An ancient peptide family buried within vicilin precursors

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Abstract

New proteins can evolve by duplication and divergence or *de novo*, from previously non-coding DNA. A recently observed mechanism is for peptides to evolve within a 'host' protein and emerge by proteolytic processing. The first examples of such interstitial peptides were ones hosted by precursors for seed storage albumin. Interstitial peptides have also been observed in precursors for seed vicilins, but current evidence for vicilin-buried peptides (VBPs) is limited to seeds of the broadleaf plants pumpkin and macadamia. Here, an extensive sequence analysis of vicilin precursors suggested that peptides buried within the N-terminal region of preprovicilins are widespread and truly ancient. Gene sequences indicative of interstitial peptides were found in species from *Amborellales* to eudicots and include important grass and legume crop species. We show the first protein evidence for a monocot VBP in date palm seeds as well as protein evidence from other crops including the common tomato, sesame and pumpkin relatives, cucumber and the sponge loofah (*Luffa aegyptiaca*). Their excision was consistent with asparaginyl endopeptidase-mediated maturation and sequences were confirmed by tandem mass spectrometry. Our findings suggest the family is large and ancient and, that based on the NMR solution structures for loofah Luffin P1 and tomato VBP-8, VBPs adopt a helical hairpin fold stapled by two internal disulfide bonds. The first VBPs characterized were a protease inhibitor, anti-microbials, and a ribosome inactivator. The age and evolutionary retention of this peptide family suggests its members play important roles in plant biology.

Introduction

A recently found and unusual mechanism for protein evolution is the appearance of new, small proteins inside existing ‘host’ proteins. These ‘interstitial’ peptides emerge during the proteolytic processing of the host protein. The first example was a protein from seeds of the common sunflower *Helianthus annuus* called Preproalbumin with SFTI-1 (PawS1). This dual destiny protein is simultaneously matured into a seed storage albumin and a cyclic peptide called SunFlower Trypsin Inhibitor-1 (SFTI-1).[1, 2] The sequence for SFTI-1 was encoded within the N-terminal region of an albumin precursor.[2] Albumins are abundant seed storage proteins typically composed of a heterodimer with small and large subunits. Most mature albumins contain cysteine and methionine residues and provide nutrition during seed germination and early seedling growth.[3, 4] Both the mature albumin and the cyclic SFTI-1 peptide are cleaved from PawS1 by an asparaginyl endopeptidase (AEP), which is also known as vacuolar processing enzyme and is heavily involved in seed storage protein processing.[5-7] PawS1 is not unique to the common sunflower; PCR-based discovery of *PawS1* genes from Asteraceae species coupled with liquid chromatography/tandem mass spectrometry (LC-MS/MS) revealed a new family of disulfide-containing and mostly cyclic PawS-Derived Peptides (PDPs) whose distribution suggested the PDP family is at least 18 My old.[8] A subsequent survey of over 110 Asteraceae seed transcriptomes, to pursue their evolutionary origin in more detail, showed the peptide family has evolved stepwise over about 45 million years within the N-terminal region of preproalbumin.[9, 10]

SFTI-1 and its family of related peptides is not the only example of peptides that emerge from within a usually latent region of a host protein. In 1999 two different groups reported genes encoding Cys-rich peptides whose sequences were located within precursors for vicilin, a different type of seed storage protein also known as a 7S globulin. These genes were discovered in pumpkin[11] and macadamia.[12] Pumpkin seeds (*Cucurbita maxima*) contain a peptide called C2 that is buried within the N-terminal region of a preprovicilin.[11] This C2-containing preprovicilin called PV100 is matured by AEP into a 50 kDa vicilin, the 5 kDa trypsin inhibitor C2, and three Arg/Glu-rich cytotoxic peptides of 4-5 kDa.[11] C2 has four Cys residues that consist of two pairs of Cys residues interspersed by three variable residues. The Cys residues form disulfide bonds with the two connecting ‘CXXXC’ motifs thought to confer a hairpin-structure on C2.[11] There are some interesting parallels between PV100 and PawS1; both have AEP-processed, bioactive peptides buried in their N-terminal pro-regions and both are precursors for seed storage proteins.[2, 11] In the same year as the discovery of C2, another group isolated C2-like peptides from macadamia nuts (*Macadamia integrifolia*) named MiAMP2b-d (MiAMP2b to MiAMP2d: *Macadamia integrifolia* Antimicrobial Protein 2b-d) that displayed antimicrobial activity.[12] The sequences encoding the three MiAMP2 peptides were also buried in the N-terminal region of a preprovicilin, although a role for AEP was not proposed for these macadamia peptides. The C2 and the MiAMP2 peptides potentially represent a second buried peptide family that has evolved within protein precursors for vicilins.

C2 and the MiAMP2 peptides are similar to another 4-Cys peptide called Luffin P1, extracted from the seeds of *Luffa aegyptiaca* (common names Vietnamese loofah, sponge loofah), which has been shown to inhibit protein synthesis in a cell-free rabbit reticulocyte lysate.[13] Although Luffin P1 is a 4-Cys peptide similar to C2, the Luffin P1 precursor is unknown. Only a small fragment was amplified from *L. aegyptiaca* genomic DNA using degenerate primers designed against the Luffin P1 protein sequence.[13] The 82 bp of sequence amplified from *L. aegyptiaca* genomic DNA was short, but its closest match by BLASTN analysis is an 87% identity match to the C2 region of pumpkin PV100. We hypothesized that, just like C2, Luffin P1 is a vicilin-buried peptide; however if processed by AEP, Luffin P1 should be longer than previously described.

Evidence was mounting that these peptides, known to have valuable bioactivities, might be the first examples of an ancient, large, peptide family buried in vicilins and so we sought to test this hypothesis. BLAST searches initially using PV100 as bait, followed by subsequent searches, found hundreds of preprovicilin genes. These included a sub-group with insertions on the N-terminal side of vicilin containing typically even numbers of CXXXC motifs indicative of buried C2-like and MiAMP2-like peptides. We performed liquid chromatography/mass spectrometry (LC-MS) and tandem mass spectrometry (LC-MS/MS) in several evolutionarily distant species and were able to fully sequence five VBPs from the monocot date palm and the dicots tomato, sesame, loofah and cucumber. We also cloned the full open reading frame for the precursor for Luffin P1 and found it was also a preprovicilin. These data demonstrate that C2, MiAMP2, Luffin P1 and the VBPs we discover herein are all members of an ancient peptide family buried in vicilin precursors, each possessing two CXXXC motifs.

Results

Vicilin precursors with potentially buried peptides are widespread in the plant kingdom

To find preprovicilins that might contain buried peptides, sequence similarity searches of GenBank and UniprotKB were performed using PV100 as the input sequence. This resulted in the identification of hundreds of homologs and, after removing duplicates, we generated an alignment of 252 preprovicilin sequences from 91 species and 22 orders, from ferns to flowering plants. This revealed substantial variation on the N- and C-terminal sides of the mature vicilin region (**Fig. 1**).

Preprovicilins can be clustered into four main types based on the different types of N- or C-terminal expansion: Class I is the simplest and widely conserved throughout the plant kingdom from *Polypodiales* to *Brassicales* (**Fig. 2**, **Table S1**) so likely to represent the ancestral form. Class I preprovicilins possess an ER targeting signal and a vicilin domain only. Class II preprovicilins are similar to Class I, but with an additional Arg/Glu-rich domain C-terminal to the vicilin domain (**Fig. 1**). Class III preprovicilins are also similar to Class I, but have an additional Arg/Glu-rich domain on the N-terminal side of the vicilin. Class IV preprovicilins (such as PV100 and the MiAMP2 precursor) resemble Class III, but have an additional Cys-rich domain with one to twelve $CX_3C(X)_{10\text{-}14}CX_3C$ motifs. Some preprovicilins of Class IV lack the Arg/Glu-rich domain, with just the additional Cys-rich domain at the N-terminal region (**Fig. 1**). The existence of Class IV preprovicilins in 60 species suggested more vicilin-buried peptides awaited discovery.

Using pumpkin C2 and its precursor PV100 [11] as the prototypic vicilin-buried peptide, we made several assumptions for the discovery of C2 relatives. We assumed that VBPs would (i) contain two disulfide bonds; (ii) be processed at both proto-termini by asparaginyl endopeptidase, which cleaves at Asp and Asn residues, and (iii) if the proto-N-terminal residue was a Glu or Gln, that it would be pyrolated to become pyro-Glu. Based on these assumptions we searched peptide extracts for a sub-set of the 60 species with Class IV preprovicilins for the expected masses using mass spectrometry. Peptide extracts from those species with masses that matched the expectations based on C2 were digested separately with trypsin or chymotrypsin, subjected to proteomics by LC-MS/MS and compared to a custom database containing the 252 preprovicilin sequences. In addition to searching for tryptic or chymotryptic fragments, MASCOT was instructed to search for non-tryptic and non-chymotryptic matches to the database of 252 pre-pro vicilin sequences.

A vicilin-buried peptide from date palm seeds

Phoenix dactylifera, commonly known as the date palm, had one Class IV preprovicilin (**Fig. 3A**) that, based on AEP-mediated cleavage at Asn and Asp residues, was predicted to produce three main candidate masses with $CX_3CX_nCX_3C$ motifs. We calculated their monoisotopic masses assuming two disulfide bonds and an N-terminal pyro-Glu. The first candidate was a 40-residue peptide predicted to begin at Pro32 and end at Asp71 with a theoretical mass of 4899.25 Da. The second candidate was a 51-residue peptide beginning at Pro32 and ending with Asp82 giving a theoretical mass of 6066.76 Da. The third candidate was 57-residues from Pro83 to Asp139 with a mass of 7063.27 Da (**Fig. 3A**).

Proteins extracted from date palm seeds were analyzed by LC-MS. Peaks for the first, 40-residue candidate were observed in an extracted ion chromatogram (EIC) corresponding to 5+, 6+ (**Fig. 3B**) and 7+ protonated molecules. No peaks were seen for the other two candidates. Reduction of the disulfide bonds and addition of an iodoacetamide moiety to the thiol group for the cysteine residues increased the mass of the 40-residue candidate by the expected 232.12 Da (**Fig. 3C**), confirming the existence of four cysteine residues involved in two disulfide bonds.

To sequence the putative peptide, the initial extract was reduced, alkylated, digested with trypsin and then analyzed by tandem mass spectrometry. Six fragments were of a size expected to be detectable after trypsin digestion, whereas two others were expected to be too small for detection. The expected monoisotopic mass with $[M+H]^+$ for each fragment was calculated with alkylation of cysteines (**Fig. S1A**). Five of the six fragments were identified by a, b and y ions (**Fig. S1B-F**). Overall, these results confirmed the 40-residue peptide as a VBP from the N-terminal region of a preprovicilin from date palm seeds (PKRQIERCKQECRESRQGEQQERQCVRQCEEQEEKRGQGD).

Two vicilin-buried peptides from tomato seeds

The common tomato (*Solanum lycopersicum*) also contain a Class IV preprovicilin (**Fig. 4A**). From its sequence we predicted four candidate VBPs. Three candidates began with Pro30 but varied in length depended on the proto-C-terminal AEP cleavage sites, namely Asp82, Asp83 and Asn86, which would produce 53-, 54- and 57-residue peptides, respectively (**Fig. 4A**). The fourth candidate was a 49-residue peptide beginning with Arg87 and ending with Asn135. Performing LC-MS, we observed peaks in the EICs at m/z values consistent with $[M+7H]^{7+}$ ions from the 53-residue (Pro30-Asp82) and the 49-residue (Arg87-Asn135) candidates (**Fig. 4B** and **4D**). To test for the existence of two disulfide bonds in these two candidates, peptides were reduced and alkylated, giving the expected increased mass of 232.12 Da for each candidate (**Fig. 4C, 3E**). Tandem mass spectrometry was used to sequence both candidates. The tomato seed peptide extract was reduced and alkylated and then divided into two aliquots. One was digested by trypsin and the other by chymotrypsin. Trypsin digestion of the 53-residue candidate was predicted to yield five primary fragments (**Fig. S2A**) for which a, b and y ion series were identified (**Fig. S2B-F**). Chymotrypsin digestion of the 53-residue candidate should yield four fragments, two of which were confirmed (**Fig. S2G-J**). Combining the results of trypsin and chymotrypsin-based sequencing, the 53-residue candidate was confirmed as a VBP (PRGYQDPQEKLRECQQRCERQQPGQQKQLCKQRCEQQYRKEQQQQHGGETGED).

For the 49-residue candidate, five tryptic fragments were expected and four were sequenced (**Fig. S3A-E**). Four chymotryptic fragments were predicted and two were confirmed (**Fig. S3F-H**). Combining results, the 49-residue candidate was confirmed as a second tomato VBP (RGPDKSYKRLQECQRRCQSEQQGQRLQECQQRCQQEYQREKGQHQGETN).

A vicilin-buried peptide from sesame seeds

A sequence encoding a Class IV vicilin precursor was found for *Sesamum indicum* (**Fig. 5A**). From this single sequence, four candidate VBPs were predicted. These range from Arg82 to Asp123, Asp124, Asp125 or Asn126 and give 42-, 43-, 44- and 45-residue peptides respectively (**Fig. 5A**). LC-MS detected m/z values consistent with 5+, 6+ (**Fig. 5B**) and 7+ ions for the 42-residue candidate. Reduction and alkylation confirmed changes in mass of the $[M+6H]^{6+}$ ions consistent with two disulfide bonds (**Fig. 5C**).

To confirm the sequence of this 42-residue candidate, trypsin and chymotrypsin digestion were performed and subjected to LC-MS/MS. Masses were found corresponding to two of the four tryptic fragments (**Fig. S4C-D**), of which one was further confirmed with b and y ions (**Fig. S4B**). For the expected four chymotryptic fragments, their corresponding masses were discovered (**Fig. S4G-J**) but only one fragment was sequenced (**Fig. S4F**). Consistent with these MS/MS results, the mass is likely to be a 42-residue VBP (RKSPIERLRECSRGCEQQHGEQREECLRRCQEEYQREKGRQD).

VBPs identified from cucumber

We also discovered a VBP in the seeds of cucumber (*Cucumis sativus*), which like pumpkin and loofah belongs to the gourd family (Cucurbitaceae). The sequence from cucumber was similar to PV100 and from it four candidates were predicted to start from Gln68 and end with Asp102, Asp108, Asp111 or Asp115 giving respectively a 35-, 41-, 44- or 48-residue peptide (**Fig. 6A**). The expected average masses for the four candidates were calculated with two disulfide bonds and a pyro-Glu at the N-terminus, resulting in 4317.79, 5004.42, 5347.76 and 5933.42 Da, respectively. Unlike the previous LC-MS based VBP discovery pathways, the peptide extract from cucumber seeds was fractionated crudely from the C18-column by different acetonitrile concentrations and each fraction analyzed by MALDI-TOF mass spectrometry. In MALDI-TOF MS, we observed a major peak at m/z 4320.16 close to the predicted m/z ($[M+H]^{+}$) of the 35-residue candidate (4318.80 Da). No masses close to the other three candidates were observed (**Fig. 6B**). To sequence the 35-residue candidate, the crude fraction was digested by trypsin and then subjected to LC-MS/MS analysis. Three fragments were expected and the monoisotopic mass for each was calculated as $[M+2H]^{2+}$ with alkylated cysteines and an N-terminal pyro-Glu (Z) modification (**Fig. 6C**). Tandem LC-MS analysis identified all three fragments (**Fig. 6D-I**), but a missed cleavage at the first Lys residue from the peptide N-terminus gave the fragment pyro-GluKETEICR instead of ETEICR (**Fig. 6D, 5E**). Our MS/MS gave 83% coverage for the 35-residue candidate. Overall, these data confirmed the 35-residue candidate from cucumber seeds is another VBP, this time with a pyro-Glu at its N-terminus which transcript data resolve as a Gln (QKETEICRQWCQVMKPQGGEEQRRCQQECEERLRD).

Luffin P1 is matured from preprovicilin

The seeds of *Luffa aegyptiaca* (loofah) contain the 4-Cys peptide Luffin P1, which exhibits 69% sequence identity to C2 (**Fig. 7A**). The genetic origin of Luffin P1 is not known, but a small 123 bp fragment was amplified from *L. aegyptiaca* genomic DNA using degenerate primers designed against the Luffin P1 protein sequence.[13] The 82 bp amplified from *L. aegyptiaca* genomic DNA in this 123 bp PCR product was short, but its closest match by BLASTN analysis is an 87% identity match to the C2 region of pumpkin PV100.

To determine the full sequence of the Luffin P1 precursor we extracted RNA from *L. aegyptiaca* seeds, assembled a transcriptome *de novo* and searched it for sequences encoding Luffin P1. In this way, we found a preprovicilin sequence with the sequence for Luffin P1 within it. Some of the assembled contig around Luffin P1 was repetitive and the read length of the RNA-seq was short (85 bp reads) so to confirm the sequence we designed PCR primers and amplified the full-length genomic sequence (**Fig. S5**). Aligning the RNA-seq raw reads against the genomic clone sequence provided a perfect match, after removing the sequences for five introns.

The encoded protein sequence of the Luffin P1 precursor consists of 871 residues (**Fig. 7C**, **Fig. S5**). The primary structure of the protein was similar to pumpkin PV100 with 73% identity and 80% similarity in a pairwise alignment. Both precursor proteins have an ER targeting signal, a region coding their CXXXC buried peptide (i.e. C2/Luffin P1) and a repetitive region rich in Arg/Glu followed by the last half of the predicted protein sequence that is the mature vicilin. The major difference between them is at the Arg/Glu region, which in Pro-Luffin P1 is longer (~360 vs ~250 residues). The previously reported 6.5k-arginine/glutamate rich polypeptide[14, 15] later called Luffin P1[13] begins with Gly, ends with Glu and is 43 residues long. This 43-residue sequence is present in our encoded sequence, but flanking it in the cloned precursor are conspicuous potential AEP-processing sites (**Fig. 7D**). If, in a manner consistent with PV100 and C2, Luffin P1 is AEP-matured by cleavages at Asn55 and Asp102 then it would begin with Pro, end with Asp and be 47 residues in length (5,690.80 Da, with two disulfide bonds) (**Fig. S6B**).

To determine whether this larger, AEP-processed mass was present we made a crude peptide extract from *L. aegyptiaca* seeds and analyzed it by LC-MS. Prominent ions for a 5,690.80 Da parent mass (47-residue Luffin P1) were indeed present in the corresponding EIC (**Fig. S6C**), in addition to others in the EIC for a parent mass of 5,223.55 Da (the 43-residue Luffin P1, **Fig. S6E**), although in our extracts the latter were only minor peaks in the mass spectrum (**Fig. S6G**). After reduction and alkylation, the EIC for the AEP-processed peptide showed a clear peak (**Fig. S6D**), whereas only a group of low-intensity peaks were seen in the EIC for the 43-residue Luffin P1 (**Fig. S6F**). Analysis of the mass spectrum across the retention time of both the 43-residue and 47-residue peptides showed peaks for the 47-residue peptide but not the 43-residue one (**Fig. S6H**). Overall, these data confirm Luffin P1 is a VBP and likely to be AEP-matured in the same way that C2 is from PV100.

A tomato VBP adopts a helical hairpin structure, like Luffin P1

Luffin P1 is the only member of the VBP family for which a three dimensional (3D) structure has been solved.[16] To investigate whether other VBPs adopt a folded conformation similar to the reported Luffin P1 structure, the tomato VBP (VBP-8) and the 47-residue Luffin P1 were generated through solid phase peptide synthesis, using regioselective formation of the two disulfide bonds. Two dimensional homonuclear ^{1}H NMR spectroscopy data, including TOCSY and NOESY, were recorded for both peptides at 700 MHz. The data were of excellent quality with sharp lines and good dispersion, allowing resonance assignments using standard sequential assignment methods. Secondary Hα shifts (i.e. the difference between observed chemical shifts and chemical shifts observed in random coil conformations) are sensitive indicators of secondary structure. Stretches of negative secondary shifts are indicative of helical structure and the profile of Luffin P1 is consistent with its reported structure showing two significant stretches of negative shifts covering the helical regions between residues 3-16 and 21-39 (**Fig. S7A**). Strikingly similar data were obtained for VBP-8, where again stretches of negative shifts were seen for residues 5-19 and 24-45, confirming it adopts a conserved helix-turn-helix hairpin, like Luffin P1 (**Fig. S7B**). Structural restraints including inter-proton distances, dihedral angles and hydrogen bonds were derived from the NMR data and used to model the 3D structures of the 47-residue Luffin P1 and VBP-8. Both peptides demonstrated well-defined structures with backbone RMSD values less than 0.75 Å and good stereochemical quality (**Table 1**). The structures define the helix-loop-helix motif and despite substantial deviations in sequence between VBP-8 and Luffin P1, both peptides share strong similarities in their 3D structures, including a short 2-3 residue loop between the helical segments and a longer C-terminal than N-terminal segment (**Fig. 8**). The fold is stabilized by the disulfide bonds and hydrophobic interactions at the helical interface. The structure of Luffin P1 presented here is consistent with the structure of the originally discovered truncated version of Luffin P1.[16]

Luffin P1 and VBP-8 have no trypsin inhibitory activity

To test if the VBPs shared a similar function with the previously characterized C2 we tested Luffin P1, which has the highest sequence identity to C2, and VBP-8 for trypsin inhibitory activity. As a positive control a commercial Bowman-Birk inhibitor from soybean was used and showed 50% trypsin inhibition at 0.25 µM and 90% inhibition at 0.4 µM. By contrast, Luffin P1 and VBP-8 showed no effect on trypsin activity, even at 8 µM (**Fig. 9**).

Luffin P1 and VBP-8 are not antimicrobial

Studies on VBPs such as MiAMP2c have demonstrated antimicrobial activity.[12, 17] To determine whether synthetic Luffin P1 and VBP-8 shared this characteristic, each peptide was incubated with five different fungi at concentrations ranging from 9.4 to 2,400 µg/mL in yeast extract, peptone and dextrose (YPD) liquid medium. No inhibition of fungal growth was observed after 72 h incubation. The gram-negative bacterium, *Escherichia coli* K-12 wild-type strain was used to test whether Luffin P1 and VBP-8 had any antibacterial activity (**Fig. 10**). Pre-incubation of the LB agar plates was done to ensure no contamination existed (**Fig. 10A**). The positive control disc contained 10 to 50 µg kanamycin and produced a clear growth inhibition zone from 20 µg (**Fig. 10B**). By contrast, no growth inhibition of *E. coli* K-12 was observed on discs containing synthetic Luffin P1 and VBP-8 up to 120 µg (**Fig. 10C-D**).

Discussion

In this paper, mass spectrometry evidence of vicilin-buried peptides from five distant plant species including the dicots cucumber, tomato, sesame, loofah and the monocot date palm combined with the published VBPs from pumpkin and macadamia revealed a family of peptides produced from within a latent region of an existing protein (**Table 2**). The other example of this kind of unusual dual biosynthesis are cyclic peptides such as SFTI-1 matured alongside albumin from within preproalbumins. These cyclic peptides evolved *de novo* within the N-terminal region between the ER targeting signal and the mature albumin.[9, 10]

VBPs are an ancient family of buried peptides

Based on the alignment of preprovicilin sequences from GenBank and Uniprot, four main classes of preprovicilins revealed genetic expansion in the open reading frames at their N- or C-terminal regions (**Fig. 1**). Class I preprovicilins are present already in ferns and gymnosperms and in most angiosperms, whereas Class II preprovicilins appear restricted to a subgroup of the legumes (*Fabaceae*). Class III and IV preprovicilins were found throughout the flowering plants but not in gymnosperms or ferns. Many species contain Class I, III and IV preprovicilins so the evolution of Class I to III/IV has been interspersed by gene duplication. No preprovicilin contains additional sequence regions both N- and C- terminally of the vicilin suggesting Class II and Class III/IV each evolved independently from Class I. It is not possible to discern the evolutionary origin of Class III/IV preprovicilins without further work refining their distribution. It is apparent though, that there has been significant internal genetic expansion of preprovicilins genes N- and C- terminally of the vicilin domain that has in at least seven species, been proven to be matured into separate, novel peptides (**Fig. 2**, **Table 2**).

The date palm (*Phoenix dactylifera*) is a member of the ancient Palmae family and is cultivated as a staple food for people in arid and semi-arid areas. Date seeds have potential use as a source of dietary fiber and have economic value in cosmetic, pharmaceutical and food products.[18, 19] Date seeds are thought to be some of the most long-lived seeds known, with at least one case of >2,000 year old material still germinating in a recent study.[20] From the date Class IV preprovicilin sequence, two CXXXC pairs were predicted, but only one VBP was found. This might be because the second pair of CXXXC motifs is followed by a long sequence before another AEP site (29 amino acids), which might make such an excised peptide unstable.

Looking more broadly, we found evidence for two VBPs that are buried within a preprovicilin in the seeds of tomato, which belong to the nightshade family Solanaceae that also contains potato, tobacco and other economically important species. Two tomato preprovicilins could be shown to be Class IV, but we found VBPs originating from only one of them.

Another interesting VBP was identified in the dicot species sesame. Sesame seeds are rich in oil and a common ingredient in cuisines across the world. The mass spectra for native and modified peptides combined with MS/MS data matched one of these VBPs. However, some tryptic and chymotryptic fragments of sesame VBP were low abundance and could not generate detectable fragmentation spectra.

We also found VBPs in other cucurbit family members, in addition to the already known C2. In cucumber seeds, two sequences for Class IV preprovicilin were found. One sequence was very similar to the preprovicilin in pumpkin seeds, in which two pairs of CXXXC are seen, but only a peptide with the second pair was matured. Pumpkin PV100 similarly has the C1 region that has Asp and Asn residues between the first CXXXC pair.[11] These Asp and Asn sites might be sensitive to AEP and so this potential peptide could be degraded.

Conservation of the helix-turn-helix fold between VBPs

Of the VBPs, only Luffin P1 had previously had its tertiary structure solved [16].The Luffin P1 structure (**Fig. 7b**) showed a helix-loop-helix motif stapled together by a pair of disulfide bonds in a ladder confirmation of CysI-CysIV and CysII-CysIII.[16] After confirming the precursor of Luffin P1 is indeed a precursor for vicilin, we speculated that other VBPs might adopt a similar fold. As we found we were unable to purify VBPs in sufficient quantities for biochemical studies, we used solid phase peptide synthesis (with regio-selective disulfide bond formation to ensure a laddered disulfide bond network) to produce both the full-length 47-residue Luffin P1 and VBP-8 from tomato. A pairwise comparison shows Luffin P1 and VBP-8 share only 29% sequence identity and 52% similarity. Using

NMR spectroscopy, we compared their structures. Both displayed chemical shifts consistent with helix-turn-helix folds, a fold we confirmed by solving the full structures using NMR restraints and structure calculations. Given the clear conservation of the fold, even in the absence of high sequence homology, we predict other members of the family should adopt similar folds.

VBPs appear absent from wheat, maize and legumes

Within the 252 sequences in our alignment, 113 were Class IV preprovicilins and so had the potential to encode VBPs. There were six Class IV sequences from wheat and five Class IV sequences from maize, but no peptides were detectable using the aforementioned approaches that successfully confirmed VBPs in the seeds of the date palm, tomato, cucumber and sesame. As grains feature prominently in human diets, we were curious what might explain the lack of VBPs in these species. We observed that for all wheat and maize genes, an Asp residue was present between the CXXXC pair. Similarly, 23 Class IV genes from legumes were in our alignment, but no peptidic evidence was found for VBPs here either. We observed that most legume genes, like wheat and maize, have an Asp residue between the CXXXC pair (**Fig. S8**). We performed trypsin digestion of peptide extracts from legumes including chick pea (*Cicer aerietinum*), broad bean (*Vicia faba*), pea (*Pisum sativum*) and common bean (*Phaseolus vulgaris*) and searched MS/MS data against their preprovicilins. None of the fragments found were specific to potential VBPs. The Asp residues are likely to be targeted by AEP for cleavage, which would render the peptides susceptible to further degradation.

In some cases genes potentially encoding two VBPs produced just one. For many, a possible explanation is that following the Cys rich domain there was no obvious AEP cleavage site close to the second CXXXC pair. Using date as an example (**Fig. 3**), following the second pair of CXXXC motifs there is no obvious AEP cleavage site, so a long tail therefore might make a VBP unstable. In most cases the number of residues following the second CXXXC motif was 6-20. For the VBPs for which we obtained evidence, the longest was 19 (VBP-7).

One of the assumptions we made was that VBPs were AEP-processed, so without evidence of an AEP-cleaved mass, VBPs could have been missed. Most seed storage proteins are processed by AEP,[5, 21] but knock out of all endogenous *AEP* genes[6, 7] showed that seed storage proteins were processed by alternative proteases, rather than no processing occurring. Also, although most seed storage proteins are processed by AEP, some are also processed in an AEP-independent manner at some positions. For example one of the four SEED STORAGE ALBUMIN precursors from *A. thaliana,* SESA3 (At4g27160, At2S-3), was not fully dependent upon AEP for its maturation. The SESA3 small albumin subunit is cleaved at its proto-N-terminus by AEP, but the SESA3 large albumin subunit is N-terminally matured in an AEP-independent fashion by an as yet unidentified protease.[6, 7] In the future, a less restrictive approach, using shotgun proteomics and samples from more species, might unearth additional VBPs.

The evolutionary origin and function of VBPs

More work is required to understand the evolutionary origin of the vicilin-buried peptides. Unlike SFTI-1 and its relatives whose common ancestor is estimated to have evolved 45 Mya,[9, 10] the CXXXC-rich region in preprovicilins is far more ancient, which makes it more challenging to retrodict its evolution. The relatively recent origin for the preproalbumin events and the rapid speciation of the sunflower family Asteraceae from 2-20 million years ago[22] made it possible to document and estimate dates for the stepwise evolution of these peptides.[9, 10] The provenance of vicilin-buried peptides is confounded by the existence of CXXXC motifs in a range of unrelated plant proteins and animal proteins.[23-25] Consequently, it is not possible to know whether vicilin-buried peptide arose stepwise by gradual genetic expansion events or by a transfer of CXXXC motifs from elsewhere.

Both genetic and proteomic evidence showed that VBPs are ancient and remain widespread in the plant kingdom. According to the alignment of these known VBPs, although the identities are low among distant species, they share a conserved CX3CXnCX3C motif and have two disulfide bonds. Also, of the known VBPs, C2 has trypsin inhibitory activity,[11] MiAMPs show antimicrobial activities[12] and Luffin P1 is a ribosome inactivator.[13] We were unable to detect antimicrobial or trypsin inhibitory activity for two of the VBPs featured in this work, namely VBP-8 and Luffin P1 suggesting VBPs might have evolved specialized functions instead of serving a conserved, generic function.

To extract these VBPs we found that the typical polar extraction method for peptides, which relies on methanol and dichloromethane, was largely unsuccessful and so instead we used ammonium sulfate to purify VBPs. Even with this method, we could not purify large quantities of VBP and so systematic assays with the VBP family were beyond the scope of this work. We have however demonstrated that solid phase peptide synthesis of VBPs using regioselective disulfide formation is an efficient approach to producing correctly folded VBPs. Further work with synthetic VBPs is required to establish whether they play the important roles in plant biology that their age and evolutionary retention suggest they might.

Methods

Biological material

Seeds of the sponge loofah (*Luffa aegyptiaca*) were supplied by Green Harvest (Cat. No. SL202), cucumber (*Cucumis sativus*) seeds were from Mr. Fothergill's (Cat. No. 5381). Tomato (*Solanum* *lycopersicum*) and pumpkin (*Cucubita maxima*) seeds were bought from Royston Petrie Seeds (Stock No. 117/15 and 229M29 respectively). Sesame (*Sesamum indicum*) and dates (*Phoenix dactylifera*) were bought from a supermarket.

Vicilin alignment

GenBank and UniprotKB databases were searched for protein sequences annotated to contain the term "vicilin". Using default BLASTP parameters plus restricting the search to green plants (Viridiplantae), GenBank and UniprotKB were queried for protein sequences using the full amino acid sequence of PV100. All results were gathered (983 unique entries) and only unique and full ORF sequences (424 sequences) were retained. These sequences were further filtered manually to eliminate, in a given species, multiple entries of the same sequences with minor variations possibly due to either sequencing errors or recent gene duplication. Such sequences would bring little information and could introduce a bias in the alignment. In this way, the number of sequences was reduced to 252 including PV100 and MiAMP2 precursors (**table S1**). These sequences were aligned with CLC Genomics Workbench (QIAGEN Aarhus A/S) and additional modifications to the alignment were made manually. For the sequences aligned see **Dataset 1** and for a high-resolution alignment used in **Figure 1**, see **Dataset 2**.

