized protein OS=Triticum urartu
GN=TRIUR3_25994 PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGSSRGGSRFGCTGVKAWMRSHAADRSGAG
EPCSMSRGELQLMLGVIGAPLIPLPVSHAKQSPSSVLCEQLKGDPIVRPALFLLLTQEED
WFLTIVVTELAWQESSSAKYIVQQYIAASGGEWALNKVTSMYAMGKILTSRQGNIWGRPY
AGYNAITIAMSGLDPMLTASLFADSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEI
IRHTVWGYFSQRTGLLVQLEDSHLLQIKSGGPAGGGSVFWETTMESRLRDYRAVDGVNIA
HSGRTAVSLVRFGDTHDGGNTRTRMEEHWDIEEVDFNIWGLSMDCFLPPSDLRDAKESQQ
QELAVVKPARPPPLRIPAVAVVRVGPSQVAAVNLDETESLLAR
>tr|N1R329|N1R329_AEGTA Uncharacterized protein OS=Aegilops tauschii
GN=F775_16944 PE=4 SV=1
MRKVCPNLDREDGLDTVLEVPVPELHQEVPARRRRTVNLKAWMRSHMHIDHQHMHRRDGV
QAMLGVMGAPLVPQPVQPRRPMGGRDSKEPLELSKARYIVEQYVAAAGGEAALSAATSMF
AMGKVRMSSTTSKSSKATKKGMGEWHQDERRQDGKVAWRQTPWQQQAHASRGLPRPIRRC
VQGLDPKSTADLFSSAASVGEEAVDGVDCFVLRVDAEPSALHARSGADVEVIRHALWGSV
SQRTGLLARLEDSHLLRIPRPADAASASMYWETTMASTIGDYRPVDGINIAHAGRTVVSV
SPFTRAAGAVDEADADVDARRKRPCTCMEETWSIEEVEFNIAGLSTECFLPPRDLVLSDS
KDQPRHNKEQGDKAAKGARDGDGGCGIRAAVPRKPLVPVVTGLGWFGPAKVAAVDTLDAA
DESKDTTYASTR
>tr|B9SMM5|B9SMM5_RICCO Putative uncharacterized protein OS=Ricinus
communis GN=RCOM_0231830 PE=4 SV=1
MRKLCPNIDKDDGLETVLEVPIPEEMFTSMGSNVTLRWHNMLTWMRAQTSDKWSQPVIAG
RINELRFLLYMVGSPLIPLQVQVGHSVYKPVKDCSIQASTAKYIVQQYIAATGGQQALNA
VHSMCVTGEVKISASEFHQGDQTINVKSSEEAGGFVLWQKDPDLWILELVVSGCKVISGS

NGKISWRHSSNQQTPISKGPPRPLRRFLQGLDPRSTANLFIDATCIGEKIINDEDCFILK
LETSPAIREAQSGPNYEIIHHTIWGYFSQRSGLLIQFEDSRC
>tr|D5ADQ9|D5ADQ9_PICSI Putative uncharacterized protein OS=Picea
sitchensis PE=2 SV=1
MFVNARCVGEKRIGEEDCFILKLAASPAALAERNDGSAEIIRHALFGYFNQKTGFLVYVE
DSHLTRIESTGNDAVYWETTIETTIDHYKPVDGVMIAHSGRSVVTVFKFGGQFGMTSTKT
RIEETWTIEEIVFNVPGLSMDFFIPPAEIRKGSASGGPSELTSGKFGNGKAWQNSLGKLK
>tr|B9FNH9|B9FNH9_ORYSJ Uncharacterized protein OS=Oryza sativa subsp.
japonica GN=OsJ_17817 PE=4 SV=1
MGKVRIRTTTTSKANKGKVMGVAAGGEVAGGFVVWQKKPDLWCVEMVVAGGVKMSAGSDG
KVAWRQTPWQEAHASRGPPRPLRRCIQGLDPKSTADLFSSAAWVGERCVDGDDCFVLRVD
ADHAALRARSSGDVEVVRHAVLGYFSQRTGLLVRLEDSHLLRIGLAHAAAESAYWETTME
SSIGDYRAVDGINIAHAGRTAVSLSRFESADDAAAAARGSNKRSWAPPPWRRRGASRSKQ
QQKEDAAAAVVVKDAAAAVDVKDAAGAAANAKGGSDDGKTNGGDVGRGVVVKKALVPAVT
GLGWFGPAKVVAVDDTVDDGVAAAADDDK
>tr|Q0IMB2|Q0IMB2_ORYSJ Os12g0581300 protein (Fragment) OS=Oryza sativa
subsp. japonica GN=Os12g0581300 PE=4 SV=1
RHVLFGYFSQKTGLLVHLEDSHLTRIQSTTGGDAVYWETTINSFIEDYRPVEGIMVAHAG
RSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTDIKSGSISETVELP
HGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFK
>tr|B4FR41|B4FR41_MAIZE Uncharacterized protein OS=Zea mays GN=umc2185
PE=2 SV=1
MALIDMQGLDPQLTASLFADSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHT
VWGYFSQRTGLLVQLEDSHLLQIRSSGGGAGGSVFWETTMESRLGDYRAVDGVNIAHAGR
TAVSLVRFGDCQDGNTRTRMEEEWNIEEVDFNIWGLSMDCFLPPSDLREGKESQDVAVVK
ADARPPPLRIPAVTVRVGPSQVAAVNMDDSDSLVARS
>tr|A0A0A9DKU8|A0A0A9DKU8_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MAFHVQGLDPQLTASLFADSVCIGERSVDGEDCFVLKVEAEASSLRARNSSSVEIIRHTV
WGYFSQRTGLLVQLEDSHLLQIRSSGGAGGSVFWETTMESRLEDYRAVDGVNIAHAGRTA
VSLVRFGDCHDGNTRTRMEEAWNIEEVDFNIWGLSMDCFLPPSDLREGKESQDVAIVKAD
ARPPPIRIPAVTVRVGPSQVAAVNMDDSDSLIARS
>tr|W5E4B9|W5E4B9_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MDVQGLDPMLTASLFAEDSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVW
GYFSQRTGLLVQLEDSHLLQIKSGGGSVFWETTMESRLRDYRAVDGVNIAHSGRTAVSLV
RFGDTQDGNTRTRMEEHWDIEEVDFNIWGLSMDCFLPPSDLRDGGKESQQQQQEELAVVK
AARPPPLRIPAVAVVRVGPSQVAAVNLDETESLLAR
>tr|A0A0E0CYI8|A0A0E0CYI8_9ORYZ Uncharacterized protein OS=Oryza
meridionalis PE=4 SV=1
MSLNRDATHAINRLGLDPMLTASLFADAVCIGERSVDGEDCFVLKVEAEASSLRARNSSS
VEIIRHTVWGYFSQRTGLLVQLEDSHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIA
HAGRTAVSLVRFGDSSDGNTRTRMEEVWNIEEVDFNIWGLSMDCFLPPSDLKESKEDKDV
STAVKPARPPPIRIPAVAVRVGPSQVAAVNMDDSDSLIARS
>tr|M7Y7Z0|M7Y7Z0_TRIUA Uncharacterized protein OS=Triticum urartu
GN=TRIUR3_09969 PE=4 SV=1
MKQASTAKYIMHQYIAATGGQAALQGVQSMYAVGKVKMCASEFHLGDQTVTAAQGRAEVG
GFVLWQKCPEVWYFELIMAGHKMSAGSDGKVAWRQSAAENSHASRGPPRPLRRSLQARPR
ILPIGLDPRSIANLFSDAVCIGEKVINGEECFILKLEASAATLRARSAAAFDIIHHTVWG
YFSQRTGLLIQLEDNHLLRMKSGKGARRSENIFWETSMELRRARYYKHGSHDPTFRAYQT
KHMRKLNMSEYRHLQMKKAKKLDYLPDPAEGTIS
>tr|M1CL42|M1CL42_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG401027132 PE=4 SV=1
MFSDSICIGEKPVHGEDCFVLKFEADPSSLKARSSSNVEIMRHTVWGYFSQRTGLLVQLE

DSHLLRLKSPKDDVFWETTMESLIQEYRTIDGVNIAHAGKTCVSLFRFGENSEGHTRTRM
EEVWTIEEVDFNIKGLSLDCFLPPSDLKKDDDQEIISDDDDINKNSRLESKNIIHHVNNP
RFITAIKGAAKIVAIDQDSED
>tr|W5ELX2|W5ELX2_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MDVQGLDPMLTASLFAEDSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVW
GYFSQRTGLLVQLEDSHLLQIKSGAGGGSVFWETTMESRLRDYRAVDGVNIAHSGRTAVS
LVRFGDTHDGGNTRTRMEEHWDIEEVDFNIWGLSMDCFLPPSDLRDAKESQQQQELAVV
KAARPPPLRIPAVAVVRVGPSQVAAVNLDETESLLAR
>tr|W5DXR2|W5DXR2_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MDVQGLDPMLTASLFAEDSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVW
GYFSQRTGLLVQLEDSHLLQIKSGGPAGGGSVFWETTMESRLRDYRAVDGVNIAHSGRTA
VSLVRFGDTHDGGNTRTRMEEHWDIEEVDFNIWGLSMDCFLPPSDLRDAKESQQQELAVV
KPARPPPLRIPAVAVVRVGPSQVAAVNLDETESLLAR
>tr|M1CL43|M1CL43_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG402027132 PE=4 SV=1
MFSDSICIGEKPVHGEDCFVLKFEAEPSSLKARSSSNVEIMRHTVWGYFSQRTGLLVQLE
DSHLLRLKSPKDDVFWETTMESLIQEYRTIDGVNIAHAGKTCVSLFRFGENSEGHTRTRM
EEVWTIEEVDFNIKGLSLDCFLPPSDMKKDDDQEIISDDDDINKNSRLESKNITHHVNNP
RFITAIKGAAKIVAIDQDSED
>tr|M8C0S9|M8C0S9_AEGTA Uncharacterized protein OS=Aegilops tauschii
GN=F775_15588 PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGGSRGSRSRAMSGIRSDGAGDPGISPGLD
PMLTASLFAEDSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRT
GLLVQLEDSHLLQIKSGAGGGSVFWETTMESRLRDYRAVDGVNIAHSGRTAVSLVRFGDT
HDGGNTRTRMEEHWDIEEVDFNIWGLSMDCFLPPSDLRDAKESQQQQQELAVVKAARPPP
LRIPAVAVVRVGPSQVAAVNLDETESLLAR
>tr|M0XTE8|M0XTE8_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MLTASLFAEDSVCIGERSIDGEDCFVLKVEAEASSLRARNSSSVEIIRHTVWGYFSQRTG
LLVQLEDSHLLQIKSGNGAGGSVFWETTMESRLRDYRAVDGVNIAHSGRTAVSLVRFGDT
QDGNTRTRMEEHWDIEEVDFNIWGLSMDCFLPPSDLRDAKESQDQDVAVVKAARPPPLRI
PAVAVIRVGPSQVAAVNLDETESLLARIPTPHP
>tr|G3LNQ9|G3LNQ9_9BRAS AT3G55720-like protein (Fragment) OS=Capsella
grandiflora PE=4 SV=1
VLWKKGMSQWSLELVVSGCKVSAGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPK
TTANMFAGSVCVGEKAVNDEECFVLKLETQPAGLKSRSKSGMETVKHTVWGCFSQRTGLL
VQLEDTYLVRIKTGPEEEDVVFWETTSETLIQDYKSVDGIQIAHRGKTRVS
>tr|G3LNR1|G3LNR1_9BRAS AT3G55720-like protein (Fragment) OS=Capsella
grandiflora PE=4 SV=1
VLWKKGMSQWSLELVVSGCKVSAGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPK
TTANMFAGSVCVGEKAVNDEECFVLKLETQPAGLKSRSKSGMETVKHTVWGCFSQRTGLL
VQLEDTYLVRIKTGPEEEDVVFWETTSETLIQDYKSIDGIQIAHRGKTRVS
>tr|G3LNR7|G3LNR7_9BRAS AT3G55720-like protein (Fragment) OS=Capsella
rubella PE=4 SV=1
VLWKKGMSQWSLELVVSGCKVSAGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPK
TTANMFAGSVCVGEKAVNDEECFVLQLETQPAGLKSRSKSGMETVKHTVWGCFSQRTGLL
VQLEDTYLVRIKTGPEEEDVVFWETTSETLIQDYKSVDGIQIAHRGKTRVS
>tr|G3LNR3|G3LNR3_9BRAS AT3G55720-like protein (Fragment) OS=Capsella
grandiflora PE=4 SV=1
VLWKKGMSQWSLELVVSGCKVSXGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPK
TTANMFAGSVCVGEKAVNDEECFVLKLETQPAXLKSRSKSGMETVKHTVWGCFSQRTGLL
VQLEDTYLVRIKTGPEEEDVVFWETTSETLIQDYKSVDGIQIAHRGKTRVX

>tr|G3LNR0|G3LNR0_9BRAS AT3G55720-like protein (Fragment) OS=Capsella grandiflora PE=4 SV=1
VLWKKGMSQWSLELVVSGCKVSAGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPK
TTANMFAGSVCVGEKAVNDEECFVLKLETQPAGLKSRSKSGMETVKHTVWGCFSQRTGLL
VQLEDTYLVRIKTGPEEEDVVFWETTSETLIQDYKSXDGIQIAHRGKTRVS
>tr|G3LNR2|G3LNR2_9BRAS AT3G55720-like protein (Fragment) OS=Capsella grandiflora PE=4 SV=1
VLWKKGMSQWSLELVVSGCKVSAGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPK
TTANMFAGSVCVGEKAVNDEECFVLXLETQPAGLKSRSKSGMETVKHTVWGCFSQRTGLL
VQLEDTYLVRIKTGPEEEDVVFWETTSETLIQDYKSVDGIQIAHRGKTRVS
>tr|G3LNR8|G3LNR8_9BRAS AT3G55720-like protein (Fragment) OS=Capsella rubella PE=4 SV=1
VLWKKGMSQWSLELVVSGCKVSAGCDGNVAWRQSPWLAHSHASNEPSGPLRRFLQGLDPK
TTANMFAGSVCVGEKAVNDEECFVLQLETQPAGLKSRSKSGMKTVKHTVWGCFSQRTGLL
VQLEDTYLVRIKTGPEEEDVVFWETTSETLIQDYKSVDGIQIAHRGKTRVS
>tr|A0A0B2QL36|A0A0B2QL36_GLYSO Uncharacterized protein OS=Glycine soja GN=glysoja_042945 PE=4 SV=1
MGRLAPLSEEPINEENEGYNNNSNPKKCLQSWRNWNWIKTHFSLVLNKKSNLKILLSVLG
CPLFPVSSSAQYIIQHFRAATGCRKLEGTVKNVFTTGKVTMDVVDELGSAGGSVNLEKGC
FVMWQMVPDKWQIELVLGGQKVVAGSNGAIAWRHTPWLGVHAAKGGVRPLRRALQASSSS
SSCLVLNFLTNLVLSLLLYCYVVGWCDGIHCLPDPLCSDSEIELISIYNCILGLDPLAVS
SVFCAAQYMGEKEISGMDCFVLKLSAEQKDLVERSDSKAEMIKHAIFGYFSQRSGLLVYL
GDSYLTRIQAPGSHPTYWETTMSTKIEDYRIVDGVMIAHAGSSTTLITRFGDNLKAGPSI
TRLEESWTIDDVAFYVKGLSLDCFIPPQELQRDCSSDDELGWRSHA
>tr|H9MAB9|H9MAB9_PINRA Uncharacterized protein (Fragment) OS=Pinus radiata GN=0_18178_02 PE=4 SV=1
ILKVAASPAALAERNDGSAEVIRHALFGYFSQKTGFLVYVEDSHLTRIEYTGNDAVYWET
TIETTIDNYKPVDGVMIAHSGRSVVTVFKFGGQLGMTSTKTRIEETWTIEEIVFNVPGLS
MDFFIPPAEIRKGSASGDPPELTSGKFGN
>tr|H9V0V4|H9V0V4_PINTA Uncharacterized protein (Fragment) OS=Pinus taeda GN=0_18178_02 PE=4 SV=1
ILKVAASPAALAERNDGSAEVIRHALFGYFSQKTGFLVYVEDSHLTRIEYTGNDAVYWET
TIETTIDNYKPVDGVMIAHSGRSVVTVFKFGGQLGMTSTKTRIEETWTIEEIVFNVPGLS
MDFFIPPAEIRKGSASGDPTELTSGKFGN
>tr|H9V0V5|H9V0V5_PINTA Uncharacterized protein (Fragment) OS=Pinus taeda GN=0_18178_02 PE=4 SV=1
ILKVAASPAALAERNDGSAEVIRHALFGYFSQKTGFLVYVEDSHLTRIEYTGNDAVYWET
TIETTIDNYKPVDGVMIAHSGRSVVTVFKFGGQLGMTSTKTRIEETWTIEEIVFNVPGLS
MDFFIPPAEIRKGSASGDPPELTSGKFGN
>tr|W1PQV8|W1PQV8_AMBTC Uncharacterized protein OS=Amborella trichopoda GN=AMTR_s00029p00180180 PE=4 SV=1
MINNEDCFILKLEVGAGTLKSRSSSSVEIMRHTVWGYFSQRTGLLCQFEDCHLLRIKANS
GDESYWETSMESLIDDYRLIDGIAIAHSGRTVVSLLRYGETSTTHSRTRMEETWSIEEVD
FNIWGLSGDCFLPPADLRKEQDSYDVVVGGGGGARGTTLGRSKSARIVAPENGARNHQDS
TDEEDED
>tr|W5DZD2|W5DZD2_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1
MSILSMHMQGLDPVMIASIFSTAEHAGEKQVDGEDCFVLRLDVGPSTLSSWSDGTAEVIR
HGLTGFFSQRSGLLARLEDSQLTRIQSPGAAAMYWETTIASTLADYRAVDGGVTVAHAGR
STAHLARFGVGVRAARVVTRMEESWTIDDVAFDVPGLGPDAFIPPEEVRRSRFYDAMAAG
GGK
>tr|M0YHS7|M0YHS7_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1
MHMQGLDPVMIASIFSTAEHAGEKQVDGEDCFVLRLDVGPSTLSSWSDGTAEVIRHGLTG