Phylogenetic analysis of vicilin distribution

To infer a phylogeny that can be used to visualize the distribution of the four preprovicilin classes across the plant tree of life we downloaded sequences of the barcoding chloroplast DNA region *rbcL* for all taxa listed in **Table S1** from GenBank. The only missing species was *Citrus clementina*, for which no *rbcL* sequence was found in the database. The *rbcL* sequences were aligned in Geneious v. 11 (Biomatters Ltd., Auckland, NZ) and the resulting alignment used to infer an ultrametric tree in BEAST v. 1.8.4[26] under the GTR+G model with six gamma rate categories. To calibrate the tree, we used the following seven secondary age constraints based on the crown node ages of major plant families estimated by Bell *et al.*[27]: (a) Poaceae - 23 +/- 6 Mio. years; (b) Arecaceae - 35 +/- 3 Mio. years; (c) Solanaceae - 35 +/- 5 Mio. years; (d) Brassicaceae - 37 +/- 4.5 Mio. years; (e) Rosaceae - 38 +/- 6 Mio. years; (f) Fagales - Cucurbitales split - 84 +/- 1 Mio. years; (g) angiosperms - 151 +/- 5.5 Mio. years. The root age of the tree was constrained to 383 +/- 5 Mio. years based on Klaus *et al.*[28] BEAST was run for 50 million generations and the performance checked using Tracer v. 1.6.0.[29] The resulting trees were combined using TreeAnnotator v. 1.8.4 (part of the BEAST package) after discarding the first 5,000 trees. The final consensus tree was edited in FigTree v. 1.4.2 (http://tree.bio.ed.ac.uk/software/figtree).

Peptide extraction and purification

Seeds were de-hulled and ground to a fine tissue powder in liquid nitrogen. For cucumber, methanol and dichloromethane were used to extract proteins. About 0.3 mL of frozen tissue powder in a 1.5 mL tube was defatted by suspension in 1 mL of hexane before being centrifuged for 5 min at 20,000 x g. The supernatant was removed and the pellet extracted with 1 mL of hexane and dried. The now defatted tissue was suspended in 0.4 mL methanol and 0.4 mL dichloromethane for 5 min, mixed with 0.2 mL of 0.05% trifluoroacetic acid solution and centrifuged for 5 min at 20,000 x g at room temperature. The upper aqueous phase was kept and desiccated by vacuum centrifugation. For separation, proteins were dissolved in 0.3 mL of 5% acetonitrile (v/v) and 0.1% formic acid (v/v). Samples were separated on MicroSpin C18 columns in a 5% to 80% acetonitrile gradient with 5% increments, followed by desiccation.

Ammonium sulfate was used to precipitate proteins from tomato, date, loofah and sesame. Initially, 1.5 g of seed flour was blended with 30 mL of 10 mM phosphate buffer (pH 7.5) containing 0.15 M sodium chloride. The mixture was frozen and thawed three times, centrifuged, and the supernatant retained. Ammonium sulfate was added to 85% saturation at 4°C to precipitate proteins. For purification, the precipitate was dissolved in 10 mM phosphate buffer (pH 7.5) and purified by Amicon Ultra 30,000 molecular weight cut-off (MWCO) and 3,000 MWCO filter units (Merck). The filtrate from the 30,000 MWCO filter was loaded onto a 3,000 MWCO filter and the 3 kDa filter retentate was collected and dried by centrifugation under vacuum. To remove salts that might affect LC-MS analysis, proteins were dissolved in 5% acetonitrile 0.1% formic acid, loaded onto Strata-X 33 µm polymeric solid phase extraction columns (10 mg/1 mL, Phenomenex), washed with 1 mL of 5% acetonitrile 0.1% formic acid twice, eluted with 0.5 mL 100% acetonitrile 0.1% formic acid three times and dried by vacuum centrifuge.

Peptide modification and digestion

After isolation, separation and purification, all peptide candidates were reduced, alkylated and digested as described previously.[30] Dried peptides were dissolved in HPLC-grade water, reduced with dithiothreitol to break disulfide bonds, alkylated with iodoacetamide, which binds covalently with the thiol group of cysteine to prevent the reformation of disulfide bonds, and then digested with chymotrypsin or trypsin. All modified or digested samples were further analyzed by tandem mass spectrometry.

MALDI-MS, LC-ESI-MS and LC-MS/MS analyses with cucumber extracts

Cucumber peptide extract was fractionated crudely from a C18-column in 5% steps of acetonitrile, with the 25% and 30% acetonitrile fractions containing the cucumber VBP. To find it, each fraction was analyzed using an UltraFlex III MALDI-TOF/TOF mass spectrometer (Bruker Daltonics). The dried fractions were resuspended in 0.2 mL 50% acetonitrile 0.1% formic acid (v/v). The matrix used was saturated α-cyano-4-hydroxycinnamic acid (Fluka) in 0.1% formic acid in acetonitrile and 0.1% formic acid in water (v/v 1:2). For each peptide fraction, a mixture of 1 µL matrix and 1 µL sample was spotted onto an MTP AnchorChip™ 384 plate (Bruker). Protein Calibration Standard I (Bruker) was used for calibration.

The 25% fraction was analyzed by liquid chromatography/electrospray-ionization mass spectrometry (LC-ESI-MS) after in-solution trypsin digestion. The digested solution was mixed with 50% acetonitrile and 10% formic acid to a final concentration of 5% acetonitrile, 0.1% formic acid. Four microlitre aliquots of this solution were loaded onto the enrichment column of a Large Capacity Chip II (Enrichment: 9 mm, 160 nL; Agilent Technologies) in 95% solvent A (0.1% formic acid in water) and 5% solvent B (0.1% formic acid in acetonitrile) and switched into the analytical column of the chip (Separation: 150 mm x 75 µm). Using a gradient of 5% solvent B to 45% solvent B over 30 min, peptides were eluted into an Agilent 6520 Q-TOF mass spectrometer by electrospray ionization at 2175 V. Spectra were analyzed with MassHunter Qualitative Analysis B.07.00 (Agilent Technologies) as well as MASCOT software (version 2.5.1, Matrix Science).

Q-TOF LC-MS and Orbitrap LC-MS with date, tomato, sesame and loofah extracts

To identify the predicted VBPs from seeds of tomato, sesame, loofah and date, both native and reduced-alkylated peptides from each species were analyzed by LC-ESI-MS as previously described.[10] Briefly, native and alkylated peptide extract were dissolved in 5% acetonitrile and 0.1% formic acid and loaded into the mass spectrometer. Then chymotrypsin and trypsin-digested peptides were dissolved in the same solvent and analyzed by tandem mass spectrometry. The flow rate was 0.2 µL/min for a gradient from 5% to 95% acetonitrile in 40 min and the injection volume was 3 µL. The mass spectrometer was operated in positive, data-dependent mode with a scan range from 400 to 1600 m/z and Orbitrap resolution set to 60,000 for both MS and MS/MS.

MS/MS analysis

All MS/MS data were analyzed using MASCOT version 2.5.1 (Matrix Science). The analyses were performed using a custom in-house database of 252 vicilin precursors and predicted VBPs. Proteomics parameters were standard, but included the following settings: trypsin (or chymotrypsin) with up to 2 missed cleavages; carbamidomethyl (C) as a fixed modification; pyro-Glu (N-term E) and pyro-Glu (N-term Q) as variable modification; 50 ppm peptide tolerance and 50 ppm MS/MS tolerance, peptide charges of 1+, 2+ or 3+.

Luffa aegyptiaca RNA extraction and sequencing

RNA was extracted from 0.2 g of whole de-hulled seeds using the phenol-based method described by Mylne *et al.*[31] Total RNA (60 µL volume) was treated with DNase (New England Biolabs) and further purified with a NucleoSpin RNA Clean-up kit (Macherey-Nagel). Sequencing libraries were generated using the TruSeq Stranded Total RNA LT with Ribo-Zero Plant kit (Illumina) with 2 µg of purified total RNA according to the manufacturer's instructions. RNA sequencing was then performed on an Illumina HiSeq 1500 platform as 85 bp single read runs.

De novo transcriptome assembly and search for the Luffin P1 precursor

Transcriptomes were assembled *de novo* as previously described,[32] using CLC Genomics Workbench 8.5.1. Filtered reads were assembled with five different word sizes (23, 30, 40, 50 and 64), keeping all other parameters as default. Each transcriptome assembly was analyzed by tBLASTn using Luffin P1 and PV100 sequences as queries and each search found significant matches, but to different transcript contigs. These contigs had a 21 bp overlap that was extended by performing a second round of assembly, using a word size of 20. This led to the assembly of a single transcript contig containing a 5′ UTR, start methionine, endoplasmic reticulum signal sequence, Luffin P1, mature vicilin, stop codon and 3′ UTR. Some of the sequence around Luffin P1 was repetitive and the RNA-seq read length was only 85 bp, which could explain why it could not be assembled initially into a single contig. To confirm the sequence of this putative transcript the gene was cloned by PCR.

To amplify the gene and include the full ORF, a forward PCR primer JM793 (5′-CGA TCT CAA ACA TGG CGT CGT-3′, start ATG underlined) and reverse PCR primer JM797 (5′-CCT TCA GAA GTA ACC GGC GAG T-3′, stop codon underlined) were designed against the assembled contig. Genomic DNA was purified from 0.1 g of seeds using the DNeasy Plant Mini Kit (QIAGEN). PCR with *L. aegyptiaca* genomic DNA as template using *Taq* DNA polymerase amplified a DNA fragment that was purified from an agarose gel with a QIAquick Gel Extraction Kit (QIAGEN) and cloned into pGEM-T Easy (Promega). Four independent clones were fully sequenced to identify errors introduced by *Taq* DNA polymerase. The intron spans were identified by comparing the transcript contig and RNA-seq reads with the genomic DNA sequence and the sequence deposited in GenBank under accession MF351606.

Peptide synthesis

Luffin P1 and VBP-8 (tomato) were synthesized on a 0.125 mmol scale using fluorenylmethyloxycarbonyl-based solid phase peptide synthesis. Both peptides were assembled on Tentagel XV 4-hydroxymethyl phenoxyacetic acid resin (Rapp Polymere GmbH), using the same protocols for all steps. Prior to loading, the resin was swollen in dimethylformamide for 24 h. Ten equivalents of the C-terminal residue dissolved in dichloromethane and five equivalents of N,N′-diisopropylcarbodiimide were stirred at 4°C for 30 min, before the dichloromethane was removed via rotary-evaporation. The dried amino acid was dissolved in minimal dimethylformamide and added to the resin together with 0.1 M 4-dimethylaminopyridine and shaken for 12 h. The resin was washed and the loading protocol repeated before the remaining residues were added to the peptide chain using a CS336X automatic peptide synthesizer (CSBio). Each subsequent residue was added by first deprotecting the N-terminal residue with 20% (v/v) piperidine, washing with dimethylformamide, then coupling using eight equivalents of amino acid, four equivalents of N,N,N′,N′-tetramethyl-O-(1H-benzotriazol-1-yl)uronium hexafluorophosphate and 16 equivalents of N,N-diisopropylethylamine. After the final deprotection the resin was washed with dimethylformamide followed by dichloromethane and dried under nitrogen. The resin was cleaved using a 50 mL solution of trifluoroacetic acid, triisopropylsilane, 3,6-dioxa-1,8-octanedithiol and water (95:2:1.5:1.5) for 2 h. The trifluoroacetic acid was removed via rotary-evaporation, after which the peptide was precipitated with cold diethyl ether, dissolved in a solution of acetonitrile/water (50:50) and lyophilized. Crude purification was conducted by reverse phase high performance liquid chromatography using 90% acetonitrile 0.05% trifluoroacetic acid at a gradient of 1% /min on a preparative C18 column (300 Å, 10 µm, 21.20 mm i.d x 250 mm, Phenomenex). ESI-MS was used to confirm peptide mass.

Disulfide bonds were formed regioselectively using pairs of acetamidomethyl and trityl Cys protecting groups to generate the connectivity of 1-4, 2-3. The first disulfide bond was formed by oxidation in 0.1 M ammonium carbonate pH 8.1 at a peptide concentration of 0.25 mg/mL with 2 mM reduced glutathione for 24 h, after which further purification was conducted using a semi-preparative C18 column (300 Å, 5 µm, 10 mm i.d. x 250 mm, Vydac).

The acetamidomethyl groups were removed and the second disulfide bond was formed by iodolysis in acetonitrile/water (50:50) at a concentration of 0.25 mg/mL. A 0.1 M iodine solution was added until a noticeable change in color was observed, from clear to dark yellow. The solution was stirred in the dark under nitrogen for 4 h, and the reaction subsequently quenched with ascorbic acid. Final purification was conducted as above and purity was determined using an analytical column (Agilent).

NMR spectroscopy

Samples for NMR analysis contained 1.5 mg peptide in a 550 µL solution of (90:10) H_2O/D_2O, at pH ~3.5. Two-dimensional datasets including TOCSY[33] (Total Correlation Spectroscopy) using a mixing time of 80 ms and NOESY[34] (Nuclear Overhauser Spectroscopy) using a mixing time of 150 ms were recorded at 298 K on a 700 MHz Bruker Avance III spectrometer equipped with a cryo-probe.

Topspin 4.0.3 (Bruker) was used for data processing. The data were referenced to the solvent signal at 4.77 ppm. The TOCSY and NOESY data were analyzed and assigned in the program CARA [35] using sequential assignment strategies.[36] Secondary structure was identified by the determination of secondary ^{1}Hα shifts through comparison to equivalent values determined for random coil peptides.[37]

Structure calculations

Interproton distance restraints were determined from the peak volumes of the cross peaks present in the NOESY spectra. TALOS-N (Torsion Angle Likelihood Obtained from Shift and sequence similarity)[38] was used in conjunction with the shift data generated from all recorded spectra to predict the φ (C^{-1}-N-Cα-C) and ψ (N-Cα-C-N^{+1}) backbone dihedral angles. For the cystine residues chemical shifts were also used to predict χ^1 (N-Cα-Cβ-Sx) and χ^2 (Cα-Cβ-Sx-Sy) dihedral angles using the program DISH (di-sulfide di-hedral prediction).[39] Hydrogen bond restraints were based on the determination and assessment of amide proton temperature coefficients. TOCSY data were recorded at 288, 293, 298, 303 and 308 K to monitor temperature dependence of the amide proton resonance frequency. Temperature coefficient values > -4.6 ppb/K were taken as indicative of a hydrogen bond being donated by the particular residue.[40] Using restraints initially 50 structures were calculated by torsion angle simulated annealing, performed by CYANA,[41] which also allowed for the automatic assignment of NOESY data. The final structures were generated and water minimized by the program CNS.[42] Structures with no violations > 0.2 Å as well as low energy were selected for stereochemical analysis by MolProbity.[43] Structure images were generated using MOLMOL.[44]

Trypsin inhibitory assay

The inhibition was determined as previously described.[45] Briefly, synthetic peptides were dissolved in water at stock concentration 10 mg/mL. The assay buffer was 50 mM Tris-HCl, pH 7.8 containing 20 mM calcium chloride. The 20 µL of 25 µg/mL trypsin from bovine pancreas (Sigma Aldrich) and 5 µL of increasing concentrations of peptide (giving final concentrations of 0-8 µM) was pre-incubated at 37 °C for 15 min. The reaction was initiated by adding 125 µL of 1 mM N-α-benzoyl-L-arginine-p-nitroanilide substrate (Sigma Aldrich) and incubated for 30 min at 37°C. A Bowman-Birk inhibitor protein from soybean (Sigma Aldrich) was used as the positive control and each reaction was performed in triplicate. The well with no inhibitor or peptide was designated 100% trypsin activity. To stop the reactions, 25 µL of 30% acetic acid was added. Absorbance was measured at 410 nm.

Antifungal and antibacterial activity assay

The antifungal assay was carried out as previously described.[10] Briefly, cultures of *Phaeophaeria nodorum, Bipolaris sorokiniana, Zymoseptoria tritici*, *Pyrenophora tritici-pepentis* and *Aspergillus* *fumigatus* were grown on YPD plates. The plate with *A. fumigatus* was incubated at 37°C for whereas the others were incubated at 23°C. After two days, the spores were harvested and diluted into YPD medium until the OD_{600} reached 0.05. A 96-well microplate was used for the assay. Each well was filled with 180 µL of diluted culture and 20 µL of each peptide solution at one of nine concentrations. Fungal growth was measured by OD_{600} after 24, 48 and 72h.

For the antibacterial activity test, a liquid culture of wild type *Escherichia coli* K-12 was diluted with sterile LB to an OD_{600} of 0.1. Luffin P1 and VBP-8 solutions were dispensed onto sterile 8 mm diameter filter papers to contain 10, 30, 60 or 120 µg of peptide. The bacteria were spread evenly onto the sterile LB agar plate with a sterile swab and dried filter papers with different amounts of peptide were placed onto the plates. Sterile water was used as negative control and 50 µg of kanamycin was used as the positive control. The plates were incubated at 37°C overnight, after which bacterial growth was imaged.

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Author contributions

J.S.M conceived the study. J.Z. designed and performed all experiments with the exception of the following: B.P. produced the alignment of vicilin precursors and confirmed the presence of VBP-10; H.S. performed the phylogenetic analysis; N.L.T. and M.F.F. helped to perform LC-MS/MS; O.B. and J.W. prepared libraries and performed RNA-seq, C.P. synthesized Luffin P1 and VBP-8; C.P. and K.J.R.

performed NMR spectroscopy analysis; all authors analyzed data; J.Z. and J.S.M. wrote the manuscript with contributions from all authors.

Supporting Information

Supporting information is available and includes: MS/MS spectra of VBP-6 from date palm seeds (*P. dactylifera*) (Fig. S1); MS/MS spectra for tryptic and chymotryptic fragments of VBP-7 from tomato seeds (*S. lycopersicum*) (Fig. S2); MS/MS evidence of VBP-8 from tomato seeds (*S. lycopersicum*) (Fig. S3); MS/MS evidence of VBP-9 from sesame (*S. indicum*) (Fig. S4); *Preprovicilin with Luffin P1* gene and its encoded protein containing Luffin P1 and vicilin (Fig. S5); Evidence for Luffin P1 (VBP-5) from *L. aegyptiaca* (Fig. S6); Tomato VBP-8 adopts a similar helix-turn-helix structure as Luffin P1 (Fig. S7); Alignment of Cys-rich domain of Class IV preprovicilins in cereal crops and legumes (Fig S8); The 252 preprovicilin sequences used for the alignment (Table S1) as well as the raw sequence alignment (Dataset 1) and a high-resolution alignment from in Figure 1 (Dataset 2). This material is available free of charge via the internet at http://pubs.acs.org.

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Tables

Table 1 | NMR statistics. Energies, restraints and structural statistics for the families of 20 structures for Luffin P1 and VBP-8.

Energies (kcal/mol)	**Luffin P1**	**VBP-8**
Overall	-1702.37 ± 101.45	-2053.03 ± 79.11
Bonds	14.44 ± 1.53	15.59 ± 1.22
Angles	60.70 ± 4.35	52.63 ± 4.13
Improper	19.93 ± 2.93	21.28 ± 2.56
Dihedral	215.64 ± 2.12	220.64 ± 3.05
Van der Waals	-174.38 ± 16.63	-205.48 ± 8.15
Electrostatic	-1838.78 ± 114.86	-2157.94 ± 86.74
NOE	0.046 ± 0.027	0.098 ± 0.024
Cdih	0.044 ± 0.073	0.16 ± 0.18
MolProbity Statistics		
Clashes (>0.4 Å / 1000 atoms)	8.74 ± 4.22	11.98 ± 2.91
Poor rotamers	0.25 ± 0.55	0.3 ± 0.66
Ramachandran Outliers (%)	1.33 ± 1.12	0.21 ± 0.66
Ramachandran Favoured (%)	94.78 ± 2.73	96.59 ± 2.23
MolProbity score	1.79 ± 0.28	1.85 ± 0.22
Molprobity score percentile	83.4 ± 9.65	81.85 ± 9.01
Residues with bad bonds	0.05 ± 0.22	0
Residues with bad angles	1.05 ± 0.22	0
Atomic RMSD (Å)		
Mean global backbone (helical regions)	0.74 ± 0.20	0.46 ± 0.12
Mean global heavy (helical regions)	1.96 ± 0.21	1.75 ± 0.19
Experimental Restraints		
Distance restraints		
Short range (i-j < 2)	329	431
Medium range (/i-j/ < 5)	25	100
Long range (/i-j/ > 5)	33	73
Hydrogen bonds	42 (21 Hydrogen bonds)	48 (24 Hydrogen bonds)
Total	429	652
Dihedral angle restraints		
φ	34	37
ψ	34	36
χ1	4	4
χ2		4
Total	72	81
Violations from experimental restraints		
Total NOE violations exceeding 0.2 Å	0	0
Total Dihedral violations exceeding 2.0°	0	0

Table 2 | Summary of vicilin-buried peptides. Luffin P1 was revealed as VBP-5, the new VBPs from this work are VBP-6 to VBP-10; Z = pyro-Glu. * Longer versions of MiAMP2c were also isolated with 2 and 22 additional residues at the C-terminus.

Vicilin-buried Peptide	Common name	Size (aa)	Species		Ref
C2 (VBP-1)	pumpkin	49	*Cucurbita maxima*	ZRGSPRAEYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQGRGEDVD	[11]
MiAMP2b (VBP-2)	macadamia	41	*Macadamia integrifolia*	DPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYN	[12]
MiAMP2c (VBP-3)	macadamia	45/47/67*	*Macadamia integrifolia*	RQRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQ(KRYEEQQREDEEKYEERMKEED)	[12]
MiAMP2d (VBP-4)	macadamia	35	*Macadamia integrifolia*	KRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQ	[12]
Luffin P1 (VBP-5)	loofah	47	*Luffa aegyptiaca*	PRGSPRTEYEACRVRCQVAEHGVERQRRCQQVCEKRLREREGRREVD	[13], this work
VBP-6	date palm	40	*Phoenix dactylifera*	PKRQIERCKQECRESRQGEQQERQCVRQCEEQEEKRGQGD	This work
VBP-7	tomato	53	*Solanum lycopersicum*	PRGYQDPQEKLRECQQRCERQQPGQQKQLCKQRCEQQYRKEQQQQHGGETGED	This work
VBP-8	tomato	49	*Solanum lycopersicum*	RGPDKSYKRLQECQRRCQSEQQGQRLQECQQRCQQEYQREKGQHQGETN	This work
VBP-9	sesame	49	*Sesamum indicum*	RKSPIERLRECSRGCEQQHGEQREECLRRCQEEYQREKGRQD	This work
VBP-10	cucumber	35	*Cucumis sativus*	ZKETEICRQWCQVMKPQGGEEQRRCQQECEERLRD	This work

Figures

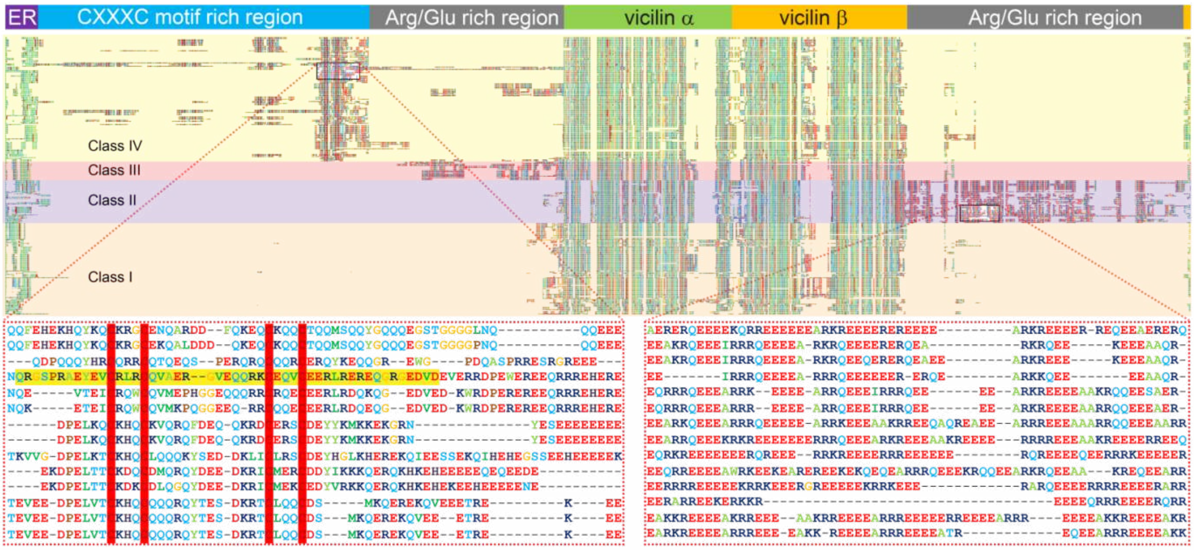


Fig. 1 | Potential for a family of CXXC-containing hairpin peptides buried in preprovicilins. Alignment of 252 preprovicilin sequences reveals there are four classes based on internal, N- and C-terminal expansions. Class I are typical preprovicilins with an ER targeting signal and vicilin domain. Class II have an Arg/Glu rich C-terminal expansion (zoom, lower right) and are restricted to legumes. Class III have an N-terminal Arg/Glu-rich region, whereas Class IV sequences also have a Cys-rich expansion on the N-terminal side (zoom, lower left) with repeating pairs of CXXXC (Cys are highlighted in red). The sequence of the first vicilin-buried peptide, C2 in PV100[11], is highlighted in yellow in the lower left panel. We predicted the Cys-rich regions of Class IV preprovicilins harbor a large and ancient family of buried peptides. For the sequences see **Dataset 1** and for a high-resolution alignment see **Dataset 2**.

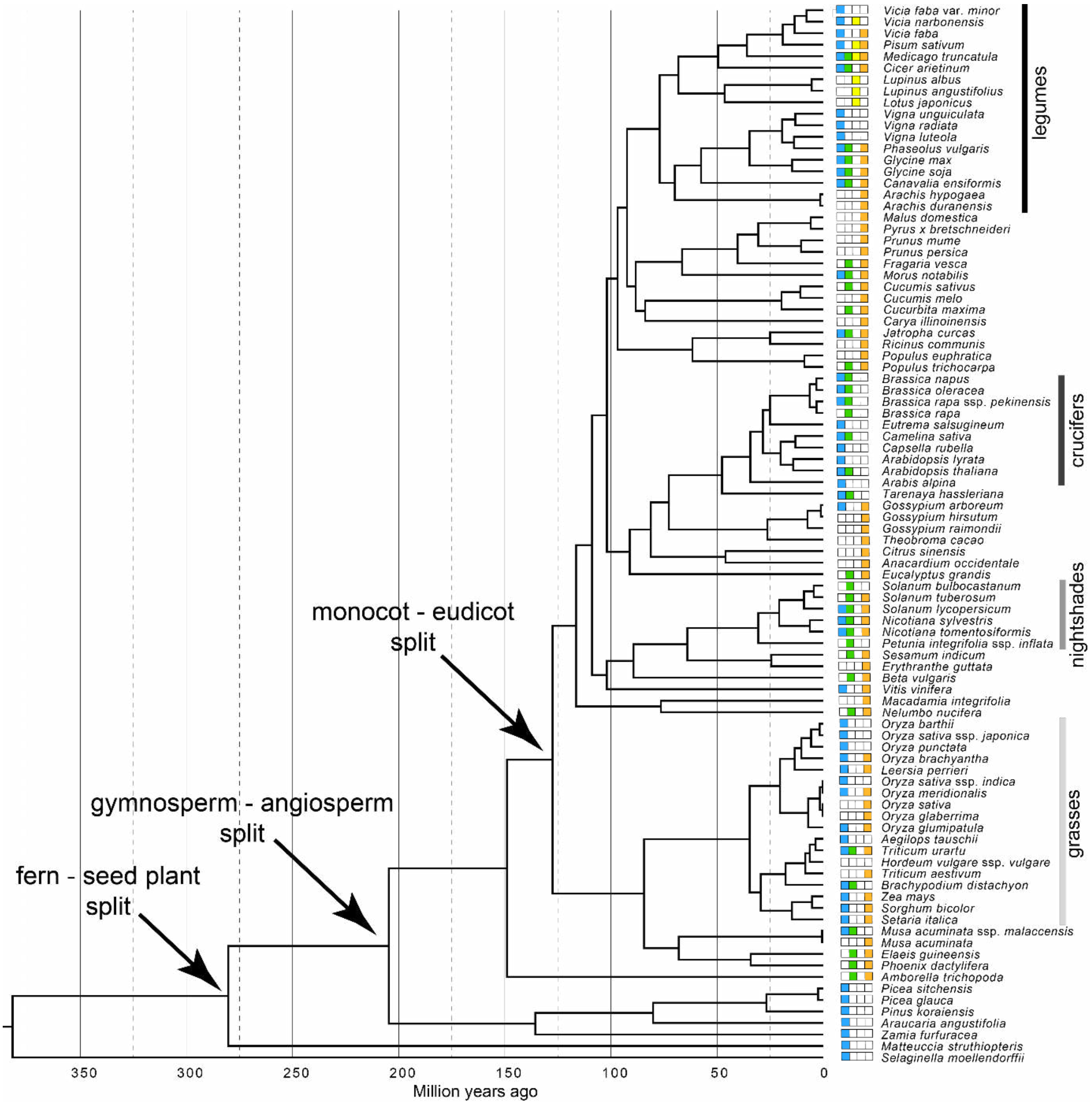


Fig. 2 | Distribution of the four preprovicilin classes across the plant tree of life. Phylogeny built from *rbcL* sequences for species containing preprovicilin sequences in **Fig. 1**. Colored boxes indicate presence of Class I (blue), Class II (green), Class III (yellow) and Class IV (orange) preprovicilins.

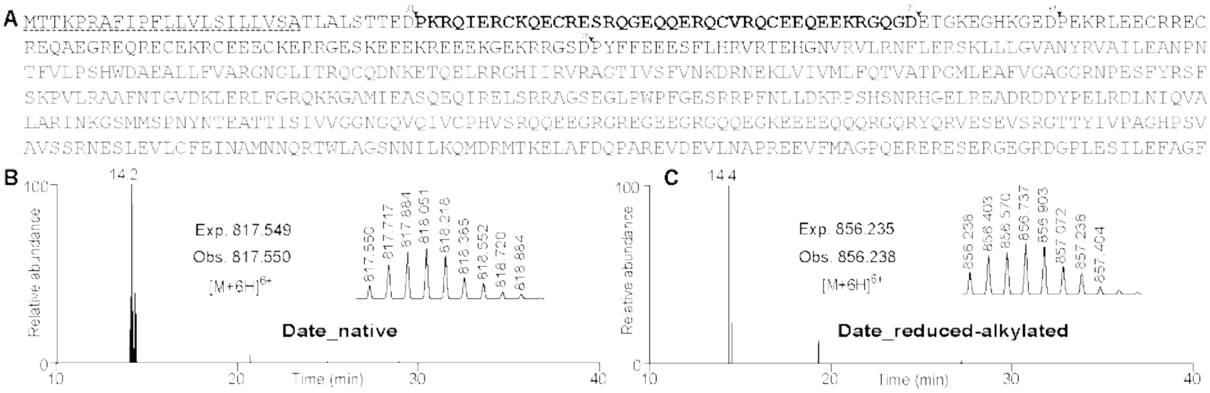


Fig. 3 | LC-MS for peptide extract from date palm seeds. (**A**) The vicilin precursor of date from GenBank (code: 008775109), which contains an ER targeting signal (dashed underline), a predicted vicilin-buried peptide (VBP) (in bold) and a vicilin protein (in gray). Variable AEP processed sites are labelled by arrows. (**B**) Extracted-ion chromatogram (EIC) for native *m/z* 817.549 at $[M+6H]^{6+}$ of the predicted VBP with two disulfide bonds showing a peak at 14.2 min. The inset is the corresponding mass spectrum. (**C**) EIC for the reduced-alkylated *m/z* 856.235 for the predicted VBP indicating a peak at 14.4 min. The corresponding mass spectrum is inset. Note: Exp. means expected m/z while Obs. is observed m/z. For sequencing of date palm VBP-6 by MS/MS see **Fig. S1**.

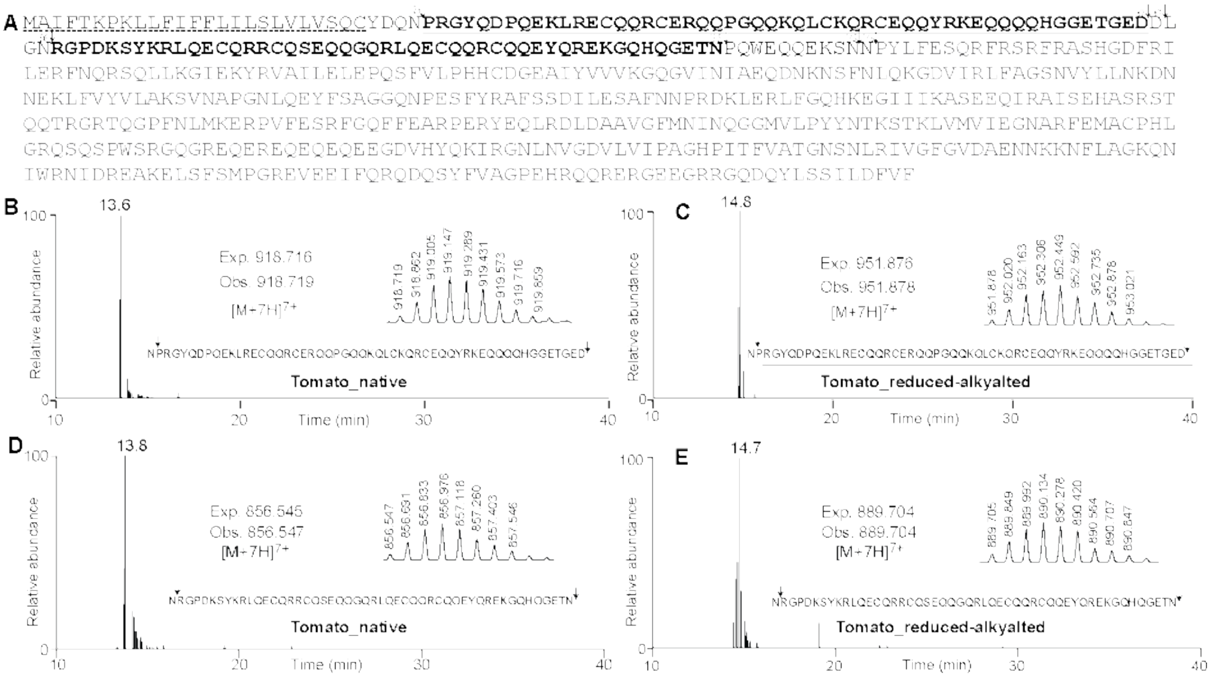


Fig. 4 | LC-MS for peptide extract from tomato seeds. (**A**) The sequence of vicilin precursor of tomato from UniprotKB (code: B0JEU3). The precursor belongs to Class IV, which contains an ER-targeting signal (dashed underline), predicted 53-residue peptide (underlined), predicted 49-residue peptide (doubly underlined) and a vicilin protein (in gray). Possible AEP-processed sites are labelled (arrows). (**B-C**) EICs at $[M+7H]^{7+}$ and corresponding mass spectra (insets) of (**B**) native predicted 53-residue peptide with two disulfide bonds and (**C**) reduced-alkylated 53-residue peptide. (**D-E**) EICs at $[M+7H]^{7+}$ of (**D**) native predicted 49-residue peptide with two disulfide bonds and (**E**) reduced-alkylated 49-residue peptide. For sequencing of tomato VBP-7 and VBP-8 by MS/MS see **Fig. S2-S3**.

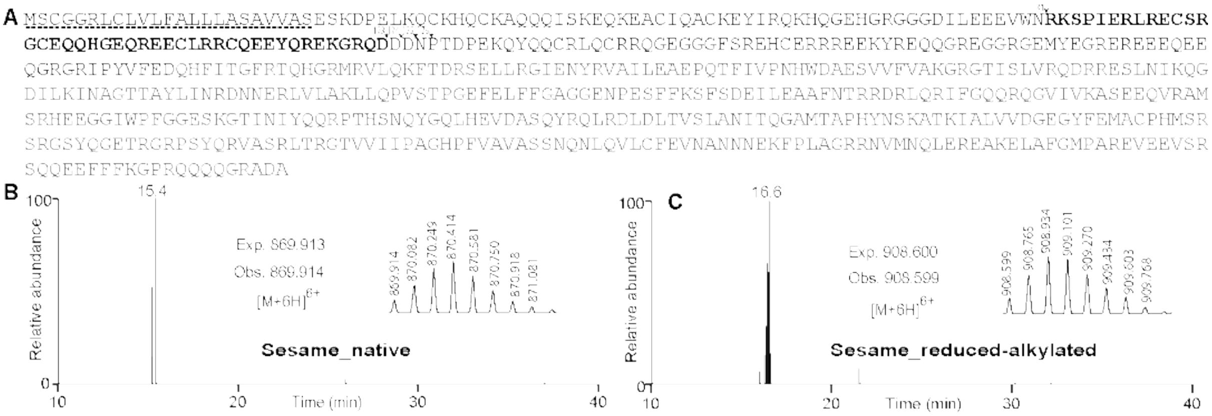
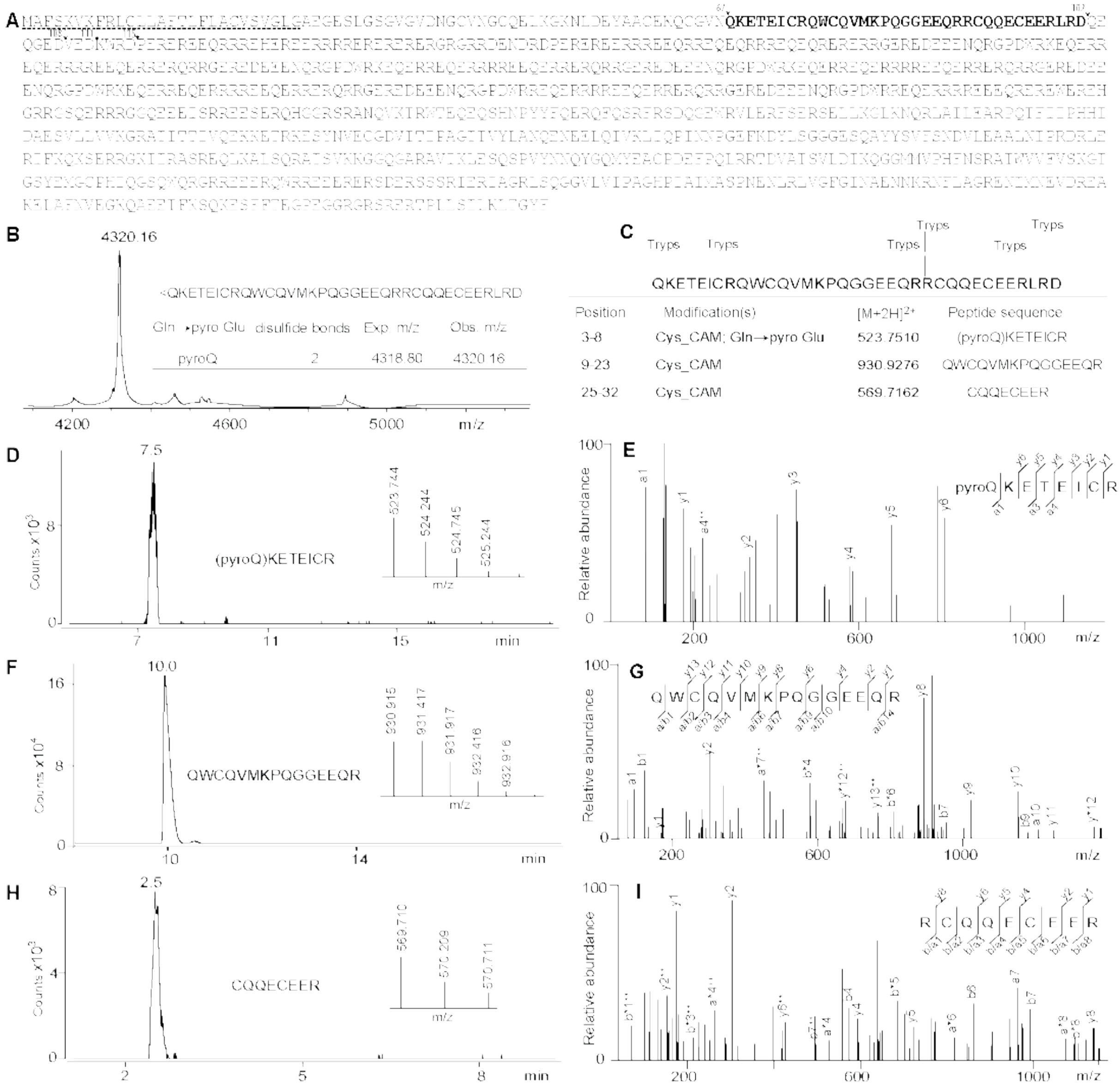


Fig. 5 | LC-MS for peptide extract from sesame seeds (VBP-9). (**A**) A vicilin precursor of sesame from UniprotKB (code: Q9AUD0) including an ER-targeting signal (dashed underline), predicted VBP sequence (42-residue, bold) and vicilin protein (in grey). Possible AEP-processed sites are numerically labelled (solid arrows). (**B-C**) EICs at $[M+6H]^{6+}$ and (insets) corresponding mass spectra of (**B**) native 42-residue and (**C**) Reduced-alkylated 42-residue peptide. For sequencing of sesame VBP-9 by MS/MS see **Fig. S4**.



Gln →pyro Glu	disulfide bonds	Exp. m/z	Obs. m/z
pyroQ	2	4318.80	4320.16

Position	Modification(s)	[M+2H]$^{2+}$	Peptide sequence
3-8	Cys_CAM; Gln→pyro Glu	523.7510	(pyroQ)KETEICR
9-23	Cys_CAM	930.9276	QWCQVMKPQGGEEQR
25-32	Cys_CAM	569.7162	CQQECEER

Fig. 6 | Mass spectrometry evidence for a 35-residue VBP from cucumber seeds (VBP-10). (**A**) The sequence of the vicilin precursor of cucumber (GenBank code: 778678441). A predicted vicilin-buried peptide (35-residue) is highlighted in bold and possible AEP-cleavage sites are labelled with arrows. (**B**) MALDI-TOF-mass spectrum of the 35-residue peptide. Inset is its theoretical m/z calculated with two disulfide bonds and a pyroglutamate (pyro-Glu/pyroQ) from N-terminal Gln as described by Yamada *et al.*[11] (**C**) Trypsin cleavage sites of the 35-residue peptide and calculated fragment masses which account for carbamidomethyl modifications of cysteine residues (alkylation: Cys_CAM) and/or a variable pyroGlu at the N-terminus Gln. All m/z ratios are shown as [M+2H]$^{2+}$ ions. (**D**, **F**, **H**) EICs from LC-MS at [M+2H]$^{2+}$ (insets: corresponding mass spectra) and (**E**, **G**, **I**) corresponding MS/MS spectra (insets: fragment sequences with y, b and a ions) of (**D**, **E**) “pyroQKETEICR”, (**F**, **G**) “QWCQVMKPQGGEEQR” and (**H**, **I**) “CQQECEER”.

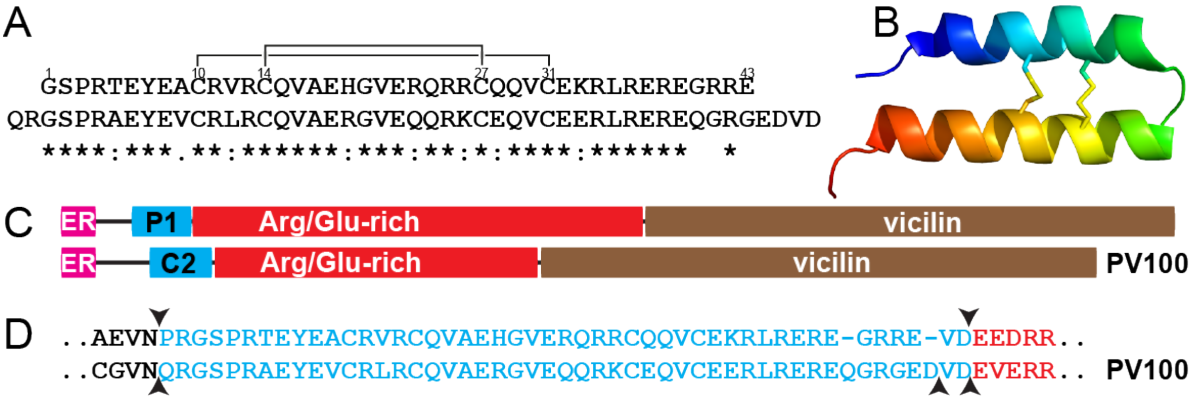


Fig. 7 | The α-helical hairpin peptide Luffin P1 is a vicilin-buried peptide. (**A**) The published sequence of the 43-residue Luffin P1 (top) is similar to the vicilin-buried peptide C2 (bottom). The disulfide connectivity of Luffin P1 (lines) was established when its NMR solution structure (**B**) was determined by Li *et al.*,[13] here shown in ribbon format. (**C**) A summary of the structure of the Luffin P1 precursor protein that we determined and found to be similar in primary structure to the pumpkin preprovicilin PV100 with Luffin P1 buried in an equivalent region, the main difference being a longer Arg/Glu-rich region. (**D**) Luffin P1 is likely to be 47-residues and AEP-processed based on conserved Asn/Asp cleavage sites (arrows). Support for a 47-residue Luffin P1 mass was found by mass spectrometry (**Fig. S6**).

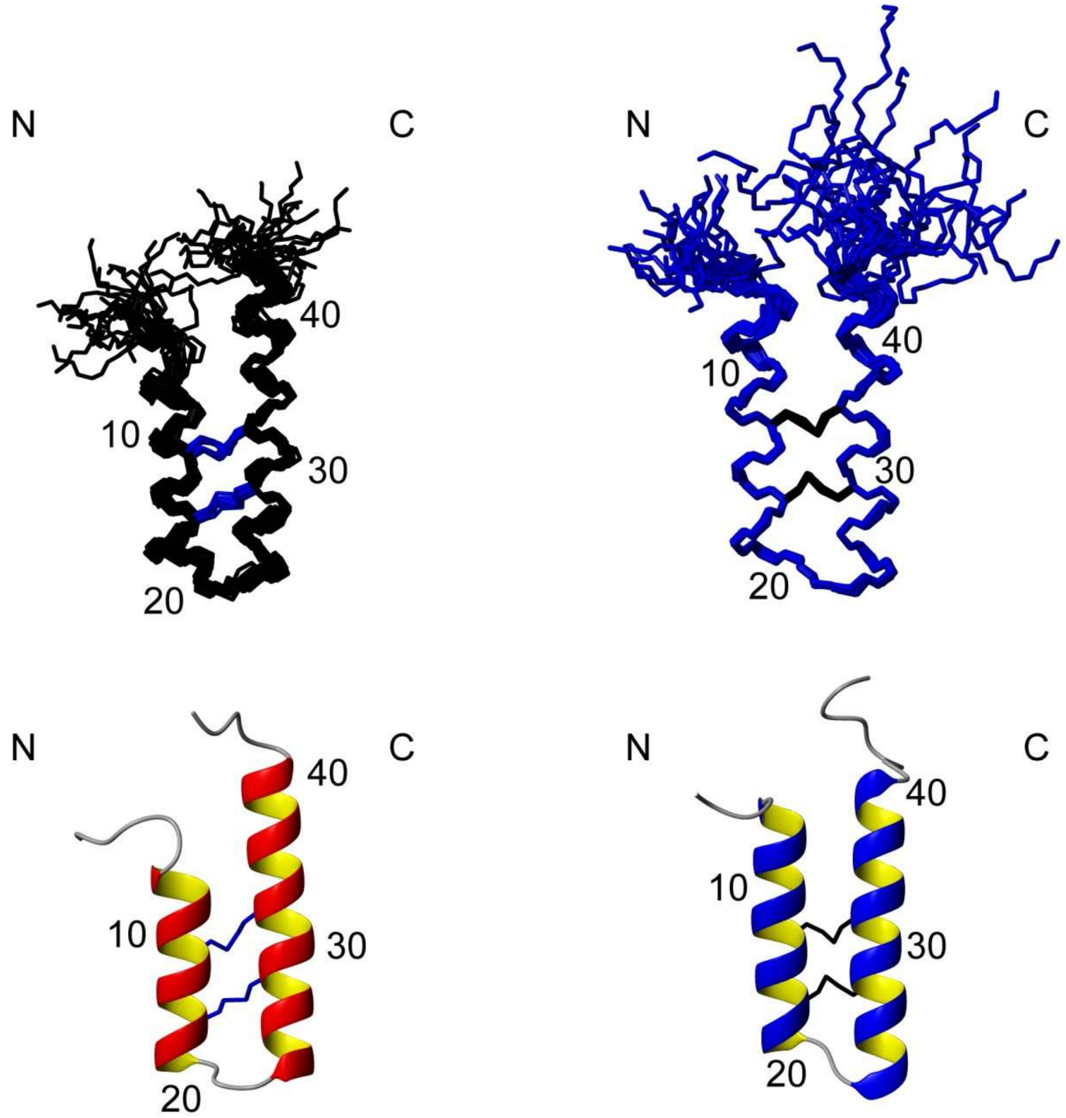


Fig. 8 | Tomato VBP-8 adopts a similar helix-turn-helix structure as Luffin P1. Nuclear magnetic resonance structures for Luffin P1 (left) and VBP-8 (right). Top panels show the superposition of the structural ensembles, while the lower panels show the lowest energy structure in ribbon format. Both peptides adopt two helical regions, which are separated by a linker. Sidechains of cysteine residues that cross brace the helical hairpin are shown and selected residues labelled with residue numbers.

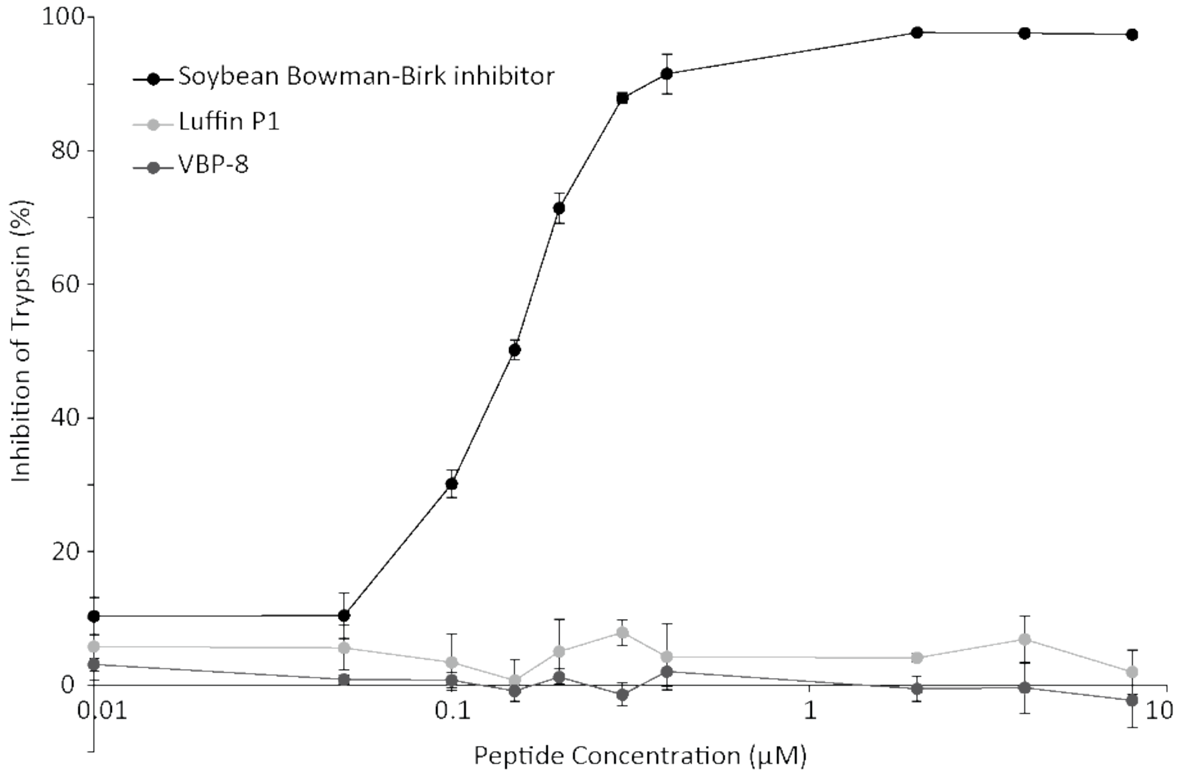


Fig. 9 | Inhibition of bovine trypsin. The inhibition of trypsin activity was tested for Luffin P1 (light gray) and VBP-8 (dark gray) at different concentrations ranging from 0.01 to 8 µM. The positive control was soybean Bowman-Birk inhibitor (black). The standard error of the mean is shown for each reaction.

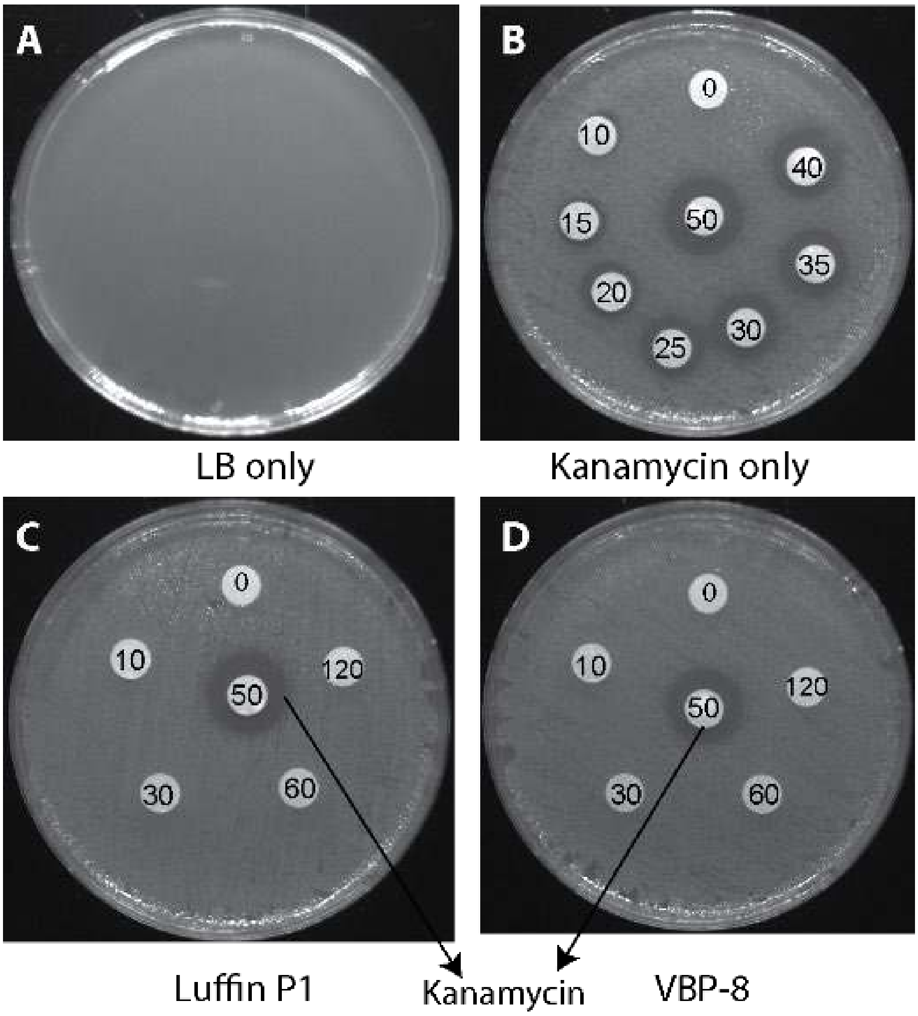


Fig. 10 | Antibacterial activity testing. Agar plates with (**A**) LB only; (**B**) a positive control plate with discs containing 10, 15, 20, 25, 30, 35, 40 or 50 µg of kanamycin, (**C**) one test plate with 50 µg of kanamycin (middle filter paper) and discs containing 10, 30, 60, or 120 µg of Luffin P1; (**D**) a plate with 50 µg of kanamycin (middle filter paper) and discs containing 10, 30, 60 or 120 µg of VBP-8.

Supporting Information

An ancient peptide family buried within vicilin precursors

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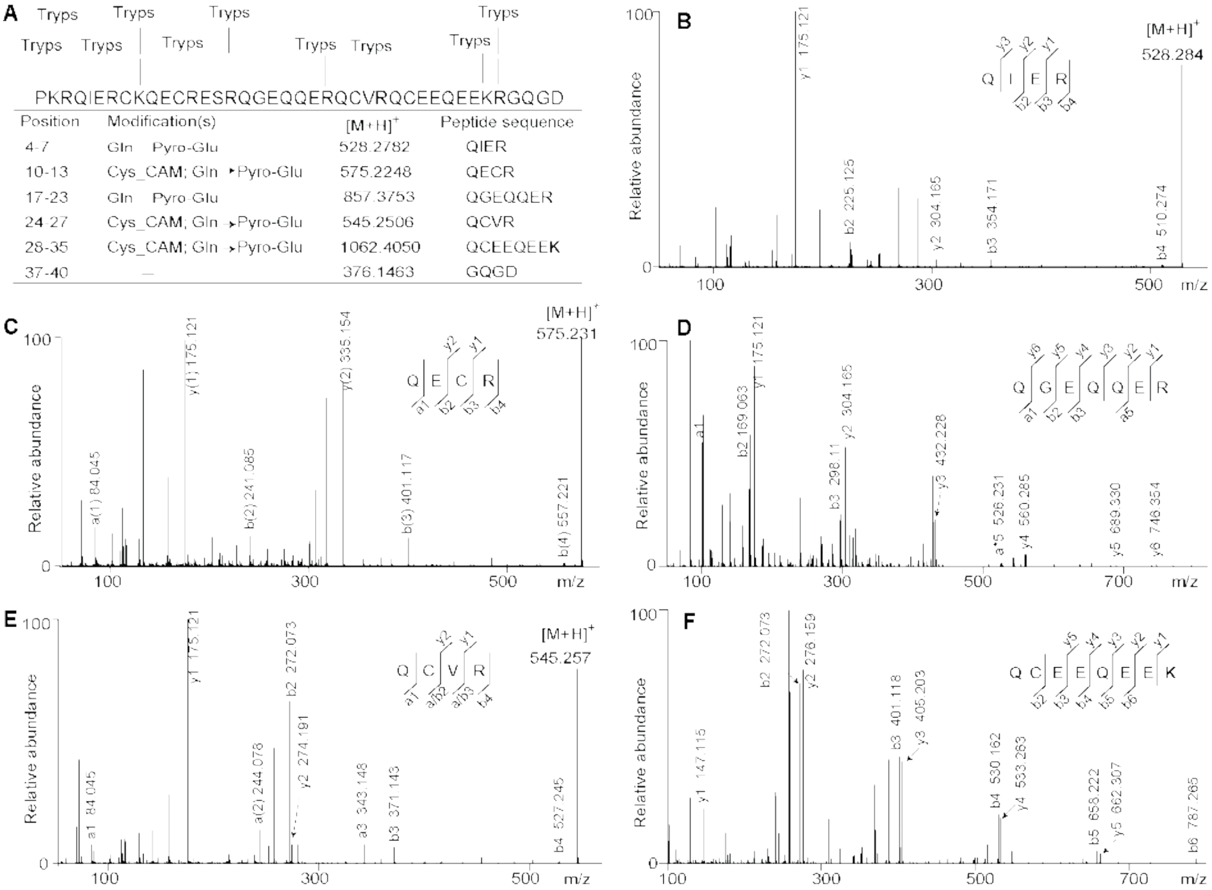
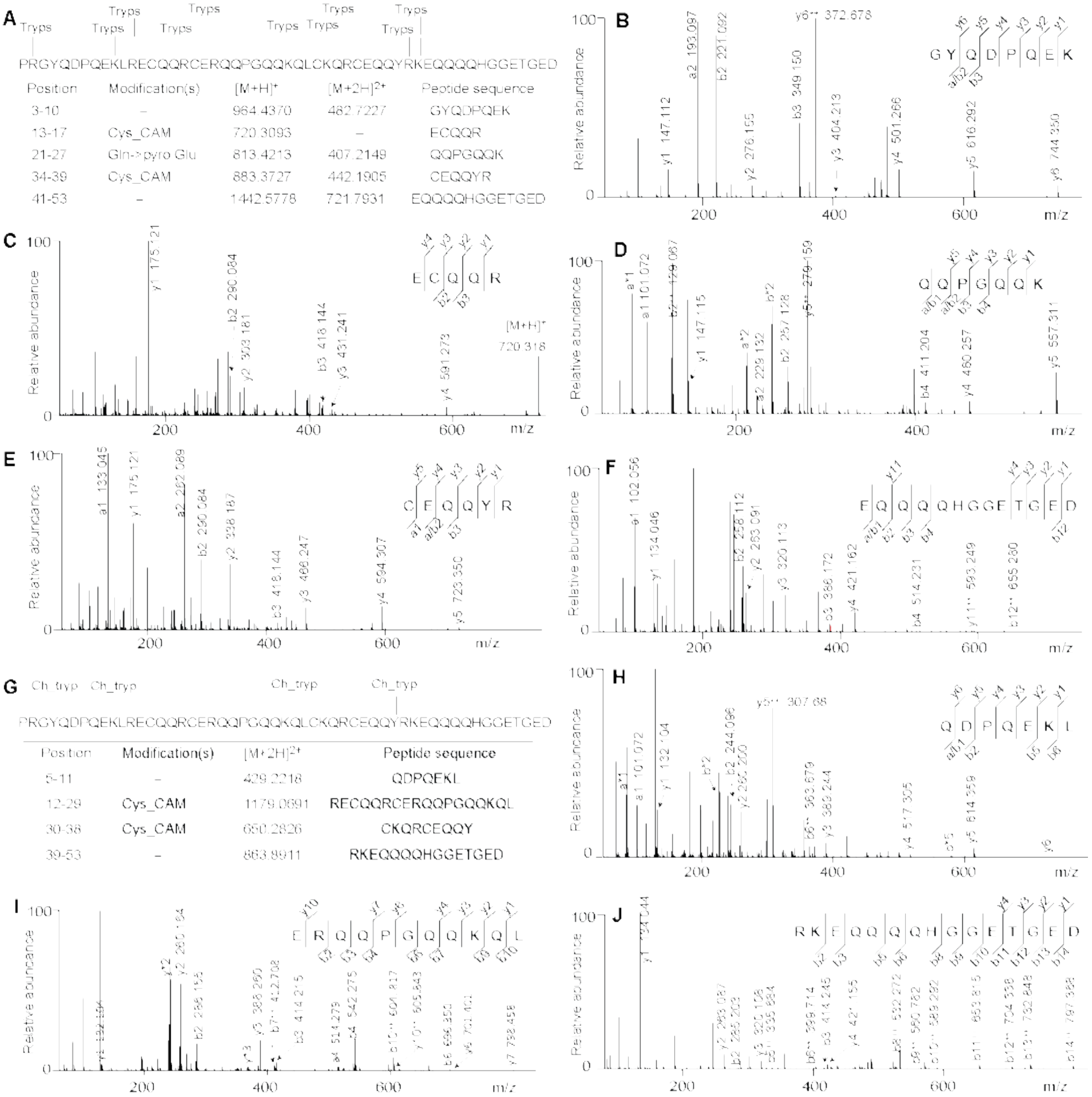


Position	Modification(s)	$[M+H]^+$	Peptide sequence
4-7	Gln Pyro-Glu	528.2782	QIER
10-13	Cys_CAM; Gln →Pyro-Glu	575.2248	QECR
17-23	Gln Pyro-Glu	857.3753	QGEQQER
24-27	Cys_CAM; Gln →Pyro-Glu	545.2506	QCVR
28-35	Cys_CAM; Gln →Pyro-Glu	1062.4050	QCEEQEEK
37-40	—	376.1463	GQGD

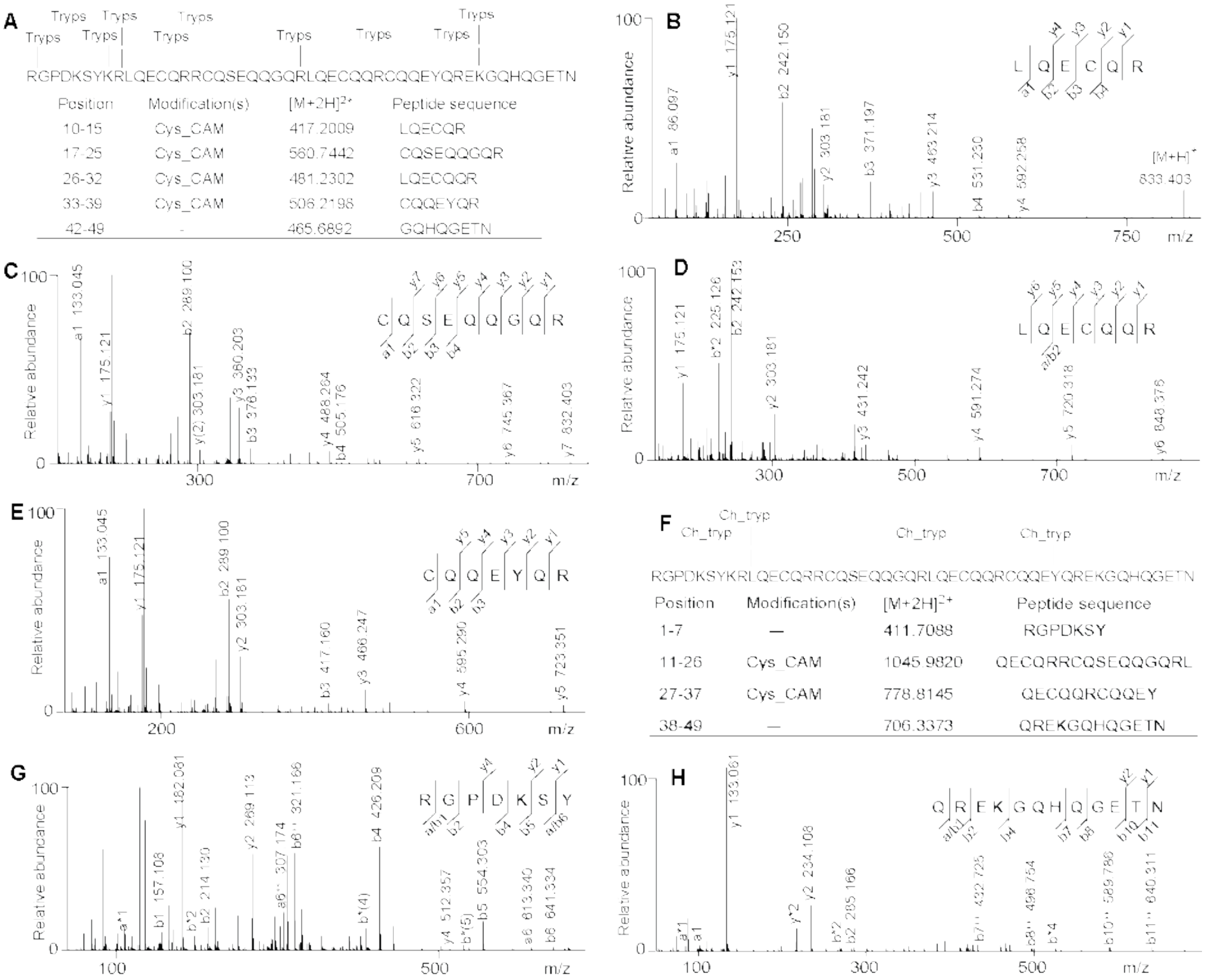
Supporting Fig. 1 | MS/MS spectra of VBP-6 from date palm seeds (*P. dactylifera*). (**A**) Tryptic fragments of VBP-6 and corresponding *m/z* values at $[M+H]^+$ are shown. The *m/z* is calculated with alkylation of Cys residues (Cys_CAM), and/or pyro-Glu from N-terminal Gln (Pyro-Glu). (**B-F**) MS/MS fragmentation spectra for corresponding tryptic fragments (**B**) QIER, (**C**) QECR, (**D**) QGEQQER, (**E**) QCVR, and (**F**) QCEEQEEK.