FFSQRSGLLARLEDSQLTRIQSPGAAAMYWETTIASTMADYRAVDGGVTVAHAGRSTAHL
ARFGVGVRAARVVTRMEESWTIDDVAFDVPGLGPDAFIPPEEVRRSRFYDAMAAGGK
>tr|A0A067FTV8|A0A067FTV8_CITSI Uncharacterized protein (Fragment)
OS=Citrus sinensis GN=CISIN_1g0168361mg PE=4 SV=1
GLDPIAVASVFSTAQYVGEKRISDIDCFVLKLAANQTDLADRSDSTAEMIKHVIFGYFSQ
RSGLLVYLEDSYLTRIQSPGTQPTYWETTMATKIEDYRAIEGVMIAHSGQSSVIITRFGD
NLKAGLSITRMEETWTIDDLAFNVAGLSLDCFIPPKEVQKDSYPVDENLDWRSPLR
>tr|H9MAC0|H9MAC0_PINLA Uncharacterized protein (Fragment) OS=Pinus
lambertiana GN=0_18178_02 PE=4 SV=1
ILKVAASPAALAERNDGSAEVIRHALFGYFSQKTGFLVYVEDSHLTRIEYTGNDAVYWET
TIETTIDNYKLVDGVMIAHSGRSVVTVFKFGGQLGMTSSKTRIEETWTIEEIVFNVPGLS
MDFFTPPAEIRKGTASGDPPELTSGKFGN
>tr|A0A0D3HDK4|A0A0D3HDK4_9ORYZ Uncharacterized protein OS=Oryza barthii
PE=4 SV=1
MEMEHIIVPMSEYRQCICTNEKRPRVHADEVSVLTIVHVCMAVRVQGLDPVTIASVFSAA
EHVGEKAVDGEDCFALRLDVAPSVLSAWGDGAAEVIRHGMTGYFSQRSGLLARLDDSQLT
RIQTPGAPAMYWETTVSSRLGDYRAADGAVVAHAGTSVAHLARFGADVGAARAVTRMEEA
WTIDDVAFNVAGLCPESFIAPEEVRSGGGGGSSSRRYDGGGGAIAKKK
>tr|B9TEF2|B9TEF2_RICCO Putative uncharacterized protein (Fragment)
OS=Ricinus communis GN=RCOM_1927320 PE=4 SV=1
GLDPMTISGVFSQAQYMGEKCMSGTDCFILKLSADQADLADRSDTTAEMIKHVIFGYFSQ
RSGLLVYLEDSYLTRIQTPGTYPTYWETTIATRIEDYRTVEGVMIAHSGQSSVMITRFGD
NLKAGLSITRMEETWAIDDFAFNVAGLSMDCFIPPREVQKDNSQEDLDWRSTLH
>tr|A0A067CYY7|A0A067CYY7_CITSI Uncharacterized protein (Fragment)
OS=Citrus sinensis GN=CISIN_1g046391mg PE=4 SV=1
GLDPIAVASVFSTAQYMGEKRISDIDCFVLKLAANQTDLADRSDSTAEMIKHVIFGYFSQ
RSGLLVYLEDSYLTRIQSPGSLPTYWETTMATKIEDYRAIEGVMIAHSGQSSVIITRFGD
NLKAGLSITRMEEIWTIDDLAFNVAGLSLDCFIPPKEVQKDSYPVDENLDWRSPLH
>tr|A0A068V162|A0A068V162_COFCA Uncharacterized protein OS=Coffea
canephora GN=GSCOC_T00040592001 PE=4 SV=1
MLPCPHFAIFANVTPSKALTLMWYIPFLLGLDPVAISTIFSQAEYMGEKQIFGVDCFVLK
LSANHTDLVERSDNTAEMIKHAVFGYFSQRSGLLIYLEDSYLTRIQSPGSLPSYWETTMA
TKMEDYRSVEGVKIAHSGQSTVIITRFGDNLKFGPSFTRMEETWTIDDIAFNVPGLSMDC
FISPKELQKDYPEENLDWISPLHQ
>tr|A0A0B2SLX7|A0A0B2SLX7_GLYSO Uncharacterized protein (Fragment)
OS=Glycine soja GN=glysoja_023066 PE=4 SV=1
RKLCPNFDKEDGLDTVLEVPIPEEMLISMGTNGFNSWQNLRTLMNAQFVDKSSGLSTPSN
NEFMVLLKLVGAPLIPLQVPSDHTLTRPLKDCSINILQGDEYDDSVQSRGKTEVGGFVLW
QKNPDLWCLELVVSGFKVGAGINGKLAWNHSSSQPFHANKGPSRPLRRFFQGLDSSYKRL
QAQSTSNTEIVMHTILGYFGQRTGAFKGKGSVFWETSIESMIDDYRYIDGINIAHGGRTI
ATLYRYGVAHNHKHMIEETWTIEEVDFNIVGLSMDCFLPPSGGEREHEGAEQAWDRILLR
FSLFCSPQP
>tr|M0YHS8|M0YHS8_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MIASIFSTAEHAGEKQVDGEDCFVLRLDVGPSTLSSWSDGTAEVIRHGLTGFFSQRSGLL
ARLEDSQLTRIQSPGAAAMYWETTIASTMADYRAVDGGVTVAHAGRSTAHLARFGVGVRA
ARVVTRMEESWTIDDVAFDVPGLGPDAFIPPEEVRRSRFYDAMAAGGK
>tr|A0A0D9VPY4|A0A0D9VPY4_9ORYZ Uncharacterized protein OS=Leersia
perrieri PE=4 SV=1
MKGLDPVTIASIFATAEHAGEKLVDGEDCFVLRIDVGPSVLSSWSDGTAEVIRHGLTGFF
SHRSGLLARLEDSQLTRIQSPGAPAMYWETTISSSLSDYRPVPVSSDDNGGVAVVAHAGR
STAHLARFGVGVRAPRVVTRMEEEWTIDDVVFDVPGLGPDAFIPPEEVRRTRFYDAMAAG
GGGGK

>tr|V7CV36|V7CV36_PHAVU Uncharacterized protein (Fragment) OS=Phaseolus vulgaris GN=PHAVU_001G0152001g PE=4 SV=1
GLHPRCTANLFIDAVCVGEETVNKEDCFLLKVETAHYILQAQNTSNSETLRHTMWGYFSQ
RTGLLVKFEDTKLVRLQPSKEKDSIFWETTMESVIEDYRCVDGIKIAHCGKTVTILYRYG
MAHNKHWKTEETWRIEEVDFNICGLSMDCFLPPSDQVVH
>tr|W1PPM1|W1PPM1_AMBTC Uncharacterized protein (Fragment) OS=Amborella trichopoda GN=AMTR_s00165p00000750 PE=4 SV=1
MRKLCPNFDREDGLDTVLEVPIPEEMFGNSSPRGLNSWQNMRAWMRAHAPGGGEQRPLFG
GRSTDLQLLLNVIGAPLIPLPVHSDPPPNHSIKDHPIEVSTAKYIVQQYIAATGGQAVLN
SVHSMYAVGKVRMLASEFHTGDRVVKAAAAATNNSKGGNGNGILGEVGAFVLWQKNPDLW
CLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQ
>tr|Q7XER0|Q7XER0_ORYSJ Lipase, putative, expressed OS=Oryza sativa subsp. japonica GN=LOC_Os10g27110 PE=4 SV=2
MEMEHIIVPMSEYRQCICTNEKRPRVHADEVSVLTIVHHVGEKAVDGEDCFALRLDVAPS
VLSAWGDGAAEVIRHGMTGYFSQRSGLLARLDDSQLTRIQTPGAPAMYWETTVSSRLGDY
RAADGAVVAHAGTSVAHLARFGADVGAARAVTRMEEAWTIDDVAFNVAGLCPESFIAPEE
VRSGGGGGSSSRRYDGGGGAIAKKK
>tr|I1QUF1|I1QUF1_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1
HNXLYFRMDXVEYRQCICTNEKRPRVHADEVSVLTIVHHVGEKAVDGEDCFALRLDVAPS
VLSAWGDGAAEVIRHGMTGYFSQRSGLLARLDDSQLTRIQTPGAPAMYWETTVSSRLGDY
RAADGAVVAHAGTSVAHLARFGADVGAARAVTRMEEAWTIDDVAFNVAGLCPESFIAPEE
VRSGGGGGSSSRRYDGGGGAIAKKK
>tr|M4CG87|M4CG87_BRARP Uncharacterized protein OS=Brassica rapa subsp. pekinensis GN=Bra003220 PE=4 SV=1
MFPLPFPGHFNPLVQLARIFHHRGFSITIIHTSFNFPDTTHYPNFTFRTIHHHNEGEEEE
DPLSKPDASGMDLVTFIRQLREGYANPFRESLKAEVGGGERACCLVSDVVWGRTTEVAAE
EVGIRRMVLTTSGVASFCAFAAYPLLRDKHYLPIQDSRLDELVTELPPLRVKDLPVMETN
EPEELYRVVNNMVEGAKSSSGIIWNTFEDLERIIVLMNFSTEFQVLVFPVGPFYKHSENI
LPTTKNKEDHVTTDWLNKQDPRTVVYVSFGSLADIEEKEFLEIAWGLRNTKQPFLWVVRP
GMVQGTEWLESLPCGFLENIGQKGQIVKWVNQLEVLAHPAVGAFWTHCGWNSTLESICEG
VPMICTPFFTDQRVNARYIVDVWQVGMILERSKLDRKEIEKLLRKEMGEEIRESCLKWKD
RANVCLSKDGSSSKYLEKLEAAVAKYVVKQYTAAAEGETALAGVESMYAIEKVKMGVTEF
CAAKALNGKRKKKMVRIRNINNGNGGEMGGFVLWNKGSCQWSLELVVSGCKVSVGCDGNL
ACKQSPWAVNDEECFVLMLETQPSGLTTRSKSGMETLKHTVWGCFSQRTGLLVQLEDSYL
VRIKTGPEEEDVLWETTSETMIQGYKRVDGIQIAHRGRTRVALLRLDESLENHSKTTMEE
SWEIEEVGLNKWL
>tr|A0A096QKT9|A0A096QKT9_MAIZE Uncharacterized protein OS=Zea mays GN=Zm.1917 PE=4 SV=1
MDAKRQGFFSALREEVARGLSPGRARRRSASNAAEVAAALRRLGGGGEALAPLMEGPDPE
AGPGATCGGSARKEGGWGRWVRGQLQLTRAPALEAGAGAGSGAAAAAAAAGRRNDLRLLL
GVMGAPLAPVHVCAAEPLPHLSIKDTPIETSSAQYILQQYLAASGGQRLLSSIRNSYAMG
KVRMVATEFEA
>tr|Q5XV50|Q5XV50_ARATH Putative uncharacterized protein OS=Arabidopsis thaliana PE=2 SV=1
MTNVFFLISISFKFSSNPNFPQIASLSSLSLNFSLRNPFFFVFANMRKLCPNYNLEDGLE
TVLEVPMPEELFAASKTKPGWNQMKSYWSKPTATATGTATATNMTRLFGGRNAEIQLLLG
VVGAPLIPLPVQPDHHNDYENPIHKDIKDQPLEMSMAQYIVKQYIAAVGGDRALNAVESM
YAMGKVRMTASEFCTGEGSLNSKMVKARSIKSGGGEVGGFVLWQKGIELWCLELVVSGCK
ISAGSDAKVAWRQTPWHPSHASRGPPRPLRRFLQVIHFSFYFLFRCLLVKSIQSYNI
>tr|A0A0E0CYI9|A0A0E0CYI9_9ORYZ Uncharacterized protein OS=Oryza meridionalis PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSGG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY

IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRGGKKSSKNCGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQV
>tr|A5BWJ6|A5BWJ6_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VITISV_032040 PE=4 SV=1
MDHPRIECGEGDGSDEAGNNWMKVLIKRRIKIQMNRLAPLSEEPTNDEEEDNNNSSKKVS
SSAEYIIQHFTAATGCRKLEGKVKNVFATGKVRMAMVDELGSSGSSTAVGPTGVSQKGCF
VMWQMVPDKWLIELVVGGHKVVAGSDGNVAWRHTPWIGAHAAKGGVRPLPASSSRSNLNL
RIVGTYYHSSSQSPNIPGIGPTGGISCVLLSPIHGGEANHGRRLLRLEIRQHSGDDQARD
LRLLQSTEWTAGVPRRFLFNAHTITWVPPHVLGDHHGHQDRGLSDGRGRDDRSRRSNQAP
FITRFGDNLKVGPAITRMEETWTIDDLAFNVPGLSMDCFIPPEEVQKDYPEENLDWRSPL
HR
>tr|A0A067DE12|A0A067DE12_CITSI Uncharacterized protein OS=Citrus
sinensis GN=CISIN_1g040059mg PE=4 SV=1
MSRLAPLSEEPINEEEQHSNSSNSGNNTKYSSKKGLSWKHWLKNHLSLVFFINKKSDLKT
LLSVLGCPLFPVPLLPKQPLNQVCSSAQYIIQHFTAAAGCRKLEGRVKNIFATGKVTMGM
GDDFGGSAGSVAIAGAGASASLGGVSEKGCFVMWQMVPNKWLIELVVGGHKVVAGSDGNL
AWRHTPWLGSHAAKGSIRPLRRALQASL
>tr|A0A0E0KBR1|A0A0E0KBR1_ORYPU Uncharacterized protein OS=Oryza punctata
PE=4 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSRGSGGGGSRGSRFGCTNVKSWVRPNASDRSCG
AGEPCSMSRGELQLMLGVIGAPLIPLPVDHAKQSPCSVLCEQLKADPIESSTAKYIIQQY
IAASGGEWALNKVTSMYAMGKVRMTAAELNSSDADGGGGGGGGGHRAGKKNSKNGGEVGG
FVLWQKKPELWSLELVVSGCKISAGSDGKVAWRQTPWHQSHASRGPPRPLRRSLQV
>tr|A0A0E0ERC8|A0A0E0ERC8_9ORYZ Uncharacterized protein OS=Oryza
meridionalis PE=4 SV=1
MAASGGYRLLQSVRNAYAMGKVRMVASEFETATRVVKNSGPSGRDVASVEQGGFVLWQMA
PDMWYVELPVGGSKVHMGSNGRLVWHHTPWLGAHAAKGPVRLLRRVPASSRSEHLTFSTS
PPGPVAARAGEEGRGRRRLGGGVRRWRAWSPPRQGRRGRCLAEVVAGLARLQEEKMDRGE
ERREGERRREQCNYH
>tr|A0A067FTZ8|A0A067FTZ8_CITSI Uncharacterized protein (Fragment)
OS=Citrus sinensis GN=CISIN_1g0168362mg PE=4 SV=1
MSRLAPLSEEPINEEEQHSNSSNGSNNTKYSSKKGLSWKHWLKNHLSLVFFINKKSDLKT
LLSVLGCPLFPVPLLPKQPLNQVCSSAQYIIQHFTAATGCRKLEGRVKNIFATGKVTMGM
GDDFGGSAGSVPVAGAGASASLGGVSEKGCFVMWQMVPNKWLIELVVGGHKVVAGSDGNF
AWRHTPWLGSHAAKGSVRPLRRALQ
>tr|M1CEZ2|M1CEZ2_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG400025725 PE=4 SV=1
MIRLAPLSEVPTNDEETHPSSSSSSWRNWLKTHFSLIFITKKSDLRILLSVLGCPLFPVS
SNPKIPISQVSSSAEYIIEHFTAASGCRKIQGVVKNMYVSGKVSMAIVDTSSPASTISQK
GCFVLWQMVPNKWLIELVVAAHKVVAGSDGNVAWRHTPWLGSHAAKGAIRPLRRALQASV
LGGGGETILQKRHMLIVPY
>tr|A0A068V340|A0A068V340_COFCA Uncharacterized protein OS=Coffea
canephora GN=GSCOC_T00040593001 PE=4 SV=1
MSRLAPLSEEPVNEEDTKNCSSKAQTWRKWLRAHFSLQLFNRKSDLRLLLSVLGCPLFPL
PVHPKHPITEVSSSAQYIIHHFTAATGCRKLEGMVKNIYATGKVAMAMVDHDQLGGGLAA
SASAANVSDAALQKGCFVMWQMLPNKWLIELAVAGHKVVAGSDGHLAWRHTPWLGVHAAK
GGARPLRRSFQARNAPSP
>tr|W5E758|W5E758_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MQKTCRVTLFACGLNVDLVHAYAGPGPGDDRVHLLDGRARRREXXXXXXXXXXXXXXXXX
XDGTAEVIRHGLTGFFSQRSGLLARLEDSQLTRIQSPGAAAMYWETTIASTLADYRPVDG
GVTVAHAGRSTAHLARFGVGVRAARVVTRMEESWTIDDVAFDVPGLGPDAFIPPEEVRRS
RLYDAMAAGGGK

>tr|A0A0B0P0Y2|A0A0B0P0Y2_GOSAR Dephospho-CoA kinase OS=Gossypium arboreum GN=F383_20751 PE=4 SV=1
MSRLAPLSEEPINEDNSANCSKKGLSWKNWLKTHLSLVFNKKSDLKILLSVLGCPLFPVS
ALSKPPINECLSTDMVASKSPLASHHESIQKEKKVSSSAQYIIQHFTAATGCRKSEGTVK
NIFVTGKVTMAMVDELGATVGSVAGAAGVAQKGCFVMWQMVPNKWLIELVVGGHKVIAGS
DGNVAWRRTPWLGAHAAKGGVRPLRRALQANPTTQDIGSGFPDTF
>tr|A0A078ETK0|A0A078ETK0_BRANA BnaC07g11640D protein OS=Brassica napus GN=BnaC07g11640D PE=4 SV=1
MDINMQPSLTRIQNIGGEAVYWETTINSYLEDYKPVEGIVIAHSGRSVATLLRFGDVSSG
YNTKTTMQEEWVIDEIAFNVPGLSMDCFIPPSDLRFDSHVEHLSQGPKIKTLQQGSDR
>tr|H9M9A0|H9M9A0_PINRA Uncharacterized protein (Fragment) OS=Pinus radiata GN=0_9197_01 PE=4 SV=1
ETVYWESKMESAMEDYKMVDGVNIAHAGRSVITLFKFGEAALHHTRTKMEESWTIKETAF
NVQGLSMDCFLPPADLKDQTPFSEACDLIVEDRGRSHSNGVSRNAKVAAVERSMDTFDDS
>tr|H9M9A1|H9M9A1_PINLA Uncharacterized protein (Fragment) OS=Pinus lambertiana GN=0_9197_01 PE=4 SV=1
ETVYWESKMESTMEDYKMVDGVNIAHAGRSVITLFKFGEAALHHTRTKMEESWTIKETAF
NVQGLSMDCFLPPADLKDQTPFSEACDLIVEDRGRSHSNGVSRNAKVAALDRSMDTFDDS
>tr|M1CEZ3|M1CEZ3_SOLTU Uncharacterized protein OS=Solanum tuberosum GN=PGSC0003DMG400025725 PE=4 SV=1
MIKHVVFGYFSQRSGLLVYVEDSYLTRIQSPGSPPTYWETTMGTKVEDYRPVEGVMIAHS
GCSSVIITRFGDNLKAGPAITRMEETYTIDDVAFNVPGLSIDSFIPPQGLIKGYPEENLD
WRSPIDR
>tr|H9VSZ6|H9VSZ6_PINTA Uncharacterized protein (Fragment) OS=Pinus taeda GN=0_9197_01 PE=4 SV=1
ETVYWESKMESAMEDYKMVDGVNIAHAGRSVITLFKFGEAALHHTRTKMEESWTIKETAF
NVQGLSMDCFLPPADLKDQTPFSEACDLIVEDRGRSHSNGVSRNAKVAAVDRSMDTFDDS
>tr|A0A0A9NZ75|A0A0A9NZ75_ARUDO Uncharacterized protein OS=Arundo donax PE=4 SV=1
MGKVRMVASEFETATRVVKNRGPSGRGAAAVEQGGFVLWQMAPDMWYVELAVGGSKVHAG
SNGRLVWRHTPWLGAHAAKGPVRSLRRVLQVPQHFEISLPICVSNLPLPEQITSPSSCQL
AMPGP
>tr|A0A0A9JGA4|A0A0A9JGA4_ARUDO Uncharacterized protein OS=Arundo donax PE=4 SV=1
MIAHAGRSAVTLFRFGEAAMSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGSVG
EACELPSHGERAKTGAVHPSRVAAVERTHAHAHNANAGVGGRGEKIVWRVEV
>tr|I1R910|I1R910_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1
MVAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTDIKSGSIS
ETVELPHGEKSKVGLLQCHSAKVAALEKADDNVAWSGALQRDFK
>tr|W5F5V9|W5F5V9_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1
MIAHAGRSAVTLFRFGEVAMSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSIS
ETMELPQSGKSKAGGLLPCHGAKVAALEKADDNVAWSGALQRDCK
>tr|J3M5A8|J3M5A8_ORYBR Uncharacterized protein OS=Oryza brachyantha GN=OB05G17820 PE=4 SV=1
MVYRSGQPGRTNVLPCACKPGLDPKSTADLFSSAAWVCERCIDGDDCFVLRVDASHAALR
ARSSGGVEDSHLLRVRLHGAAAGESAYWETTMESSVGDYRAVDGINIAHAGRTVVSLSRF
DSAGDADADAAARGKRSCTTMEETWSIEEVDFNVVGLSMDCFLPPRDLVLNECKKQQHHH
QKVEDAAGDKDIAGAAAAAKGGSDEGKANGGDTGRGTVARKALVPAVTGLGWFGPAKVVA
VDDTVDDAAPAATDDDKLDHVICSRSRATGGDTGRGTVARKALVPAVTGLGWFGPAKVVA
VDDTVDDAAPAATDDDK
>tr|J3N2K4|J3N2K4_ORYBR Uncharacterized protein OS=Oryza brachyantha GN=OB10G17520 PE=4 SV=1

MRSVHVCMHGASCAVVTKCRCADVAWMQGLDPVTIASVFSAAEHVGEKQVEGEDCFALRL
DVGPSVLSTWSDGAAEVIRHGMTGYFSQRSGLLARLEDSQLTRIQAPGAPAMYWETTVAS
SVADYRAVDGGAVVAXXXAAPSPTWRASAPTSAPPAPSRGWRRPGPSTTSPSTSPGSARS
RSSHRRRGGSAAAATTTPPPSPRSSDVIWDKSDQMVILITLSLS
>tr|B9TME7|B9TME7_RICCO Putative uncharacterized protein (Fragment)
OS=Ricinus communis GN=RCOM_2024700 PE=4 SV=1
VSSSAQYIIQHFTAATGCRKLEGGVKNIFTTGKVSMAMVDELGGSPGLAAGSTGEAQKGC
FVMWQMVPNKWLIELVVNGQKVVAGSDGNVAWRHTPWLGAHAAKGGVRPLRRALQASDIN
>tr|I1QUF2|I1QUF2_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4
SV=1
MAPQLATLAEEPGGGEEAARARRKTGLHAALHRWARARIPLRFLSGGGGGGGVGGGGGGG
RPSPDLRVLLSVLACPLSPVPVLPRHPRNVASSAQYILEQFRATTGCAKIEGAAKSMYAA
GRVRMAMAPEPGGGIGIGGGGGDGHEGCFVVWQLVPDMWLVEMAVAGHAVAAGCDGRVAW
RRTPWLGAHAARGGGARPLRRALQVGTPHVPAIWPF
>tr|Q7XEQ9|Q7XEQ9_ORYSJ Lipase, putative, expressed OS=Oryza sativa
subsp. japonica GN=Os10g0411100 PE=4 SV=1
MAPQLATLAEEPGGGEEAARARRKTGLHAALHRWARARIPLRFLSGGGGGGGVGGGGGGG
RPSPDLRVLLSVLACPLSPVPVLPRHPRNVASSAQYILEQFRATTGCAKIEGAAKSMYAA
GRVRMAMAPEPGGGIGIGGGGGGGHEGCFVVWQLVPDMWLVEMAVAGHAVAAGCDGRVAW
RRTPWLDAHAARGGGARPLRRALQVGTPHVPAIWPF
>tr|A0A0A9E753|A0A0A9E753_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MIAHAGRSAVTLFRFGEMAMSHTKTRMEEAWTIDEAAFNVPGLSTDCFIPPADIRRGAVG
EPCELPPRAKAGAMHPSRVAAVEHMHPRRNAAGDKMHWRVEV
>tr|A0A096SRL3|A0A096SRL3_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.32789 PE=4 SV=1
MHARRNGGITTRASRTSRKLTRLLERSVEASVDGQVHHPAVHCGDGQAALQGVRIMYAVR
RVRMRASEFHLGDQTVTAAQGRGEVGGFVLWQKTPEVWFFEFELIMAGHKMSAGSDGKVA
WRQSAAEHSHVSRGPPRPLRRSPQVTKGGPCAGNVAEDGVQPEASPIVFLLFAGPGSTLH
REPLLGRGAHRREDPQRRGVLHRFILKVEAGAATLRARSAPAFDIITTRPAKALAAARTS
FGTWEASMESVISDYRYIDGINIAHGGHTNVTLFRYGEGSVNRKRKLEETWTLEEADFSV
QCARPHHGLLSAAGRPQGGRRSE
>tr|V7CRE8|V7CRE8_PHAVU Uncharacterized protein (Fragment) OS=Phaseolus
vulgaris GN=PHAVU_001G0152000g PE=4 SV=1
MSALMRKLCPNFDNVDGLETVLDVPIPEAMWTNIGNSGSNRWQNLRSLMRAQTSSPSPSP
SSSSSNPTRVSASSNHEFIALLKLVGSPLIPLQVQSDRTLTRPLKDSSIKASSAKYIVQQ
YIASIGGVGAMDSLKSMCAVGQVRISGSEMRQSGESIKQVGGTEVGGFLLWQKNPDLWHF
ELVVSGLKVSSGSDGKVAWNQSSSQPSRAHRGPPRPLRRFFQ
>tr|J3KUI0|J3KUI0_ORYBR Uncharacterized protein OS=Oryza brachyantha
GN=OB0054G10040 PE=4 SV=1
MEAGGWSAGGGNRRGRGRLGRGTARSLGLDPVTIASVFSAAVHVGEKQVEGEDCFALQLD
VGPSILSTWSDDAVEVIRHGMTGYFSQRSDLLARLEDSQLTHSQALEAPAIYWKTTIASS
VANYRTVDGDAVRTEIHRMH
>tr|A0A096T3K8|A0A096T3K8_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.56627 PE=4 SV=1
MDKERKQGFFAALKEEVVRGLSPSRSRGKSPAPPRSASPARMLIPRRRKAPAAPPPPPPE
KVLEQYLGEQLVARSGSLRPGGEALAPLIEGPDAERLAAGDPDAEDSGRREGFGHWVRGH
LTRTPSMASSAAGGGGGPGGSSGSFRRSDLRLLLGVMGAPLAPIPSKTAEPLPLLSIKGT
PIVRPLVA
>tr|M0Z485|M0Z485_HORVD Uncharacterized protein OS=Hordeum vulgare var.
distichum PE=4 SV=1
MDKERKQGFFAALKEEVVRGLSPARSRGKTPARSASPARMLIPRRRKAQPPPPDKQQQQQ
YLPEQLIPRSGSLRPGGEVLEPLIEGPDADRLAAGDFVGEDSGRREGFGHWVRGHLTRTP
SMASASAGPGGSSGSFRHSDLRLLLGVMGAPLAPISSNLADPLPLLSIKGTPIVRPHLLL

VRVQVMPLLVVHPVLTSPLWEFAGVVVRAVHPAAVHGGVRRLQDAAVGEERLRHGQGADG
GVRVRDGDARRQEPRAQRPRHRCRRAGRLRALDDGPRHVVRRASRRRQQGPRRLQRPPRL
APHPLARRPRR
>tr|A5AJ07|A5AJ07_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VITISV_031060 PE=4 SV=1
MHISTTDPLPHLSIKDTPIEISSAQYILQQYTXXFGGQKLQNSIRNAYAMGKVKMIAYEF
EIATRVLKNWDASKDVDSCGFVLWSEGPAEIIRHVFFDYFSQKMGLLVHVEVSHFTHIQS
NGGNVVYWETIINSFLEDYRPVEGIMVAQSRCSIVTLFKFGEDGFSNAPVXLTVHFSRLL
SVESYESFHHRKPPGMLSFAAWDDLEGILVASLSTKFRMPDIERYTSLCMMLRMAFREDY
GQILPLLMLRGRNQPDDDIYFIDFAELDDHIHMLSWDESKLEPIVADEIYEVGGVTLGPR
IPTPLRLVPDVTPIQSATIKAFTFPYVDEVHTPYVDDVHTLDIQYVIRGGRVALSQIRVE
TTTTLEGLIHMMTAGKATCIVFFDDDLPPESLDHTRPLYISVGCSGHRVSFILLDNGPTL
KVCLLAIAITLSYAPFIHDGQRLGRRQHEPSEFIAIPDHDVPFGLRFIPTEADYRYMARL
RKEMMRARLTHTPFDYLVHPYNMSLADYFVRAPKLQXPSDGIIDLNDGAPNIYASALVAP
SSPDRMSLMTLYFLDEIDEHRTFSEIWDKVNGAVPHNEYIDEMVAMSMSQIDGIVQPEFA
SPFDLFEYLEWLANVVSIPKKDDKVKVCVGFRDLNKASLKDDFPLPHIDMLVDSTIGHSM
LCFMDGFFGYSQILMAPKDMGKMSFIIEWGTYYYRRAATTIFHDMIHRDVXVYVDDMIVK
SQDKADHLAALERFFERIRQFRLRLNPNKCTFRVTSRKLLGYMVSERGIEADLDKIRSIL
DMLAPTIEREIKGFLGRLQYISRFIARLTNIYYETRYVMIERLCLALVWATWRLRHYMTK
YSVHLISCLNPLRCLFDRSALVGRLMRWLVLLTRFDIHYVTQKSIKGSIVAYHSFSLPVF
DGRAIDDDFVDEDIVVVTSLSGWRMYFDGVANHLGYEIGVLLISPHGDHGKWKTRDVKLR
PYHTYFELLVGRFDDLRYTHLPRAQNQFADALATLTSMINIPMDTNVLHFLIELRSVPTY
CCLIDEVELDDGLPWYHDIYRFFRLGAYLEAGTTKDKRALRQLATRFVICRKTLYRQSAD
GMLLXCLDRASVDRVMREVHVGVYGPHMEGHMLARKIMRAGYF
>tr|A0A096SRL2|A0A096SRL2_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.32789 PE=4 SV=1
MYAVRRVRMRASEFHLGDQTVTAAQGRGEVGGFVLWQKTPEVWFFEFELIMAGHKMSAGS
DGKVAWRQSAAEHSHVSRGPPRPLRRSPQGLDPRSIANLFSVAVRTGEKILNDEECFIGS
S
>tr|C4JB27|C4JB27_MAIZE Uncharacterized protein OS=Zea mays PE=2 SV=1
MSPDMWYVELAVGGSKVRAGCNGRLVWRHTPWLGAHAAKGPVRPLRRALQVAFPSRARLD
ACHWLVPTIVCVCVRARVYCAGSGSAVDCGAVRGGAVRGREEGGRRGVLHPEAVGGRGDA
AAAERGSGGDHPARGVRVLQPAHGPAGAGGGLAPDAHPAARRRGRRVLGDHHQLVPGGLP
RGGRRGDRARGAVRRDAVPVRRDGHEPHQDAHGGGVDHPGGRLRRAGPVHRLLHPAGRRP
ARLRLRGRALRAPAARRQGRRRAPRVRRGALAAAAGCGPGRWGAGDKIYRTVEMRFLTVG
DGTDRADSYRKSSTITSS
>tr|A0A0A9NF68|A0A0A9NF68_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MESRLEDYRAVDGVNIAHAGRTAVSLVRFGDCHDGNTRTRMEEAWTIEEVDFNIWGLSMD
CFLPPSDLREGKENQEVAVVKADARPPPIRIPAVTVRVGPSQVAAVNMDDSDSLIARS
>tr|A0A0A9MJ71|A0A0A9MJ71_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MSHTKTRMEEAWSIEEVAFNVPGLSVDCFIPPADIRSGSVGEACELPAHGERAKTGAVHP
SRVAAVERAHAHNAGANAAGGGRGEKIVWRVEV
>tr|M1CL41|M1CL41_SOLTU Uncharacterized protein OS=Solanum tuberosum
GN=PGSC0003DMG401027132 PE=4 SV=1
MGKVKMMASEFIEGDGLGLNNGKVMKIKTAKNGTGEMGGFVLWQKRPDLWSIELVVSGCK
ISAGSDGKVSWRQTPWHHSHASRGPARPLRRSLQVLFFNLDNKN
>tr|A0A0A9PM80|A0A0A9PM80_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MESRLEDYRAVDGVNIAHAGRTAVSLVRFGDCHDGNTRTRMEEAWNIEEVDFNIWGLSMD
CFLPPSDLREGKESQDVAIVKADARPPPIRIPAVTVRVGPSQVAAVNMDDSDSLIARS
>tr|A0A0A9JIE5|A0A0A9JIE5_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1

MSHTKTRMEEAWSIEEVAFNVPGLSIDCFIPPTDIKSGSVSETAELPHGEKSKVCLLPCH
RAKVAALEKADDNVAWSGALQLDCK
>tr|A0A0A9HNW1|A0A0A9HNW1_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MESRLEDYRAIDGVNIAHTGRTAVSLVRFGDCHDGNTRTRMEEAWNIEEVDFNIWGLSMD
CFLPPSDLREGKECQDVAIVKANARPTPIRIPEVTLRVGPSQVAAVNMDDSDSLIARS
>tr|A0A0A9JD11|A0A0A9JD11_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MSHTKTRMEEAWSIEEVAFNVPGLSMDCFIPPTDIKSGSVSETVELPHGEKSKVGLLPCH
RAKVAALEKADDNVAWSGALQLDCK
>tr|A0A0A9ENW7|A0A0A9ENW7_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MSHTKTRMEEAWNIEEVAFNVPGLSIDCFIPPTDVKSGSVGETMELSYGNKSKAVPPAGH
RAKVAALEKAEEDKVAWGGTILENHN
>tr|A0A096RVF4|A0A096RVF4_MAIZE Uncharacterized protein OS=Zea mays
GN=Zm.24093 PE=4 SV=1
MYWETTIASAVSDYRAVDGGVAVAHAGTSTAHLARFGVGVRAARVVTRMEESWTIDDVAF
NVPGLGPDAFIPPEEVRRSRSYGAAIAGGK
>tr|A0A0L9TWT4|A0A0L9TWT4_PHAAN Uncharacterized protein OS=Phaseolus
angularis GN=LR48_Vigan02g109600 PE=4 SV=1
MGKVKVKKMQKKGEVGGFVVWQKKPELWCLELVVSGYKISAGSDGKVAWRQTPWHHSHAS
RGPPRPLRRLLQVVVAAGVDIVERVVALDQMNQSKQLHEATSWLA
>tr|I1JTC3|I1JTC3_SOYBN Uncharacterized protein (Fragment) OS=Glycine max
PE=4 SV=1
KLCPNFDKEDGLDTVLEVPIPEEMLISMGTNGFNSWQNLRTLMNAQFVDKSSGLSTPSNN
EFMVLLKLVGAPLIPLQVPSDHTLTRPLKDCSIRFYCKVHSSAVRGGDGRSSCIEFTGKH
VMNTMIAFNQEAKLKLEALCYGRRTLIYGAWNWLFPLAWNHSSSQPFHANKGPSRPLRRF
FQGLDSSYKRLQAQSTIESMIDDYRYIDGINIAHGGRTIATLYRYGVAHNHKHMIEETWT
IEEVDFNIVGLSMDCFLPPS
>tr|A0A0B2S430|A0A0B2S430_GLYSO 60S ribosomal protein L12 OS=Glycine soja
GN=glysoja_017373 PE=3 SV=1
MAMSHTKTRMEEAWTIDEVVFNVRGLSIDCFIPPAGLRTTSISEACELPQDERAKVSEST
WGTVETWFNSEYAVKSGKDESDVKKEEYLLNEEGHNVVDVFVRVTGGEVGAASSLAPKIG
PLGLSPKKIGEDIAKETAKDWKGLRVTEPERDRKKTKNIKHSGNISLDDVVEIARVMSPR
SMAKDLSGTIKEILGTCVSVGCTVDGKDPKDLQQEISDGDVEVPLE
>tr|W5AN06|W5AN06_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MYWETTMASTIGDYRPVDGINIAHAGRTVVSVSPFTRAAGAVDEADADADARRKRPCTCM
EETWSIEEVEFNIAGLSTECFLPPRDLVLSDSKDQPRHNKEQGDKAAKGARDGDGGCGIR
AAVPKKPLVPVVTGLGWFGPAKVAAVDTLDAADESKDTTYASTR
>tr|A0A0A8Y8P4|A0A0A8Y8P4_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MESSIGDYRPVDGINVAHAGRTVVSLSRFGGGADTEARGKRTCTCMEETWSIEEVDFNIV
GLTKECFLPPRDLIPCESKPVQKKDCAVDHRSKKDAAVVVSDKSAVGAGGPALELKGKNG
DSGVVRPAAARKVLVPAATGLGWFGPAKVVAVETVDADE
>tr|B9SMM4|B9SMM4_RICCO Putative uncharacterized protein OS=Ricinus
communis GN=RCOM_0231820 PE=4 SV=1
MEDYKYVDGVNIAHSGKTRVTVFRYGEQSANHKRQMEEKWKIEDVDFNVWGLTNEHFLPP
SSLKYEKI
>tr|A0A0A9AB25|A0A0A9AB25_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MESSIGDYRPVDGINVAHAGRTVVSLSRFGGGAEDDADARGKRTCTCMEETWSIEEADFN
IVGLSKECFLPPRDLVPGESKPVQKKDCAVDHSGKKDDAVVDAAKSAIGACGQEIEVKGK
NGEGVVCPAAGRKVLVSAATGLGWFGPAKVVAVDTVDADE

>tr|Q657Z7|Q657Z7_ORYSJ Putative uncharacterized protein P0005A05.1
OS=Oryza sativa subsp. japonica GN=P0005A05.1 PE=4 SV=1
MGTPLAPIPLKLADPLPLLSIKGTLIQYMAASGGYQLLQPWAQRPRRRLRRAGRLRFVLW
QMALNMWYVELAVGGSKVHAGSNSRLVWRHTPAAARAGEGKGRRRLRGGVRRRVTEVTAR
LARMRKRR
>tr|C0PN12|C0PN12_MAIZE Uncharacterized protein OS=Zea mays GN=umc2185
PE=2 SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGSRGSTRFGCTNVKAWMRSHAADRSGAGE
PCSMTRGELQLMLGVIGAPLIPLPVYHANQSPCSVLCEQLKADPIESSSAKYIVQQYIAA
SGGEWALNKVKSMYAMGKVRMTAAELNSSDADGHGGSTGNGHHRGGKKGSKGGGVAPDAV
APVARIPRSPAPAPPFAPGPRSAADREPVRGLGVHRRAEHRRRGLLRAQGGGGGVQPARA
QQQQRRDHPAHGVGLLQPAHGPAGAAGGLAPAADQVQRRRRRRERLLGDHHGVPPRRLPR
RRRRQHRPRRPHRRLARQVRRLPGRQHQDAHGGGVEHRGGGLQHLGPLHGLLPAAQRPQG
GQGEPGRRRRQGRRAPAAAEDTGGHRARRALAGGCRQHGRLGLARREVMTTRHVPYVRTY
VLAVLSEEHVFVRDTCVTIRSYMSQDL
>tr|A0A0D3CIA1|A0A0D3CIA1_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MSSFEVSVPSVICSSADWDNKKTKKRNKKKKKGSYEEGSVRFLSESRDVDGSGGCVAVPD
VWCGDKLLLRVRGAPLALIHVSSSDPLPHLSIKNIPIETSSAQFIRQWYTAASSGQKLQN
SITNAYGEAHDDHF
>tr|A0A078CVW5|A0A078CVW5_BRANA BnaC06g19850D protein OS=Brassica napus
GN=BnaC06g19850D PE=4 SV=1
MYATGIMKMSCCETEIAAGKSVKTLSGGGNGRSGDSELALGGTKLISGSDGKTVWRHTPW
LSTHAAKGPQRPLRRLIQATMYQFTF
>tr|A0A0D3CVT7|A0A0D3CVT7_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MYATGIMKMSCCETEIAAGKSVKTLSGGGNGRSGDSELALGGTKLISGSDGKTVWRHTPW
LSTHAAKGPQRPLRRLIQATMYQFTF
>tr|A0A0D3B6V4|A0A0D3B6V4_BRAOL Uncharacterized protein (Fragment)
OS=Brassica oleracea var. oleracea PE=4 SV=1
PIASVIRDVNGSGGCVAVSDVWCSKGLGFSTDAVSMILRGGIFRRRVATRGQEQFEPNRG
DKLLLRVRGAPLALIHVSSSDPLPHLSIKNTPIETSSAQFIHQRYTAASSGQKLQNSIIS
AYGEAQDDH
>tr|A0A0A9NTB9|A0A0A9NTB9_ARUDO Uncharacterized protein OS=Arundo donax
PE=4 SV=1
MLIPRRRKTPPPPPPEKVLQQYLGEQLIARSGSLRPGGEALEPLIEGPDAERLAAGDPDG
EDSGRREGFGNWVRGHLTRTPSMASAAAGPGGSSGSFRRSDLRLLLGVMGAPLAPIPSKL
AEPLPLLSIKGAPIVRPHLDHLLSPVGCCFASTRCVASRRCGLCSCIWYQSLTIPS
>tr|A0A078GW92|A0A078GW92_BRANA BnaA06g13990D protein OS=Brassica napus
GN=BnaA06g13990D PE=4 SV=1
MSSFSLLPTSSNEPTKKKQLGFPRAASFLGMNCTVAAETRVRGAPLALIHVSSSDPLPHL
SIKNTPIETSSAQFIRQRYTAASSGQKLQNSITNAYGEAQDDHF
>tr|M4EAG3|M4EAG3_BRARP Uncharacterized protein OS=Brassica rapa subsp.
pekinensis GN=Bra025771 PE=4 SV=1
MSSFSLLPTSSNEPTKKKQLGFPRAASFLGMNCTVAAETRVRGAPLALIHVSSSDPLPHL
SIKNTPIETSSAQFIRQRYTAASSGQKLQNSITNAYGEAQDDHF
>tr|A0A078ERJ1|A0A078ERJ1_BRANA BnaC09g10290D protein OS=Brassica napus
GN=BnaC09g10290D PE=4 SV=1
MGFHVTNSSLDNVTRVHGVKALRFIKGMSCCILRMSSTTISEHIKLRRVRHQTIRHIAAD
EDLPLTHVVPPIFQPNRFCRDKLLLRVRGALLALIHVSSSDPLPHLSIKNTPIETSSAQF
IRQRYTAASSGQKFQNSIISAYGEAQDDH
>tr|A0A0D3E3L3|A0A0D3E3L3_BRAOL Uncharacterized protein OS=Brassica
oleracea var. oleracea PE=4 SV=1
MAKTASTFVHPIIFLVMFALGCHMGFHVTNSSLDNVTRVHGVKALRFIKGMSCCILRMSS