Position	Modification(s)	[M+H]+	[M+2H]2+	Peptide sequence
3-10	–	964.4370	482.7227	GYQDPQEK
13-17	Cys_CAM	720.3093	–	ECQQR
21-27	Gln->pyro Glu	813.4213	407.2149	QQPGQQK
34-39	Cys_CAM	883.3727	442.1905	CEQQYR
41-53	–	1442.5778	721.7931	EQQQQHGGETGED

Position	Modification(s)	[M+2H]2+	Peptide sequence
5-11	–	429.2218	QDPQEKL
12-29	Cys_CAM	1179.0691	RECQQRCERQQPGQQKQL
30-38	Cys_CAM	650.2826	CKQRCEQQY
39-53	–	863.8911	RKEQQQQHGGETGED

Supporting Fig. 2 | MS/MS spectra for tryptic and chymotryptic fragments of VBP-7 from tomato seeds (*S. lycopersicum*). (**A**) Possible trypsin cleavage sites and corresponding theoretical m/z are calculated with the alkylation of cysteine residues (Cys_CAM), and/or pyroGlu from N-terminal Gln (Pyro-Glu) and are given as $[M+H]^+$ and $[M+2H]^{2+}$ ions. (**B-F)** MS/MS spectra corresponding to tryptic fragments of VBP-7 identified by y ions and b ions, which are presented as in: (**B**) GYQDPQEK, (**C**) ECQQR, (**D**) QQPGQQK, (**E**) CEQQYR, (**F**) EQQQQHGGETGED. (**G**) Possible chymotrypsin cleavage sites of VBP-7 and the corresponding theoretical fragmental masses which are given as $[M+2H]^{2+}$ ions and calculated with alkylation of cysteine residues (Cys_CAM), and/or pyroGlu from N-terminal Gln (Pyro-Glu). (**H-J**) MS/MS spectra corresponding to fragments (**H**) QDPQEKL, (**I**) ERQQPGQQKQL, (**J**) RKEQQQQHGGETGED.



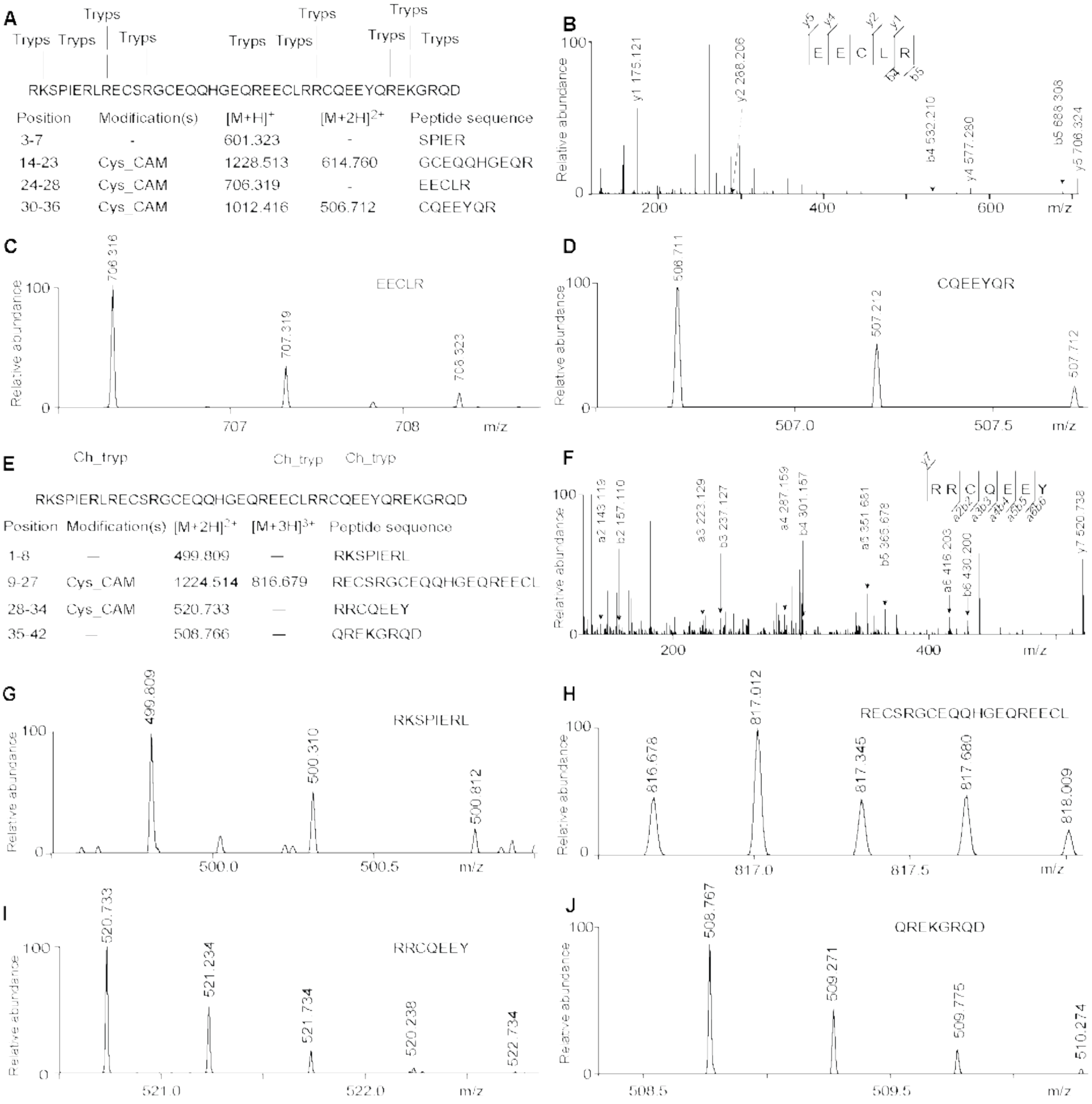
A

Position	Modification(s)	$[M+2H]^{2+}$	Peptide sequence
10-15	Cys_CAM	417.2009	LQECQR
17-25	Cys_CAM	560.7442	CQSEQQGQR
26-32	Cys_CAM	481.2302	LQECQQR
33-39	Cys_CAM	506.2198	CQQEYQR
42-49	-	465.6892	GQHQGETN

F

Position	Modification(s)	$[M+2H]^{2+}$	Peptide sequence
1-7	—	411.7088	RGPDKSY
11-26	Cys_CAM	1045.9820	QECQRRCQSEQQGQRL
27-37	Cys_CAM	778.8145	QECQQRCQQEY
38-49	—	706.3373	QREKGQHQGETN

Supporting Fig. 3 | MS/MS evidence of VBP-8 from tomato seeds (*S. lycopersicum*). (**A**) Trypsin cleavage sites and theoretical m/z of five main fragments with alkylation of cysteine residues (Cys_CAM). All m/z are given for $[M+2H]^{2+}$ ions. (**B-E**) MS/MS fragmentation spectra of tryptic fragments (**B**) LQECQR (**C**) CQSEQQGQR (**D**) LQECQQR (**E**) CQQEYQR. (**F**) Predicted chymotrypsin cutting sites and calculated m/z for chymotryptic fragments with alkylation of cysteine residues (Cys_CAM) as $[M+2H]^{2+}$ ions. (**G-H**) MS/MS spectra of chymotryptic fragments (**G**) RGPDKSY (**H**) QREKGQHQGETN.



Position	Modification(s)	[M+H]$^+$	[M+2H]$^{2+}$	Peptide sequence
3-7	-	601.323	-	SPIER
14-23	Cys_CAM	1228.513	614.760	GCEQQHGEQR
24-28	Cys_CAM	706.319	-	EECLR
30-36	Cys_CAM	1012.416	506.712	CQEEYQR

Position	Modification(s)	[M+2H]$^{2+}$	[M+3H]$^{3+}$	Peptide sequence
1-8	—	499.809	—	RKSPIERL
9-27	Cys_CAM	1224.514	816.679	RECSRGCEQQHGEQREECL
28-34	Cys_CAM	520.733	—	RRCQEEY
35-42	—	508.766	—	QREKGRQD

Supporting Fig. 4 | MS/MS evidence of VBP-9 from sesame (*S. indicum*). (**A**) Predicted tryptic fragments of VBP-9 and corresponding m/z values are calculated with alkylation of cysteine residues (Cys_CAM) and are shown as [M+H]$^+$ and [M+2H]$^{2+}$. (**B-D**) MS fragmentation spectra of two tryptic fragments found corresponding to (**C**) EECLR and (**D**) CQEEYQR, and MS/MS evidence for (**B**) EECLR. (**E**) Chymotryptic fragments of VBP-9. The m/z value for each fragment is calculated with [M+2H]$^{2+}$ and [M+3H]$^{3+}$ and alkylation of cysteine residues (Cys_CAM) residues. (**F-J**) MS spectra corresponding for all four chymotryptic fragments (**G**) RKSPIERL, (**H**) RECSRGCEQQHGEQREECL, (**I**) RRCQEEY and (**J**) QREKGRQD and one MS/MS spectrum is found corresponding to (**F**) RRCQEEY.

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....|...10....|...20....|...30....|...40....|...50....|...60....|...70....|...80....|...90
ATGGCGTCGTCTAAAGTAAAGTTTCGTTTGTGTCTATTGGCGTTTACCCTTTTTCTTGCTTCTGTGTCTGTTGGTTTGGGTGCTGAGAGT
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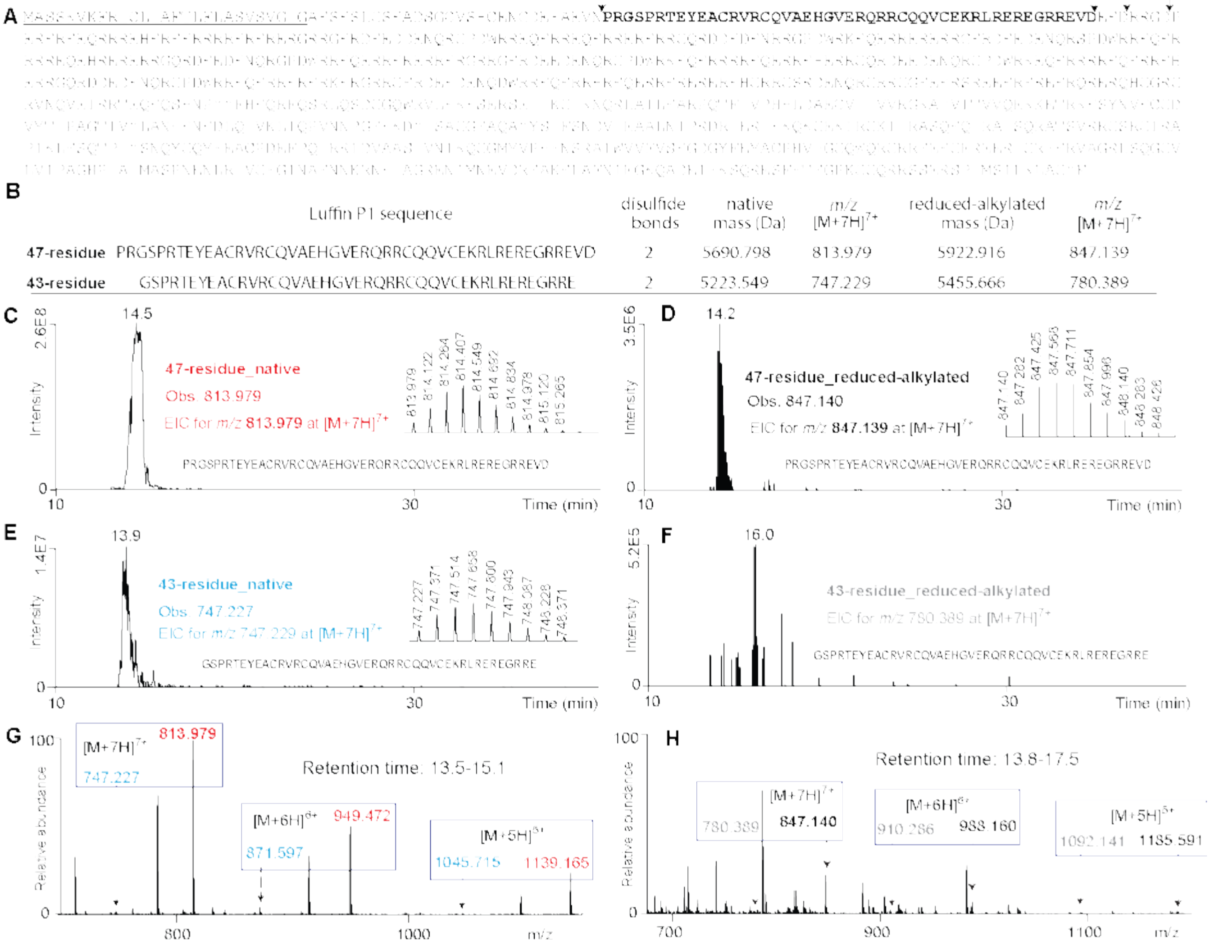
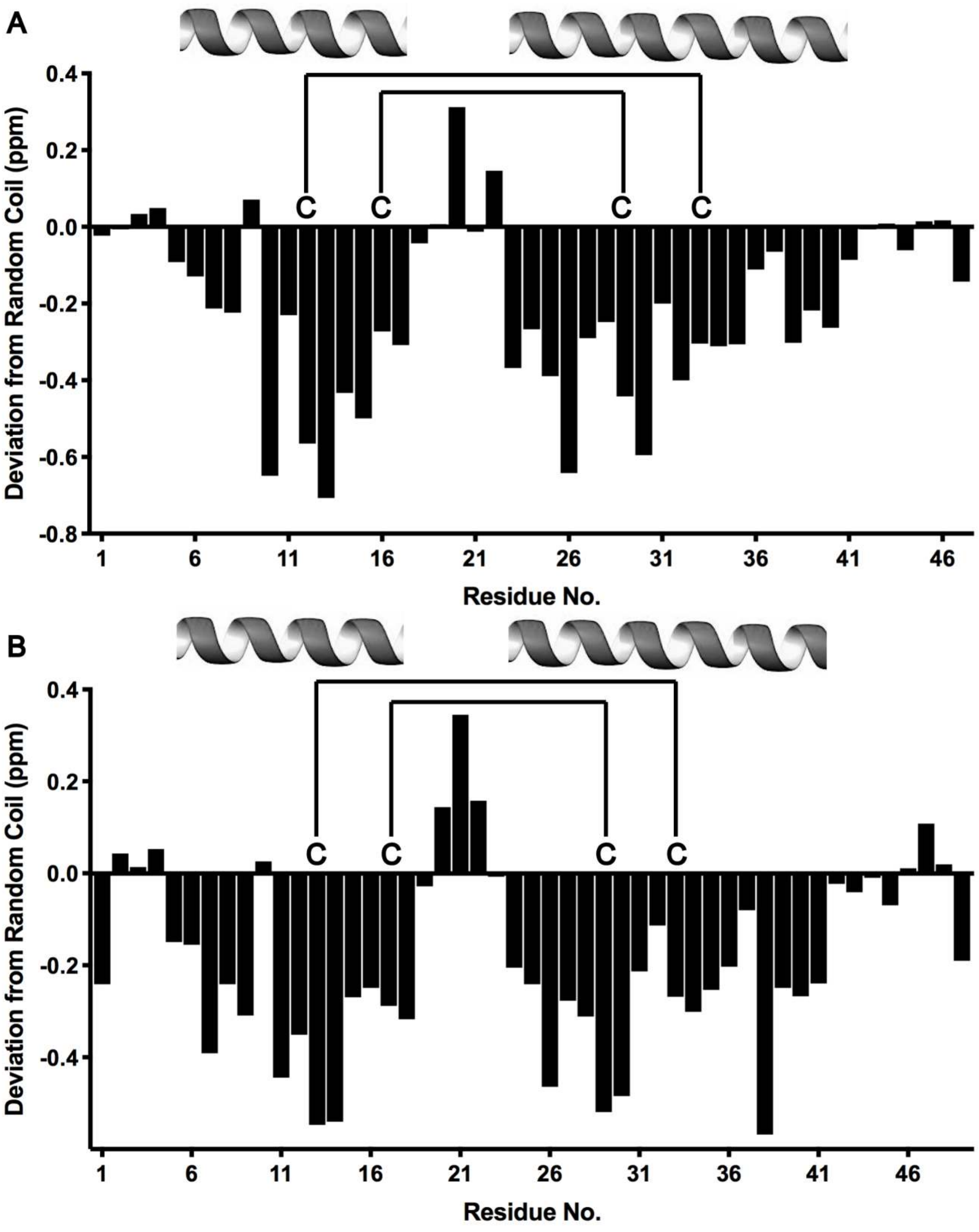
  Q  R  R  S  S  E  R  S  P  L  M  S  I  L  K  L  A  G  Y  F  *
....|...10....|...20....|...30....|...40....|...50....|...60....|...70....|...80....|...90
```

Supporting Fig. 5 | *Preprovicilin with Luffin P1* gene and its encoded protein containing Luffin P1 and vicilin. Colours indicate ER targeting signal (rose), Luffin P1 (cyan), and the predicted vicilin region (brown) Pro458-Phe871. A candidate site for AEP-mediated cleavage of the vicilin region into α and β domains is the bond between Asn673 and Gln674. The five introns are in lower case (purple).

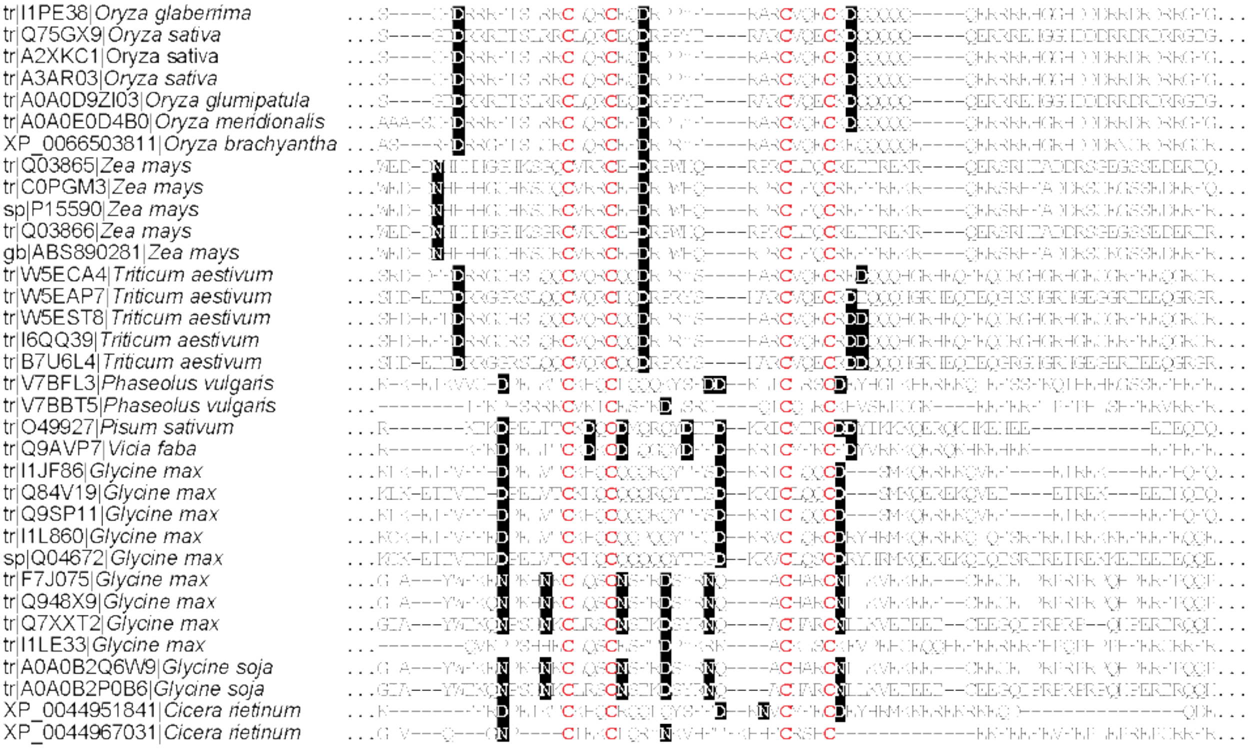


	Luffin P1 sequence	disulfide bonds	native mass (Da)	m/z $[M+7H]^{7+}$	reduced-alkylated mass (Da)	m/z $[M+7H]^{7+}$
47-residue	PRGSPRTEYEACRVRCQVAEHGVERQRRCQQVCEKRLREREGRREVD	2	5690.798	813.979	5922.916	847.139
43-residue	GSPRTEYEACRVRCQVAEHGVERQRRCQQVCEKRLREREGRRE	2	5223.549	747.229	5455.666	780.389

Supporting Fig. 6 | Evidence for Luffin P1 (VBP-5) from *L. aegyptiaca*. (**A**) The deduced amino acid sequence of the Luffin P1 precursor consisting of an ER-targeting signal (underlined), Luffin P1 with CXXXC motifs (bold), an Arg/Glu-rich domain, and a vicilin protein (light gray).(**B**) Our predicted sequence of AEP-processed Luffin P1 (47-residue Luffin P1) and previously published Luffin P1 sequence [13] (43-residue Luffin P1). The monoisotopic masses for both sequences were calculated with two disulfide bonds and mass-to-charge ratios (m/z) were calculated for $[M+7H]^{7+}$ ions. Also, the monoisotopic masses for reduced-alkylated 47- and 43-residue Luffin P1 and their corresponding *m/z* at $[M+7H]^{7+}$ ions are shown. (**C-F**) EICs at $[M+7H]^{7+}$ and (inset) mass spectra for (**C**) Native 47-residue Luffin P1 (red) (**D**) Reduced-alkylated 47-residue Luffin P1 (black) (**E**) Native 43-residue Luffin P1 (blue) (**F**) Reduced-alkylated 43-residue Luffin P1 (light gray) (**G**) Mass spectrum from 13.5 to 15.1 min retention time in which both native 47- and 43-residue Luffin P1 peaks appear. The masses for native 47-residue (red, solid lines) and 43-residue Luffin P1 (blue, dashed lines) at 5+, 6+ and 7+ charge are enclosed by rectangles. (**H**) Mass spectrum from 13.8 to 17.5 min retention time in which reduced and alkylated 47- and 43-residue Luffin P1 peaks appear. The masses for reduced and alkylated 47- (bold, solid lines) and 43-residue Luffin P1 (light gray, dashed lines) at charge 5+, 6+ and 7+ are shown in rectangles.



Supporting Fig. 7 | Tomato VBP-8 adopts a similar helix-turn-helix structure to Luffin P1. Nuclear magnetic resonance secondary Hα shifts for (**A**) 47-residue Luffin P1 and (**B**) VBP-8. Stretches of negative chemical shifts are indicative of helical secondary structure. Both peptides adopt two helical regions as indicated by schematic helices, which are separated by a turn or loop linker. Positions and connectivities of cysteine residues that cross brace the helical hairpin are indicated by connecting lines.



Supporting Fig.8 | Alignment of Cys-rich domain of Class IV preprovicilins in cereal crops and legumes. Cysteine residues are in red, Asp and Asn residues are in black solid.

Supporting Table 1 |252 preprovicilin sequences used for alignment. The sequences are listed in the order they appear in the alignment. The first three columns are species, order and a unique ID code (SP = UniprotKBKB; TR= UniprotKBKB, REF/GB/EMB = GenBank). The fourth column is the class of preprovicilin.

Species	**Order**	**Identifier**	**Class**
Gossypium raimondii	Malvales	>TR|A0A0D2R6E8|	IV
Gossypium arboreum	Malvales	>TR|A0A0B0PET1|	IV
Gossypium arboreum	Malvales	>TR|A0A0B0N1K7|	IV
Gossypium hirsutum	Malvales	>SP|P09801|	IV
Gossypium raimondii	Malvales	>TR|A0A0D2NXS4|	IV
Gossypium raimondii	Malvales	>TR|A0A0D2S8U5|	IV
Gossypium hirsutum	Malvales	>SP|P09799|	IV
Gossypium arboreum	Malvales	>TR|A0A0B0MWH7|	IV
Theobroma cacao	Malvales	>TR|A0A061EM85|	IV
Anacardium occidentale	Sapindales	>TR|Q8L5L5|	IV
Citrus sinensis	Sapindales	>TR|A0A067FZ38|	IV
Citrus clementina	Sapindales	>TR|V4TAE4|	IV
Eucalyptus grandis	Myrtales	>REF|XP_010026941.1|	IV
Eucalyptus grandis	Myrtales	>TR|A0A059CFS8|	IV
Pyrus x bretschneideri	Rosales	>REF|XP_009367697.1|	IV
Malus domestica	Rosales	>REF|XP_008386543.1|	IV
Pyrus x bretschneideri	Rosales	>REF|XP_009370838.1|	IV
Prunus persica	Rosales	>TR|M5VLX9|	IV
Prunus mume	Rosales	>REF|XP_008235388.1|	IV
Prunus persica	Rosales	>TR|M5Y4Q9|	IV
Prunus mume	Rosales	>REF|XP_008224282.1|	IV
Fragaria vesca	Rosales	>REF|XP_004292578.1|	IV
Morus notabilis	Rosales	>TR|W9QBD2|	IV
Morus notabilis	Rosales	>TR|W9RZA0|	IV
Prunus persica	Rosales	>TR|M5Y3W2|	IV
Prunus mume	Rosales	>REF|XP_008224279.1|	IV
Carya illinoinensis	Fagales	>TR|B3STU4|	IV
Cucurbita maxima	Cucurbitales	>TR|Q9ZWI3|	IV
Cucumis melo	Cucurbitales	>REF|XP_008439368.1|	IV
Cucumis sativus	Cucurbitales	>REF|XP_011650968.1|	IV
Cucumis melo	Cucurbitales	>REF|XP_008451293.1|	IV
Cucumis sativus	Cucurbitales	>REF|XP_011659275.1|	IV
Phaseolus vulgaris	Fabales	>TR|V7BFL3|	IV
Pisum sativum	Fabales	>TR|O49927|	IV
Vicia faba	Fabales	>TR|Q9AVP7|	IV
Glycine max	Fabales	>TR|I1JF86|	IV
Glycine max	Fabales	>TR|Q84V19|	IV
Glycine max	Fabales	>TR|Q9SP11|	IV
Glycine max	Fabales	>TR|I1L860|	IV
Glycine max	Fabales	>SP|Q04672|	IV
Medicago truncatula	Fabales	>TR|G7IDM5|	IV
Cicer arietinum	Fabales	>REF|XP_004495184.1|	IV
Arachis hypogaea	Fabales	>TR|B3IXL2|	IV
Arachis duranensis	Fabales	>TR|N1NEW2|	IV
Arachis hypogaea	Fabales	>TR|Q6PSU3|	IV
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Arachis hypogaea	Fabales	>TR|E5G076|	IV
Glycine soja	Fabales	>TR|A0A0B2Q6W9|	IV
Glycine max	Fabales	>TR|F7J075|	IV
Glycine max	Fabales	>TR|Q948X9|	IV
Glycine max	Fabales	>TR|Q7XXT2|	IV
Glycine max	Fabales	>TR|I1LE33|	IV
Glycine soja	Fabales	>TR|A0A0B2P0B6|	IV
Phaseolus vulgaris	Fabales	>TR|V7BBT5|	IV
Populus trichocarpa	Malpighiales	>TR|B9H8B1|	IV
Populus euphratica	Malpighiales	>REF|XP_011032788.1|	IV
Ricinus communis	Malpighiales	>TR|B9SFI3|	IV
Jatropha curcas	Malpighiales	>TR|A0A067JF64|	IV
Ricinus communis	Malpighiales	>TR|B9RTM9|	IV
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Vitis vinifera	Vitales	>TR|F6HI56|	IV
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Solanum tuberosum	Solanales	>REF|XP_006349767.1|	IV

Solanum lycopersicum	Solanales	>TR|K4CUH3|	IV
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Nicotiana tomentosiformis	Solanales	>REF|XP_009595711.1|	IV
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Solanum lycopersicum	Solanales	>TR|B0JEU3|	IV
Solanum tuberosum	Solanales	>TR|M1D5K3|	IV
Solanum lycopersicum	Solanales	>REF|XP_004247581.2|	IV
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Sesamum indicum	Lamiales	>TR|Q9AUD0|	IV
Erythranthe guttata	Lamiales	>TR|A0A022RN45|	IV
Sesamum indicum	Lamiales	>REF|XP_011090693.1|	IV
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Nelumbo nucifera	Proteales	>REF|XP_010256229.1|	IV
Macadamia integrifolia	Proteales	>SP|Q9SPL5.1	IV
Oryza glaberrima	Poales	>TR|I1PE38|	IV
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Oryza meridionalis	Poales	>TR|A0A0E0D4B0|	IV
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Phoenix dactylifera	Arecales	>REF|XP_008775109.1|	IV
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Lupinus angustifolius	Fabales	>TR|F5B8V9|	III
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Arabidopsis thaliana	Brassicales	>TR|F4IQK5|	II
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Brassica oleracea var. oleracea	Brassicales	>TR|A0A0D3BEH9|	II
Brassica napus	Brassicales	>TR|A0A078HFA1|	II
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Eucalyptus grandis	Myrtales	>REF|XP_010026166.1|	II
Fragaria vesca subsp. vesca	Rosales	>REF|XP_004300614.1|	II
Morus notabilis	Rosales	>TR|W9RZX9|	II
Cucurbita maxima	Cucurbitales	>TR|Q8W3X8|	II
Cucumis sativus	Cucurbitales	>TR|A0A0A0KGF2|	II
Glycine max	Fabales	>TR|I1LHP6|	II
Glycine soja	Fabales	>TR|A0A0B2RSR0|	II
Phaseolus vulgaris	Fabales	>TR|V7CFI9|	II
Medicago truncatula	Fabales	>TR|G7ZW34|	II
Cicer arietinum	Fabales	>REF|XP_004512222.1|	II
Jatropha curcas	Malpighiales	>TR|A0A067KHS0|	II
Populus trichocarpa	Malpighiales	>TR|U5GAT4|	II
Solanum bulbocastanum	Solanales	>TR|A9XLG8|	II
Solanum tuberosum	Solanales	>REF|XP_006363154.1|	II
Solanum lycopersicum	Solanales	>TR|K4BB70|	II
Nicotiana sylvestris	Solanales	>REF|XP_009803271.1|	II
Nicotiana tomentosiformis	Solanales	>REF|XP_009590474.1|	II
Petunia integrifolia subsp. inflata	Solanales	>TR|A9XLF3|	II
Sesamum indicum	Lamiales	>REF|XP_011100121.1|	II
Beta vulgaris subsp. vulgaris	Caryophyllales	>REF|XP_010680893.1|	II
Nelumbo nucifera	Proteales	>REF|XP_010254919.1|	II
Brachypodium distachyon	Poales	>TR|I1H8K5|	II
Triticum urartu	Poales	>TR|M7YE46|	II
Musa acuminata subsp. malaccensis	Zingiberales	>REF|XP_009396731.1|	II
Phoenix dactylifera	Arecales	>REF|XP_008798757.1|	II
Elaeis guineensis	Arecales	>REF|XP_010905079.1|	II
Amborella trichopoda	Amborellales	>REF|XP_011627755.1|	II
Camelina sativa	Brassicales	>REF|XP_010488296.1|	I
Camelina sativa	Brassicales	>REF|XP_010466550.1|	I
Camelina sativa	Brassicales	>REF|XP_010511540.1|	I
Capsella rubella	Brassicales	>TR|R0I7W9|	I
Camelina sativa	Brassicales	>REF|XP_010466552.1|	I
Arabidopsis lyrata subsp. lyrata	Brassicales	>TR|D7L1S0|	I
Arabidopsis thaliana	Brassicales	>TR|Q9LUJ7|	I
Brassica napus	Brassicales	>TR|A0A078H9R3|	I
Brassica rapa subsp. pekinensis	Brassicales	>TR|M4E4V9|	I
Brassica napus	Brassicales	>TR|A0A078J095|	I
Brassica oleracea var. oleracea	Brassicales	>TR|A0A0D3ABI5|	I
Eutrema salsugineum	Brassicales	>TR|V4LB10|	I
Eutrema salsugineum	Brassicales	>TR|V4LUV6|	I
Arabis alpina	Brassicales	>TR|A0A087HEI1|	I
Tarenaya hassleriana	Brassicales	>REF|XP_010551719.1|	I
Arabidopsis thaliana	Brassicales	>TR|Q9SK09|	I
Gossypium arboreum	Malvales	>TR|A0A0B0PUP3|	I
Morus notabilis	Rosales	>TR|W9SCA8|	I
Glycine max	Fabales	>TR|I1NGF4|	I
Glycine soja	Fabales	>TR|A0A0B2QNP6|	I
Glycine soja	Fabales	>TR|A0A0B2QQS2|	I
Phaseolus vulgaris	Fabales	>GB|AAC23610.1|	I
Vigna radiata	Fabales	>TR|Q198W3|	I
Vigna luteola	Fabales	>TR|A5WYF9|	I
Vigna radiata	Fabales	>TR|Q198W5|	I
Vigna radiata	Fabales	>TR|Q198W4|	I
Vigna unguiculata	Fabales	>TR|A8YQH5|	I
Canavalia ensiformis	Fabales	>SP|P50477|	I
Pisum sativum	Fabales	>TR|Q43626|	I
Pisum sativum	Fabales	>TR|D3VNE1|	I
Pisum sativum	Fabales	>TR|D3VNE0|	I
Pisum sativum	Fabales	>TR|D3VND7|	I
Pisum sativum	Fabales	>SP|P13918|	I
Vicia narbonensis	Fabales	>TR|Q41677|	I
Vicia faba	Fabales	>TR|I0B569|	I
Vicia faba var. minor	Fabales	>EMB|CAA68525.1|	I

Vicia faba	Fabales	>PRF|1502201A|	I
Medicago truncatula	Fabales	>TR|Q2HW19|	I
Medicago truncatula	Fabales	>TR|Q2HW18|	I
Medicago truncatula	Fabales	>TR|Q2HW22|	I
Cicer arietinum	Fabales	>REF|XP_004493035.1|	I
Cicer arietinum	Fabales	>REF|XP_004493034.1|	I
Cicer arietinum	Fabales	>REF|XP_004492829.1|	I
Cicer arietinum	Fabales	>TR|Q304D4|	I
Jatropha curcas	Malpighiales	>TR|A0A067L245|	I
Vitis vinifera	Vitales	>TR|F6GTY5|	I
Nicotiana tomentosiformis	Solanales	>REF|XP_009605859.1|	I
Nicotiana sylvestris	Solanales	>REF|XP_009771135.1|	I
Solanum lycopersicum	Solanales	>TR|K4CVL0|	I
Aegilops tauschii	Poales	>TR|M8BGV8|	I
Oryza sativa subsp. indica	Poales	>TR|B8AL97|	I
Oryza nivara	Poales	>TR|A0A0E0GUU5|	I
Oryza sativa subsp. japonica	Poales	>TR|Q852L2|	I
Oryza sativa subsp. japonica	Poales	>TR|Q8L8I0|	I
Oryza glumipatula	Poales	>TR|A0A0D9ZEA9|	I
Oryza meridionalis	Poales	>TR|A0A0E0D840|	I
Oryza barthii	Poales	>TR|A0A0D3FQ29|	I
Oryza punctata	Poales	>TR|A0A0E0KK37|	I
Oryza brachyantha	Poales	>TR|J3LTM2|	I
Leersia perrieri	Poales	>TR|A0A0D9W021|	I
Zea mays	Poales	>TR|B6UGJ0|	I
Zea mays	Poales	>TR|Q7M1Z8|	I
Sorghum bicolor	Poales	>TR|C5WY16|	I
Setaria italica	Poales	>TR|K4A9S8|	I
Brachypodium distachyon	Poales	>TR|I1GMC8|	I
Triticum urartu	Poales	>TR|M7ZQM3|	I
Aegilops tauschii	Poales	>TR|M8B8C6|	I
Hordeum vulgare var. distichum	Poales	>TR|M0XUU4|	I
Brachypodium distachyon	Poales	>TR|I1GMD1|	I
Aegilops tauschii	Poales	>TR|M8C814|	I
Brachypodium distachyon	Poales	>REF|XP_003557965.1|	I
Musa acuminata subsp. malaccensis	Zingiberales	>TR|M0TXJ0|	I
Musa acuminata subsp. malaccensis	Zingiberales	>TR|M0SMF3|	I
Araucaria angustifolia	Pinales	>TR|Q8LKI7|	I
Picea sitchensis	Pinales	>TR|A9NW52|	I
Picea sitchensis	Pinales	>TR|B8LLB1|	I
Picea glauca	Pinales	>TR|Q40873|	I
Picea glauca	Pinales	>TR|Q40844|	I
Pinus koraiensis	Pinales	>TR|V9VGU0|	I
Zamia furfuracea	Cycadales	>TR|Q41727|	I
Selaginella moellendorffii	Selaginellales	>TR|D8RUY4|	I
Selaginella moellendorffii	Selaginellales	>TR|D8T005|	I
Matteuccia struthiopteris	Polypodiales	>TR|Q40371|	I

Dataset 1 | Raw sequence alignment for alignment in Figure 1 **(NOTE: 124 pages)**.