TTISEHIKLRRVRHQTIRHIAADEDLPLTHVVPPIFQPNRFCRDKLLLRVRGALLALIHV
SSSDPLPHLSIKNTPIETSSAQFIRQRYTAASSGQKFQNSIISAYGEAQDDH
>tr|K7VF36|K7VF36_MAIZE Uncharacterized protein OS=Zea mays
GN=ZEAMMB73_289594 PE=4 SV=1
MSMDFGAPADDPKAFRNICRDRILKDLLKPDKDKETKSSWKVLIMDKFTVKIMAYACKMA
EITDAGISLVEDLFKRREPMPSMDAIYFLQPLKENVIMLLSDMSGRCPLYRKAYIFFSSP
IPKDLVTYIKNDSSMNLEFFTIDMQGFVTDHDTALIDLYGPSEQNSKKFNDTISTMATRI
ATTFASLKLIISRKFHVFCYAKEFPCVRYRAPKGDASTTTKFDMVPKWLATAVWEIVSKY
KSTIPEFPQKETCELLIVDRPIDQIAPVIHEWTYDAMCHDLLEMDGNKYIYEVSKMGSEP
EKKESLLEDHDPLWLELRHAHIADASERLYEKMNNFVAKNKAAQLSRDGGEVSTRDLQKI
VQALPQYSDQVEKLTLHIEIAGKMNRCIREYGLRDIGQLEQDLVFGDAGAKEVISILRSK
QDMSPENKMRLLIIYAIVYPEKFEGDKGEKLMQLAKLPHDDMDIINCLGYLDGSNTKKSS
RTGTFSLKFDAQKKKNAARTDKQDGEETWALSRFFPLIEAPDRGILPLRKPWLYALRVSG
SAQLQDEAILPVHLPLTNTPRTNKHASRHQRIQALEGTWKRANRALDRMGTEPWMLLGVM
VCATEPLPHLNVKDTPIETSSVQYILQQYLAASGGHKLLASLPSTYAMGMVATEFETADR
LTKNNAGHGGAWPFRAVADGP
>tr|A0A0E0MXN0|A0A0E0MXN0_ORYRU Uncharacterized protein OS=Oryza
rufipogon PE=4 SV=1
MAIHPYFRSLMVLGLGYIWYSLAVKNAGVIVGAVYSAAVDGGVGRLPAAALPVGGSKVHV
GSNEGLIWHHTPWLGAHAAKGPVRLLRPRARVLQVRTSHVLNLTPGTGGGEGGGGGERKA
VARRWSSAVAREVAASPRSPRSSPASLACRKRR
>tr|W5ELI2|W5ELI2_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
MRKLCPNLERDDALDTVLEVPIPEEMFSGGGGGSRGSRFGCTGVKAWMRSHAADRSGAGE
PCSMSRGELQLMLGVIGAPLIPLPVSHAKQSPSSVLCEQLKGDPIESSSAKYIVQQYIAA
SGGEWALNRV
>tr|Q5JL79|Q5JL79_ORYSJ Putative uncharacterized protein OSJNBa0047D12.25
OS=Oryza sativa subsp. japonica GN=OSJNBa0047D12.25 PE=4 SV=1
MAASGDYRLLQSVRNVYAMGKGGFVLWQMAPDMWYVELPVGGSKVRTSHVLNLTPGTGGG
EGGGGGERKAVARRWSSAVAREVAASPRSPRSSPASLACRKRRWIGERKEEREREEEMFP
RRGWCCCRTGIRQREAQKHVDKMSKCPDFKGFHRIADAEIQKRFLWFH
>tr|F6I4Q6|F6I4Q6_VITVI Putative uncharacterized protein OS=Vitis
vinifera GN=VIT_14s0060g01650 PE=4 SV=1
MEHCQREGPVEIMRHVSFDYFSWKTSLLDHVEGVHFIRIKFNGGDVVHWEITINLFLEYW
PVEEVLSFEKMALNCGELRKKDRSDLGSLVLPELNRLKDLRLDHENSLGHSLQGREGTGS
AKAKEDSATILGNLCNHSEDIRACVESANVVPALLWLLKNGSSNVKEIAAKTLNHLIHKS
DITTISQFTALLTNDLLESKVYVLDALKSISLNMLPSSLNIYYMCIYKHGFGILFHDDSG
GSGKNLWLTVCFMEGEVIET
>tr|K7K941|K7K941_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1
MDRKQGFFSALKDEVVHGISPAWSRAKSPARSASPISSLLRCRSKHHVPLPKLFIVRSRS
LRPAHMFLPIYLDGDIALPFFLVFSGVGACQCFTPFYPSRLPTLLPFCHSLKNATLYVLL
Y
>tr|W5E2M7|W5E2M7_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4
SV=1
LGVIGAPLIPLPVSHAKQSPSSVLCEQLKGDPIESSSAKYIVQQYIAASGGGG
>tr|A0A0B2PLE6|A0A0B2PLE6_GLYSO Uncharacterized protein OS=Glycine soja
GN=glysoja_049159 PE=4 SV=1
MERKQGFFIVLKDEVVCGLSLVRSRAKSPARSASPMSLLLCCCRKHHVPPPELFIARSRS
LRLARYQ
>tr|J3LW92|J3LW92_ORYBR Uncharacterized protein OS=Oryza brachyantha
GN=OB04G14170 PE=4 SV=1
MRRPAAALPQSPYAAPPTWSSPQSPSTPLGSVAPVPSTAPRPAVAALARLCCPVASAALA
WRTHKHLLQIKSSGHGSVFWETTMESHLHDYRAVDGVNIAHVGRTAISSTSVTAATTTPG
HDTGVAIRIGPSQATDCRNYTRRELPARERREEEERE

>tr|A0A078C7Q1|A0A078C7Q1_ECHMU BnaC08g26650D protein OS=Echinococcus multilocularis GN=BnaC08g26650D PE=4 SV=1
MEESWEIEEVGFNVKGLSSDFFLPPGDLCTKENEESGFSFGDYTSPMMIPLKSQLLKILE
ILND
>tr|A0A087G5C5|A0A087G5C5_ARAAL Uncharacterized protein OS=Arabis alpina GN=AALP_AA8G063100 PE=4 SV=1
MVLEESCRRMVVGEICSQPLEKESSMEEGESCRRMVVEKESSMKEEESCRRMVVEEICSQ
PLEKENSMVKEVVMATQYIIQHFAAATGCKKLAKNTFVTGKITMNMVNDPNFSAAVGTAS
HVSHKGCFVMWQMLPEKWKIAWRYTPCLGDRCSVKHQMNISKNKQEHIN
>tr|M0Z484|M0Z484_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1
MASASAGPGGSSGSFRHSDLRLLLGVMGAPLAPISSNLADPLPLLSIKGTPIVRPHLLLV
RVQVMPLLVVHPVLTSPLWEFAGVVVRAVHPAAVHGGVRRLQDAAVGEERLRHGQGADGG
VRVRDGDARRQEPRAQRPRHRCRRAGRLRALDDGPRHVVRRASRRRQQGPRRLQRPPRLA
PHPLARRPRR
>tr|D2HUX3|D2HUX3_AILME Uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=TOB2 PE=4 SV=1
MQLEIKVALNFIISYLYNKLPRRRADLFGEELERLLKKKYEGHWYPDKPLKGSGFRCVHI
GEIVDPVVELAARRSGLAVEDVRANVPEELSVWIDPFEVSYQIGEKGAVKVLYLDDSEGC
VAPELDKEFKSSFNPDAQVFVPIGSQDSSLSNSPSPSFGQSPSPTFIPRSAQPITFTTAS
FAATKFGSTKMKKGGGAAGGGGVAGGGASGPQPPQPQPRLARSPTNGLLKHRSLSLSLHS
LNFIAAAPAPQSQLSPNAKEFVYNGGGSPSLFFDGADSGGSGAGSCNSSSFDVAQVFGGG
ANSLFLEKTPFVEGLSYNLNTMQYPSQPFQPVVLAN
>tr|A0A0B2SB96|A0A0B2SB96_GLYSO Uncharacterized protein OS=Glycine soja GN=glysoja_037881 PE=4 SV=1
MDRKQGFFSALKDEVVHGISPAWSRCIAHILAAPLSQFV
>tr|A0A058ZFM5|A0A058ZFM5_9EUKA Uncharacterized protein OS=Fonticula alba GN=H696_01675 PE=4 SV=1
MPLDSPAPYNDSSNFSIYSHVRTRAPASGRRGDSHPSPIGSPGSLAPVAPASGGSLGLKP
AGQPPLSQQSDALLGFAHQPPHTLTTNQILARMAILPEPMPAVVFEQIRRFDAIFSSQKA
ALADKHMPDRKRISDSPTQGLSPGSLGETTDAESPSDSGGSISKGTGLLSSTTPPTTAEH
SPPPLKRQRSDRRSSSTGTGTGTGTSAAEGGGASHPSSPDLRSVAAFPARDPSPRRHLGS
DVSRFHRGATAHAGDSGTGPGTATSRLRPDSASEIDTLDRPRSRSQSDATRDLDRPAASR
PRRPEIRVTPSRSPSPRPRSRSRTLRSWSRSRSRSRSRSRSPSRPHSQSQSRSRSRSPPS
VARRASASRRGAEPESRLPPRPSPRSRASSDEMDHLRRPSPSSSSSSSSSSSSSSSSSSV
PSRGRRPSISPSSPRSRRSISPGPVTARRRRSASPVPSSSRGRRSVSPASDLRRSRHPRR
AADQVPFNWESDDEAPDAERFDRARADQQAFTATDTRPARPNSAPAGRPAGRTTNRGLSS
DLDNGGNSTDEESDTPRGRARSGPTRLAASDDRVSRRDRVIGNGRSRSVSPGDRPRKRPA
GTRPGSRLRDSSTHDPRDDPPPRQARTGRVSGGDGMSAVAPASAVGPPSPERDHLLLSRQ
LRSLGDAVISTQIFLQRFREARNIPAMVTRLQERMRSAPADRDYSSEGLLQILRRYLFLY
LCSAVLFLQHDQKNATLWPAFSRYIFRLRNQGYDLIQQLGLADVASANGRALAISLQLLS
LITSCYLKAHFSLRVTHLLQKRIPSDPICSLDMDEDDEPAEQLASLLLGCDTSADWALVA
GLRQDHTSIFQQLFGRLRPFSLHDQPSAFGTFVEEAIERLNQLHPPTSPADLASDDALFR
TGPVPDFSPLNHVQLR
>tr|Q02AR5|Q02AR5_SOLUE Uncharacterized protein OS=Solibacter usitatus (strain Ellin6076) GN=Acid_0852 PE=4 SV=1
MTRSLKLGAALAFAAAIVCAADLPKGEALLDKYIEATGGKAAYAKIHSDMTTGTMEFKAM
GLKGKVTTWAAEPDKKYSEVVLGGIGKMQEGVNDGVAWSLSSMQGPHIKDGDEKAETLLQ
AKFNSDLNWREQFKSAETVGVETVDGKECYKVVMTPKTGSPSTRWFDKDTNLLVKLSMTT
KSAMGEVQSESVVSDYRKEGEVLMPHKINSKVATMELVMTVESVQHNPEIPKDKFDIPEE
VKALVKK
>tr|M4ERY7|M4ERY7_BRARP Uncharacterized protein OS=Brassica rapa subsp. pekinensis GN=Bra031564 PE=4 SV=1
MDGGFPNNRAIEGSEVVIAHSGRTDVLISRFGENLKGGISVTRMEERWTLHRLFYSA

>tr|W7Z8T8|W7Z8T8_9BACL Endonuclease OS=Paenibacillus pini JCM 16418
GN=JCM16418_5109 PE=4 SV=1
MARKGDYYPLNDYSIKGDYAALHFINKKREELEILVDMAVLDYLIKINHHWRATYRKKTD
SYYAQTILHNQKLIEQYKTRTPYLHKIVLEADASQNQYVHHKNHNTLDNRISNLEVTTNE
NNSKDRNGQNKNNTSGYRNVCWNKNVEMWMVQLQIDGENTRLGYFDDVHEAGKFAERMRK
KYYGKYAGKNRV
>tr|A0A022TUW5|A0A022TUW5_TRIRU Uncharacterized protein OS=Trichophyton
rubrum MR850 GN=H100_02390 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A022XZV0|A0A022XZV0_TRISD Uncharacterized protein OS=Trichophyton
soudanense CBS 452.61 GN=H105_02408 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A022VEZ7|A0A022VEZ7_TRIRU Uncharacterized protein OS=Trichophyton
rubrum CBS 100081 GN=H102_02387 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A022YWA7|A0A022YWA7_TRIRU Uncharacterized protein OS=Trichophyton
rubrum MR1448 GN=H110_02393 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG

YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A022W998|A0A022W998_TRIRU Uncharacterized protein OS=Trichophyton
rubrum CBS 288.86 GN=H103_02398 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A022X4B8|A0A022X4B8_TRIRU Uncharacterized protein OS=Trichophyton
rubrum CBS 289.86 GN=H104_02374 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A028JXE2|A0A028JXE2_TRIRU Uncharacterized protein OS=Trichophyton
rubrum CBS 735.88 GN=H106_02178 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRH

QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A059K7N2|A0A059K7N2_TRIRU Uncharacterized protein OS=Trichophyton
rubrum D6 GN=H112_02389 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A023ALR2|A0A023ALR2_TRIRU Uncharacterized protein OS=Trichophyton
rubrum CBS 202.88 GN=H107_02470 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMQYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSSYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGHVKGKRRLHLSLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPISLFILFTLAAFALLVTYIILSYLHERRVGAGYDPRGHYYGP
EVIDDDERSHRNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSRS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLVGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRHHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPGGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKQQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRTPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHPPSQSRAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|W5QJ97|W5QJ97_SHEEP Uncharacterized protein OS=Ovis aries GN=TOB2
PE=4 SV=1
MQLEIKVALNFIISYLYNKLPRRRADLFGEELERLLKKKYEGHWYPDKPLKGSGFRCVHI
GEIVDPVVELAAKRSGLAVEDVRANVPEELSVWIDPFEVSYQIGEKGAVKVLYVDDSEGC
VAPELDKEIKSSFNPDAQVFVPIGSQDSSLSNSPSPSFGQSPSPTFIPRSAQPITFTTAS
FAATKFGSTKMKKGGGATGGGGVASGGAGGPQPPQQQPRLARSPTNNLLKQKSLSLSLHS
LNFITANPAPQSQLSPNAKEEGADGPGSGSPASFGGSGAGTCNSSSFDVAQVFGGGANSL
FLEKTPFVEGLSYNLNTMQYPSQPFQPVVLAN
>tr|D4D6S9|D4D6S9_TRIVH Uncharacterized protein OS=Trichophyton
verrucosum (strain HKI 0517) GN=TRV_02806 PE=4 SV=1
MQILTLFLTTVVFTLGWFAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGRVKGKRR
LHLSLELMQIHHWLGRALALLGIAQIPLGLTLYGSPLSLFILFALAAFALLVTYIILSYL
HERRVSAGYDPRGHYHGPEVIDDGERSHGNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRS
RSRSRSRSRSRSRSRSHSPDTAVTPYINEKESHHGGWGKKLLGVGALAGLMGLGKKAFNK
RREDDYSESGYHPAHTVTDSYDDSISRVEEGRPPQPPPHRHQGQYHGAPSEDQTTSYTDT
DYYTHTEDSRPGGGGGGGHPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHER
IARANSKRKHQGERRYDRPHSPSSELAASDAAPGPSGTAGRPPPPAASSVTDRPPSPGRK
HRSHHRYPSTLGVGTAVAGAAETAGSGHRRRSGNRGEDAYDSPQVAITVKPEGRHVTLRQ
LTKEEKRAEREARRREHRRQGREGSFSEDEHWRRVEERERQQAQEELHPPSQSHAPSHSP
IPAPAHSHVPSHSQVPESQLNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHS
PGTVSTDLSGSYASRSGRRRAERRIARSQRQHSVDWT

>tr|D4AJU8|D4AJU8_ARTBC Uncharacterized protein OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) GN=ARB_04548 PE=4 SV=1
MQILTLFLTTVVFTLGWFAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWVIHGRVKGKRR
LHFSLELMQIHHWLGRSLALLGIAQIPLGLTLYGSPLSLFILFALAAFALLVTYIILSYL
HERRVSAGYDPRGHYHGPEVIDDDERSHGNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRS
RSRSRSRSRSRSRSRSHSPDTAVTPYINEKESHHGGWGKKLLGVGALAGLMGLGKKAFNK
RREDDYSESGYHPAHTVTDSYDDSISRVEEGRPPQPPPHRHQGQYHGAPSEDQTTSYTDT
DYYNHTEDSRPGGGGGGGHPVRNALLGAGAFAAVKSFFGRKSREDRRVEQIRQEDLEHER
IARANSKRKHQGDRRYDRPHSPSSELAASDAAPGPSGTAGRPPPPAASSVTDRPPSPGRK
HRSHHRYPSTLGVGTAVAGAAETAGSGHRRRSGNRGEDAYDSPQVAITVKPEGRHVTLRQ
LTKEEKRAEREARRREHRRQGREGSFSEDEHWRRVEERERQQAQEELHPPSQSHAPSHSP
VPAPAHSHVPSHSQVPESQLNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHS
PGTVSTDLSGSYASRSGRRRAERRIARSQRQHSVDWT
>tr|F4MJ47|F4MJ47_SHEEP Transducer of erbB-2 2 OS=Ovis aries GN=TOB2 PE=2 SV=1
MQLEIKVALNFIISYLYNKLPRRRADLFGEELERLLKKKYEGHWYPDKPLKGSGFRCVHI
GEIVDPVVELAAKRSGLAVEDVRANVPEELSVWIDPFEVSYQIGEKGAVKVLYVDDSEGC
VAPELDKEIKSSFNPDAQVFVPIGSQDSSLSNSPSPSFGQSPSPTFIPRSAQPITFTTAS
FAATKFGSTKMKKGGGATGGGGVASGGAGGPQPPQQQPRLARSPTNNLLKQKSLSLSLHS
LNFITANPAPQSQLSPNAKEFVYNGGGSPSLFFDGADGPGSGSPASFGGSGAGTCNSSSF
DVAQVFGGGANSLFLEKTPFVEGLSYNLNTMQYPSQPFQPVVLAN
>tr|A4FUY5|A4FUY5_BOVIN TOB2 protein OS=Bos taurus GN=TOB2 PE=2 SV=1
MQLEIKVALNFIISYLYNKLPRRRADLFGEELERLLKKKYEGHWYPDKPLKGSGFRCVHI
GEIVDPVVELAAKRSGLAVEDVRANVPEELSVWIDPFEVSYQIGEKGAVKVLYVDDSEGC
VAPELDKEIKSSFNPDAQVFVPIGSQDSSLSNSPSPSFGQSPSPTFIPRSAQPITFTTAS
FAATKFGSTKMKKGGGAAGGGGVASGGAGGPQPPQQQPRLARSPTNNLLKQKSLSLSLHS
LNFITANPAPQSQLSPNAKEFVYNGGGSPSLFFDGADGPGSGSPASFGGSGAGTCNSSSF
DVAQVFGGGANSLFLEKTPFVEGLSYNLNTMQYPSQPFQPVVLAN
>tr|B0W710|B0W710_CULQU Putative uncharacterized protein OS=Culex quinquefasciatus GN=CpipJ_CPIJ003108 PE=4 SV=1
MPLLLLAKAASAGSVSSNCSSSSSSVSSDGNGLVISICATIAFMDIKSASKAHTAEHKFD
DRILTTEYYEPSLLLNMPPAVAPSTAPQTTNAPPTVNCSTTTPSGDSNNGSAMQKYAGNT
AAGSLGSNSNLQYSSSVTAAAAASNAISNNCINGGSVVVCKSDSLSHPCSSSSSTSGKLL
GFSDDQPQLQQQHNSSLYECSNNGNSGTGVSSSIRTANFTRLQGDLDAGQCNAGPGNING
RRLSVIDGGLLNRGRPRDRQHYRNGPYAAPPTTANPTTTTLLPESWYNGNNSSSGSNSGD
NASISGPAVAAAPATGPVTPTGSNPPPPPPSSAATLGASVINVNNNNSYDSFLVKSQNHV
VVGGHFAANHNRSRSRSRSHSPSSSCSSTNSTTTSQSNETSSTTRSPANVLLLGGGGNSR
EARSDRLDQQQQSAVRGSLQSAVASVSSTNNGGNSSGASSSSGSGGGNLNCHSDDNRPLA
ICVRNLPARSSDTSLKDGLFHEYKKHGKVTWVKVVGQSTDRYALVCFKKPEDVEKALEVS
HDKLFFGCKIEVAPYQGYDVDDNEFRPYEAELDEYHPKSTRTLFIGNLEKDITAGELRKH
FDCFGEIIEIDIKKQGVSAYAFCQYSDIVSVVKAMRKMDGEHLGSNRIKLGFGKSMPTNC
VWIDGIADNFGEGYLKSQFDHFGAVSQVTIDRERKLALVFFEQVQCAQAAVKEMRGTTLR
GRKLQVDFASRECQEAFFDKLDKQLSVSFGSPRFEAGTGSRYANNRYVDNPGRSRATSFS
RPGNPLSLSGAVSPRHDPSPVASSRGGAGGNSSSRSRIVRYSSEDYYLDGGGGGGSGGGG
PNSHGNSERRFRSYDEYSQGSAASSHEDVYDHESYGGASGTHPRSSAHDRPQPTSTSDSP
PPSVTSSSGLSSSIQSRLGDVDPSVALSRKRSEKSPASASEAVSSGDPAALSGTNNSSGG
GGGHHHYSGSNNSSNHYNSHHHHHHHNNSESGVQSSGHRNGSGGHSYSHSLNKRRKTILN
SDNSMTVIASAGSTSVSSNEHHHSSRGRGHQLHSIHSHEASGGESADGSRPGTPLCDERP
ENLPPSEPRRIPTSRSYNQEPLSLPLPRFAIQFLQQYRLQQQQSSSASSSSTASSSSATS
ALPSSTTSTLFPSAAVSSSSSTALSSSLHSASAATVIAASSGALPAALSSNSSLLHNTLS
SPPPTHSSKLSLLIPPSVGVAAGSGSGSSITTGNTPASASTTNSLEHGSNQAPASPLRPP
SISSNSSDSESGPSTSPSLEERINKLDEMYEKWSGNSQTRLNNAGNEHHFNNDRHHIQPA
QPLPQLQLQHVYAGHNHIGSGNNNTGSLNQSPISNVSSSSTSSFRHKFLELDVKEVPPSD
IVKSLLSRKSIFDEDLKRLENIGDKYEPGVLVNFPKNPVTTTLNTVAIASTTNPTVVSPV

VNTAILASQSPLHALKAQTPPAPSLQRIGSCSTSGSPMNSPQPYNSPNPSVKSGLQYPFP
SHPPSTGSVTPPAPPPATTTTGPTVAPPPPPAEAKPSSEPSTSEQQQVPPPKHNKINKVN
HHGHGHRHSCDSTSSSSSSSSSAPHKAGHHSRNATDNSSSTDFDRLKQDVRPNAVVNCRS
ASVEKREQEPRKTSTSSSSEGKPEEEPKRKVEETPVKEPEVSKPKEPEEREHQATQNHCE
DMEIGEQQQDKQCDKEEPLDDGQHKERRDRVSSVGSNSSVRNSSKRRHNSHDSNDSPTED
SHAQKKHKQNNLDSSRIFERRDSGKDGKKEKHHKSHNRSEKSSKCSSVSSCSSEKSVSHL
NALAKHDNHDEKQQFLLDERRKEITFSNEGQLQQHSHHQKKKERYHDKHKSKKDHESCRD
KENTQSVNFPQESFTGNRSTSDEEDHTRTHHKADRKCPKDYAAKRYHSESGGDTKKYDRK
LSRAESSADEEGRKKKNRPNHTRAKTANNSSDTDDSDEPKKHSIFDIPDDPMPNISMYDK
VKARSCKNMQKQEEEKKIKEKFSKLKQCRAKREGKNRSKSWDDDSDSDANSDTTINSKYN
HKDQLNKSGMITTSDDDDQMPSTPRFRRHNKEHLASDSEDENHRIRFNRDRLNNLCDDES
SDGDRPKKENMPHTPRRSSSEKKMSRKNSRSTRIQSDSDSENESTMDQAKTAHENQDSEC
DKPKPAVEDPEKAQSAIPKIEPSSIKQEIKCEEDTPAEETKKVEIKVETKVQPPSALVTS
DVSDDETVKPAVVKSEFIPSTMIKKEPIDDGYSYSKERLNQLCDASSEGEPNMTPVVASA
EIDNTVNSAVDQLMYGHPEAAKRKHKKKQKRHKTNDGSEGENKPDKEHSPTSDGLAGSTF
DNLKKTADDQLYVSSKKKHGGKKEKRRERCKEDYDKPGKSKKSKNKHKENNNKVPEVPNP
NTKREEKMEDIFGPISDDESQHSSVETEVSVKQEPVDADNEVKPAEEESKQADDRPNDSE
VSEKDKLKEESRKRKERKRREREKLRTTMTMKEEENSVDLDEAGRALEAQLMSDSDQKAE
DASPTSTVGTSGKRSSVDVMDVFRFTDGDDSMENSFSEKKESDHGRKEKKKKKKRGKDEK
HKHHHGSSNNIPPTTTPISPTTSKLSLDIISAQQDDSKNSISKPSPSLPCLLDESPPSSN
LHHASTTASGPMSPPTPTGREMACSTPTNLEEATVTKEENPSAREVESCSKQAKQQRKPD
KLIPGFGTDMDEQIHEKAVLSISGDFINEKIASDDRKPTDIVDPLKHKADDMKIEEKSRV
VISQEETEDAVAALLGESFGTSNTPDFSIDYSIDPVEESSSQLVADTPQIPEEDDEEMKN
AILSLNTEEHIKLDIKPDTPQSEHDLQIDTDTDDQAEDEHPASLLRFDNPPKTPDVDLSQ
IGKPLSESITSSSAPDSVKKEDKLEMPDTPGKNVSTVSSSASTTTPIQSPIATSSVISKV
TTSTESGTIASTASCTVPTTTSTKPTVAPVQAPIIAQPPVIPPATTIAMIPESPAKIVST
ATVATASKPMTVFTSTPSPMQVKPTPVDTQKTPVVSSQPATAPPVVRNPYVMLAPPTINI
PEQHVVYQPSDAVSMSPRGSNGGDIRMQSPKLQQIQSSIPFTKATSPTSPNLLRPQQIIA
NRQSPQHSPGLNSHPTILHSASGGHMLVSSPTSSGQFAPKPNHIVQPRFPVVTASPMKIN
VPQQKPLEQQPVLLKQQQQPVTSISPVVQMARVATTMAITSMPMMETPGPTVTVSAAPMP
TKGMDVTQKTTLPGTPTKTIIHQTPVYIQHPPSKPMVTAVQSPVRLQPTHPNMVVAKPLV
VESKPLNTISTITSNPNHNVQSEMPVESKSDGKELLASTEPQRNQPEATTIQKSGPTTTG
STDASGKKSAADSLLTEENVSKIPDSSNATSSVLGIDQEDQEGDSKEDSDYWSSKDTIID
SVIKKVDALCSEDDASEGGLELNREEWSKQESEALKTSTTNPVPSMPPVPEPTKVEVVQA
PAQPEPPVVPAASPIALIQPPSQTQMQSVVQRTPPPPPAPAVHVEEAEDHEETVTTAVEC
PIPETSTRGGKRGGRRGGRKTSESLTTPVKMPELPEATTTPAKRGAKAGAKRGRGGGRGG
ARGGAANVQPTPGVGGYKGKNFNSGSDVYEFHDDSGEEVQSSDKQLQDGGRPRLILTIKN
QVTTAAPMPTTSTVPVAVTVASLAPLNVTNVTTINTSTAQLQPTTSCPAPLLPVDPHNNP
APAVDGSKDDFVHPSSNTRKSRRLLEKDGRTTVDDIIDDVIRNGPSSVEPPTPPMQQQPP
PMPTPPVGGFGQFQPQPVSIPTSQPGNQPLPQQQIQTQLQPLPVAADQPGRRATRQNVTP
VTGAGTDARKSPRAGRKGKNRTISESSSVDSSDEKPVGLAARPNLGDAKTEEKTQTATTP
ITPTLPVTRPNETASLADKSKEKPKSAEDFKMEFGNSQALGPLTLIDPVTGELTVMRTGK
EGQYVPLPNANAPQPLKKVIAAAAQSAEQMKSNASSPTPPISASASPVQHRTPTPGSVPS
PGMTRVPTPNAYPVQQQLEVQKMNKQSSPLPLTLQNQMNPTASAVVVPSPHSNTGTMVIQ
HSQGPPQVQQPVGVMQQQQQGPPSSKPHPLKQHVLNAQQIMSQQQPPNAGKHIQQQQQHP
VGNQQQIIFKSAIPMTSQTPSSGAIHTTTGKQIHPSSNIKMAPQIIQQGGPPPQHTQQII
IQNAMSQQSMTINKHTTTIINKQGQPQGHHQPGSGNLLINIPQNMQQQLGNVPMSPRMQQ
QQQQHHQVVITNSKPGPMSNQQQQQQQQQHSPHIIHKLPPGQSQPQPQQIIIQGGKIPPG
HHQIPMGYTTVVQSGTKIIHQSTLQPGQGQPGGPQQQPMPGKHATQTIQIGQFHGTQTSQ
PPTTVVQKTITTSHGGQQQHIRIQQQKIGGPEALSHLQPVHMIGKQQLIQPPMGTAVGSK
MLPQQPSQMHQPVGLTKLNHVGPVGNQQQQQQPQQLTIQQQQGKGGMPSHLHQQPPQGIP
GQIMTGAVASPPLKHMHSQQPVGASSSRVAHPAISPQGMPPGPQQQPPPGSSSTLRHVQG
PGLNVPPQVAYEANPTDAAFRSGMPRDYVKYIYARNTIHMPSRSPLLPGSVEQRELSEME
DSVAASPPLELRRPSSGPRPTTSVPPSLQSPGDRSTDSPQVAQVYIGSARIPHTYSDSLN

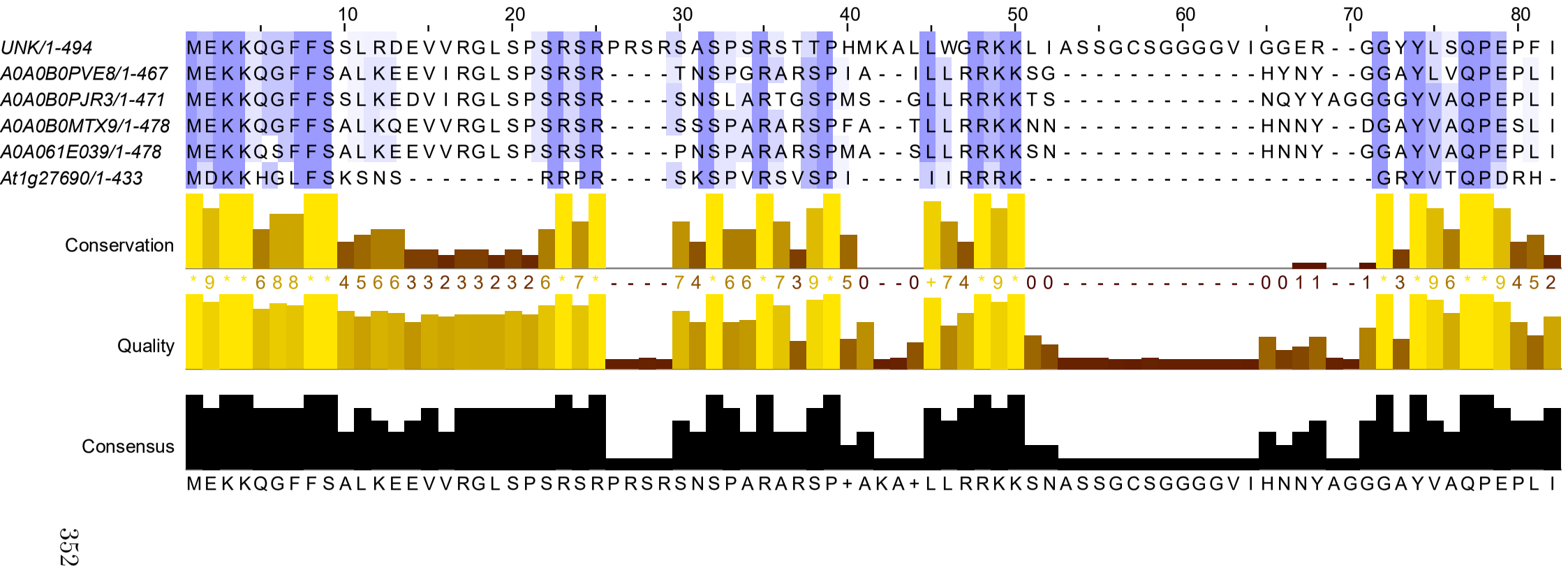
TRFYDPAASGPNGPPRALSTEPPPAHHRPHNLSTSGGSGFPPGSSYPGTPSQTPPPASPA
NLSQLQPQQQQQQQQQQRDRDLLQQRDRVTMPGSYDQLSDRYSYSLSEYECNDYINPPDS
GHAAAATVGAGAIPIQASPLPAHSGGLPGVIPNTGRNAVVPPISVASGSSSNTGTLVPSG
QQQPTAVPSQSDSLDQLLQRYPVMWQGLLALKNDQAAVQMHFVHGNPGVAGSSLPSNSDG
TTPPLRIAQRMRLEPAQIDGVARKMQMDQEHCMLLALPCGRDRMDVLQQQNNLQTGFITY
LQQKQAAGIVNIAAPGSSQAAYVVHIFPSCEFANENLARIAPDLMHRVANIQYLLIVIAT
V
>tr|A0A058Z0R8|A0A058Z0R8_9EUKA Uncharacterized protein OS=Fonticula alba
GN=H696_05845 PE=4 SV=1
MPDLLACPALRQTPERLEPKRAYRKEKLLGMSTGSAGSLAKRFTSLLRPSSSKHSSAGTP
VPDAGRPSAGGRPLTRTHSGSSYSSGTFNQYEEPSSRKSSSSSGSFFRQHHHHHHHVGPD
GAGVFHSQPSLSSPGSALGSGSALHQPQPQPSAGPWFKRNHSASSHHLHGGFAAGHTQNA
LPMGDPGPEERAGYAVHPRGLSDTTDPASSSSSSLSSSSGGAGGSRKRSGNWSFSMARSS
TRSSFNEGSFSPPGGTSMGSGWPGASSEPRRMSEDSSAASMHTTIIEEPTSEGRFAGIPA
GGPSATTPSTTAAMVVPPPCSFLHDREADFDVAHTGAEGGDHGRQDRRGSVSSAASASLG
LGTVSPPPGGLHASAENPATSAPEMDPALSWKKRISISVKKKRRDPALSQ
>tr|A8M3S5|A8M3S5_SALAI Uncharacterized protein OS=Salinispora arenicola
(strain CNS-205) GN=Sare_0933 PE=4 SV=1
MAPSTAVATRKREWGMVKAKELTGDESSWNWKQIKAAVNGGSEIPAGDSSAHEEARGVSN
PESFFRLAQSFARVQATLALCRDVTQLHSHAIAGDDRPWQGGAADAFNRSMKWTVGVLDS
HIDQITAAADKDRPEQGSIIESLVAAGNRLAYSRAVLDAIDSHYASEARRLGVEPMDNGL
IPVSKRPDIVAMMDRDMRAEFERLNEQYSLTVNDLRPPPPEEPPTTDPLAPPGEGPVTDP
PPLPDRDPSTRPDMPADWIPNGASPDSFPTTEPPGGLSDSSSIGSPEPVSGTGLEGPFVR
PFDSPNGADPLLDEPATPFSEPTLGPGDTPAMDFTPATTLAGADALTSPTAFPGGTVSPA
SSTGIGSFPGGAGSPAAAPMSHSAPLPAVPLSTPAFNARESPAARAPKLGGVGGGAPVPF
VPGGAPGSGSGGGAGSRRPRVSGVGGGAPVPFVPGGAPGSGSGGGAGSRRPRVSGVGGGA
PTPFVPGGGPASGGNGGSSLRRTRPFVGGPGGIRSSSTGSAPAPGAGKVEGTDRLRPGSG
GTGVPFAGAPATTATGKEASRERKTWLVEEDDVWGADPDSPAGPIGRPGA
>tr|A0A022U6E5|A0A022U6E5_9EURO Uncharacterized protein OS=Trichophyton
interdigitale H6 GN=H101_06902 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMRYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSPYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGRVKGKRRLHISLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPLSLFILFALAAFALLVTYIILSYLHERRVGARYDPRGHYHGP
EVIDDDERSHGNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSHS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLMGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRRHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPDGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKHQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRPPSPGRKHRSHHRYPSTLGVGTAVA
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHAPSQSHAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|A0A059JG69|A0A059JG69_9EURO Uncharacterized protein OS=Trichophyton
interdigitale MR816 GN=H109_01712 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGLNFEAMRYNGMGNRFKNLPG
YHSIIRAHGALAAITFLGLVPISILLARFYSRSPYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGRVKGKRRLHISLKLMIHHWLGRAL
ALLGIAQIPLGLTLYGSPLSLFILFALAAFALLVTYIILSYLHERRVGARYDPRGHYHGP
EVIDDDERSHGNFGRLAAAGAAGAGLAMLGNQLRGGRGRSRSRSRSRSRSRSRSRSHS
PDTAVTPYINEKESHHGGWGKKLLGIGALAGLMGLGKKAFNKRREDDYSESGYHPAHTVT
DSYDDSISRVEEGRPPQPPPHRRHGQYHGAPSEDQTTSYTDTDYYTHTEDSRPDGGGGGG
HPVRNALLGAGAFAAVKSFFGRKSKEDRRVEQIRQEDLEHERIARANSKRKHQGDRRYDR
PHSPSSELVASDAAPGPSGTAGRPPPPAASSVTDRPPSPGRKHRSHHRYPSTLGVGTAVA