```
Gossypium raimondii                     >TR|A0A0D2R6E8|          MSA-------
------------------KSKLSTLILIL-SL-VFLYAGCLAFAKQ-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELKQCTHQCRVQQQYDEK--QKEECVKTC-
EEYHREKKDRESLKEVGQDPDVEF---------------------------------------------------
----HPGGE-LSECQSRC-V---GLAGEVRQLCLFRCQQKWRRDYASRWEEEGKK--QSKE------DAEDEG--
------EE---EKH-------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------NPYVFE-DK-H-FST-
AIKTGKGRVDL-LTKFTHD-SDILRG-IEN-----------YRLALLVASPKSFVVPNHFDANAIFVVTQG-
RGTLTLIHED-KRES---FNIETG-DII----HVRAGTPLYLINRD-DN-----EKLFIVKLLQP---
INQPDHYEVFY--GAGG-AKPESFYETFSTEILEAALKT---SRDKLERFFDKQ---------------------
-------------------------------GKGPFLEASREQIEAMS--S-HEE-GSKGGGLWP--FGSE----
----SKSKSAFNLFRKREPS-HCNRYGQLFEVEEDEF-K-RLKD--FDLRVSYANITK-
GCMSAPFYNSRAIKIAIVVKGEG---YFEMVSPPVS------PKSS------QEDSG------GRK---------
------------S-----GSRYQKISSRLRSDTVFVVPAGHPFVTVASR--NNNLEILCFEVNIEN-----
NVRYLLAGE-GNYVQQFEK-----EAKELAFKS-K---EEEVDRIFG-N-QDEEFFFPGP----RQ---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------Q--RGRDYE

Gossypium arboreum                      >TR|A0A0B0PET1|          MSA-------
------------------KSKLSTLILIL-SL-VFLYAGCLAFAKQ-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELTQCTHQCRVQQQYDEK--QKEECVRTC-
EEYHREKKDRESLKEVGQDPDVEF---------------------------------------------------
----HPGDG-LSECRSRC-A---GLAGEVRQLCLFRCQQKWRRDYASRWEEEGKK--QSKE------DAEDEG--
------EE---EKH-------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------NPYVFE-DK-H-FST-
AIKTGKGRVDL-LTKFTHN-SDILRG-IEN-----------YRLALLVASPKSFVVPNHFDANAIFVVTQG-
RGTLTLIHED-KRES---FNIETG-DII----YVRAGTPLYLINRD-DD-----EKLFIVKLLQP---
INQPDHYEVFY--GAGG-AKPESFYETFSTEILEAALKT---SRDKLEKFFDKQ---------------------
-------------------------------GKGPFLEASKEQIEAMS--S-HEE-GSKGGGLWP--FGSE----
----SKSESAFNLFRKRQPS-HCNRYGQLFEVEEDEF-K-RLKD--FDLRVSYVNITK-
GCMSAPFYNSRAIKIAIVVKGEG---YFEMVSPPVS------PKSS------QEDSA------GRK---------
------------S-----GSRYQKISSRLRSDTVFVVPAGHPFVTVASR--NNNLEILCFEVNIEN-----
NVRYLLAGE-GNYVQQFEK-----EAKELAFKS-K---EEEVDRIFG-N-QDEEFFFPGP----RQ---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------Q--RGRNYE
```

```
Gossypium arboreum                      >TR|A0A0B0N1K7|          MVRNKS----
-------------------------ACVVLLFSLFLSFGLLCSAKDFPGRRG-DD--------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------
DPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQFGEKDQQQRHR-------------------------------
-----------------------------------------------------PEDPQRRYEECQQECRQQEE--
---RQRPQCQQSCLKRFE-QEQQQ---------------------------------------------------
--------------------SQRQFQECQQHCHQQEQ--RPERKQQCVRECRERYQENPWRREREE---------
------------EAEEEETEEGEQQQSH-----------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------NPFHF-HRR-S-
FQS-RFREEHGNFRV-LQRFASR-HPILRG-INE-----------
FRLSILEANPNTFVLPHHCDAEKIYLVTNG-RGTLTFLTHE-NKES---YNVVPG-VVV----
RVPAGSTVYLANQD-NK-----EKLIIAVLHRP---VNNPGQFEEFF--PAGS-
QRPQSYLRAFSREILEPAFNT---RSEQLDELFGGR---------------QSHRRQ------------------
-----------QGQ-GMFRKASQEQIRALSQEATSP----------------------REKSGERFAFNLLYQT-
PR-YSNQNGRFYEACPREFRQ--LRD--INVTVSALQLNQ-GSIFVPHYNSKATFVVLVNEGNG---
YVEMVSPHLP------RQSS-YEEEEEQEQEQEQEQEEERR--------------------------
SGQYRKIRSQLSRGDIFVVPANFPVTFVASQ--NQNLRMTGFGLYNQNINPDHNQRIFVAGKINHV-RQWDS---
--QAKELAFGL-S---SRLVDEIFNNN-PQESYFVS--RQRQRASE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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Gossypium hirsutum                      >SP|P09801|              MVRNKS----
-------------------------ACVVLLFSLFLSFGLLCSAKDFPGRRG-DD--------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------
DPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHR-------------------------------
-----------------------------------------------------PEDPQRRYEECQQECRQQEE--
---RQRPQCQQRCLKRFE-QEQQQ---------------------------------------------------
--------------------SQRQFQECQQHCHQQEQ--RPERKQQCVRECRERYQENPWRREREE---------
------------EAEEEETEEGEQEQSH-----------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------NPFHF-HRR-S-
FQS-RFREEHGNFRV-LQRFASR-HPILRG-INE-----------
FRLSILEANPNTFVLPHHCDAEKIYLVTNG-RGTLTFLTHE-NKES---YNVVPG-VVV----
RVPAGSTVYLANQD-NK-----EKLIIAVLHRP---VNNPRQFEEFF--PAGS-
QRPQSYLRAFSREILEPAFNT---RSEQLDELFGGR---------------QSHRRQ------------------
-----------QGQ-GMFRKASQEQIRALSQEATSP----------------------REKSGERFAFNLLYRT-
PR-YSNQNGRFYEACPREFRQ--LSD--INVTVSALQLNQ-GSIFVPHYNSKATFVVLVNEGNG---
YVEMVSPHLP------RQSS-FEEEEEQQQEQEQE--EERR--------------------------
SGQYRKIRSQLSRGDIFVVPANFPVTFVASQ--NQNLRMTGFGLYNQNINPDHNQRIFVAGKINHV-RQWDS---
--QAKELAFGV-S---SRLVDEIFNNN-PQESYFVS--RQRQRASE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
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```

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Gossypium raimondii                    >TR|A0A0D2NXS4|          MVRNKS----
-------------------------ACVVLLFSLFLSFGLLCSAKDFPGRRG-DD--------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------
DPSKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHR-------------------------------
-----------------------------------------------------PEDPQRRYEECKQECRQQEE--
---RQQPQCQQRCLKRFE-QEQQQ---------------------------------------------------
--------------------SQRQFQECQQHCHQQEQ--RPEKKQQCVRECREKYQENPWRGEREE---------
------------EAEEEETEEGEQEQSH-----------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------NPFHF-HRR-S-
FQS-RFREEHGNFRV-LQRFASR-HPILRG-INE-----------
FRLSILEANPNTFVLPHHCDAEKIYLVTNG-RGTLTFLTHE-NKES---YNIVPG-VVV----
SVPAGSTVYLANQD-NK-----EKLIIAVLHRP---VNNPGQFEEFF--PAGS-
QRPQSYLRAFSREILEPAFNT---RSEQLDELFGGR---------------QSRRRQ------------------
-----------QGQ-GMFRKASQEQIRALSQEATSP----------------------REKSGERFAFNLLSQT-
PR-YSNQNGRFFEACPREFRQ--LRD--INVTVSALQLNQ-GSIFVPHYNSKATFVILVTEGNG---
YAEMVSPHLP------RQSS-YEEEEEQEEEQEQEQEEERR--------------------------
SGQYRKIRSRLSRGDIFVVPANFPVTFVASQ--NQNLRMTGFGLYNQNINPDHNQRIFVAGKINHV-RQWDS---
--QAKELAFGV-S---SRLVDEIFNNN-PQESYFVS--RQRQRASE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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Gossypium raimondii                    >TR|A0A0D2S8U5|          MVRNKS----
-------------------------VFVVLLFSLFLSFGLLCSAKDFPGRRS-ED--------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------
DPQQRYEDCRKRCQLETRGQTEQDKCEDRCETQF--KEEQQRDG-------------------------------
------------------------------------------------------EDPQRRYQDCRQHCQQEER--
---RLRPHCEQSCREQYEKQQQQQ---------------------------------------------------
--------------------PDKRFKECQQRCQWQEQ--RPERKQQCVKECREQYQEDPWKGERENKW-------
-----------REEEEEESDEGEQQQRN-----------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------NPYYF-HRR-S-
FQE-RFREEHGNFRV-LQRFADK-HHLLRG-INE-----------
FRIAILEANPNTFVLPHHCDAEKIYVVTNG-RGTITFVTHE-NKES---YNVVPG-VVV----
RIPAGSTVYLANQD-NR-----EKLTIAVLHRP---VNNPGQFQKFF--PAGQ-
ENPQSYLRIFSREILEAVFNT---RSELLDELFGGR---------------QSHRRQ------------------
-----------QGQ-GMFRKASQEQIRALSQGATSP----------------------RGKGSEGYAFNLLSQT-
PR-YSNQNGRFYEACPRNFQQ-QLRE--VDSSVVAFEINK-GSIFVPHYNSKATFVVLVTEGNG---
HVEMVCPHLS------RQSSHWSSREEEEQEEQE---DERR--------------------------
SGQYKRVRAQLSTGDLFVVPAGHPVTFVASQ--NEDLGLLGFGLYNGQ----DNKRIFVAGKTNNV-RQWDR---
--QAKELAFGV-E---SRLVDEVFNNN-PQESYFVS--GQSRRGFDERR--------------------------
------------------------------------------------------------------G--------
---------------------SNN---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----PLSPFLDFARLF
```

```
Gossypium hirsutum                      >SP|P09799|              MVRNKS----
-------------------------VFVVLLFSLFLSFGLLCSAKDFPGRRS-ED--------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------
DPQQRYEDCRKRCQLETRGQTEQDKCEDRSETQL--KEEQQRDG-------------------------------
------------------------------------------------------EDPQRRYQDCRQHCQQEER--
---RLRPHCEQSCREQYEKQQQQQ---------------------------------------------------
--------------------PDKQFKECQQRCQWQEQ--RPERKQQCVKECREQYQEDPWKGERENKW-------
-----------REEEEEESDEGEQQQRN-----------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------NPYYF-HRR-S-
FQE-RFREEHGNFRV-LQRFADK-HHLLRG-INE-----------
FRIAILEANPNTFVLPHHCDAEKIYVVTNG-RGTVTFVTHE-NKES---YNVVPG-VVV----
RIPAGSTVYLANQD-NR-----EKLTIAVLHRP---VNNPGQFQKFF--PAGQ-
ENPQSYLRIFSREILEAVFNT---RSEQLDELPGGR---------------QSHRRQ------------------
-----------QGQ-GMFRKASQEQIRALSQGATSP----------------------RGKGSEGYAFNLLSQT-
PR-YSNQNGRFYEACPRNFQQ-QLRE--VDSSVVAFEINK-GSIFVPHYNSKATFVVLVTEGNG---
HVEMVCPHLS------RQSSDWSSREEEEQEEQE---VERR--------------------------
SGQYKRVRAQLSTGNLFVVPAGHPVTFVASQ--NEDLGLLGFGLYNGQ----DNKRIFVAGKTNNV-RQWDR---
--QAKELAFGV-E---SRLVDEVFNNN-PQESYFVS--GRDRRGFDERR--------------------------
------------------------------------------------------------------G--------
---------------------SNN---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----PLSPFLDFARLF

Gossypium arboreum                      >TR|A0A0B0MWH7|          MVRNKS----
-------------------------VFVVLLFSLFLSFGLLCSAKDFPGRRS-ED--------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------
DPRQRYEDCQRRCQSETRGQTEQDKCEDRCERQF--KEEQQRDG-------------------------------
------------------------------------------------------DDPQRRYQDCRQHCQQEER--
---RLRPQCEQSCQEQYERQQQQQ---------------------------------------------------
--------------------PDKRFKECQHRCQRQEQ--GPERKQQCVKECREQYQEDPGKGERENKW-------
-----------REEEEEESDEGEQQQRN-----------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------NPYYF-HRR-S-
FQE-RFREEHGNFRV-LQRFADK-HHLLRG-INE-----------
FRIAILEANPNTFVLPHHCDAEKIYVVTNG-RGTITFVTHE-NKES---YNVAPG-VVV----
RIPAGSTVYLANQD-NR-----EKLTIAVLHRP---VNNPGQFQKFF--PAGQ-
ENPQSYLRIFSREILEAVFNT---RSEQLDELFGGR---------------QSHRRQ------------------
-----------QGQ-GMFRKASQEQIRALSQEATSP----------------------RGKGSEGYAFNLLSQT-
PR-YSNQNGRFYEACPRNFQQ-QLQE--VDSSVVAFEINK-GSIFVPHYNSKATFVVLVTDGNG---
HVEMVCPHLS------RQSSHWSSREEEEQEEQEEQEDERR--------------------------
SGQYKRVRAQLSTGDIFVVPAGHPVTFVASQ--NKNLGLLGFGLYNGQ----DNKRIFVAGKTNNV-RQWDR---
--QAKELAFGV-E---SRLVDEVFNNN-PQESYFVS--GQSRRGFDERR--------------------------
------------------------------------------------------------------G--------
---------------------SNN---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----PLSSFLDFARLF
```

```
Theobroma cacao                         >TR|A0A061EM85|          MVISKS----
-------------------------PFIVLIFSLLLSFALLCSGVSAYGRKQYER--------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------DPRQQYEQCQRRCESEATEERE---
QEQCEQRCEREYKEQQRQQEEE-----------------------------------------------------
---------------LQRQYQQCQGRCQEQQQ--GQREQQQCQRKCWEQYKEQE-RGEHEN-Y------------
------HNHKKNRSEEEEGQQRN----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------NPYYFPKRR-S-FQT-
RFRDEEGNFKI-LQRFAEN-SPPLKG-IND-----------YRLAMFEANPNTFILPHHCDAEAIYFVTNG-
KGTITFVTHE-NKES---YNVQRG-TVV----SVPAGSTVYVVSQD-NQ-----EKLTIAVLALP---
VNSPGKYELFF--PAGN-NKPESYYGAFSYEVLETVFNT---QREKLEEILEEQ---------------
RGQKRQ-----------------------------QGQQGMFRKAKPEQIRAISQQATSP---------------
-------RHRGGERLAINLLSQS-PV-YSNQNGRFFEACPEDFSQ--FQN--MDVAVSAFKLNQ-
GAIFVPHYNSKATFVVFVTDGYG---YAQMACPHLS------RQSQGSQSGRQDRREQEEESEEET---------
------------------FGEFQQVKAPLSPGDVFVAPAGHAVTFFASK--DQPLNAVAFGLNAQN-----
NQRIFLAGKKNLV-RQMDS-----EAKELSFGV-P---SKLVDNIFN-N-PDESYFMSFSQQRQRGDERR-----
---------------------------------------------------------------------------
--------------------------------------------GN-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------PLASILDFARLF

Anacardium occidentale                  >TR|Q8L5L5|              MGP-------
------------------PTKFSFSLFLV-SV-LVLCLG-FALAKI-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELKQCKHQCKVQRQYDEQ--QKEQCVKEC-
EKYYKEKKGREREHE---------------------------------------------EEEEEWGTGGV--
DEPSTHEPAEKHLSQCMRQCERQE---GGQQKQLCRFRCQERYKKER----GQHNYK--REDD------
EDEDED--------EA-EEEDE-----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------NPYVFE-DE-D-FTT-
KVKTEQGKVVL-LPKFTQK-SKLLHA-LEK-----------YRLAVLVANPQAFVVPSHMDADSIFFVSWG-
RGTITKILEN-KRES---INVRQG-DIV----SISSGTPFYIANND-EN-----EKLYLVQFLRP---
VNLPGHFEVFH--GPGG-ENPESFYRAFSWEILEAALKT---SKDTLEKLFEKQ---------------------
-------------------------------DQGTIMKASKEQIRAMS--R-RGE-GPK---IWP--FTEE----
----STG--SFKLFKKD-PS-QSNKYGQLFEAERIDY-P-PLEK--LDMVVSYANITK-
GGMSVPFYNSRATKIAIVVSGEG---CVEIACPHLS------SSKS---------SH------------------
-------------------PSYKKLRARIRKDTVFIVPAGHPFATVASG--NENLEIVCFEVNAEG-----
NIRYTLAGK-KNIIKVMEK-----EAKELAFKM-E---GEEVDKVFG-K-QDEEFFFQGP-EWRKE---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------K--EGRADE

Citrus sinensis                         >TR|A0A067FZ38|          MN--------
-------------------RKLCFTLFTL-SV-LVLCAG-LALATK-----------------------------
```

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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELKQCKHQCRARQQYDEK--QKEQCARTC-
EEYYKEKEQRERHREG------------------------------------------ESEEEKEWG---
GRHEWMNPGEPAEKHLRQCQRECDRQEE--GGQQRALCRFRCQEKYRREKEGEGGQHN-T--QEEE------
EEEEGD--------EE-----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------SS-
RVTSQHGRVAF-LPKFTQR-SKLLRG-LEK-----------YRLGILIANPQTFVTPTHLDADAVFFVSWG-
QGTITVIREN-NRES---YNVKRG-DII----RVPSGNTFYVTNTD-DD-----EKLYIVKFIKS---
INLPGQYEAFY--GAGG-ENPESFLRAFSWEILESAFKT---KRDSLERVLFQQ---------------------
-------------------------------DQGAMVKASKQQIRALS--R-SQE-GPS---IWP--FAGE----
----SRG--TFNLFGKR-PS-HSNNFGELFEADSNDF-R-PLED--LDITVSYANISK-
GAMAAPFYNSRSTKVAVVVAGDG---YIEIACPHVS------RSSSERRH--QGSST------REE---------
------------G-----SATYHKVSSRIRTDSAYIVPAGHPVVTVASQ--NNNLEVVCFEINAEG-----
NIRFPLAGR-NKIFKVMES-----EAKELAFNT-R---ADEVERVFG-N-QDQDWFFKGPSRWHQQ---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------Q--QGRAYE

Citrus clementina                       >TR|V4TAE4|              MN--------
-------------------RKLCFTLFTL-SV-LVLCAG-LALATK-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELKQCKHQCRARQQYDEK--QKEQCARTC-
EEYYKEKEQRERHREG------------------------------------------ESEEEKEWG---
GRHEWMNPGEPAEKHLRQCQRECDRQEE--GGQQRALCRFRCQEKYRREKEGEGGQHN-T--QEEE------
EEEEGD--------EE-----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------SS-
RVTSQHGRVAF-LPKFTQR-SKLLRG-LEK-----------YRLGILIANPQTFVTPTHLDADAVFFVSWG-
QGTITVIREN-NRES---YNVKRG-DII----RVPSGNTFYVTNTD-DD-----EKLYIVKFIKS---
INLPGQYEAFY--GAGG-ENPESFLRAFSWEILESAFKT---KRDSLERVLFQQ---------------------
-------------------------------DQGAMVKASKQQIRALS--R-SQE-GPS---IWP--FAGE----
----SRG--TFNLFGKR-PS-HSNNFGELFEADSNDF-R-PLED--LDITVSYANISK-
GAMAAPFYNSRSTKAAVVVAGDG---YIEIACPHVS------RSSSERRH--QGSST------REE---------
------------G-----SATYHKVSSRIRTDSAYIVPAGHPVVTVASQ--NNNLEVVCFEINAEG-----
NIRFPLAGR-NKIFKVMES-----EAKELAFNT-R---ADEVERVFG-N-QDQDWFFKGPSRWHQQ---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------Q--QGRAYE

Eucalyptus grandis                      >REF|XP_010026941.1|
MVFKVPRLLP-------------------------LLILFHSLCLTSLAL-------------------------
---------------------------------------------------------------------------
-------------RRGPETEVLRCLDDCDDED--------------
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VQEYITCHKECELRYREREERREEEGRPGSRELDPRWQRGRGRRRGGGGGGGEREPEGPRGEREPAW--------
------------------------GPGGEYDQCRRLCEPY---
KPRERERCWEQCEERERARERRRDREREREVKD------------------------------------------
---------------------------GVRNSSGDASRSERYERCERACERQA-GGQ---
QRQLCKFRCRQQREREERETPGGRDAKLL----------------------------------------------
---------LATTTEDPQQQFQHCQQRCERQQG--REPQRRQCLQECERQFQEQQR----------------
GKRRSTNPREQEEEEEE----VGESGD------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------------NPYYFH-SR-M-
LHS-RFRAEEGQIRV-LERFDKR-SRLLRG-LKN-----------
YRLEIFEANPNTFVLPHHVDADCILIVLKG-EGTISLVWQD-KKQS---YHLEGG-DVM----
RVPAGTTVYFISSG-RD-----GQVQIAKLIQP---VNIPGTFKEFY--PVGTENPE-
SYYKVFSSEILESSLKT---SRDQIERLFGQQ-------------------------------------------
---------RQGVMIRASEEQRQALSEHSGW------------------LKNKGHGLR---GPFNLLGRE-PI-
YSNEFGRFFQASPGEFK--QLLD--LGVS---------GSTMVPHYNSKSMTVVLVVEGNG---WFEMACPHL--
------AQAQQRWGSGGEREEEEEEEEEQETEQ----------------GG-----
SARYQKVTSQLSPGDIFVIPAGHPIAIVAGQ--NEDLRMVGFGINAHK-----NERIFLAGK-ENIINRMDT---
--EAKELSFDL-P---AREVDRVFR-N-QEKSYFVSSSVQQQPQRERRERRSIEKIE------------------
---------------------------------------------GSQQLRQSKRMDKSDTKGSEGS--------
---------------------SSS---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----AMASILNLAGLS

Eucalyptus grandis                      >TR|A0A059CFS8|          MG--------
---------------------LKASLVVL-SL-LLALALASASAKQ-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELKQCRHQCKVQQQFSEE--
QQRQCEQRCEDYYLQKQERKREEGREEEKGGGDD-----------------------------------------
-----------------RKQLKECQKQCERRQQ--
KGRSREGCQQRCVEAYGRKGEDQPRNRRGKEDQEKERGREWVNDRYEEEEEEEGGESEGREESD-----------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------NPYVFD-RE-H-FKA-IVETEHGRVSV-LPKFTKR-SKLLRG-IEN------
-----FRLALLEAEPNTFEVPSHWDTDAVLFIVEG-RGTITLVRQN-KRQS---INIEEG-DIV----
RVEAGTPVYMINRD-QN-----QKLIIAQLLRP---VNLPSQFEAFY--GTGG-
QNPESFYTAFSWEVLEAALKT---DRNKLERLFGQQ---------------------------------------
-------------QQGAIVKASREQIEALS--G-HEEGGR-----WP--FGGGESHG----SKGSRSFNLFNKH-
PS-HANQHGQLYIADRDDF-K-ELED--MDVMISFANITQ-GSMIGPYYNSRATKISFVTEGEG---
YLEMGCPHLS------SSRSKHSRHQKQ-QG------GGG---------------------G-----
GRTYQKVRAQLRRGTAFIVPAGHPVAAIASK--NSNLQIACFEVNAEN-----NVRYPLAGK-RNIIDLMER---
--EAKELAFNF-P---SRDVDRIFK-S-QDEEFFFAGPEEWQEQ-------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------E--KGYADE

Pyrus x bretschneideri                  >REF|XP_009367697.1|     MDL-------
------------------KGRVLVVCLLL-SA-FFLSAF-VAVALE-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------DPELKQCKHQCKHQRGFEEW-QKKQCERKC-EDYIKQKREQEEQRG-------------
REEFEGRGQQQ--QEEG----DE----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------NPYFFE-DQ-H-FET-
RVQTEEGRVQV-LQKFNER-SDLLRG-IEN-----------FRVGFLVTEPHAFVAPTHLDADCVLFVFQG-
RPTITVVKEE-KKES---HNLERG-DLF----RIPAGTPFYILNRD-EN-----ERLHIVKLLKT---
VSTPGEYEAFY--SAGG-QDPESFFKAFSPEVLQAAFKT---DRNKLDRLFGQQ---------------------
-------------------------------RRGSIIRASKEQVQRMS--QQHGHGGSEG--IWPLPFHGG-ES-
-----SSKDSFNLFKKH-AS-QENKFGRLFEADFKDF-K-QLQE--FDLLVSFANITR-
GAMEGPFFNSRATKISVVLDGEG---HFEMACPH-----------------------------RQK---------
------------S-----SPTYQKMSGDLRRGAVFVAPAGHPVTIIASR--NNNLQLLCFEVNARD-----
NIRFPLVGK-NNVVSQFDR-----QAKELSFNV-P---ASEVESIFN-N-QKDELFFEGPN---EQPQ-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------H--GWAY-A

Malus domestica                         >REF|XP_008386543.1|     MDL-------
------------------KGRVLVVCLLL-SA-FFLSAFAVAVALE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------DPELKQCKHQCKHQRG--------RGNRRT-SGGGGKEEEEEEEGG----
EGGSFYIREREEFEGRGQQQ--QQQG----DE-------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------------NPYFFE-
DQ-H-FET-RVQTEEGRVQV-LQKFNER-SDLLRG-IEN-----------
FRVGFLVTEPHAFVAPTHLDADCVLFVCQG-RPTITLVREE-KKES---HNLERG-DLF----
RIPAGTPFYILNRD-DN-----ERLHIVQLLKA---VSTPGEYEAFH--SAGG-
QDPESFFKAFSPEVLQAAFKT---DRNKLDRLFGQQ---------------------------------------
-------------TRGSIIRASKEQVQRMS--QQHGHGGSEG--IWPLPFHGG-EL------TSKDSFNLFKKH-
PS-QENKFGRLFEADFKDF-K-QLQE--FDLLVSFANITR-GAMEGPFFNSRATKISVVLDGEG---
HFEMACPH-----------------------------RQK---------------------S-----
SPTYQKMRGDLRRGAVFVAPAGHPVTTIASR--NNNLQLLCFEVNARD-----NIMFPLVGK-NNVVSQFDR---
--QAKELSFDV-P---ASEVESIFN-N-QKDELFFEGPN---EQPQ-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------N--GLMHES

Pyrus x bretschneideri                  >REF|XP_009370838.1|     MEL-------
------------------KSKVFVVLLLL-SA-FVLSAFAASVVLE-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------DPELKQCQHQCKHQRGFDER-QKQQCERKC-EDYTGE----------------------
REEFEGRGQQQHQQQQG----DE----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------NPYFFE-DQ-H-FET-
RIQTEEGSVQV-LQKFNER-SDLLRG-IEN-----------FRVGFLVTEPHAFVSPTHLDADSILFVFQG-
GPTITMVRGE-KKES---HNLERG-DLF----RIPAGTPFYVLNRD-EN-----EKLHIVELFKT---
VSTPGEYASFH--SSGG-QDPESFFRAFSPEVLQAAFKT---DRNKLDRLFGQQ---------------------
-------------------------------RRGSIIRASKEQVQRMS--QQHGHGGGEG--IWPLPFHGGDES-
-----SSKDSFNLFKKH-PS-HENKFGRLFEADFNDF-K-QLQE--FNLVVSFANITR-
GGMAGPYFNSRATKISVVLDGEG---YFEMACPH-----------------------------RQK---------
------------S-----SPTYQKMSGDLRRGAVFVAPAGHPVTTIASR--NNNLQVLCFEVNAHD-----
NIRFPLVGK-NNVVSQFDR-----QAKELSFNV-P---ASEVESIFN-N-QKDELFFEGPN---DQLE-------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------H--GRAH-A

Prunus persica                          >TR|M5VLX9|              MAL-------
------------------KSKLLLVALLL-SV-LFLSVY-VASATQ-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------DPELKQCRHQCEHQQGFDSK-QREQCEQGC-DKYIKQKREEEKHRR----
KSEGGGSFYPIPETGRAQEEEEEFQGRQQQDQ-------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------------NPYFFE-
DE-H-FET-RVQTEEGRFQL-LQKFTER-SDLLRA-IEN-----------
YRIGFLVTKPHAFVAPCHFDADTVLFVFQG-RPAVTIVRGE-KRET---HNLEHG-DLF----
RIPAGTPVYMVNRD-EN-----EKLFIVNFMKP---VSVPGEYEAFY--AAGG-
ENPESFFKAFSPQVLQAALKT---EINKLERLFGQQ---------------------------------------
-------------RQGSITRASKEQIKKLS--QQHGQGGSEG--FWP--FHGG--Q------SSSDAFNLFSKH-
PS-QANKFGRLFEADFNDF-K-QLQD--LDLLVSFANITQ-GAMVGPYFNSRATKISFVLDGEG---
YFEMACPHVS------STGRQEPQPQPQPQQ------RRK---------------------S-----
SPRYQKISGNLRRGAVFVAPAGHPMTAIASR--NSNLQIICFEVNAHD-----NIRVPLVGK-KNVVSQFDR---
--EAKQLAFNV-P---AREVDRIFN-N-QDDEFFFEGPN---EQPE-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------H--GRAF-A

Prunus mume                             >REF|XP_008235388.1|     MAL-------
------------------KSKLLLVALLL-SV-MFLSVY-VASATQ-----------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------DPELKQCRHQCEHQQGFDSK-QREQCEQGC-DKYIKQKREEEKHRG----
KSGGGGSFYPISETGRAQEEEEEFQGRQQEDQ-------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------------NPYFFE-
DE-H-FET-RVQTEEGRFQL-LQKFTER-SDLLRA-IEN-----------
YRIGFLVTKPHAFVAPSHFDADTVLFVFQG-RPAVTIVRGE-KRET---HNLERG-DLF----
RIPAGTPVYMVNRD-EN-----EKLFIVNFMKP---VSVPGEYEAFY--AAGG-
ENPESFFKAFSPQVLQAALKT---EMNKLERLFGQQ---------------------------------------
-------------RQGSITRASKEQIKKLS--QQHGQGGSEG--FWP--FHGG--Q------SSSDAFNLFSKH-
PS-QANKFGRLFEADFNDF-K-QLQD--LDLLVSFANITQ-GAMVGPFFNSRATKISFVLDGEG---
YFEMACPHVS------STGRQEQQPQPQ--Q------RQK---------------------S-----
SPRYQKISGNLRRGAVFVAPAGHPMTAIASR--NSNLQIICFEVNAHD-----NIRVPLAGK-KNVVSQFDR---
--EAKELAFNV-P---AREVDRIFN-N-QDDEFFFEGPN---EQPE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
--------H--GRAY-A

Prunus persica                          >TR|M5Y4Q9|
MAIKITIKASYKLPF---------------------FFFFLSTLFLA----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------------------------
SSSVTPLINALSDYHNQKCQQSICRGVGGRHSLLRSKDHPQDAREEYFYCSQSCGTSEEPEQ------
CETECRERFDEQLKKEA----------------------EEQQKGQEEEEEGPTFNP------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------NPYYFP-KF-G-LRP-RFLAEEGAYFV-LGSFA-RLSHLLRGRIQN-----------
YRAALLQTTPGTFVLPYHLDAESIFVVWNG-RGTLTLVMKD-TKQS---FKIENG-DVI----
RVPAGATTYLINNH-TT-----ENLSLVHLFQP---VNTPDLFEEFF--PAGYKGPE-
SYYSVFSNDLLEAAFDV---PREQLEKAFGQQ---------------K---------------------------
---------REGMIIRASKEQLEALSKQASPW-----------------WRKLVPWSMGSDLNFNLLSQR-PL-
HSNNYGKFYEASPQEFK--QLQD--MNVSVAMLDINP-EAMMVPHYNSKATYLMMVVDGMG---YFEMACPKFT-
-----IPASEEEMEYQEEQADQQ---------------------------------
SGVYSKVSGKLSLGDVFVIPAGHPVSIVAQQ--NQNLRIVGFGINAGN-----NMRNFLAGQEGNIMKQMER---
--EATQLTF-------GQEMEQVLT-S-QKQSYFVPASRRGSSTEK-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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----------------A

Prunus mume                             >REF|XP_008224282.1|
MAIKITIKASYKLPF---------------------FFFFLSTLFLA----------------------------
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------------------------------------------------
SSSVTPLINALSDYHNQKCQQSICRGLGGRHSLLRSKDHPQDAREEYFYCSQSCGTSEDPEQ------
CETECRKRFDEQLRKEA----------------------EEQ-KGQEEE--GPTFNP------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------NPYYFP-KF-E-LRP-RFLAEEGAYFV-LESFA-RLSHLLRGRIQN-----------
YRTALLQTTPGTFVLPYHLDAESIFVVWNG-RGTLTLVMKD-TKES---FKIENG-DVI----
RVPAGATTYLINNH-TT-----ENLSLVQLFQP---VNTPDLFEEFF--PAGYKDPE-
SYYSVFSSDLLEAAFDV---PREQLEKAFGQQ---------------K---------------------------
---------REGMIIRASKEQLEALSKQPSPW-----------------WRKLVPWSMDSDLNFNLLSQR-PL-
HSNNYGKFYEAPPQEFN--QLQD--MNVSVAMLDINP-EAMMVPHYNTKATYLMMVVDGMG---YFEMACPKFT-
-----IPASEEEMKYQEEQADQQ---------------------------------
SGAYVKVSGKLSLGDVFVIPAGHPVSIVAQQ--NQNLRIVGFGINAGN-----NIRNFLAGQEGNIMKQMER---
--EATELTF-------GQEMEQILT-S-QKHSYFVPASRRGSSTEK-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
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----------------A

Fragaria vesca                          >REF|XP_004292578.1|     MEL-------
------------------KSKLCLVVLVF-SV-LLAVSSGLDYKER-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------DPGLRQCMHQCQHQEGYDEQ-QKQICEQRC-DDYIKQKRQEERQRR----RGGGDTSFVRYDEN---
MEQYQGGQQHQQFDQ------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------NPYLFE-DQ-D-FDT-
IVETDQGRVQI-LQKFTEK-SDLLRG-IAN-----------FRIGALITKPHSFVAPHHFDADCVFFVFHG-
RPTISMVRGD-KRES---HNLERG-DIL----RVPAGTPVYIINRD-EN-----EKLFVVKLLHP---
VNLPDQFEAFY--EGGG-ENPQSFFKAFSPEVLEAAFKT---ERDELRRLFGQQ---------------------
-------------------------------RQGSIMKASREQIEKMS----HSSRSSEG--LWP--
FHGDQPSTPFSTSSKSGPFNLLRKR-PS-QSNRHGRLFEADSSDY-K-QLEE--LDLQISFANITR-
GSMIAPFFNSRATKISFVLDGEG---FFEMACPHLA------S---QESSQGGSQRQ------QRS---------
------------S-----SPSYQNVRGDLRRGTVFIVPAGHPATAIASR--NNNLQILCFEVNAKD-----
NVRLPLTGK-KNVVSQFER-----EAKELAFGV-P---GREVDRIFN-K-QDGEFFLEGPN---NQQQ-------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------G--RIRSVV

Morus notabilis                         >TR|W9QBD2|              MAC-------
------------------LNKLSLV--IL-SV-LVLTA-SLASATQ-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
------DPELKQCRHQCKHQRGFEEE-QRQQCEQRC-EEYIREKKHREREEE----------
GYSRRSRESREEEEEKEESGERIEQN-------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------NPYLFE-AE-H-
FDT-SVRTEEGRVHI-LKKFTER-SKLLKG-IEN-----------
YRVGFLEANPHAFVAPVHFDADVIFFVASG-RPTVTLLREE-KRET---FNLERG-DVV----
HIPAGTPAYIVNRD-ER-----EKLFIVNLINP---VYLPGEFESFH--GPGG-
EDPESFYKAFSWKVLKAAFKR---DRDEIERLFGQQ---------------------------------------
-------------KRGGITKASREQVEELS--R-HAEGGGGGGPIWP--FKG----------ETKGPFNLFRKH-
PV-SSNRYGSLFEANTEDC-K-DLED--LNLMISFANITK-GAMIAPNYNSKATKMSFVVDGEG---
WFEMACPHTP------SEQGRQ-RGGGSAWQ------GEK---------------------S-----
GKKFKRITGRLRRGMVFVVPAGHPVTAIASQ--NTNLQILCFEVNAKG-----NTRYPLAGR-KNIVNNMDN---
--VAKELAFGV-P---AREVERIFK-S-QNEEFFFPGPT---QQEE-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
--------G--GHRAYM

Morus notabilis                         >TR|W9RZA0|             M---------
----A--------------IKSSLPLFLLLSSLFVASFALSYDE-------------------------------
--------------
ENDQHRISPRQEYQQCQSRCQDQQLHGQERQLCQHRCEQQLREREREREQSEHGGRGRGSRESKERELREEFEQC
RQDCERREKGQQQQ-
QQCQRRCQQEYEERRREEQQREERERRRRQEGGRSVYDEEENDYHRTSPRQEYQQCQSRCQDQQLHGQERQLCQH
RCEQQLREREREREQSEHGGRGGGSRESKERELREEFEQCRQDCERREKGQQQQ-
QQCQRRCQQEYEERQREEQQREERERRRRQEGGRSVYDEEENDYHRTSPRQEYQQCQSRCQDQQLHGQERQLCQH
RCEQQLREREREREQSEHGGRGGGSRESKERELREEFEQCRQDCERREKGQQ---
QQQQCQRRCQQEYEERQREEQQREER-------------------------------------------
ERRRRQEGGRSEYEEVETASRDPEEKFRRCQQRCQEQQHV--QERRRECQQECERKYREEERR----
ERRRRDDDDD--EEMYNPEREREGEEREREISPRSEGE-------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------------------
NPYHFR-SH-R-LQS-RYRTEEGHLKV-LEMLSRR-SELLKG-LKN-----------
YRIVVLEANPNTFVVPHHCDADSVLVVTRG-KGTISIVRQN-NKES---YNIERA-DVI----
TVLAGSTVYLVNDQ--N-----EPLQITKLVTP---VNIPGQFEEYY--PGGGENPQ-
SYFKAFSTNILKSTLSA---TEEQIERLIGEQ---------------REGRRQ----------------------
-------LQRPGFIKRASQEQLQALTQHAS--------------------SPRRKGGRQTTGPISLHSLS-PT-
YSNNYGKFYEATPEDNK--QLEE--MDVLVAWTDLKQ-GSIFVPHFNSKTTTVLVMVVEGEG---RMEMACPHLA-
-----RQKRQ-QWGGREEEEKER-----QT-------------------ST-----W-
QYQKVTSHLSAGDVFIIPAGHPISVVASS--NQNLRMVGFGVNARN-----NERTFIAGK-DNVIKQLER-----
EAKELAFNM-P---GREVEQIFN-K-PKLSYFV--PQE-SQEEES-R----------------------------
---------------------------------------------------------------------------
-------------------QSH-----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---PLNSILNLAGFA

Prunus persica                          >TR|M5Y3W2|
MVIHIKPRLPLFLFL--------------S----
LLFLAFSVSFTLGQDREQHCQKQCQDFKRPIIHSECIYQCRMWGPWSLPPAESSNHHHKQQQQHEQEQQCKQRCQS
QHGHRQQQQQCQQECYEQIRQQREREEMQQMCQQSCEMQGSGGQQQQRQQCQRQCEQQVEQLKQCQLRCQMQGQG
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QQQE--QCQRTCRQELEDQQRRQQQEQG-----------------------------------------------
---------------------PGGGDNKLEDETLNGEPRRRFEQCMQGCERQQQGQGEQ-
EQCPRQCREQFDKEKSQ----------------------------------------------------------
------------------------------------YQQCKQSCEKSSQHDD---EKRQCKQQCKQQISLQQ---
-GGGNQEEDDDALNGSGYGGA----------------KERFEQCKLSCQSQQG-
QGQQERCPKQCKQQFEHEKHQYKQCKRGCENQARDD--FQKEQCKQQCTQQMSQQYGQQQEGSTGGGGLNQ----
------QQEEEGQMGSQGQSQSQSN--------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------------NPYYFP-SH-R-FQP-
RFQSNEGGLYV-LERFTQRQSEVLRG-IKN-----------YRLAIFEAKPNTFVLPHHCDAEAIYVVLSG-
QCTCTLLMQD-RKES---FNMEHG-DVI----RVPAGATTYLVNNN-SD-----ETLRIAKLLQP---
VNNPGRFEEFF--PAGSRNPE-SYFSVFSNDILESAFNT---PREQLEHGFKQG----------------QQQQG-
--------------------------------QGIVMRAPREQLQALSQAAS--------------------S-
RRRGDRQSQGPFNLRQQR-PV-HSNNYGQFFEARPEEFN--QLQD--MDASVSCIEINQ-
QAMMVPHFNSKATHLIMVVEGNG---LVEMACPYLA------SQ--SQEIMGQQEQQGEP---------------
------------------SGRYMKVTAQLSRGDVFVIPAGHPVALVAQ---NQSLRILGFGLNAQN-----
NKRNFLAGQEDNIIMHMDR-----EARQLAF-------GPEMEQIFS-K-QQQSYFV--PTQQGRSRN-------
---------------------------------------------------------------------------
---------------------------------------------Q-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------HLSSILEFAGVI

Prunus mume                             >REF|XP_008224279.1|
MVIHIKPRLPLFLFL--------------S----
LLFLAFSVSFTLGQDREQQCEKQCQDFKRPVIHSECIYQCRMWGPWSLSPAESSNHHKKQQQHEQEQQCKQRCQS
QHGHRQQQQ-
CQQECHEKIRQQKEREEMQQMCQQRCEMQGSGGQQQQRQQCQRQCEEQVEQLKQCQLRCQMQGQGQQQE--
QCQRTCRQELEDQQRRQQQEQG-----------------------------------------------------
---------------PGAGDNKLEDETLNGEPRRRFEQCMQGCERQQQGQGEQ-EQCPRQCREQFDKEKKQ----
---------------------------------------------------------------------------
---------------YQQCKQSCEKSSQHDD---EKRQCKQQCKQQISLQQ----
GGGNQEEDDDALNGSGYGGA----------------KERFEQCKLSCQSQQG-
QGQQEQCPKQCKQQFEHEKHQYKQCKRGCEKQALDDD--QKEQCKQQCTQQMSQQYGQQQEGSTGGGGPNQ----
------QQEEEGQMGSQGQSQSQSN--------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------------NPFYFP-SH-R-FQP-
RFQSNEGGLYV-LERFTQRQSEVLRG-IKN-----------YRLAIFEARPNTFVLPHHCDAEAIYVVLSG-
QCTCTLLMQD-RKES---FNMEHG-DVI----RVPAGATTYLVNNN-SD-----NTLRIAKLLQT---
VNNPGRFEEFF--PAGSGNPE-SYFSVFSNDILESAFNT---PREQLEHGFKQG----------------QQQQG-
--------------------------------QGIVMRAPREQLQALSQAAS--------------------S-
RRRGDRQSQGPFNLRQQR-PV-HSNNYGQLCEARPEEYN--QLQD--MDASVSCIEINQ-
QAMMVPHFNSKATHLIMVVEGNG---LVEMAYPYLA------SQ--SQEIMGQQEQQGEQ---------------
------------------SGRYMKVTAQLSPGDVFVIPAGHPVALVAQ---NQNLRILGFGLNAQN-----
NTRNFLAGQEDNIIMQMDR-----EARQLAF-------GPEMEQIFS-K-QQQSYFV--PTQQGRSRN-------
---------------------------------------------------------------------------
---------------------------------------------H-----------------------------
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---------------------------------------------------------------------------
---------------------------HLSSILEFAGMI

Carya illinoinensis                     >TR|B3STU4|              M---------
----V--------------TKAKIPLFLFLSALFLALVCSSLAL-------------------------------
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ETEDLSNELNPHHDPESHRWEFQQCQERCQHEERGQRQAQQCQRRCEEQLREREREREREEIVDPREPRKQYEQC
RETCEKQDPRQQPQ---CERRCERQF---QEQQERERRERRRGRDDDDKENPRDPREQYR---------
QCEEHCRRQGQGQRQQQQCQSRCEERFEEEQRRQEERERRRGRDNDDEENPRDPREQYRQCQEHCRRQGQGQRQQ
-QQCQSRCEERLEEEQRKQEERERRRGRDEDDQNPRDP-------------------------------------
----------------------------------EQRYEQCQQQCERQRRG-Q---
EQQLCRRRCEQQRQQEERERQRGRDR-------------------------------------------------
--------------QDPQQQYHRCQRRCQTQEQS--PERQRQCQQRCERQYKEQQGR--EWG----
PDQASPRRESRGREEE-----------QQRH--------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------------------NPYYFH-
SQ-G-LRS-RHESGEGEVKY-LERFTER-TELLRG-IEN-----------
YRVVILEANPNTFVLPYHKDAESVIVVTRG-RATLTFVSQE-RRES---FNLEYG-DVI----
RVPAGATEYVINQD-SN-----ERLEMVKLLQP---VNNPGQFREYY--AAGAQSTE-
SYLRVFSNDILVAALNT---PRDRLERFFDQQ---------------E---------------------------
--------QREGVIIRASQEKLRALSQHA-MS-----------------AGQRPWGRRSSGGPISLKSQR-SS-
YSNQFGQFFEACPEEHR--QLQE--MDVLVNYAEIKR-GAMMVPHYNSKATVVVYVVEGTG---RFEMACPHDV-
-----SSQSYEY---KGRREQE-----EEE-------------------SS-----
TGQFQKVTARLARGDIFVIPAGHPIAITASQ--NENLRLVGFGINGKN-----NQRNFLAGQ-NNIINQLER---
--EAKELSFNM-P---REEIEEIFE-R-QVESYFV--PMERQSRRGQ----------------------------
------------------------------------------------------------------G--------
---------------------RDH---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----PLASILDFAGFF

Cucurbita maxima                        >TR|Q9ZWI3|
MALSKVKLRCLLAFTLFLACLSVG---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------LGDKGESLSSGAGVDHDGCVNRC-EE-
LKGKNVDEFAACKKGCGV---------------------------------------------------------
------------------NQRGSPRAEYEVCRLRCQVAER--
GVEQQRKCEQVCEERLREREQGRGEDVDEVERRDPEWEREEQRRREHEREERRRRERERERERGRGRRDENERDP
KREQEER----QRREQERRRRREQEQRERERRGERDEEDDENQRDPDWRREQERREQERRRREQ-----------
---------------------------EQERRERQRRGGRDDEDENQRDPDWRREQKRREQ--------------
--------------------------------
EQERRERERRGGRDDEDENQRDPDWRREQERREQERRRREREQERREREHRGGRDVEDENQRDPDWRREQERRRR
EEEQREREWEREHGRRGREEQR--------SREDE----RRRHERQHGGRSRVNQVAIRRTEQEQSNNPYYFQ-
EQ-R-FQS-RYRSDEGHWRV-LERFSERSELLKG-IKN-----------
QRLALLEARPHTFIVPHHLDAECVLLVVRG-RATITTVVQEKRETRKESYNVESG-DVM----
TIPAGTTLYLANQE--N-----EDLQIVKLVQP---VNNPGEFKDYL--SAGGES--
QAYYSVFSNDVLEAALNI---PRDKLERIFKQR---------------RE-------------------------
----------RGGKIVRASQEQLRALSQRAT---------------------SVRKGSRGVRAPIKLESQT-PV-
YNNQYGQMFEACPDEFP--QLRR--TDVATSVVDIKQ-GGMMVPHFNSRATWVVFVSEGAG---SFEMACPHIQ-
-----SSQWQR-----GRREEERHWRREEEEER-----------------EERS--G-
RFERVAGRLSEGGVLVIPAGHPIAIMASP--NENLRLVGFGINAEN-----NHRNFLAGR-ENIMNELDR-----
EAKELAFNV-E---GKQADEIFR-S-QRESFFTEGPEGGRRRSTE--R---------------------------
---------------------------------------------------------------------------
---------------------S-----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---PLLSILKLAGYF
```

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Cucumis melo                            >REF|XP_008439368.1|
MAFSKVKFRCLLALTLFLACVSVG---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------LGAEGESLGSGVGVDN-GCVNGCQ-E-
LKGKNLDEYAACEKRCGV---------------------------------------------------------
------------------NQE-----VTEICRQWCQVMEPHGGEQQQRRCRQECEERLRDQKQG--EDVED-
KWRDPEREREEQRRREHEREERRRRERERERERGRGHRDENDRDPEREREERRREEQRREQEQRRREGKPK----
-------------GHDWRREQERREQERRRREQ------------------------------------------
---------------------------------------------------------------------------
--EQERRERERRGEREDEEENQRDPDRRREQERR------------------------------------
EQERRRREQEQREREWEREHGRGGSQERRRGGQEEEISRKEEWEREERRRERQHGGRSRANEVNSRWTEQEQSHN
PYYFQ-ER-Q-FQS-RFRSDQGQWRV-LERFSERSELLRG-LKN-----------
QRLAILEARPQTFIIPHHIDAESVLFVVKG-RATITTIVQERKETRKESYNVERG-DVV----
TIPAGTTVYLANQE--N-----EDLQIVKLIQP---VNNPGEFKDYL--SGGGEA--
QSYYSVFSNDVLEAALNI---PRDRLERIFKQR---------------GE-------------------------
----------RRGKIIRASQEQLKALSQRAT---------------------SVKKGGRGARSLIKLESQS-PV-
YNNQYGQMYEACPDEFP--QLRR--TDVATSVLDIKQ-GGMMVPHFNSRATWVVFVSEGTG---SFEMGCPHVQ-
-----GSQWQR-----GRREEERQWRREEEKEL----------------SDERS--G-
RIERIAGRLSQGGVLVIPAGHPIAIMASP--NENLRLVGFGINAEN-----NKRNFLAGR-ENIMNEVDR-----
EAKELTFNV-E---GKQAEETFK-S-QKESFFTEGPEGGRRRSTETER---------------------------
---------------------------------------------------------------------------
---------------------T-----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---PLFSILKLAGYF

Cucumis sativus                         >REF|XP_011650968.1|
MAFSKVKFRCLLAFTLFLACVSVG---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------LGAEGESLGSGVGVDN-GCVNGCQ-E-
LKGKNLDEYAACEKQCGV---------------------------------------------------------
------------------NQK-----ETEICRQWCQVMKPQGGEEQ-RRCQQECEERLRDQEQG--EDVED-
KWRDPEREREEQRRREHEREERRRRERERERERGRGRRDENDRDPEREREERRREEQRREQEQRRREQEQRERER
RGEREDEE-
ENQRGPDWRKEQERREQERRRREEQERRERQRRGEREDEEENQRGPDWRKEQERREQERRRREEQERRERQRRGE
REDEEENQRGPDWRKEQERREQERRRREEQERRERQRRGEREDEEENQRGPDWRKEQERREQERRRREEQERRER
QRRGEREDEEENQRGPDWRREQERRRRE------
EQERRERQRRGEREDEEENQRGPDWRREQERRRREEEQREREWEREHGRRGSQERRRGGQEEEISRREE------
-SERQHGGRSRANQVKTRWTEQEQSHNPYYFQ-ER-Q-FQS-RFRSDQGEWRV-LERFSERSELLKG-LKN----
-------QRLAILEARPQTFIIPHHIDAESVLLVVKG-RATITTIVQEKKETRKESYNVECG-DVI----
TIPAGTTVYLANQE--N-----EELQIVKLIQP---INNPGEFKDYL--SGGGES--
QAYYSVFSNDVLEAALNI---PRDRLERIFKQK---------------SE-------------------------
----------RRGKIIRASREQLKALSQRAT---------------------SVKKGGQGARAVIKLESQS-PV-
YNNQYGQMYEACPDEFP--QLRR--TDVATSVLDIKQ-GGMMVPHFNSRATWVVFVSKGTG---SYEMGCPHIQ-
-----GSQWQR-----GRREEERQWRREEERER----------------SDERS--
SSRIERIAGRLSQGGVLVIPAGHPIAIMASP--NENLRLVGFGINAEN-----NKRNFLAGR-ENIMNEVDR---
--EAKELAFNV-E---GKQAEETFK-S-QKESFFTEGPEGGRGRSRE--R-------------------------
---------------------------------------------------------------------------
-----------------------T---------------------------------------------------
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---------------------------------------------------------------------------
-----PLLSILKLTGYF

Cucumis melo                            >REF|XP_008451293.1|
MRLQIPSYNLHFPFIHFSLHQQQSTMAFKIKINLNLHLL-LLFL-ITALCLALASK-------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------DPELKQCKHQCKVQRQFDEQ-QKRDCERSCDEYYKMKKEKGRN--------------
YESEEEEEEEEEEEEE----EEE----------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------------------------------NPYVFD-DE-H-FVG-
KVETGEGKIKV-LQKFTQR-SQLLRG-IEN-----------FRVSIVEANPSTFVVPTHFDAEIIMFVAQG-
RGTITVIKE--KRGS---FDLKCG-DVF----RIPSGAPFYFINKD-EH-----QKLKIVKLLQS---
TSVPGHFQTFQ--PAGG-ENPESFYTAFSWDLLEAAFKI---PRDKLERFFKQQ---------------------
-------------------------------RPGTIIKASREQIRSLS--Q-HEE---IIPKIWPFSEG------
-----ETERPFNLLKQH-PW-QSNKFGRLFEAYPDEF-S-QLRD--LGVAIAFANITK-
GSMMTPHYNSKSMKIAVVLDGEG---GFQMACPHLS------SSSGRSG-------RWSEREEGRK---------
------------G-----ERTYQKIRGRLSRGVVFVVPAGHPFSVFASP--NHSLQIVCFEVNAYG-----
NTKYFLAGK-ENIVNKMES-----IARELGFNT-P---GREVERMFK-Q-QEEEFFFPGPNQQEHEW--------
---------------------------------------------------------------------------
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------------------------------------ASA

Cucumis sativus                         >REF|XP_011659275.1|
MTLHIPSYNLQFSIYSLLSSTTTSTMAFKIKINLNLHLL-LLFL-ITAVCLALASK-------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------DPELKQCKHQCKVQRQFDEQ-QKRDCERSCDEYYKMKKEKGRN--------------
YESEEEEEEEEEVE-------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------------NPYVFD-DE-H-FVG-
QIETGEGKIKV-LQKFTQR-SHLLRG-IEN-----------FRVSIVEANPSTFVVPTHFDAEIILFVAQG-
RGTITVIKE--KRGS---FELKCG-DVF----RIPSGAPFYFINKD-EH-----RKLKIVKLLQS---
TSVPGHFQTFQ--PAGG-ENPESFYTAFSWDLLEAAFKI---PRDKLERFFKQQ---------------------
-------------------------------KPGTIIKASREQIRSLS--R-HEE---IIPKIWPFSEG------
-----ETERPFNLLKQH-PC-QSNKFGRLFEAYPDEF-S-QLRD--LGVAIAFANITE-
GSMVAPHYNSKSMKIAVVLDGQG---GFQMACPHLS------SSSRRSG-------RWSEREEERK---------
------------G-----ERTYQKIRGRLSRGVVFVVPAGHPFSVFASP--NHSLQIVCFEVNAYG-----
NTKYFLAGK-ENIVNKMES-----IARELGFNT-P---GREVERMFK-Q-QEEEFFFPGPNQQEHEW--------
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------------------------------------ADA
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Phaseolus vulgaris                      >TR|V7BFL3|              M---------
------------------KINLSLPILLFFLLALF-SNLSLAK-KE-----------------------------
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---------------------------------------------------------------------------
TKVVG-DPELKTCKHQCLQQQKYSED-
DKLICLRSCDEYHGLKHEREKQIEESSEKQIHEHEGSSEEHEEEEEKEEQVEEGGEEEEE---------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
--------------------YPYIFEEDR-D-FDT-KFETEDGRIRL-LKKFTEK-SELLKG-IEN---------
--IRLTIVEAKPHTFVAPRHFDSDVVLFNIKG-RAVLGWVKES-ETEK---FILESG-DML----
AIPAGTPLYIVNRD-EN-----EKLFLAMLHVP-VS--TPGKFQEFF--GPGG-
RDPESFLSAFGWNVLQAALQS---PKGQLEKLFNQQ---------------------------------------
-------------NGGSIFEISRKKVQEMAP-KKTS--------WWP--FGGP----------STAEFNLFTKP-
PT-FSNRHGRLTEVGPPD-SRSLLEK--LNIMLSFTNITM-KSMSTIHYNSHATKIALVIDGKG---
HLQIVCPHIS------SRS-NS-------------KHEKS---------------------S-----P-
SNHRISADLKPGMLFVVPPGHPFVTFSSR--KENLQIISFEINARD-----NKKFTFAGK-DNIVSSMDD-----
LAKELAFNY-P---SEIVNKIF--D-RKESFFFPF--ELPQSDP-------------------------------
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-----------RADA

Pisum sativum                           >TR|O49927|              M---------
----------------AIKTKLSLTIFLFFLLALLCSNLAV--GRK-----------------------------
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---------------------------------------------------------------------------
----EKDPELTTCKDQCDMQRQYDEE-DKRICMERCDDYIKKKQERQKHKEHEEEEEQEQEEDE-----------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------------------NPYVFE-DN-D-FET-KIDTKDGRVLI-
LNKFNEK-SKLLKN-IEN-----------YGLAVLEIKANAFLSPHHYDSEAILFNIKG-RGIIGLVAED-
RTER---FNLEEG-DIM----RVPAGTPMYLVNRD-EN-----EKLYIAAFHMPPSSGSAPVNLEPFF--ESAG-
RKPESVLNTFSSKVLQAALKS---SKGELETVLDEQ---------------------------------------
-------------KKGRIFKIEKEDVRGLAP--KKS--------LWP--FGGP----------FKSPFNIFSNN-
PA-FSNKFGSLFEVGPSQ-EKSGLEG--LNLMLTLANITK-GSMSTIHYNTNANKIALVIDGEG---
ELEMACPHMP------SSSSNS-------------RQKKS---------------------S------
ISYHNINAKLRPGVMFVVPAGHPFVNIASK--KKNLIVVCFEVNAQR-----NKKLALAGK-KNIVSALDK----
-AAKEVAFDI-A---AEKVDEVF--E-RKEEFFFPYDNE-ERKEE------------------------------
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----------HGRAVV
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Vicia faba                              >TR|Q9AVP7|              M---------
----------------AIKTKLSLTIFLFFLLALLCSNLAI--ARK-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----EKDPELTTCKDKCDLQGQYDEE-DKRICMEKCEDYVRKKQERQKHKEHEKEEHEEEEENE-----------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------------------NPYVFE-NK-D-FET-KIDTKDGRILI-
LNKFHEK-SKLLKN-IEN-----------YGLAVLEIKANAFLSPHHYDSEAILFNIKG-KGIIGLVAED-
QTER---FNLEEG-DLI----RVPAGTPTYLVNRD-EN-----EKLLIAAFHLPPSSGSAPVNLEPFF--ESGG-
RRPESVLSTFSSKVLQAALKS---SERELETVLDEQ---------------------------------------
-------------QKGRIFKIAKEDVLSLAP--KRS--------LWP--FGGT----------FKGPFNIRNNN-
PA-FSNQFGTLFEVGPSL-EKTGLEG--LNLMLTFANITK-GSMSTIHYNTNANKIAFVVNGEG---
DFEMACPHMP------SSSSNS-------------KQKKS---------------------S------
ISYHNINAKLKPGMVFVVPAGHPYVNIASK--KNNLLILCFEVNAQR-----NKKLAFAGK-KNIMSALDK----
-TAKELAFDL-A---AQKVDKIF--E-RKEELFFPYD-E-ERKEE------------------------------
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----------RGRAFV