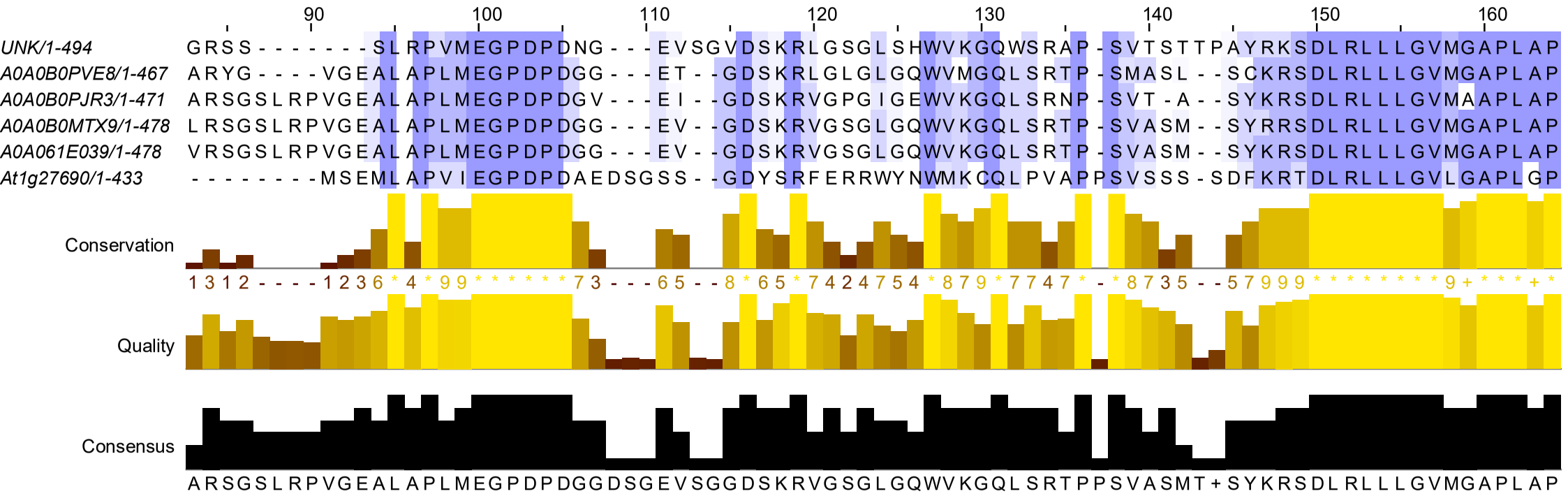
GAAETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRR
QGREGSFSEDDHWRRVEERERQQAQEELHAPSQSHAPSHSPIPAPAHSHVPSHSQVPESQ
LNPPHSPMPQSSAHPPGSVAAPSSIPAPPPPLPISHAGLHSPGTVSTDLSGSYASRSGRR
RAERRIARSQRQHSVDWT
>tr|E4V075|E4V075_ARTGP Putative uncharacterized protein OS=Arthroderma
gypseum (strain ATCC MYA-4604 / CBS 118893) GN=MGYG_06012 PE=4 SV=1
MSNSGLGPPGTGTYASNVLNVGDGTWDSQRNTFLLPNLMGINFEAMQYNGMGNRFKNLPG
YHSLIRAHGALAAITFLGLVPISILLARFYSRSPYWALRLHIWMQILTLFLTTVVFTLGW
FAVGPKRSLTNPHHGIGLAIYVMVIAQTFWGWFIHGRLKGKHRPHLSLKIMIHHWLGRAL
ALLGIAQIPLGLTLYGSPLSLFILFALAAFALFVTYFILTYLHERRVGAGYDPRGHYHGP
EVIDDDDRSHGNLGRLAAAGAAGAGLAMLGNRMRGRGRSRSRSRSRSRSRSRSRSRSRSP
DTALTPYINEKESHHGGWGKKLLGIGALAGVFGLGKKAFDKRREDDYSESGYHPAQTVTD
SYDDSISRVEEGRPPPPPSHRRHGQYHGAPSEDHTATYTDTDYYTHTEDSRHDGGGGHPV
RNALLGAGAFAAVKSFFGRKSKEDRRVEQLRQEDLEHERIARANSKRKHQGDRRHARPHS
PSSELVASEAAAGPSGTAGRPPPPAASSVTDRPSSPGRARRSHHRYPSTLGVGTAVAGAA
ETAGSGHRRRSGNREDAYDSPQVAITVKPEGRHVTLRQLTKEEKRAEREARRREHRRQGR
EGSFSEDDHWRRVEERERQQAQEELHAPSQSHAPSHSPAPAPSHSHVPSHSQAPAHSQAP
GSQLNPPLSPMPQGSTLHPPGSIAAPSSIPVPPPPLPISHAGLHSPGTVSTELSGSYASR
SGRRRAERRIARSQRQHSVDWT
>tr|G9NIF3|G9NIF3_HYPAI Uncharacterized protein OS=Hypocrea atroviridis
(strain ATCC 20476 / IMI 206040) GN=TRIATDRAFT_315102 PE=4 SV=1
MDFWSRLLSPLSSGSSRQEQAKDPAKRLHRFEKEYAGLLSIWRKSTNLSQDIDAAETVEI
RLQELTNILSDESRRPLPHPCIQYASIKQIYVPIGKIATSSYNEWIIKEAVLFFATLIES
EEEAFVENHTFSASLTNLLVRITGVNSARLGLDTESRVVELAFNITTKIRLDPEILPAWF
KTQQDVNRPSDRAASVRDKFAGRTKRADFPLFYILMDYIHHEGKVGDFARTGLLYIIEAA
SSSESLEQWIVESDLSTLMATGLGALYSQLSRKLVIDHLPNNLPPILALSDYQHPTSNYE
IVSSCSGEFQSHLETFLSHLLFWQDVLNHCKSVEVKSTLLEHFQVIFLQQLLYPSLLESS
DIDGGSSVAVLTYLRRIIESLDHPDMINLILHYLLALPETVTSNSPPSGTAISAARQRKS
MDLATMMAEKPDTTATPLLFNLVDLILACLRSRNQQTIYVTLQLVSAIVKRHHRYAVLTL
LQTDMFPSNNINRTVGAHEQEIEYLMALAETIGGRGDFDETYESILKDTMARLESHPCSL
RLVAPRLSQHNHKTPTIPDSLPGAPKDVREHTLRSDDLLLNSILDLMENFFMNPVETNLS
VTDTIVDMAICGYMSIEGWLARNPKSYTYAGDEQQPEPEKGIETKSQQEGEGEEETETET
ETETEKGDDADTEPGNKSLADELGSQDGDSSDGGFSTFTDDTEAERLESMEKCRRRPKWT
QQSLPRILIVLKRLCDQVEAFKQTVPRFDELLQQRREAFQTANAIMDNPPAPVQPRTPER
PSSTLDEVIRSVSPSRPTGLEGFAQRLLSELSTPSRSVTPRGRKNSTRTSGASTPGYNVS
DLLSPSPFPNTSKPLPDPTRNALNRSLSPSSAQSGASGGREGRQSQASIQPAEFTAMDQS
ILARRVALPGEQVKLMPLDSERKPVHDAPESLFSGDELASLDGDDSSADRSEVATEPTVT
TETTDNAEPTSPTSDENMVSVSHVITNVLIYQSFLLELASLMQVRAGLFNEVRFV
>tr|Q4RJP9|Q4RJP9_TETNG Chromosome 13 SCAF15035, whole genome shotgun
sequence (Fragment) OS=Tetraodon nigroviridis GN=GSTENG00033335001 PE=4
SV=1
LQMTEGRRCQVHLLDDRKLELLVQPKLMAKDLLDLVASHFNLKEKEYFGIAYTDETGHFS
WLQLDRRVLELDRRVLEHEFPKKSGPIVLYFCVKFYIESISYLKDNATIELFFLNAKSII
YKELIEVDSDVVFELASYILQEAKGDFTSNDATRSDLKKLPALPTQALKEHPSLAYCEDR
VIEHYKKLSGQSRGQAIVNYMSIVESLPTYGVHYYAVKDKQGIPWWLGLSYKGIFQYDHQ
DKVKPRKVFQWRQLENLYFREKKFSVEVHDPRRASVTRRTFGHSGIAVHTWYACPALIKS
IWAMAISQHQFYLDRKQSKSKIHAARSLSEIAIDLTETGTLKTSKLANMGSKGKIISGTC
GSLLSSGSQESDSSQTAKKDMLAALRARQEALEETLKQRIEELKSICIREAELTGKLPKE
YPLDPGEEPPTVRRKIGTAFKLDEQKILPKGEEEELERLEREFAIQSQITEAARRLASDP
HVNSKKLKKQRKTSYLNALKKLQEIENSINEYRVRSGKKPTQRASLIIEEANIGSEDSSL
SDALVLDDDDPQITGTPTFSPVASPHKGLPPRPPSHSRPPPPQSLDGLRHMHYTRSDYDK
SPIKPKMWSESSLDEPYEKVKKRSSHSSHRRFPSSGSAEAGGSNSLQSSPIRNPPHWNSQ
SSMPSTPDLKTRDPTLRTFHQHFRNRSSSLESQAKLLVSDSDAHPHALGTLGSPDFFLGP
GRSSNGSDPLDDCSSCTSQSSSEHYYPSGGPPGSNPNYSTLGEDSPSKARQRQRQRHRSA

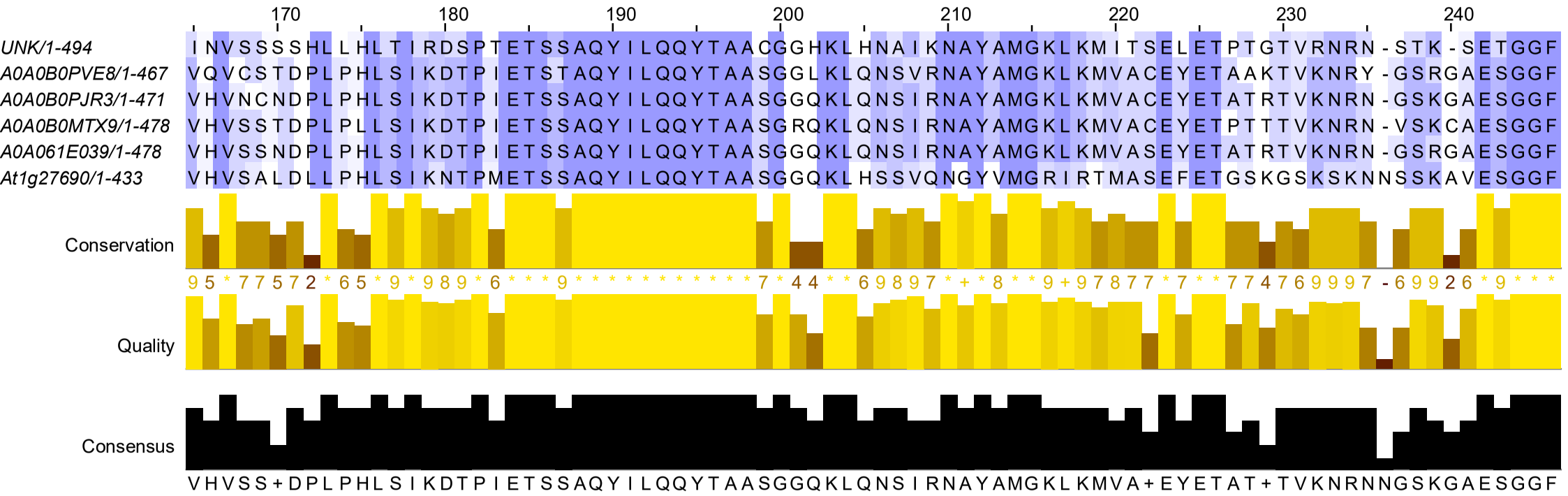
GHLGSSNSGSMPNLAAKNGTGGCSGGGGMGGGQHGIYLHSQSQPSSQYRIKEYPLYVEGS
PNPVVVRSLESDQEGHYSVKAQFKTSSSYTAGGLYKEAWGGDEGGEGSGRLTPSRSQIVR
TPSLGREGSGGGRAAVSEELRCWYQRSSGSLKDRNHSHSGSTSSETGSQQGTLGHGRGSR
VGTLAKGSPAASPHSQRNMPPSGEQAVTPTPPCSPQHILNWQSGSFSDSCFLGSPLCSEL
ADVQWYGHDKAKPGTLV
>tr|H3DKS5|H3DKS5_TETNG Uncharacterized protein OS=Tetraodon nigroviridis
GN=FRMD4A PE=4 SV=1
VWKMLVIIFSLLNLQMTEGRRCQVHLLDDRKLELLVQPKLMAKDLLDLVASHFNLKEKEY
FGIAYTDETGHFSWLQLDRRVLELDRRVLEHEFPKKSGPIVLYFCVKFYIESISYLKDNA
TIELFFLNAKSIIYKELIEVDSDVVFELASYILQEAKGDFTSNDATRSDLKKLPALPTQA
LKEHPSLAYCEDRVIEHYKKLSGQSRGQAIVNYMSIVESLPTYGVHYYAVKDKQGIPWWL
GLSYKGIFQYDHQDKVKPRKVFQWRQLENLYFREKKFSVEVHDPRRASVTRRTFGHSGIA
VHTWYACPALIKSIWAMAISQHQFYLDRKQSKSKIHAARSLSEIAIDLTETGTLKTSKLA
NMGSKGKIISGTCGSLLSSGSQESDSSQTAKKDMLAALRARQEALEETLKQRIEELKSIC
IREAELTGKLPKEYPLDPGEEPPTVRRKIGTAFKLDEQKILPKGEEEELERLEREFAIQS
QITEAARRLASDPHVNSKKLKKQRKTSYLNALKKLQEIENSINEYRVRSGKKPTQRASLI
IEEANIGSEDSSLSDALVLDDDDPQITGTPTFSPVASPHKGLPPRPPSHSRPPPPQSLDG
LRHMHYTRSDYDKSPIKPKMWSESSLDEPYEKVKKRSSHSSHRRFPSSGSAEAGGSNSLQ
SSPIRNPPHWNSQSSMPSTPDLKTRPHYVHSTRSVDISPTRLHSLAQHFRNRSSSLESQA
KLLVSDSDAHPHALGTLGSPDFFLGPGRSSNGSDPLDDCSSCTSQSSSEHYYPSGGPPGS
NPNYSTLGEDSPSKARQRQRQRHRSAGHLGSSNSGSMPNLAAKNGTGGCSGGGGMGGGQH
GIYLHSQSQPSSQYRIKEYPLYVEGSPNPVVVRSLESDQEGHYSVKAQFKTSSSYTAGGL
YKEAWGGDEGGEGSGRLTPSRSQIVRTPSLGREGSGGGRAAVSEELRCWYQRSSGSLKDR
NHSHSGSTSSETGSQQGTLGHGRGSRVGTLAKGSPAASPHSQRNMPPSGEQAVTPTPPCS
PQHILNWQSGGTADSSPTEDTCQSPPQPSSDA
>tr|A0A0N0BG55|A0A0N0BG55_9HYME Heterogeneous nuclear ribonucleoprotein K
OS=Melipona quadrifasciata GN=WN51_00655 PE=4 SV=1
MAAFIAFSPTLCLKAHSLEKEEDWLLTSSRHAIRPDHWRLKNRHDATFELSNATTPRSVS
KTGARIKIYSHCCPHSTDRLISICGKPTTCIECIRELIATIKTSPLKGVNNPYDPHNFDD
YYADDYGGYGTGDGGQGKGGGFGGPGGGPRGGGSGGGGMSGGPPDRGYGGNSRGGGGAGG
GYEGGRGGYGGNRGGPPPYAGNYNGDGWGMQGGAPNGLGGGANSGMSGPPMGGNNQGNQG
NMGGNKTTTQVTIPKDLAGAIIGKGGARIRKVRSDSGAGITIDEPLSGSNDRIITITGLP
SQIQMAQYLLQQR
>tr|Q6ZFB4|Q6ZFB4_ORYSJ Putative uncharacterized protein OJ1126_D10.15
OS=Oryza sativa subsp. japonica GN=OJ1126_D10.15 PE=4 SV=1
MKSGKGARRSENIFCETTMKSTISDYYHINSINIAHGGHTVVMLFCSPTAAHCRSARISA
PLHCHAGQPPAGLPY
>tr|A0A0M2MKK7|A0A0M2MKK7_9ACTN Type IV secretion protein Rhs
OS=Streptomyces sp. MUSC136T GN=VT52_32745 PE=4 SV=1
MTTPEARGGRSFAADPVVEAPGELPRIWAAQLVSCVVDENVGLPDTAQLTYRDPDNEFLG
STGITLGTPLKVSVVTVTGQAREQLFSGEVTAVEIDRDGTGSFTVVRAYSKAHRLQRGRK
VVAYRNMTAAAIVRKVAAGAGLPVGKVQAAPVTYKQLSQANVSDWDFLQYLAGESGAQVR
VDDKGVLQFTRPEPASGAPAPSTPATQNPMVLEYGRNLLALRAALSGADGASQVEVRGWD
VTTKTPLVARQPSVTSRTVRPGLSPSLASAFGADAKLTVTDTPYRTQAETTAAATAISAQ
VASAFGELEVVVEGSPRLRAGVPVALGNVGPAFSGRYTTTAVHHSLDPHGGYRTTVWVSA
SPDRSLAGLATGANAPGRGPRIPGLAIGVVTDVREPGGAQSGAVRLKFPWLDDTYVSDWV
RTVQWGGKGGGGVVSPEVNDEVLVGFEQGLLDSPYVIGGLYNGVDTPSEHDVPLIDGTSG
KVNRRSIVSRSGHRVELLDARAPGPSGVRLRTADERMEVLLDDRDDRIELTVYAAGGRRA
LSSVRLDEHGITLDAGTGKVSVKGASVDIDGTESVNVSGLSTTVSGQSGLTLDGGLLGVL
KADLVRIN
>tr|M3Z7A3|M3Z7A3_MUSPF Uncharacterized protein OS=Mustela putorius furo
GN=TOB2 PE=4 SV=1
MQLEIKVALNFIISYLYNKLPRRRADLFGEELERLLKKKYEGHWYPDKPLKGSGFRCVHI
GELVDPVVELAARRSGLAVEDVRANVPEELSVWIDPFEVSYQIGEKGAVKVLYLDDSEGC