Glycine max                             >TR|I1JF86|              M--------
DHLKPRVSLLFLTDLTMATRAKLSLAIFLFFLLALI-SNLALGKLKE----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-TEVEE-DPELVTCKHQCQQQRQYTES-DKRTCLQQCDS-----MKQEREKQVEEETRE---------K----
EEEHQEQHEEEEDE-------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------NPYVFEEDK-D-FST-
RVETEGGSIRV-LKKFTEK-SKLLQG-IEN-----------FRLAILEARAHTFVSPRHFDSEVVLFNIKG-
RAVLGLVRES-ETEK---ITLEPG-DMI----HIPAGTPLYIVNRD-EN-----EKLLLAMLHIP-VS--
TPGKFEEFF--GPGG-RDPESVLSAFSWNVLQAALQT---PKGKLERLFNQQ-----------------------
-----------------------------NEGSIFKISRERVRALAPTKKSS--------WWP--FGGE------
----SKAQFNIFSKR-PT-FSNGYGRLTEVGPDD-EKSWLQR--LNLMLTFTNITQ-
RSMSTIHYNSHATKIALVMDGRG---HLQISCPHMS------SRS-DS-------------KHDKS---------
------------S-----P-SYHRISADLKPGMVFVVPPGHPFVTIASN--KENLLIICFEVNVRD-----
NKKFTFAGK-DNIVSSLDN-----VAKELAFNY-P---SEMVNGVF--E-RKESLFFPF--ELPSEER-------
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---------------------------------GRRAVA

Glycine max                             >TR|Q84V19|              M---------
----------------ATRAKLSLAIFLFFLLALI-SNLALGKLKE-----------------------------
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---------------------------------------------------------------------------
TEVEE-DPELVTCKHQCQQQRQYTES-DKRTCLQQCDS---MKQEREKQVEE--ETRE---------K----
EEEHQEQHEEEEDE-------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------NPYVFEEDK-D-FST-
RVETEGGSIRV-LKKFTEK-SKLLQG-IEN-----------FRLAILEARAHTFVSPRHFDSEVVLFNIKG-
RAVLGLVRES-ETEK---ITLEPG-DMI----HIPAGTPLYIVNRD-EN-----EKLLLAMLHIP-VS--
TPGKFEEFF--GPGG-RDPESVLSAFSWNVLQAALQT---PKGKLERLFNQQ-----------------------
-----------------------------NEGSIFKISRERVRALAPTKKSS--------WWP--FGGE------
----SKAQFNIFSKR-PT-FSNGYGRLTEVGPDD-EKSWLQR--LNLMLTFTNITQ-
RSMSTIHYNSHATKIALVMDGRG---HLQISCPHMS------SRS-DS-------------KHDKS---------
------------S-----P-SYHRISADLKPGMVFVVPPGHPFVTIASN--KENLLIICFEVNVRD-----
NKKFTFAGK-DNIVSSLDN-----VAKELAFNY-P---SEMVNGVS--E-RKESLFFPF--ELPSEER-------
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---------------------------------GRRAVA

Glycine max                             >TR|Q9SP11|              M---------
----------------ATRAKLSLAIFLFFLLALI-SNLALGKLKE-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
TEVEE-DPELVTCKHQCQQQRQYTES-DKRTCLQQCDS---MKQEREKQVEE--ETRE---------K----
EEEHQEQHEEEEQDQ------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------NPYVFEEDK-D-FST-
RVETEGGSIRV-LKKFTEK-SKLLQG-NEN-----------FRLAILEARAHTFVSPRHFDSEVVLFNIKG-
RAVLGLVRES-ETEK---ITLEPG-DMI----HIPAGTPLYIVNRD-EN-----EKLLLAMLHIP-VS--
TPGKFEEFF--GPGG-RDPESVLSAFSWNVLQAALQT---PKGKLERLFNQQ-----------------------
-----------------------------NEGSIFKISRERVRALAPTKKSS--------WWP--FGGE------
----SKAQFNIFSKR-PT-FSNGYGRLTEVGPDD-EKSWLQR--LNLMLTFTNITQ-
RSMSTIHYNSHATKIALVMDGRG---HLQISCPHMS------SRS-DS-------------KHDKS---------
------------S-----P-SYHRISADLKPGMVFVVPPGHPFVTIASN--KENLLIICFEVNVRD-----
NKKFTFAGK-DNIVSSLDN-----VAKELAFNY-P---SEMVNGVF--E-RKESLFFPF--ELPSEER-------
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---------------------------------GRRAVA

Glycine max                             >TR|I1L860|              M---------
----------------AMRTKLSLAIFFFFLLALF-SNLAFGKCKE-----------------------------
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---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
TEVEEEDPELVTCKHQCQQPQQYTEG-DKRVCLQRCDRYHRMKQEREKQIQESRERETRE-------
KKEEEEEEQQEQHEE-QDE--------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------NPYIFEEDK-D-FET-
RVETEGGRIRV-LKKFTEK-SKLLQG-IEN-----------FRLAILEARAHTFVSPRHFDSEVVFFNIKG-
RAVLGLVSES-ETEK---ITLEPG-DMI----HIPAGTPLYIVNRD-EN-----DKLFLAMLHIP-
VSVSTPGKFEEFF--GPGG-RDPESVLSAFSWNVLQAALQT---PKGKLEKLFDQQ-------------------
---------------------------------NEGSIFAISREQVRALAPTKKSS--------WWP--FGGE--
--------SKPQFNIFSKR-PT-ISNGYGRLTEVGPDDDEKSWLQR--LNLMLTFTNITQ-
RSMSTIHYNSHATKIALVIDGRG---HLQISCPHMS------SRSSHS-------------KHDKS---------
------------S-----P-SYHRISSDLKPGMVFVVPPGHPFVTIASN--KENLLMICFEVNARD-----
NKKFTFAGK-DNIVSSLDN-----VAKELAFNY-P---SEMVNGVF--D-RKESFFFPF--ELPREER-------
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---------------------------------GRRADA

Glycine max                             >SP|Q04672|              M---------
----------------GMRTKLSLAIFFFFLLALF-SNLAFGKCKE-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
TEVEEEDPELVTCKHQCQQQQQYTEG-DKRVCLQSCDRYHRMKQEREKQIQESRERETRE-------
KKEEEEEEQQEQHEE-QDE--------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------NPYIFEEDK-D-FET-
RVETEGGRIRV-LKKFTEK-SKLLQG-IEN-----------FRLAILEARAHTFVSPRHFDSEVVFFNIKG-
RAVLGLVSES-ETEK---ITLEPG-DMI----HIPAGTPLYIVNRD-EN-----DKLFLAMLHIP-
VSVSTPGKFEEFF--APGG-RDPESVLSAFSWNVLQAALQT---PKGKLENVFDQQ-------------------
---------------------------------NEGSIFRISREQVRALAPTKKSS--------WWP--FGGE--
--------SKPQFNIFSKR-PT-ISNGYGRLTEVGPDDDEKSWLQR--LNLMLTFTNITQ-
RSMSTIHYNSHATKIALVIDGRG---HLQISCPHMS------SRSSHS-------------KHDKS---------
------------S-----P-SYHRISSDLKPGMVFVVPPGHPFVTIASN--KENLLMICFEVNARD-----
NKKFTFAGK-DNIVSSLDN-----VAKELAFNY-P---SEMVNGVF--D-RKESFFFPF--ELPREER-------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------GRRADA

Medicago truncatula                     >TR|G7IDM5|              M---------
----------------AMKTKLSLAIFLFFLLALLCSNLAIAIGRE-----------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
----ETDPELKTCIHQCKQQRQYDE--DKGICMDKCEDYHRMKQEREKRQHQ--------------HQREH-
EHQHEREHEHEEDE-------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------NPYVFE-DR-D-FET-
KIDTDDGRVMA-LNMFDQK-SKLLRN-FEN-----------YGLTILEAKGHAFVSPHHFDSEVIFFNVKG-
RGIIGLVMED-KTER---FNLEAG-DIM----RVPAGTPMYLVNRD-EN-----
EKLFVAALHMPPSSASAPVNLEAFF--GPAG-RDPESVLTAFSSKVLQAAFKS---PKGKLESFLDEQ-------
---------------------------------------------NKGRIFKIQKEDLSGLAP--KKS-------
-IWP--FGGQ----------FKNPFNIFSNN-PA-FSNQFGSLFEVGPSE-ITSGLDG--LNLMLTFANITK-
GSMSTIYYNTNANKIALVIDGEG---EFEMACPHMS------SSSSHS-------------KQRRS---------
------------S-----STSYQKINARLRPGTVFVVPAGHPFVTIASK--NNNLKIVCFEVNAQR-----
NKKLAFAGK-NNIVSALDK-----TAKKLAFDK-S---AEKVDEIF--K-RDEEFFFPYDVEDESKEE-------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------HGRADE

Cicer arietinum                         >REF|XP_004495184.1|     M---------
----------------AIKAKVSLAFFLFFLLSLLCSNLVI--SKE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----ERDPEIKTCKHQCRQQLQYSEE-DKNVCMEECDEYHRMKKEREKRK-------------------------
-EQDQDEDENE----------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------NPYVFK-SK-D-FDT-RIDTEDGRVLV-
LNKFNDK-SKLLRN-IEN-----------YGLAVLEVKGHAFVSPHHFDSEVIIFNVKG-KAIIGLVMED-
KTER---FNLESG-DIM----RVPAGTPMYLVNRD-EN-----EKLFIAALHMPPLSASAPVNLEAFF--EPGG-
RNPESVLTAFSSKVLQAALKT---PKEKLERFFDYQ---------------------------------------
-------------RRERIFKISKEDVHGLAP--KRS--------IWP--FGGQ----------FKGPFNIFTNR-
PS-FSNQYGSLFEVGPSE-EKSGLDE--LNLMLTLANITK-GCMSTIYYNTNANKIAFVTEGEG---
DFEMACPHL--------------------------KEKKS---------------------S-----
STSYHKISGRLKAGMVFVVPAGHPFVTMASK--KNNLVIVCFEVNAER-----NKKLAFAGK-RNIVSALDK---
--RAKEVAYEY-P---AEKVDEIF--E-RDEEFFFPY----EEGEE-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------EERADA

Arachis hypogaea                        >TR|B3IXL2|              MRGRVS----
--------PL-----MLLLGILVLASVSAT---------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------QAKS-
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PY-RKTENPCAQRCLQSCQQE---PDDLKQKACESRCTKLEYDPRCVYD----TGATNQRHPPG-----------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----ERTRGRQPGDYDDDRRQPRREEGGRWGPAEPR---EREREEDW-RQPREDWRRPSHQQPRKIRP------
-------------------------EGREGEQEWGTPGSEVREETSRNNPFYFPSR--R-FST-
RYGNQNGRIRV-LQRFDQR-SK-QFQNLQN-----------HRIVQIEARPNTLVLPKHADADNILVIQQG-
QATVTVANGNNRKS----FNLDEG-----HALRIPSGFISYILNRHD-N-----QNLRVAKISMP---
VNTPGQF-EDF--FPASSRDQSSYLQGFSRNTLEAAFN-AEF--
NEIRRVLLEENAGGEQEERGQRRRSTRSSDN--------------------------------
EGVIVKVSKEHVQELTKHAKSVS-----------------KKGSEEE-DITNPINLRDGEP--
DLSNNFGRLFEVKPDK-KNPQLQD--LDMMLTCVEIKE-GALMLPHFNSKAMVIVVVNKGTG---
NLELVAVRKE------QQQRGRREQEWEEEEEDE----------------------------
EEEGSNREVRRYTARLKEGDVFIMPAAHPVAINAS----SELHLLGFGINAEN-----
NHRIFLAGDKDNVIDQIEK-----QAKDLAFP-GS---GEQVEKLI--KNQRESHFVSARPQSQSPS-------
SPEK----------------------------------------------------------------
EDQEEENQGGKGPLLSI----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------LKAFN

Arachis duranensis                      >TR|N1NEW2|              MRGRVS----
--------PL-----MLLLGILVLASVSAT---------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------HAKS-
PY-RKTENPCAQRCLQSCQQE---PDDLKQKACESRCTKLEYDPRCVYD----TGATNQRHPPG-----------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----ERTRGRQPGDYDDDRRQPRREEGGRWGPAEPR---EREREEDW-RQPREDWRRPSHQQPRKIRP------
-------------------------EGREGEQEWGTPGSEVREETSRNNPFYFPSR--R-FST-
RYGNQNGRIRV-LQRFDQR-SK-QFQNLQN-----------HRIVQIEARPNTLVLPKHADADNILVIQQG-
QATVTVANGNNRKS----FNLDEG-----HALRIPSGFISYILNRHD-N-----QNLRVAKISMP---
VNTPGQF-EDF--FPASSRDQSSYLQGFSRNTLEAAFN-AEF--
NEIRRVLLEENAGGEQEERGQRRRSTRSSDN--------------------------------
EGVIVKVSKEHVQELTKHAKSVS-----------------KKGSEEE-DITNPINLRDGEP--
DLSNNFGRLFEVKPDK-KNPQLQD--LDMMLTCVEIKE-GALMLPHFNSKAMVIVVVNKGTG---
NLELVAVRKE------QQQRGRREREWEEEEEDE----------------------------
EEEGSNREVRRYTARLKEGDVFIMPAAHPVAINAS----SELHLLGFGINAEN-----
NHRIFLAGDKDNVIDQIEK-----QAKDLAFP-GS---GEQVEKLI--KNQRESHFVSARPQSQSPS-------
SPEK----------------------------------------------------------------
EDQEEENQGGKGPLLSI----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------LKAFN

Arachis hypogaea                        >TR|Q6PSU3|              MRGRVS----
--------PL-----MLLLGILVLASVSAT---------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------QAKS-
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PY-RKTENPCAQRCLQSCQQE---PDDLKQKACESRCTKLEYDPRCVYD----TGATNQRHPPG-----------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----ERTRGRQPGDYDDDRRQPRREEGGRWGPAEPR---EREREEDW-RQPREDWRRPSHQQPRKIRP------
-------------------------EGREGEQEWGTPGSEVREETSRNNPFYFPSR--R-FST-
RYGNQNGRIRV-LQRFDQR-SK-QFQNLQN-----------HRIVQIEARPNTLVLPKHADADNILVIQQG-
QATVTVANGNNRKS----FNLDEG-----HALRIPSGFISYILNRHD-N-----QNLRVAKISMP---
VNTPGQF-EDF--FPASSRDQSSYLQGFSRNTLEAAFN-AEF--
NEIRRVLLEENAGGEQEERGQRRRSTRSSDN--------------------------------
EGVIVKVSKEHVQELTKHAKSVS-----------------KKGSEEE-DITNPINLRDGEP--
DLSNNFGRLFEVKPDK-KNPQLQD--LDMMLTCVEIKE-GALMLPHFNSKAMVIVVVNKGTG---
NLELVAVRKE------QQQRGRREQEWEEEEEDE----------------------------
EEEGSNREVRRYTARLKEGDVFIMPAAHPVAINAS----SELHLLGFGINAEN-----
NHRIFLAGDKDNVIDQIEK-----QAKDLAFP-GS---GEQVEKLI--KNQRESHFVSA----------------
---------------------------------------------------------------------------
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Arachis hypogaea                        >TR|N1NG13|              MRGRVS----
--------PL-----MLLLGILVLASVSAT---------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------
HAKSSPYQKKTENPCAQRCLQSCQQE---PDDLKQKACESRCTKLEYDPRCVYDPRGHTGTTNQRSPPG------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------ERTRGRQPGDYDDDRRQPRREEGGRWGPAGPR---EREREEDW-RQPREDWRRPSHQQPRKIRP-
------------------------------EGREGEQEWGTPGSHVREETSRNNPFYFPSR--R-FST-
RYGNQNGRIRV-LQRFDQR-SR-QFQNLQN-----------HRIVQIEAKPNTLVLPKHADADNILVIQQG-
QATVTVANGNNRKS----FNLDEG-----HALRIPSGFISYILNRHD-N-----QNLRVAKISMP---
VNTPGQF-EDF--FPASSRDQSSYLQGFSRNTLEAAFN-AEF--
NEIRRVLLEENAGGEQEERGQRRWSTRSSEN-------------------------------
NEGVIVKVSKEHVEELTKHAKSVS-----------------KKGSEEEGDITNPINLREGEP--
DLSNNFGKLFEVKPDK-KNPQLQD--LDMMLTCVEIKE-GALMLPHFNSKAMVIVVVNKGTG---
NLELVAVRKE------QQQRGRRE---EEEDEDE----------------------------
EEEGSNREVRRYTARLKEGDVFIMPAAHPVAINAS----SELHLLGFGINAEN-----
NHRIFLAGDKDNVIDQIEK-----QAKDLAFP-GS---GEQVEKLI--
KNQKESHFVSARPQSQSQSPSSPEKESPEK---------------------------------------------
-------------------EDQEEENQGGKGPLLSI---------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------------LKAFN

Arachis hypogaea                        >TR|E5G076|              MRGRVS----
--------PL-----MLLLGILVLASVSAT---------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
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HAKSSPYQKKTENPCAQRCLQSCQQE---PDDLKQKACESRCTKLEYDPRCVYDPRGHTGTTNQRSPPG------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------ERTRGRQPGDYDDDRRQPRREEGGRWGPAGPR---EREREEDW-RQPREDWRRPSHQQPRKIRP-
------------------------------EGREGEQEWGTPGSHVREETSRNNPFYFPSR--R-FST-
RYGNQNGRIRV-LQRFDQR-SR-QFQNLQN-----------HRIVQIEAKPNTLVLPKHADADNILVIQQG-
QATVTVANGNNRRA----LILTRAM----HSESHPFHF----LHLDDMT-----PELRVAK-SHA---
VNTPGQF-EDF--FPASSRDQSSYLQGFSRNTLEAAFN-AEF--
NEIRRVLLEENAGGEQEERGQRRWSTRSSEN-------------------------------
NEGVIVEVSKEHVEELTKHAKSVS-----------------KKGSEEEGDITNPINLREGEP--
DLSDNFGRLFEVKPDK-KNPQLQD--LDMMLTCVEIKE-GALMLPHFNSKAMVIVVINKGTG---
NLELVAVRKE------QQQRGRREQEWEEEEEDE----------------------------
EEEGSNREVRRYTARLKEGDVFIMPAAHPVAINAS----SELHLLGFGINAEN-----
NHRIFLAGDKDNVVDQIEK-----QAKDLAFP-GS---GEQVEKLI--KNQRESHFVSARPQSQSPS-------
SPEK----------------------------------------------------------------
EDQEEENQGGKGPLLSI----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------LKAFN

Glycine soja                            >TR|A0A0B2Q6W9|          M---------
---MRARFPLL------LLGLVFLASV-SVSFGIAY---------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--WEKENPKHNKCLQSCNSE---RDSYRNQACHARCNLLKV--EKEE-CEEGEIPRPR-----------------
---------------------------------------------------------------------------
--------------------------------------------PRPQHPEREPQQPG-------
EKEEDEDEQPRPIPFPRP-QPR-----------------------------------------------------
---------------------------QEEEHEQREEQEWPRKEEKRGEKGSEEEDE------------DEDEE-
-Q---DERQFPFPRPPHQ-KE--ERKQEEDEDEEQQQESEESEDSE----LRRHKNKNPFLF-GSN-R-FETL-
FKNQYGRIRV-LQRFNQR-SP-QLQNLRD-----------YRILEFNSKPNTLLLPNHADADYLIVILNG-
TAILSLVNNDD-RDS---YRLQSG-----DALRVPSGTTYYVVNPDN-N-----ENLRLITLAIP---
VNKPGRF-ESF--FLSSTEAQQSYLQGFSRNILEASYD-TKF--EEINKVLFSRE-E-----------
GQQQGEQ-----------------------------RLQESVIVEISKEQIRALSKRAKSSS-------------
----RKTISSE---DKPFNLRSRDP--IYSNKLGKFFEITPEK-N-PQLRD--LDIFLSIVDMNE-
GALLLPHFNSKAIVILVINEGDA---NIELVGLKEQ------QQEQQQ-----------E---------------
-------------EQ---PLEVRKYRAELSEQDIFVIPAGYPVVVNAT----SNLNFFAIGINAEN-----
NQRNFLAGSQDNVISQIPS-----QVQELAFP-GS---AQAVEKLL--KNQRESYFVDAQP--KKKEEGNKGR--
-------------------------------------------------------------------KG------
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------LRAFY

Glycine max                             >TR|F7J075|              M---------
---MRARFPLL------LLGLVFLASV-SVSFGIAY---------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
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---------------------------------------------------------------------------
--WEKENPKHNKCLQSCNSE---RDSYRNQACHARCNLLKV--EKEE-CEEGEIPRPR-----------------
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---------------------------------------------------------------------------
--------------------------------------------PRPQHPEREPQQPG-------
EKEEDEDEQPRPIPFPRP-QPR-----------------------------------------------------
---------------------------QEEEHEQSEEQEWPRKEEKRGEKGSEEEDE------------DEDEE-
-Q---DERQFPFPRPPHQ-KE--ERKQEEDEDEEQQQESEESEDSE----LRRHKNKNPFLF-GSN-R-FETL-
FKNQYGRIRV-LQRFNQR-SP-QLQNLRD-----------YRILEFNSKPNTLLLPNHADADYLIVILNG-
TAILSLVNNDD-RDS---YRLQSG-----DALRVPSGTTYYVVNPDN-N-----ENLRLITLAIP---
VNKPGRF-ESF--FLSSTEAQQSYLQGFSRNILEASYD-TKF--EEINKVLFSRE-E-----------
GQQQGEQ-----------------------------RLQESVIVEISKEQIRALSKRAKSSS-------------
----RKTISSE---DKPFNLRSRDP--IYSNKLGKFFEITPEK-N-PQLRD--LDIFLSIVDMNE-
GALLLPHFNSKAIVILVINEGDA---NIELVGLKEQ------QQEQQQ-----------E---------------
-------------EQ---PLEVRKYRAELSEQDIFVIPAGYPVVVNAT----SNLNFFAIGINAEN-----
NQRNFLAGSQDNVISQIPS-----QVQELAFP-GS---AQAVEKLL--KNQRESYFVDAQP--KKKEEGNKGR--
-------------------------------------------------------------------KG------
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------LRAFY

Glycine max                             >TR|Q948X9|              M---------
----RARFPLL------LLGVVFLASV-SVSFGIAY---------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--WEKQNPKHNKCLQSCNSE---RDSYRNQACHARCNLLKV--EKEEECEEGEIPRPR-----------------
---------------------------------------------------------------------------
--------------------------------------------PRPQHPEREPQQPG-------
EKEEDEDEQPRPIPFPRPRQPR-----------------------------------------------------
---------------------------QEEEHEQREEQEWPRKEEKRGEKGSEEEQD-GREHPRPHQPHDEDEE-
-Q---DERQFPFPRPPHQ-KESEERKQEEDEDEEQQRESEESESSESQRELRRHKNKNPFHF-GSN-R-FETL-
FKNQYGRIRV-LQRFNQR-SP-QLQNLRD-----------YRILEFNSKPNTLLLPNHADADYLIAILNG-
TAILSLVNNDD-RDS---YRLQSG-----DALRVPSGTTYYVVNPDN-N-----ENLRLITLAIP---
VNKPGRF-ESF--FLSSTEAQQSYLQGFSRNILEASYD-TKF--EEINKVLFSRE-E-----------
GQQQGEQ-----------------------------RLQESVIVEISKEQIRALSKRAKSSS-------------
----RKTISSE---DKPFNLRSRDP--IYSNKLGKFFEITPEK-N-PQLRD--LDIFLSIVDMNE-
GALLLPHFNSKAIVILVINEGDA---NIELVGLKEQ------QQEEQQ-----------E---------------
-------------EQ---PLEVRKYRAELSEQDIFVIPAGYPVVVNAT----SNLNFFAIGINAEN-----
NQRNFLAGSQDNVISQIPS-----QVQELAFL-GS---AQAVEKLL--KNQRESYFVDAQP--KKKEEGNKGR--
-------------------------------------------------------------------KG------
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------LRAFY

Glycine max                             >TR|Q7XXT2|              M---------
---MRARFPLL------LLGVVFLASV-SVSFGIAY---------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--WEKQNPSHNKCLRSCNSE---KDSYRNQACHARCNLLKV--EEEEECEEGQIPRPR-----------------
---------------------------------------------------------------------------
--------------------------------------------P--QHPERERQQHG-------
```

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EKEEDEGEQPRPFPFPRPRQPR-----------------------------------------------------
---------------------------QEEEHEQKEEHEWHRKEEKHGGKGSEEEQD-EREHPRPHQPHQKEE--
-----EKHEWQHKQEKHQGKESEEEEEDQDEDEEQDKESQESEGSESQREPRRHKNKNPFHF-NSK-R-FQTL-
FKNQYGHVRV-LQRFNKR-SQ-QLQNLRD-----------YRILEFNSKPNTLLLPHHADADYLIVILNG-
TAILTLVNNDD-RDS---YNLQSG-----DALRVPAGTTYYVVNPDN-D-----ENLRMITLAIP---
VNKPGRF-ESF--FLSSTQAQQSYLQGFSKNILEASYD-TKF--EEINKVLFGRE-E-----------
GQQQGEE-----------------------------RLQESVIVEISKKQIRELSKHAKSSS-------------
----RKTISSE---DKPFNLRSRDP--IYSNKLGKLFEITPEK-N-PQLRD--LDVFLSVVDMNE-
GALFLPHFNSKAIVVLVINEGEA---NIELVGIKEQ------QQRQQQ-----------E---------------
-------------EQ---PLEVRKYRAELSEQDIFVIPAGYPVVVNAT----SDLNFFAFGINAEN-----
NQRNFLAGSKDNVISQIPS-----QVQELAFP-GS---AKDIENLI--KSQSESYFVDAQP--QQKEEGNKGR--
-------------------------------------------------------------------KG------
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------LRAFY

Glycine max                             >TR|I1LE33|              M---------
---I-ARFPLLP---LLLLGIVFLASV-SVSL-------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---QVKPPSHHECLQSCESE---TDPYKRKACKLSCKFVPEHGEQQHEEEEREREHPQ-----------------
---------------------------------------------------------------------------
--------------------------------------------
PHPPHEERGRRERGRQEGEKEEKEQDERELQ-PRPFPRPE-----------------------------------
-------------------------------------------------
EHEGEQWKGRHRHEDPEERARMRLREAER------------------IE---
REREEQRVREEEEKLRRREKKEQREEKEEEGQGSEDSHSK---------RQNNPFHF-SSN-R-FQTL-
FKNQHGHLRV-LQRFDQR-SP-QLENLRD-----------YRVVELMAKPNTLFLPHHADADFLLLVLSG-
RALINLVKPDD-RDP---YYLDRG-----YAQRIPAGTTVYLVNPDK-K-----KDLRVIKLAIP---
VNKPGNF-EDF--FLSSTQDQQSYLQGFSENILEASFN-TKF--EEINRVLFGGE-----------------
GRR-----------------------------HQQEGVILELSKEQIRELSKRAKSSS-----------------
RSTNSFD---YEPFYLRGSQ---ISSNNFGKFYEITPEK-N-PQLRD--FDILLNTVDINE-
GGLLLPHYNSKAIVILMVTEGEA---NIELVGLKEQ------QQG------------------------------
-------------EE---TREVRKYRAELSEDDIFVIPAAYPFVVNAT----SNLNFVAFGINAEN-----
NQRNFLAGSKDNVIRQIQK-----QVKELAFPAGS---AQDIENLI--KNQRESYFADAQP--LQKEE---GK--
-------------------------------------------------------------------KGSFV---
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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--------------------------------------F

Glycine soja                            >TR|A0A0B2P0B6|          M---------
---MRARFPLL------LLGVVFLASV-SVSFGIAY---------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--WEKQNPSHNKCLRSCNSE---KDSYRNQACHARCNLLKV--EEEEECEEGQIPRPR-----------------
---------------------------------------------------------------------------
--------------------------------------------PRPQHPERERQQHG-------
EKEEDEGEQPRPFPFPRPRQPH-----------------------------------------------------
```

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---------------------------QEEEHEQKEEHEWHRKEEKHGGKGSEEEQD-
EREHPRPHQPHQKEEQKHE---
EKHEWQHKQEKHQGKESEEEEEDQDEDEEQDKESQESEGSESQREPRRHKNKNPFHF-NSK-R-FQTL-
FKNQYGHVRV-LQRFNKR-SQ-QLQNLRD-----------YRILEFNSKPNTLLLPHHADADYLIVILNG-
TAILTLVNNDD-RDS---YNLQSG-----DALRVPAGTTYYVVNPDN-D-----ENLRMITLAIP---
VNKPGRF-ESF--FLSSTQAQQSYLQGFSKNILEASYD-TKF--EEINKVLFGRE-E-----------
GQQQGEE-----------------------------RLQESVIVEISKKQIRELSKHAKSSS-------------
----RKTISSE---DKPFNLRSHDP--IYSNKLGKLFEITPEK-N-PQLRD--LDVFLSVVDMNE-
GALFLPHFNSKAIVVLVINEGEA---NIELVGIKEQ------QQRQQQ-----------E---------------
-------------EQ---PLEVRKYRAELSEQDIFVIPAGYPVVVNAT----SDLNFFAFGINAEN-----
NQRNFLAGSKDNVISQIPS-----QVQELAFP-GS---AKDIENLI--KSQSESYFVDAQP--QQKEEGNKGR--
-------------------------------------------------------------------KG------
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------LRAFY

Phaseolus vulgaris                      >TR|V7BBT5|              M---------
---G-SRFPLL-----MLLGIVFLASV-SESL-------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---TEKP-SRRKCVKICESE---KDLSRGQTCQLRCKHVSEPGGK----EEEEREIPE-----------------
---------------------------------------------------------------------------
--------------------------------------------
PHLSHEERVRRERGHQEGEKKKKEVEKEEREKPRPFPPPHPTE--------------------------------
------------------------------------------------
HEREEEQWTGRHRRGDPEERERVRQEREE--------------------E---
EIRERERKKKKGEKHWRREKKEKWEEIEED-PGFPNSDSQ---------TQNNPFHF-SSN-R-FRTL-
FKNKHGHIRV-LQRFDQR-SSTKLQNLQD-----------YRVVEFKSRPHTLLLPHRADADFLLVVLSG-
RALINFVEPED-RDC---YYLDPG-----YAQIIPAGTTFYLVNPER-N-----KNLRVIKLAIP---
VNKPGKFDENF--FLSRTQDQQFYLQGFS-GILEASFDDSKF--EEINKVLFGEE--------------------
-----------------------------RPQEGVIVELSNEKIRKLSRSAESSS-----------------
RKINSFE---YKPFDLRSSSP--IYSNKFGAFYEITPDK-N-PHLRK--LNILLNYVDINK-
GGLLLPHYNSKAIVILVVSEGEA---NIELLGLREQ------QQ-------------------------------
-------------EE---RREVQKYRAELSEDDVFIIPAAYPVAINAT----SNLNFIAFGINAEN-----
NQRNFLAGEKENVISEIPR-----QVLEV-----------NVEKLI--KKQRESYFVDAQP--QQQQKENTGR--
-------------------------------------------------------------------NGRKV---
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------LGALY

Populus trichocarpa                     >TR|B9H8B1|              MAV-------
------------------KVRLSLAVLVF-SL-LALCVG-IAKANK-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELKVCEHQCKEQLGYDER--
EVEKCLRDCTEEHFRRKE-ERERET-----------RGTEEEDDDEW----------------------------
--------R-SFMVDPAKKKPGQCLEECQRQ---EGGKQKSLCRLRCQEKYEREPGRE--EEGNM--EEKE---
E------AG------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------------------------------NPYVFE-DR-H-LKS-
EVETEHGRVRV-LQKFTKK-SKLLRG-LEN-----------IRVAIIEANPQTFIAPTHLDAGFVLFVAKG-
RGAITLIHEE-DKQT---FNLERG-DVF----GVPAGTTFYMVNKD-EN-----EKLRVAKILWP---
VNLPGNFKAFH--GAGG-EDAESFFRAFSWELLEAALKV---RR--LERIF-KQ---------------------
-------------------------------QQGGIVKASKEQIQALG--H-GEEGGHGGGGLWP--FPTG----
----GSS-GPFNIFDKD-PV-KRNNYGQLFEAKPKD--SEQLRD--LDLIVSLANITR-
GSMAGPYYNSKATMISIVLEGEG---YFEMACPRDS------SSGSSMGYIESEGSR------RGK---------
------------G-----GQTYQKTSSRLSRNSVFIVPAGHPVATVASE--NSNLEVLCFEVYAKG-----
NVRYPLAGK-WNVIGEMDR-----EAKELAYGV-P---AKEVDQIFG-K-QQEEFFFPGPRR--QR---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------R--EGRAYA