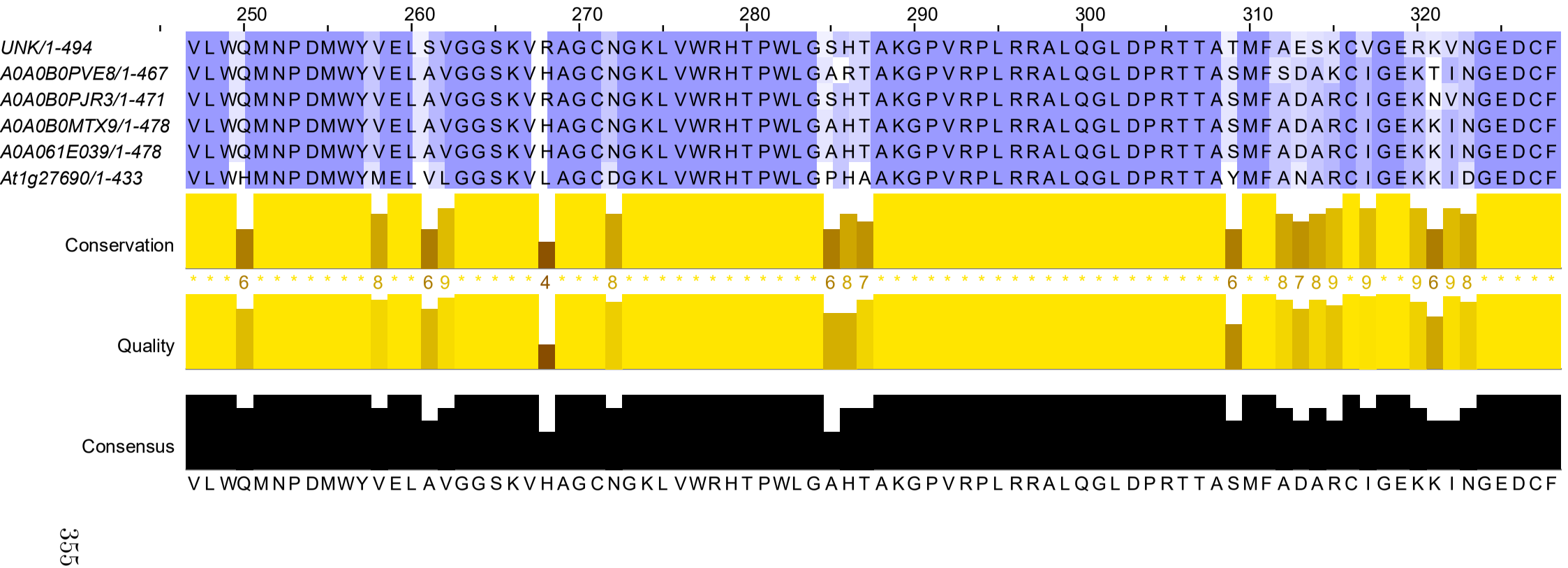
VAPELDKEFKSSFNPDAQVFVPIGSQDSSLSNSPSPSLGQSPSPTFIPRSAQPITFTTAS
FAATKFGSTKMKKGGGAASSGGVTGGGASGPQPPQPQPRLARSPTSSLLKHKSLSLSLHS
LNFMAATPGPQSQLSPNAKEFVYNGGGSPSLFFDGADSGASGASGAGSCNSSSFDVAQVF
GGGANSLFLEKTPFVEGLSYNLNTMQYPSQPFQPVVLAN
>tr|G3B5G2|G3B5G2_CANTC DUF1620-domain-containing protein OS=Candida
tenuis (strain ATCC 10573 / BCRC 21748 / CBS 615 / JCM 9827 / NBRC 10315
/ NRRL Y-1498 / VKM Y-70) GN=CANTEDRAFT_106468 PE=4 SV=1
MVRLTQFLGFVVLIATCVSGVFLEDAFTKNWVKYNHALIKSFDAIQDSSFVGVTLDGELV
KYNLTNEAVLSWKVTVPLNDVEYLINGGTILTYSTSEDTIYLWDIQSGVLLNNYQVGPVK
YISRSFGGFIVLSSNSLLTFVDGNLSKEIATSVGDIWASEFNGLTYIVTDDSKLLKLDPN
FKYTTVDINVKFSKISQIVGNRVLVNGQVFDLDKNQITTKAKVTGLFESEPAYSLEKNKF
KIIKDDKVVLEDDFEESSVKVLQNYLLVDSEDERKVIDLKGFFESLDETSINLESYNHSI
TGKDYIFGNEIVSLIVTGKFIQFSRYNILLDKVAHYNYHINTYNLNFPKALLINKPESKQ
TMDSIQHLVDEIQQNNVLSRFIKRTRRHLVEFGKSIISKVTRLDFNSDHIEITNPYDLEK
LLVFVDDSKLVAVDSLNGDGVWETVIEDGLLDLEENGDTMSLVYGDKAITVSTRDGEIID
SHDRTSSVDLPQGTIYVKQVENSIQSYKYVDGKLIPTWKFAKDKIINFAIKPNTKTGSVG
IALHDKSVLYKYLNDNSIAVIAEEDGILKLYLIDGKSGNVIYVQEHLKSDNIDTKSIKLI
LDDNWIIYSYFVTEPKYEQRISVVDLFGEAPTKGNFTVPISSSSSKSFIYPERIIDLKST
YTRFGITLKSIIALTEDGDLVELPKYILNSRRIDDRQLSQNDFKDDFRMLPYEPVVARND
YSVLNHGYKLDTGSNNLILLKDTKLESTSIICMINSRNMFCTRVQPSLSFDNLTEAFQKF
RLIITIFVLFVAYFVTKPMVIKKNLNSQWIYKA
>tr|Q4RMY6|Q4RMY6_TETNG Chromosome 6 SCAF15017, whole genome shotgun
sequence OS=Tetraodon nigroviridis GN=GSTENG00031820001 PE=4 SV=1
MATEETAGGARKATKSKLFEFLVHGVVSGAVPHSHQGLWHASVRVRVWECVSRCSGGGGG
GGGGGGGGVLSVCEGALGRAEPCEGYFQPPGSQPGGGGGGGRGGGGGGWVQRTGSRSATI
GWSRRKDGEDF
>tr|A0A072PAT1|A0A072PAT1_9EURO Uncharacterized protein OS=Exophiala
aquamarina CBS 119918 GN=A1O9_07949 PE=4 SV=1
METIKNTVANVLGSSKSDEADTATHGTLGHHGHSSNTTDTTGSHHGTSGTTTDTLSHNSG
TTTGVTGSMGDAAPSFHDQSRGGTGSTLSQGGTGTSTTGTHGTGLGRETTAASGTTGVKH
GTNEGTATTGVGHGTSDTTTTHGTKSNDLSPSQSHPDRKDAQSPDQGPDPALVGDAKDHP
KMVGQGAPGSHSAVFGLTPDGKKHKESSHGAAPIRPAHSKETTLGRKSVVGASGADSGGD
TVSGGRGGVSDQIDAPDTGKKGLERTDPAPISASNSGGKPGAGLTGLGQS
>tr|A0A0A0LH68|A0A0A0LH68_CUCSA Uncharacterized protein OS=Cucumis
sativus GN=Csa_3G873810 PE=4 SV=1
MGKATDFSSNHRSPSGTSLAGDNTNSSEFRRKNLQSPWAQVVRGEPESISPVDQSQLSSS
SSSLSSLAVSATETPAPASPPSDNFTSSENCDANDGNAASKKQAWNKPTNGVVEGGSVMG
ADSWPALAESARASPKLTVDSPPKVTVEVAVPPSQGPINVPPQRQATNNAKSNPTLKNPV
VARRSSRRGGGGGGSSVGGPRGGYYRPPPPPPPPPPPPFPVFQVSPNSYCNMIPAIPDPS
SGEPLFRSPNWDPRAVAGFVPQLNFGTDHRNFFPRGNFPLHPRGDSHYHNNRGGKRGQDR
GIYFNARDAHFQQHRPHTRGFMRPLPPFTGQFPQGVRPHLNPMAHPEFVYVPTLPLEAYR
GGLPFMPRPAMNYPTVDPTLSASIVKQIEYYFSDGNLVKDDYLRSQMDDQGWVPISLIAT
FPMVLSLTNNIQWIVESLRTSTEVEVQDYKIRRRNEWKKWTTKSNWFRTDLVSSASSGST
HDSLATSFQRVRVDEGTNQSMTNDTDPHNAERTTELQSSESGDCSQLTNGEANQDVQTDI
>tr|B9TLI7|B9TLI7_RICCO Putative uncharacterized protein OS=Ricinus
communis GN=RCOM_1983660 PE=4 SV=1
MNRLAPLSEEPIREDEESTSSSKKGQSWKNWLKTHFSLVFNKKSDLKILLSVLGCPLFPV
SVHPKLPINEHIQKQDKL

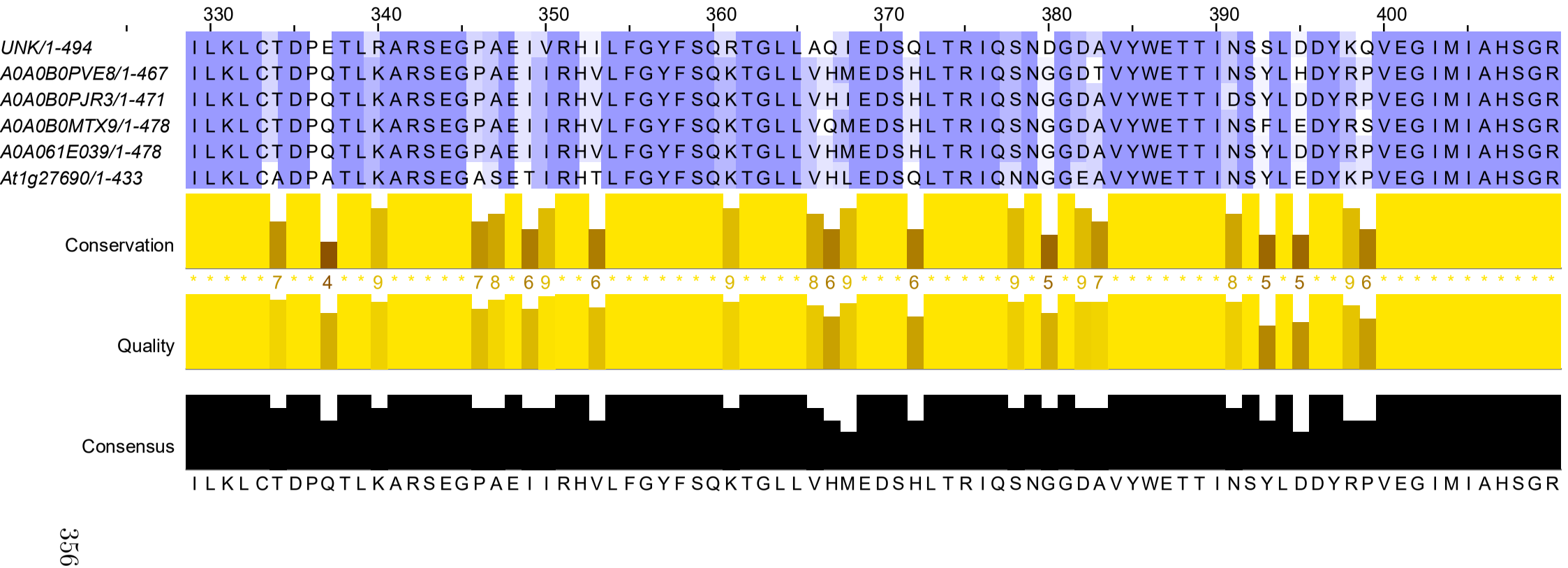
Appendix 6: Alignment of UNK and 5 Most Similar Orthologues

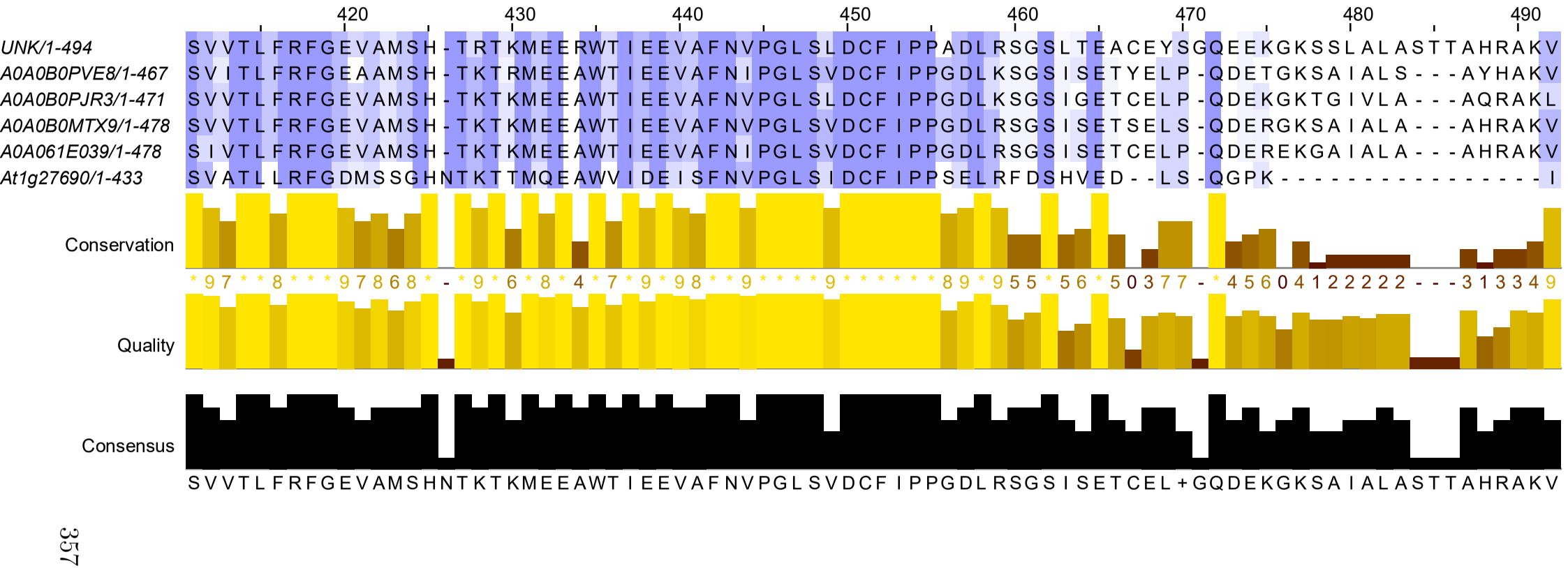

10
20
30
40
50
60
70
80
UNK/1-494 MEKKQGFFSSLRDEVVRGLSPSRSRPRSRSASPSRSTTPHMKALLWGRKKLIASSGCSGGGGVIGGER--GGYYLSQPEPFI
A0A0B0PVE8/1-467 MEKKQGFFSALKEEVIRGLSPSRSR----TNSPGRARSPIA--ILLRRKKSG----------HYNY--GGAYLVQPEPLI
A0A0B0PJR3/1-471 MEKKQGFFSSLKEDVIRGLSPSRSR----SNSLARTGSPMS--GLLRRKKTS----------NQYYAGGGGYVAQPEPLI
A0A0B0MTX9/1-478 MEKKQGFFSALKQEVVRGLSPSRSR----SSSPARARSPFA--TLLRRKKNN----------HNNY--DGAYVAQPESLI
A0A061E039/1-478 MEKKQSFFSALKEEVVRGLSPSRSR----PNSPARARSPMA--SLLRRKKSN----------HNNY--GGAYVAQPEPLI
At1g27690/1-433 MDKKHGLFSKSNS--------RRPR----SKSPVRSVSPI----IIRRRK----------GRYVTQPDRH-
Conservation
*9**688**4566332332326*7*----74*66*7399*50--0+74*9*00----------0011--1*3*96**9452
Quality
Consensus
MEKKQGFFSALKEEVVRGLSPSRSRPRSRSNSPARARSP+AKA+LLRRKKSNASSGCSGGGGVIHNNYAGGGAYVAQPEPLI

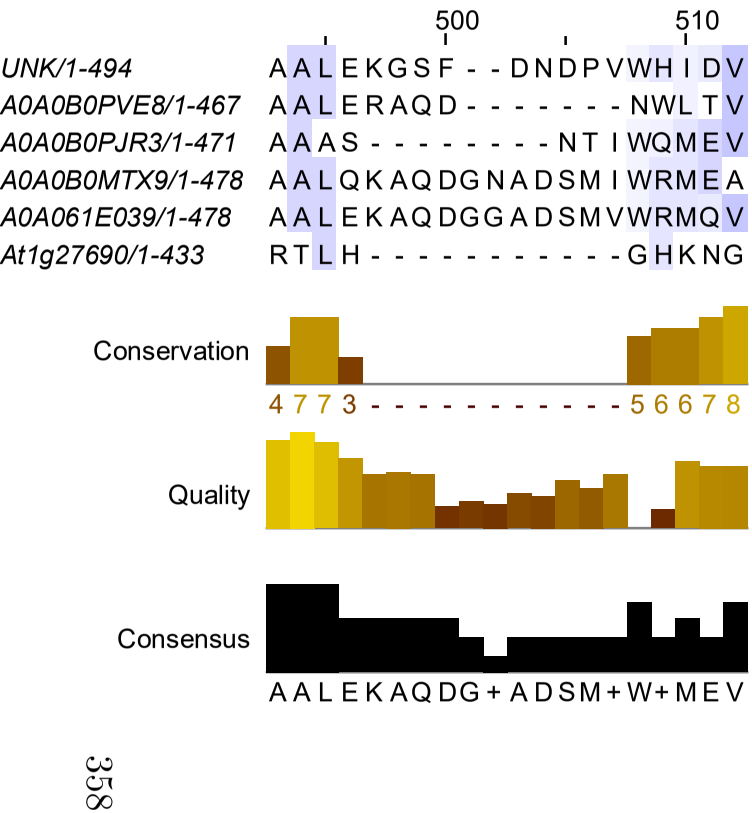

90
100
110
120
130
140
150
160
UNK/1-494 GRSS-------SLRPVMEGPDPDNG---EVSGVDSKRLGSGLSHWVKGQWSRAP-SVTSTTPAYRKSDLRLLLGVMGAPLAP
A0A0B0PVE8/1-467 ARYG----VGEALAPLMEGPDPDGG---ET--GDSKRLGLGLGQWVMGQLSRTP-SMASL--SCKRSDLRLLLGVMGAPLAP
A0A0B0PJR3/1-471 ARSGSLRPVGEALAPLMEGPDPDGV---EI--GDSKRVGPGIGEWVKGQLSRNP-SVT-A--SYKRSDLRLLLGVMAAPLAP
A0A0B0MTX9/1-478 LRSGSLRPVGEALAPLMEGPDPDGG---EV--GDSKRVGSGLGQWVKGQLSRTP-SVASM--SYRRSDLRLLLGVMGAPLAP
A0A061E039/1-478 VRSGSLRPVGEALAPLMEGPDPDGG---EV--GDSKRVGSGLGQWVKGQLSRTP-SVASM--SYKRSDLRLLLGVMGAPLAP
At1g27690/1-433 --------MSEMLAPVIEGPDPDAEDSGSS--GDYSRFERRWYNWMKCQLPVAPPSVSSS-SDFKRTDLRLLLGVLGAPLGP
Conservation
1 3 1 2 - - - - 1 2 3 6 * 4 * 9 9 * * * * * * 7 3 - - - 6 5 - - 8 * 6 5 * 7 4 2 4 7 5 4 * 8 7 9 * 7 7 4 7 * - * 8 7 3 5 - - 5 7 9 9 9 * * * * * * * * 9 + * * * + *
Quality
Consensus
ARSGSLRPVGEALAPLMEGPDPDGGDSGEVSGGDSKRVGSGLGQWVKGQLSRTPPSVASMT+SYKRSDLRLLLGVMGAPLAP


170
180
190
200
210
220
230
240
UNK/1-494 INVSSSSHLLHLTIRDSPTETSSAQYILQQYTAACGGHKLHNAIKNAYAMGKLKMITSELETPTGTVRNRN-STK-SETGGF
A0A0B0PVE8/1-467 VQVCSTDPLPHLSIKDTPIETSTAQYILQQYTAASGGLKLQNSVRNAYAMGKLKMVACEYETAAKTVKNRY-GSRGAESGGF
A0A0B0PJR3/1-471 VHVNCNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIRNAYAMGKLKMVACEYETATRTVKNRN-GSKGAESGGF
A0A0B0MTX9/1-478 VHVSSTDPLPLLSIKDTPIETSSAQYILQQYTAASGRQKLQNSIRNAYAMGKLKMVACEYETPTTTVKNRN-VSKCAESGGF
A0A061E039/1-478 VHVSSNDPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIRNAYAMGKLKMVASEYETATRTVKNRN-GSRGAESGGF
At1g27690/1-433 VHVSALDLLPHLSIKNTPMETSSAQYILQQYTAASGGQKLHSSVQNGYVMGRIRTMASEFETGSKGSKSKNNSSKAVESGGF
Conservation
95*7752*65*9*989*6***9*********7*44**6989 7*+*8**9+9787 7**7746999 7-6992 6*9***
Quality
Consensus
VHVSS+DPLPHLSIKDTPIETSSAQYILQQYTAASGGQKLQNSIRNAYAMGKLKMVA+EYETAT+TVKNRNNGSKGAESGGF


250
260
270
280
290
300
310
320
UNK/1-494 VLWQMNPDMWYVELSVGGSKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTATMFAESKCVGERKVNGEDCF
A0A0B0PVE8/1-467 VLWQMNPDMWYVELAVGGSKVHAGCNGKLVWRHTPWLGARTAKGPVRPLRRALQGLDPRTTASMFSDAKCIGEKTINGEDCF
A0A0B0PJR3/1-471 VLWQMNPDMWYVELAVGGSKVRAGCNGKLVWRHTPWLGSHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKNVNGEDCF
A0A0B0MTX9/1-478 VLWQMNPDMWYVELAVGGSKVHAGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCF
A0A061E039/1-478 VLWQMNPDMWYVELAVGGSKVHAGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCF
At1g27690/1-433 VLWHMNPDMWYMELVLGGSKVLAGCDGKLVWRHTPWLGPHAAKGPVRPLRRALQGLDPRTTAYMFANARCIGEKKIDGEDCF
Conservation
Quality
Consensus
VLWQMNPDMWYVELAVGGSKVHAGCNGKLVWRHTPWLGAHTAKGPVRPLRRALQGLDPRTTASMFADARCIGEKKINGEDCF


330
340
350
360
370
380
390
400
UNK/1-494 ILKLCTDPETLRARSEGPAEIVRHILFGYFSQRTGLLAQIEDSQLTRIQSNDGDAVYWETTINSSLDDYKQVEGIMIAHSGR
A0A0B0PVE8/1-467 ILKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDTVYWETTINSYLHDYRPVEGIMIAHSGR
A0A0B0PJR3/1-471 ILKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHIEDSHLTRIQSNGGDAVYWETTIDSYLDDYRPVEGIMIAHSGR
A0A0B0MTX9/1-478 ILKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVQMEDSHLTRIQSNGGDAVYWETTINSFLEDYRSVEGIMIAHSGR
A0A061E039/1-478 ILKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDAVYWETTINSYLDDYRPVEGIMIAHSGR
At1g27690/1-433 ILKLCADPATLKARSEGASETIRHTLFGYFSQKTGLLVHLEDSQLTRIQNNGGEAVYWETTINSYLEDYKPVEGIMIAHSGR
Conservation
* * * * * 7 * * 4 * * 9 * * * * * 7 8 * 6 9 * * 6 * * * * * * * 9 * * * * 8 6 9 * * * 6 * * * * * 9 * 5 * 9 7 * * * * * * * 8 * 5 * 5 * * 9 6 * * * * * * * * * *
Quality
Consensus
ILKLCTDPQTLKARSEGPAEIIRHVLFGYFSQKTGLLVHMEDSHLTRIQSNGGDAVYWETTINSYLDDYRPVEGIMIAHSGR


420
430
440
450
460
470
480
490
UNK/1-494 S V V T L F R F G E V A M S H - T R T K M E E R W T I E E V A F N V P G L S L D C F I P P A D L R S G S L T E A C E Y S G Q E E K G K S S L A L A S T T A H R A K V
A0A0B0PVE8/1-467 S V I T L F R F G E A A M S H - T K T R M E E A W T I E E V A F N I P G L S V D C F I P P G D L K S G S I S E T Y E L P - Q D E T G K S A I A L S - - - A Y H A K V
A0A0B0PJR3/1-471 S V V T L F R F G E V A M S H - T K T K M E E A W T I E E V A F N V P G L S L D C F I P P G D L K S G S I G E T C E L P - Q D E K G K T G I V L A - - - A Q R A K L
A0A0B0MTX9/1-478 S V V T L F R F G E V A M S H - T K T K M E E A W T I E E V A F N V P G L S V D C F I P P G D L R S G S I S E T S E L S - Q D E R G K S A I A L A - - - A H R A K V
A0A061E039/1-478 S I V T L F R F G E V A M S H - T K T K M E E A W T I E E V A F N I P G L S V D C F I P P G D L R S G S I S E T C E L P - Q D E R E K G A I A L A - - - A H R A K V
At1g27690/1-433 S V A T L L R F G D M S S G H N T K T T M Q E A W V I D E I S F N V P G L S I D C F I P P S E L R F D S H V E D - - L S - Q G P K - - - - - - - - - - - - - - - - - I
Conservation
* 9 7 * * 8 * * * 9 7 8 6 8 * - * 9 * 6 * 8 * 4 * 7 * 9 * 9 8 * * 9 * * * * 9 * * * * * * 8 9 * 9 5 5 * 5 6 * 5 0 3 7 7 - * 4 5 6 0 4 1 2 2 2 2 2 - - - 3 1 3 3 4 9
Quality
Consensus
S V V T L F R F G E V A M S H N T K T K M E E A W T I E E V A F N V P G L S V D C F I P P G D L R S G S I S E T C E L + G Q D E K G K S A I A L A S T T A H R A K V


500
510
UNK/1-494 A A L E K G S F - - D N D P V W H I D V
A0A0B0PVE8/1-467 A A L E R A Q D - - - - - - - - N W L T V
A0A0B0PJR3/1-471 A A A S - - - - - - - - - N T I W Q M E V
A0A0B0MTX9/1-478 A A L Q K A Q D G N A D S M I W R M E A
A0A061E039/1-478 A A L E K A Q D G G A D S M V W R M Q V
At1g27690/1-433 R T L H - - - - - - - - - - - G H K N G
Conservation
4 7 7 3 - - - - - - - - - - - - 5 6 6 7 8
Quality
Consensus
A A L E K A Q D G + A D S M + W + M E V

Appendix 7: Gel Images of Genotyping Analyses

Author Contribution: I conducted PCRs and captured images compiled as figures in this appendix.

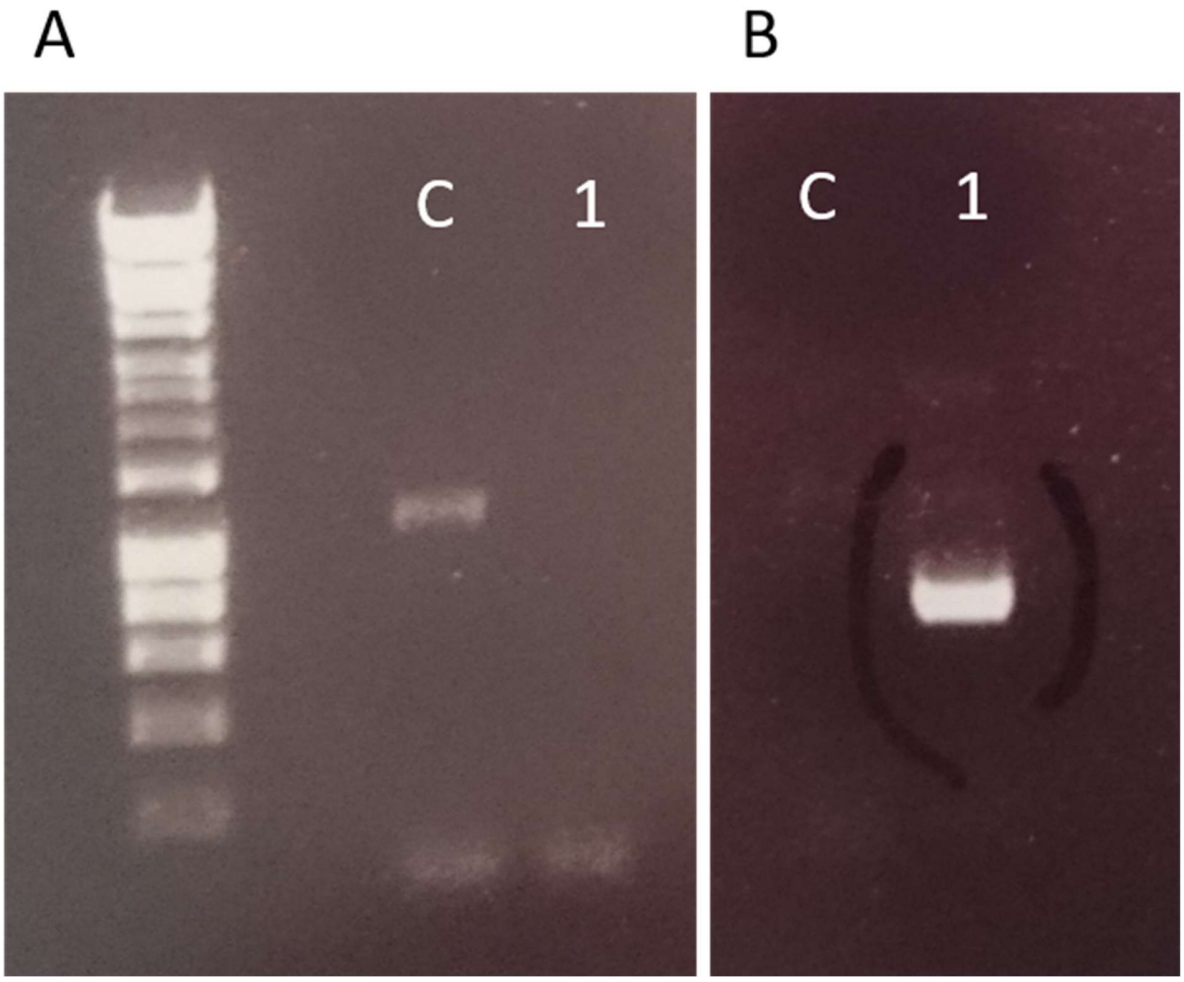


Figure 1: Genotyping gel image for *cle26* indicates identification of a homozygous mutant line using DNA isolated and combined from 10 seedlings of both Col-0 and *cle26.* **A**) CLE26 forward and reverse primers were used to amplify DNA isolated from Col-0 control (C), and *cle26* (1) samples. **B**) SALK LBb and CLE26 reverse primers were used to amplify DNA isolated from Col-0 control (C), and *cle26* (1) samples, indicating placement of a SALK T-DNA insert in the CLE26 genomic sequence.

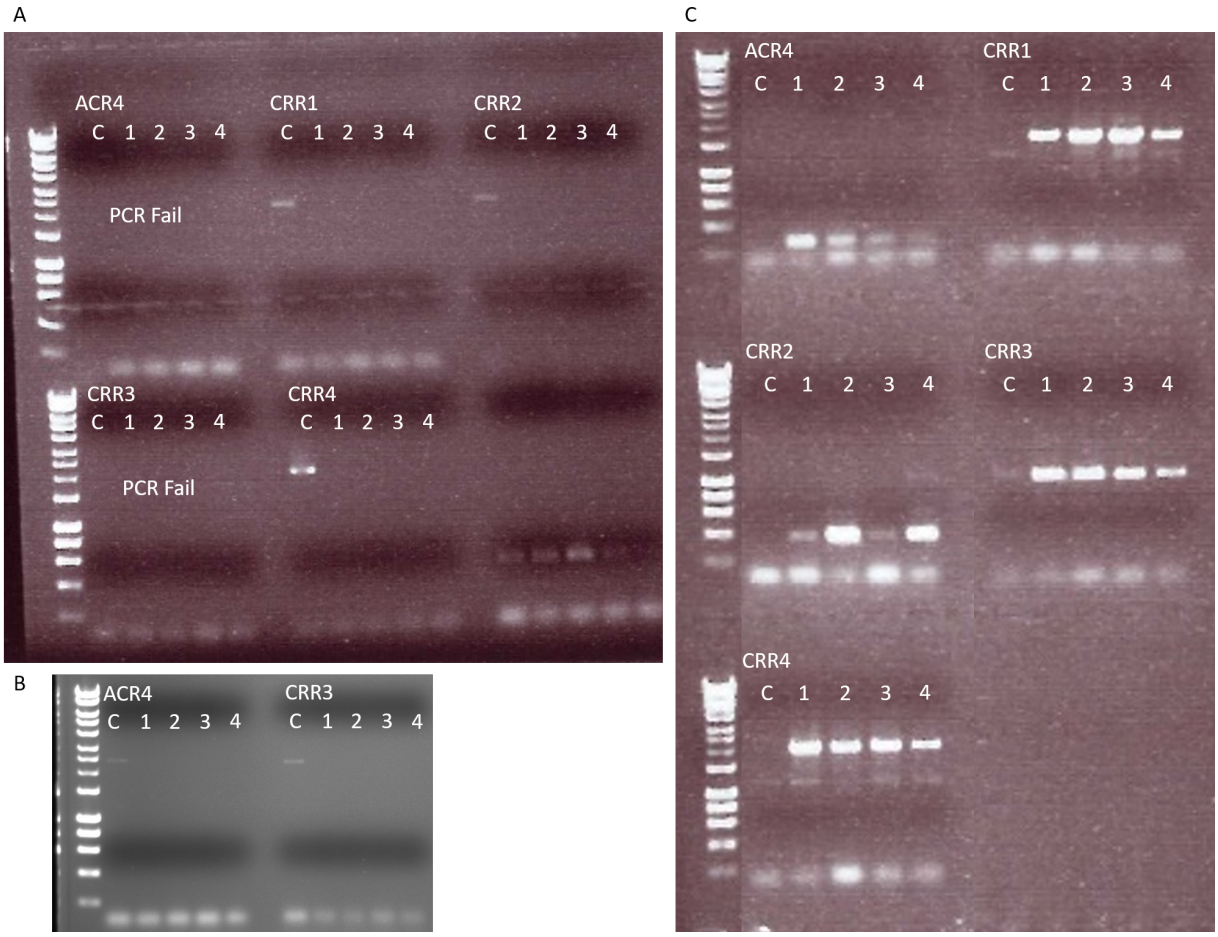


Figure 2: Genotyping gel image for *acr4-crr1-crr2-cr3-crr4* (pentuple mutant) indicates isolation of four homozygous pentuple mutant seedlings derived from the same parent. Forward and reverse primers for ACR4, CRR1, CRR2, CRR3, and CRR4 were used to amplify DNA from Col-0 (C) and four pentuple mutant samples (1-4) (**A**), however PCR failed using ACR4 and CRR3 primers, and was repeated (**B**). SALK/SAIL LBb and ACR4, CRR1, CRR2, CRR3, and CRR4 reverse primers were used to amplify DNA isolated from Col-0 (C) and four mutant samples (1-4) (**C**), indicating placement of a T-DNA insert in each of the five genes.

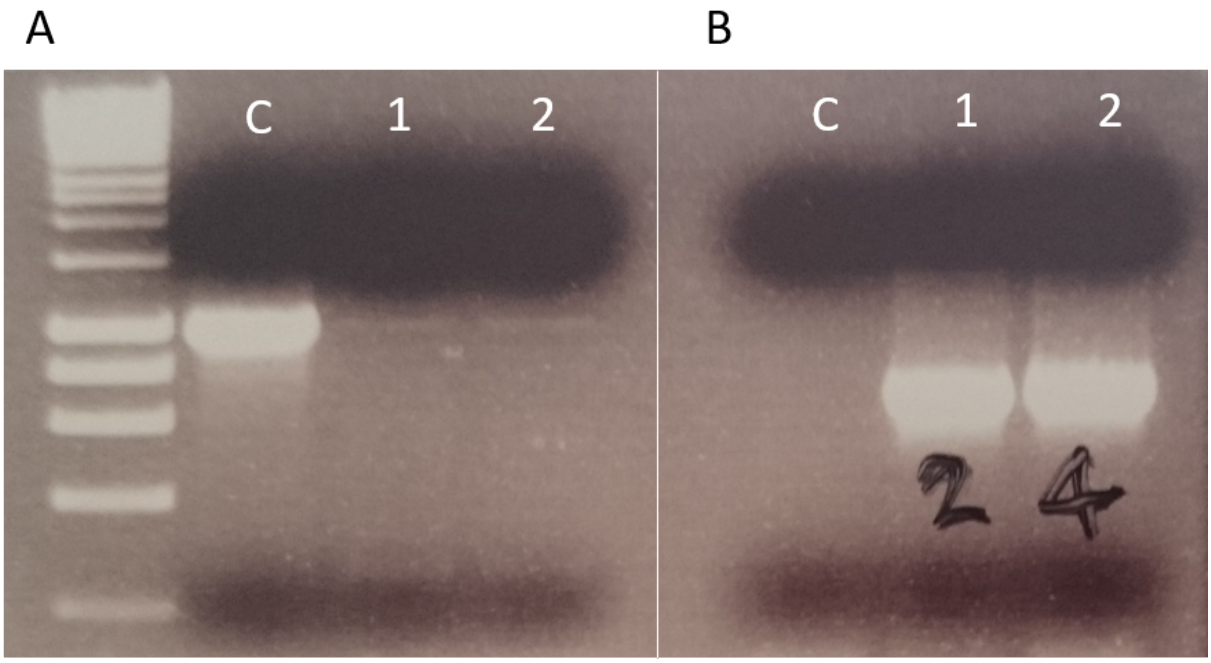


Figure 3: Genotyping gel image for *unk* indicates isolation of two homozygous mutant seedlings derived from the same parent. Forward and reverse primers for UNK were used to amplify DNA from Col-0 (C) and two *unk* samples (1, 2) (**A**). SAIL LBb and UNK reverse primers were used to amplify DNA isolated from Col-0 (C) and *unk* samples (1, 2) (**B**), indicating placement of a T-DNA insert in the UNK genomic sequence.

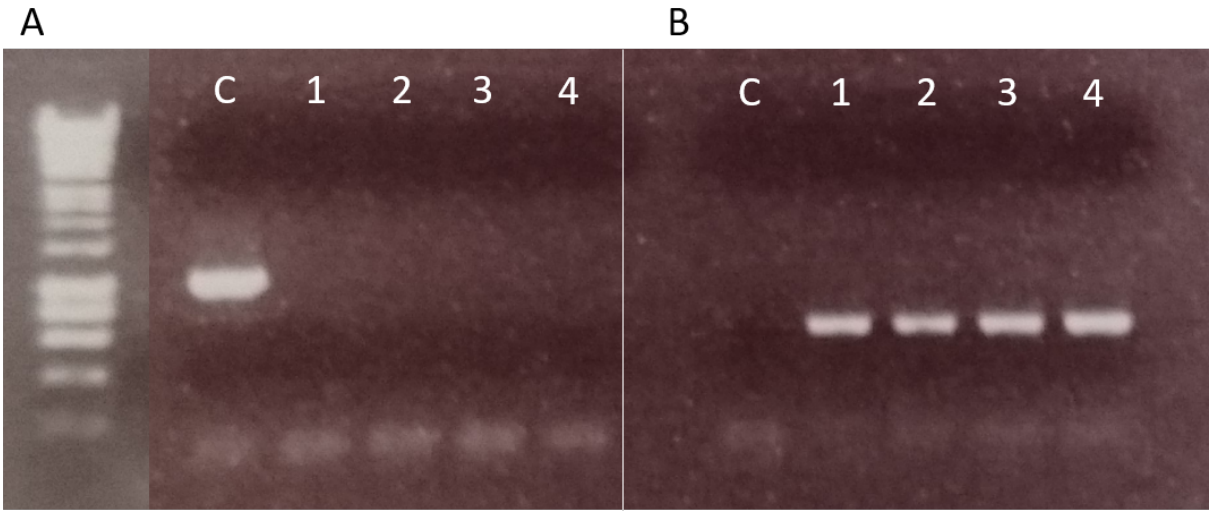


Figure 4: Genotyping gel image for *pla-iγ2* indicates isolation of four homozygous mutant seedlings derived from the same parent. Forward and reverse primers for PLA-Iγ2 were used to amplify DNA from Col-0 (C) and four *pla-iγ2* samples (1-4) (**A**). SALK LBb and PLA-Iγ2 reverse primers were used to amplify DNA isolated from Col-0 (C) and four *pla-iγ2* samples (1-4) (**B**), indicating placement of a T-DNA insert in the UNK genomic sequence.

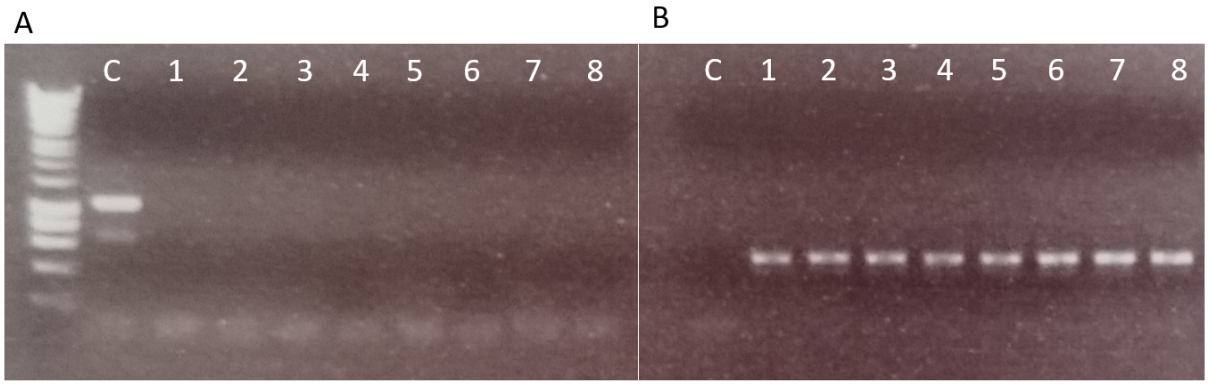


Figure 5: Genotyping gel image for *s/tpk* indicates isolation of eight homozygous mutant seedlings derived from the same parent. Forward and reverse primers for S/TPK were used to amplify DNA from Col-0 (C) and eight *s/tpk* seedlings (1-8) (**A**). SALK LBb and S/TPK reverse primers were used to amplify DNA isolated from Col-0 (C) and eight *s/tpk* samples (1-8) (**B**), indicating placement of a T-DNA insert in the S/TPK genomic sequence.