Populus euphratica                      >REF|XP_011032788.1|     MAV-------
------------------KVRLSSAVLVF-AL-LALCVG-IAKANK-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DLELKVCERQCKEQLGYDGR--
EVEKCLRDCTEEHFRRKE-EPERKT-----------SGTEEEGDGEW----------------------------
--------R-SFTVDPAKKKLGQCLEECQRQ---AGGEQKSLCSLRCQEKYERGPGRE--EVGNM--EEEE---
E------EG------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------------NPYVFE-DR-H-LKT-
EVETEHGRVRV-LQKFTKK-SKLLRG-LEN-----------IRVAIIEANPQAFIAPTHLDAGFVLFVAKG-
RGAITLIHEE-DKQT---YSLERG-DVF----RVPAGTTFYMVNKD-EN-----EKLRVAKILWP---
VNLPDNFNAFH--GAGG-EDAESFFKAFSWELLEAALKT---DRGRLERIF-KQ---------------------
-------------------------------QQGGIVKASKEQIQALG--Q-GEEGGHGGGGLWP--FPTG----
----GSS-GPFNIFDKG-PV-KRNNYGQLFEARPKD--SEQLRD--LDLIVSSANITR-
GSMAGPYYNSKATMISIVMEGEG---YFEMACPRDS------SSGSSMGYIESEGSR------RGK---------
------------G-----GQTYQRTSSRLSRSSVFIVPAGHPVATMASE--NSNLEVLSFEVYAKG-----
NVRYPLAGK-WNVIGEMDR-----EAKELAYGV-P---AKEVDQIFG-K-QQEEFFFPGPRR--QR---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------R--EGRAYA

Ricinus communis                        >TR|B9SFI3|              M---------
--------------------KLSIISVLF-VF-VLFTGT-LAQATT-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELKQCKHQCKVQRQYGED--QKRQCMRRC-
EEYYREKERERERREGEGEGEGEGGGRGSGHREEDDW------------------------------------
DVSSTTDP-EKRLRECQRQCERQ---EG-QQRTLCRRRCQESYERERERE--EEGGR--GEREHGRE------
KGGGRGGKEEETNEEAEE---------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------NPYVFD-TD-Q-FTE-
```

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KVRTEHGSISV-LPRFTKK-SKLLRG-IEN-----------YRVGILKANPQTFVAPSHWDADAVLVVAKG-
RGTVTLIHEEGEKRS---FNIEVG-DVM----RVRAGTPVYVINRD-DN-----EKLYIINFIQP---
VNLPGEFEAFR--AAGG-REDESFYNAFSWELLEAAFKT---DRRRIEQLI-TQ---------------------
-------------------------------KQEAIVKASKEQIQAMT--H-RDQEG---GTIWP--FGGE----
----SSG-APFNLLHKR-PV-QSNNHGQLFEARPNDH-KEQLQD--LDLMISFANITR-
GSMAGPLYNSRATKIAIVTQGEG---YMEMACPH-L------SGGSE---------H------QGR---------
------------K-----GQTYGRVRSRLRPGTVFIVPAGHPVATVASP--NNNLAVLCFEVNAQG-----
NIRYTLAGR-NNIVRRWER-----EAKELAFGV-R---AREVDEVFE-S-QNEVFFFPGPRR--QE---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------W--QGRASA

Jatropha curcas                         >TR|A0A067JF64|          MAM-------
------------------RMKFCLSVLLV-SL-LVLCSG-LALAKR-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELEQCQHQCRVQRHYDEG--EKKRCIQQC-
EDYYKEKKGREHGEE------------GREEEEE-----------------------------------------
------AERRVGQCQSQCERQ---KG-EERALCRFRCQQKFGRDEGEH--SWG----EEK---------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------NPYVFE-EE-H-FTS-
IIKTEHGRARV-LQKFTKR-SELLRG-IKN-----------YRVGILEANPQTFVSQGHWDADGVLYVARG-
RGTISMIIEE-KRQS---FNVQRG-DVL----RIRAGTPLYLINRD-EK-----EKLYVVSVMVP---
VNIPGEFEIFS--ASGT-EDSESFYEAFSWELLEAALKT---ERRRLEHIF-RQ---------------------
-------------------------------KQGAIVKASREQIQAMS--H-REEGG----GVWP--FGTE----
-----SI-GPISIL-KN-PV-FRNNYGQLFEVGSRDF-KQQLRD--LDLSVSVANISR-
GAMSGPYYNSRVTKISVVLDGEG---YFEMACPH--------LSGSR-------GDT------TGE---------
------------S-----QKTYQKVSSRLKRGTAVVVPAGHPAAFVASR--NNNLEVVCFEINEEG-----
NTRHLLAGK-NNIVNKMEK-----QAKELAFGV-S---EREVDQAFG-R-QNEEWFFPGPRR--GS---------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------F--EGHAVA

Ricinus communis                        >TR|B9RTM9|              MSIR------
-------------------AKPPSFMFL-LI-FLFLSYGLQSLGYEVPYPQTGKERCLQRCDEIETEVSGLVS--
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------CAVRCEHQYGDKGNGNKGG------D--------------------------------------
--------------------------------------PKSPRWEIERCQQRCRREGADQR---
ELQKCQQRCEEEPIKEREREQ--------------------------------------------------
EKGQERQPREHELDREKSDDPRKQYERCLEICERQEGR----
QKQQCKRRCYTQYEEQQKEWEEREHGGGGGNSE----TETRSREIE-----------QHKN--------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------NPYYFH-AQ-R-LRS-PFKTDEGHIRV-LEKFSES-SELLRG-IEN---------
--YRLLLLDAVPNTFIVPNHFDAESLVVVLNG-KCTISYVLRE-KRVS---YNLETG-DVI----
```

```
KIPAGATVYMSNHD-NN-----EMLRLATLIQP---VNIPGEFSSFS--AAGGGNLE-
SFYTVFSNDVLEAALDT---PRDQLDKLFGQQ-------------------------------------------
---------RQGVIVKAPQKQLKALSQRVS--------------------STRQKG----QAPLNLRNQQ-PL-
YSNRYGNLWEASPNDHK--QLQD--MDVSVSYAEIKR-GSLMVPHYNSRTTTIGLVLEGSG---RVEMACPHVA-
-----SQKQKESQQEQETK------------------------------GG-----
AEHYRKISSNLSPGGVFIMPAGHPTALLASQ--NENLLTLWFGINASN-----NHRNFLAGQRDNVMNQIEI---
--EAKELSFNV-P---AELIEKIFR-N-QKESHFVAGPQQGQRQQREE---------------------------
------------------------------------------------------------------G--------
---------------------RGH---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----SIPSILDFPGFF

Jatropha curcas                         >TR|A0A067KVT0|          MTIK------
-------------------AQPGFFLFLPIL-LLFFSFGISSLGYEVPYPKTDKERCLERCHETKKDFSGLIS--
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------CASHCERKYENHREEKREGEEISPRD--------------------------------------
--------------------------------------PKSPRWKIERCQEQCRREESDDR---
MLQRCQKRCEEEVIKEREGE-------------------------------------------------------
-------------SEDPRVQYERCQELCDRQPER----QKSQCRGRCERQFEEKQKEREERGSD-----------
RGTKSREME-----------KQRD---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------NPYYFH-AQ-R-LQS-
RHKTQEGHISV-LEKFSDR-SELLRG-IEN-----------YRLSTLEANPNTFVVPHHCDAESIIVVLRG-
KGTITCVLRD-ERRS---YNLEKG-DVI----RIPAGATLYLINRD-NN-----EKLNMVKLMQP---
VNSPGNFR-----------------TVFINDVLEAALDT---PRDQLDRLFGQQ---------------------
-------------------------------RQGVILKASQEHLKALSQHIS--------------------
STKQKGHE-SERPFNLLNRQ-PL-YSNRFGNFIEAS--------LQD--VDISVSYAEIKR-
GALMVPHYNSKATMIALVVEGAG---RFEMACPHLA------SQRMEPREEPPE---------------------
------------G-----TRQYQKISSDLSPGDVFITPAGHPVAVLASQ--NQNLILIGFAINARD-----
NQRNFLAG-RDNIMNQIER-----EAKELSFNS-P---AELIEKIFR-N-QKESHFVAARQQSHG--REE-----
---------------------------------------------------------------------------
-------------D-----------------------------RDH-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------SIPSILDFSGFF

Vitis vinifera                          >TR|F6HI56|              MVINT-----
--------------------KLSFAFLLF-SLFFLSVTFSLAVANV-----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELQLCKSQCRTYHEFSH--
RQRRECEQKCEDYHGQNHGEGEGEGGGGSRIVLNS----------------------------------------
--------------NTDPEKQLQQCQKQCER-Q---REQQKEQCRRQCQDTYERQRGEEGKGGGGQSGEKDE-
QGRQ------QEQGQEQEQEQGQEQQE------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------QNPYVFQ-DQ-H-
YTA-SLETNEGRIKI-LQRFHQR-SRLLRG-LKN-----------
YRFVYLEANPQTFVLPAHLDAEAVVYVASG-RGTLSLVSQG-KRES---FNIKQG-DIV----
RIRAGTTIYMINRD-KN-----KKLRIAKLLQP---VALPDEFQPFY--GPAG-
```

```
ENPQSFYRAFSEELLSSALKV---EQDRVQRVIKQQ---------------------------------------
-------------NKGVIVKASEQQIQALS---QREESG-----MFPFPFGSTE--------SKR-VFNLLSKE-
PS-ISNRYGRLHEADANEF-Q-QLQD--MDIAVSYSNITK-GSMEGPFFNTRATKIAVVVKGEG---
YMEMACPHVS------QQQQGQGQSTGEQRRE---QQQQS---------------------A-----
SPHYQRLSSPLKRGMLFVVPAGHPLIVVAGN--NRNLEIVCFDVNAEN-----NRRESLAGD-KNIVNALEK---
--EAKELAFSI-P---AREVDEVFA-K-QNEWWFFPGPR------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-----------GGHAYA

Vitis vinifera                          >TR|F6HI57|              MVINN-----
-------------------AKFPFAFFLC-CTFCLWVALSLVAAQE-----------------------------
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---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------------------DPELQQCKHQCRVQQQVSE--
RQSGECEHKCEDYYREHHGPV------------------------------------------------------
---------------VDPEKQLQQCRKQCELLQ---PGRQREQCHQECQEKYDQQQLEEG---------------
------------------GEEEEEN--------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------------NPYVFR-DQ-H-F-A-
FLRTNQGEVKI-LEMFDRR-SRLLRG-LKN-----------YRFICLEANPQTFVVPTHYDAEIVGFVCSG-
QGTITMVCQG-KRIS---FRIRIG-DIV----RIPAGITLHLINSH-KN-----QKLRIAYFLLP---
VGIPGRFEPFH--GAAG-ENPQSFYRAFSPKLLSSAFKV---EEGTLERVFQQQ---------------------
-------------------------------TKGHFIKASGEQIQALSGGQHGEAAG-----IWPFTSG--E---
-----SKRPVFNLLNKD-PS-VCNNYGRLHEADAEDF-R-QLKD--MDIEISYANITQ-
EGMMGPFFNSRSTMVAAVLEGEG---YLEMVCPHLS------GEK----------------QQQQG---------
------------A-----SPIYQKVSSSLRRGTLFVVPAGHPIAIVAGT--SWNLEIVCFGINAEN-----
NRREPLAGK-GNVVNGLEK-----EAKELAFAL-P---AREVDKVFR-K-QKEELFFPGPQLQKQQHH-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------HHHKGHAYA

Solanum tuberosum                       >REF|XP_006349767.1|     MML-------
------------------RSKVLPFLFCL-VV-VA-----FG-TK------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------ESDLKQCKHQCKVLQQIEEY-QREKCYEICEKLYHGEKQEKEE-INF---------YEGRE-E-GKN--
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------NPYVFN-EE-H-FIT-GIKTEHGRIRV-
LPKFSER-SKLLKG-IEN-----------YRFAILEANPKTFVVPNHWDADAVLFVAQG-RGTLSLVRKG-
KRNS---FNIGRG-DVI----KVCAGTTAYLINRD-DN-----EKLLIAKLLRP---VSTPGQFEHFF--
GPGGRENPQSFYSAFSSDILEAALNT---RKDRLQRLFGQP----------------------------------
------------------REGVIIRASEEQIRVMS--Q-HEEGG-----IWP--FGGE--------SKG--
```

```
SVNIYKQR-PL-QSNQYGQFYQVDDSTY-K-QLED--LDISLNFANITE-GGMLGPIYSSRATKIAVVVEGEG--
-YFEMACPHLA------SESES-GKRQGSKET------ETR---------------------I-----GR-
YQKVSSKLRRGMVLVIPAGHPFVAVAST--NQNLQIVGFNVNARN-----NEIVPLAGR-NNVMSQLER-----
EALELGFGL-P---AREVEQIFQ-S-QQEEFFFQGPGG-RQS---------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------GRAAA

Solanum lycopersicum                    >TR|K4CUH3|              MMK-------
------------------GAKVLPFLFCL-VV-VA-----FG-TK------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------ESDLKQCRHHCKVLQHIEEY-QREKCYDICEKLYHSEKQEKEEETNS---------YEGRE-E-GEN--
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------NPYVFN-EE-H-FIM-GIETEHGRIRV-
LPKFNER-SKLLKG-IEN-----------YRFAILEANPKTFVVPNHWDADAVLFVAQG-RGTLSLVRKG-
KRNS---FNIRRG-DVI----KVCAGTTAYLINRD-DN-----EKLLIAKLLRP---VSTPGHFEHFF--
GPGGRQNPESFYSAFSSEILEAALNT---RKDRLQRLFGQP----------------------------------
------------------REGVIIRASEEQIRVMS--Q-HEEGG-----IWP--FGGE--------SKG--
SVNIYKQR-PL-RSNQYGQFYQVDESNY-K-QLED--LDISINFANITE-GGMVGPIYNSRATKIAVVVQGEG--
-YFEMACPHLA------SKFTS-SH-------------ETR---------------------I-----
GSSYQKVRSKLRRGMVLVIPPGHPFVGVTST--NQNLQIVGFNVNARD-----NEIVPLAGR-NNVMSQLER---
--EALELGFGL-P---AREVEQIFR-S-QQEEFFFQGPGG-RQS-------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------GRAAA

Nicotiana sylvestris                    >REF|XP_009786980.1|     M-V-------
--------------------KVRPFLFCV-LL-LAVASLALG-TK------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------DPELKQCKHQCKALQQIGEH-QRKECYEMCER-YHSEKQSKEEDTSTFL------PYRGRE-
ETGEEEE-QQYGEQERE----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------NPYVFE-DQ-H-FIT-
GIKTQHGRIRV-LPKFTER-SKLLKG-IEN-----------YRVAILEANPQTFIVPNHWDADAVLFVAQG-
RGTLNLVRRG-KRNS---FNIRAG-DVI----RVHAGTTAYLINRD-NN-----EKLVIAKLLNP---
VSTPGQFEHFF--GPGGRENPESFYNAFSSEILESALNV---RRDRLQRLFGQQ---------------------
-------------------------------REGVIIRASEEQIRAMS--Q-HEEGG-----IWP--FGGE----
----SKG--SVNLYRQR-PL-QSNQYGQLYEVDGSHY-R-QLED--LDISVSLANITQ-
GGMFGPAYSSRATKIAVVVDGEG---YFEMACPHLA------SESGSRGRQSRGSER------ETR---------
```

```
------------I-----GSGYQKVRARLRRGMVVIIPAGHPVVNVASN--NQNLQVVCFNINARN-----
NEIVPLAGR-NNVMSQLER-----EAMELGFGI-P---AREVEEIFR-S-QQEEFFFQGPGG-RQQHQ-------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------E--GGRADA

Nicotiana tomentosiformis               >REF|XP_009607668.1|     MMV-------
--------------------KVRPFLFCL-LL-LAVASLSLG-TK------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------DPELKRCKHQCKALQQIGEH-QRKECYEMCEK-YDSEKQSKEEDTSTFF------PYRGKE-
ETGEEEEGQQYGEQERE----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------NPYVFE-DQ-H-FIT-
GIKTQHGRIRV-LPKFTER-SKLLKG-IEN-----------YRVAILEANPQTFIVPNHWDADAVLFVAQG-
RGTLNLVRRG-KRNS---FNIRPG-DVI----RVHAGTTAYLINRE-NN-----EKLVIAKLLNP---
VSTPGQFEHFF--GPGGRENPESFYNAFSSEILESALNV---RRDRLQRLFGQQ---------------------
-------------------------------REGVIIRASEEQIRAMS--Q-HEEGG-----IWP--FGGE----
----SKG--SVNIYRQR-PS-QSNQYGQLYEVDGSHY-R-QLED--LDISVSFANITQ-
GGMLGPVYSSRATKIAVVVDGEG---YFEMACPHLA------SESGSRGRQSRGSER------ETR---------
------------I-----GSGYQKVRARLRRGMVVIIPAGHPVVNVASN--NQNLQLVCFNINARN-----
NEIVPLAGR-NNVMSQLER-----EAMELGFGV-P---AREVEEIFR-S-QQEELFFQGPGG-RQQHQ-------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------E--GGRADA

Nicotiana tomentosiformis               >REF|XP_009595712.1|     M---------
--AIF--------------AK-PKLLFLFF---LILSLFLASQC-------------------------------
--------------DDENPRG-QDPRRELESCLRQCQVSERQESPEQQLQCQRSCVLRYEQQ-
REKSEEVIEDILTHHRDPESIYRECQQRCQRQEHGQQRQ---CQQRCEQEY---
RREQEQQHRGHQSGEDNQGRE-GRTQ-------------------------------------------------
----------------REPERRFRECQQRCQRQEQGQ-QQ-
RQCQQRCEQEYRREQEQQHGGSEEILEENQGRGQREP--------------------------------------
---------------------------------ERRFRECQQRCQRQEQG-Q---
QQRQCQQRCEQEYRREQEQQRGGSEEILEENQGRGQREPERRFRECQQRCQRQEQGQQQRQCQQRCEREYRREQE
QQRGSEEREEDNQGRDPQRIFRECQQRCQQQEQ--GRQQQRQCQQRCEEEFRREQEQ--QRR----
GQETGEERENPQRERE-----------EE-N--------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------------------NPYLFE-
SQ-R-FRS-RFRATHGDFRV-LEKFTER-SELLRG-IEN-----------
YRVAVVEFEPLSFMLPHHCDAEAIFVVVRG-RGTISIAEQD-EKNS---FNLEHG-DVI----
RVNAGSTVYMLNRD-NN-----ERFFVYVLAQA---VNTPGQFQEYF--SAGGQNPE-
SFYRAFSSDILETAFNT---PRDRLERLFGQQ-------------------------------------------
---------KQGIVIKASEEQIRAISEHASRS-----------------TKQQTKGRTT--GPFNLLKEH-PL-
FSSRFGQFFEASPDRFE--QLRD--MDAAVAFMNINQ-GGMVLPYYNTRSTRLAMVVEGNG---RFEMACPH-L-
-----GSQSQRQGSRGGRREQE----REQE-------------------GG-----
```

```
DVHYQKVRGTLSVGDVLVVPAGHPITFIATG--GSNLRIVGFGVNAHN-----SRKNFLAGQ-QNIWRNVDR---
--EAKELSFNM-P---GKEVEEILQ-R-QDQSYFVAGPEQHGQRQRERGEE------------------------
---------------------------------------------------------------GK-G--------
---------------------Q-Q---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----YLSSILDFV--F

Nicotiana tomentosiformis               >REF|XP_009595711.1|     M---------
--AIF--------------AK-PKLLFLFF---LILSLFLASQC-------------------------------
--------------DDENPRG-QDPRRELESCLRQCQVQSERQESPEQQLQCQRSCVLRYEQQ-
REKSEEVIEDILTHHRDPESIYRECQQRCQRQEHGQQRQ---CQQRCEQEY---
RREQEQQHRGHQSGEDNQGREVGRTQ-------------------------------------------------
----------------REPERRFRECQQRCQRQEQGQ-QQ-
RQCQQRCEQEYRREQEQQHGGSEEILEENQGRGQREP--------------------------------------
---------------------------------ERRFRECQQRCQRQEQG-Q---
QQRQCQQRCEQEYRREQEQQRGGSEEILEENQGRGQREPERRFRECQQRCQRQEQGQQQRQCQQRCEREYRREQE
QQRGSEEREEDNQGRDPQRIFRECQQRCQQQEQ--GRQQQRQCQQRCEEEFRREQEQ--QRR----
GQETGEERENPQRERE-----------EE-N--------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------------------NPYLFE-
SQ-R-FRS-RFRATHGDFRV-LEKFTER-SELLRG-IEN-----------
YRVAVVEFEPLSFMLPHHCDAEAIFVVVRG-RGTISIAEQD-EKNS---FNLEHG-DVI----
RVNAGSTVYMLNRD-NN-----ERFFVYVLAQA---VNTPGQFQEYF--SAGGQNPE-
SFYRAFSSDILETAFNT---PRDRLERLFGQQ-------------------------------------------
---------KQGIVIKASEEQIRAISEHASRS-----------------TKQQTKGRTT--GPFNLLKEH-PL-
FSSRFGQFFEASPDRFE--QLRD--MDAAVAFMNINQ-GGMVLPYYNTRSTRLAMVVEGNG---RFEMACPH-L-
-----GSQSQRQGSRGGRREQE----REQE-------------------GG-----
DVHYQKVRGTLSVGDVLVVPAGHPITFIATG--GSNLRIVGFGVNAHN-----SRKNFLAGQ-QNIWRNVDR---
--EAKELSFNM-P---GKEVEEILQ-R-QDQSYFVAGPEQHGQRQRERGEE------------------------
---------------------------------------------------------------GK-G--------
---------------------Q-Q---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----YLSSILDFV--F

Nicotiana sylvestris                    >REF|XP_009771136.1|       M-------
----AIF--------------TK-SKLLFLFF---LILSLFLASQC-----------------------------
----------------DDENPWG-
QDPRRELESCLRQCQVQKERQESPEQQLQCQRSCVLRYERQHREKSEEVIEDIPTHHRDPERIYRECQERCQRQE
HGQQRQ---CQQRCEQEY---RREQQQQHRGHQTGEDNQGRE----G----------------------------
-------------------------------------REPERRFRECQQRCQTQEHGQ-QQ-
KQCQQRCEQEYRREQEQQRRG------------------------------------------------------
-----------------QGEIIEENQGRGQREPEERFRECQQRCQRQEQG-Q---
QQRRCQQRCEQEYRREQEQQRGGSEEILEENQGRGQREPDRRFRECQQRCQRQEQGQQQRQCQQRCEQEYRREQE
QQRGREESEENNQGRDPQRRFRVCQQRCQQQEQ--GRQQQRRCQQRCEEEFRREQEQ--QGR----
GQETGEERENPQRERE-----------EE-N--------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------------------NPYLFE-
SQ-R-FRS-RFRATHGDFRV-LQKFTER-SELLRG-IEN-----------
YRVAVIEFEPLSFMLPHHCDAEAIFVVVRG-RGTISIAEQD-EKNS---FNLEHG-DVI----
RVNAGSTIYMLNRD-NN-----ERFFVYVLAQA---VNTPGQFQEFF--SAGGQNPE-
SFYRAFSSDILETAFNT---PRDRLERLFGQQ-------------------------------------------
---------KQGIVIKASEEQIRAISEHASRS-----------------TKQQTKGQTT--GPFNPLKER-PL-
```

```
ISNKFGKFFEASPDRFE--QLRD--LDAAVAFMNINH-GGMVLPYYNTRSTRLAMVVEGTG---RFEMACPH-L-
-----GTQSQRQGSRGGRREQE---SEEQE-------------------GG-----
DVHYQKVRGTLSAGDVLVVPAGHPITFIATG--GSNLRIVGFGVNAHN-----NRKNFLAGQ-QNIWRNVDR---
--EAKEISFNM-P---GKEVEEILQ-R-QDQSFFVAGPEQRGQRQRERGEE------------------------
---------------------------------------------------------------GR-G--------
---------------------Q-Q---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----YLSSIWDFV--F

Solanum lycopersicum                    >TR|B0JEU3|              M---------
--AIF--------------TK-PKLLFIFF---LILSLVLVSQC-------------------------------
--------------YDQNPRGYQDPQ-EK----------------------------------------------
----------LRECQQRCERQQPGQQKQ--LCKQRCEQQY---RKEQQQQHGG-ETGEDDLGN------------
-----------------------------------------------------------RGPDKSYK--------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------RLQECQRRCQSEQQG-Q--RLQECQQRCQQEYQRE-------K----GQHQGET--NPQWEQQ----
-------EKSN----------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------NPYLFE-SQ-R-FRS-RFRASHGDFRI-
LERFNQR-SQLLKG-IEK-----------YRVAILELEPQSFVLPHHCDGEAIYVVVKG-QGVINIAEQD-
NKNS---FNLQKG-DVI----RLFAGSNVYLLNKD-NN-----EKLFVYVLAKS---VNAPGNLQEYF--
SAGGQNPE-SFYRAFSSDILESAFNN---PRDKLERLFGQH----------------------------------
------------------KEGIIIKASEEQIRAISEHASRS-----------------T-QQTRGRTQ--
GPFNLMKER-PV-FESRFGQFFEARPERYE--QLRD--LDAAVGFMNINQ-GGMVLPYYNTKSTKLVMVIEGNA-
--RFEMACPH-L------GRQSQSPWSRGQGREQEREQEQEQE-------------------EG-----
DVHYQKIRGNLNVGDVLVIPAGHPITFVATG--NSNLRIVGFGVDAEN-----NKKNFLAGK-QNIWRNIDR---
--EAKELSFSM-P---GREVEEIFQ-R-QDQSYFVAGPEHR--QQRERGEE------------------------
---------------------------------------------------------------GRRG--------
---------------------QDQ---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----YLSSILDFV--F

Solanum tuberosum                       >TR|M1D5K3|              M---------
--AIF--------------TK-PKLLFVFF---LILSLVLVSQC-------------------------------
--------------YDQNPRGDQDPQQEK----------------------------------------------
----------LRECQQRCERQQPGQQRQ--LCKQRCEQQY---KKEQQQQHER-ETGEDDLGN------------
-----------------------------------------------------------RGPEKRYR--------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------KFQECQRRCQSEEQG-Q--QLQECQQRCQQEYQRE-------K----GQ-QVET--NPEWEQQ----
-------EKSN----------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------NPYLFE-SQ-R-FRS-RYRASHGDFRI-
LEKFNQR-SQLLKG-IEK-----------YRVSVLELEPQSFVLPHHCDGEAIFVVVKG-QGIISIAEQD-
NKNS---FNLQKG-DVI----RVFAGSNVYMLNKD-NN-----EKLFVYVLAKS---VNAPGNLQQYF--
SAGGQNPE-TFYKAFSSDILESAFNN---PRDKLERLFGQH----------------------------------
------------------KEGIIIKASEEQIRAISEHASRS-----------------T-QQTKGRTQ--
GPFNLLKER-PL-FESKFGQFFEACPERFE--QLRD--LDAAVGFMNINQ-GGMVLPYYNTKSTKLVMVVEGNA-
--RFEMACPH-L------GRQGQSPWSRGQGREHE--QEQEQE-------------------EG----
```

```
EVHYQKIRGNLNVGDVLVIPAGHPITFVATG--NSNVRIVGFGVDAQN-----SKKNFLAGK-QSIWRNVDR---
--EAKELSFSM-P---GREVEEILQ-K-QDQSYFVAGPEHR--QQRERGEE------------------------
---------------------------------------------------------------GRRG--------
---------------------QDQ---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----YLSSILDFV--F

Solanum lycopersicum                    >REF|XP_004247581.2|
MHACNAHFRTINFSSSSKHLITTTFSLTMPIFTKPKHLFIFFLILSLVIA-------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------SQCDDQNPQGQHPEE--KFRECQQHCERQEQ------------------------
------------QGEQEESNN------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------PYLFE-SQ-R-FKS-
SFKASHGDLRI-LEKFTQR-SQLLQG-IEK-----------IRVAVLELEPHTFLIPHHCDGEIIFVVVRG-
QGTISIAEQD-DKNS---FNLEKG-DVF----RVPAGSIIYLINRD-KE-----EKFFVYGLAKS---
INAPGKLHEYF--SAGA-ENPESFYRAFSSDIVESAFNI---QRDRLERLFELQ---------------------
-------------------------------KQGIVIKASEKQIRGISKHR------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------FALH----------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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Erythranthe guttata                     >TR|A0A022RLJ6|          MRC-------
---------------------FCLLLFAL-LL--ASATIALG-YKE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------
DPELKQCKHQCEAQKQFGEEKIRTCIQQCEDYVREKQRREHGG--------------------------------
----------------------------------EGGGSTTFFEEEDDDLNRRSPIERLRECTKGCDRS------
-KQKERCQSRCQETYEKEKERYEGGGNPVD---------------------------------------------
------------------PEQEYQECRQECRRQSREGGSR-QERCEERCQEQRREREREQPGR---
REGGGGMYMYEGRE-REEEEERRQQKQ------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------
NPYVFE-ER-H-FFT-GMETQHGRLRI-LPKFTDR-SKLLKG-IEN-----------
YRVAILEAEPQTFIVPNHWDADTLIFVANG-RGAVSLMRQE-RRES---FNIKQG-DIF----
RINAGTTAYLINRD-SN-----QKLVLAKLLQP---VNTPGQFEAFF--GAGG-
ENPESFYTAFSNDILEAAFNT---RRDRLQRLFGQQ---------------------------------------
-------------KQGVIIKASEEQVRAMS--H-HEEGG-----IWP--FGGE--------SKG--TFNLYDQR-
PS-HSNEYGQLFEVDSSQF-R-QLRD--LDIAISLANITQ-GAMIAPSYNSKSTKITVVVDGEG---
YFEMACPHIS------QSQSQGGRQQR--QQ------QGA---------------------G-----
QRGYEKVSSRLKRGTVVVVPAGHPFVAVASN--NQNLQLLCFEVNAYN-----NEKFTLAGR-RNVMNQLER---
```

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--EAKELAFGM-P---AREVDEIFR-S-QKEEFFFKGP---RQQG------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------GRSDE

Erythranthe guttata                     >TR|A0A022Q7M6|          MRC-------
---------------------FCLLFFAL-LL--ASATIALG-YKE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------
DPELKQCKHQCEAQKQFGEEKIRTCVQKCEDYVREKQRREHGG--------------------------------
-------------------------------------GSTTFFEEEDDDLNRRSPIERLRECTKGCDRS------
-KQKERCQSRCQETYEKEKERYEGGGNPVD---------------------------------------------
------------------PEQEYQECRQECRRQSREGGSRRGTS-QERCEERCQEQRREREREQPGRREGGGNM-
-YEGRE-REEEEEERQQQKKQGREN--------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------NPYVFE-ER-H-
FFT-GMETQHGRLRI-LPKFTDR-SKLLKG-IEN-----------
YRVAILEAEPQTFIVPNHWDADTLIFVANG-RGAVSLMRQE-RRES---FNIKQG-DIF----
RINAGTTAYLINRD-SN-----QKLVLAKLLQP---VNTPGQFEAFF--GAGG-
ENPESFYTAFSNEILEAAFNT---RRDRLQRLFGQQ---------------------------------------
-------------KQGVIIKASEEQVRAMS--H-HEEGG-----IWP--FGGE--------SKG--TFNLYDQR-
PS-HSNEYGQLFEVDSSQF-R-QLRD--LDIAVSLANITQ-GAMIAPSYNSKSTKITVVVDGEG---
YFEMACPHIS------Q------------QQ------QGA---------------------G-----
QRGYEKVSSRLKRGTVVVVPAGHPFVAVASN--NQNLQLLCFEVNAYN-----NEKFTLAGR-RNVMNQLER---
--EAKELAFGM-P---AREVDEIFR-N-QKEEFFFKGP---RQQG------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------GRSDE

Sesamum indicum                         >TR|Q9AUD0|              MSC-------
------------------GGRLCLVLFAL-LL--ASAVVASE-SK------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------
DPELKQCKHQCKAQQQISKEQKEACIQACKEYIRQKHQGEHGR---GGGDILEEE--------------------
----------------------------------------------V--WNRKSPIERLRECSRGCEQQHGE---
--QREECLRRCQEEYQREKGRQDDD-NPTD---------------------------------------------
------------------PEKQYQQCRLQCRRQGEGGGFSR-----EHCERRREEKYREQQGR---EGGRGEM--
YEGRE-REEEQEE------QGRGR---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------------------------IPYVFE-DQ-H-
FIT-GFRTQHGRMRV-LQKFTDR-SELLRG-IEN-----------
YRVAILEAEPQTFIVPNHWDAESVVFVAKG-RGTISLVRQD-RRES---LNIKQG-DIL----
KINAGTTAYLINRD-NN-----ERLVLAKLLQP---VSTPGEFELFF--GAGG-
ENPESFFKSFSDEILEAAFNT---RRDRLQRIFGQQ---------------------------------------
-------------RQGVIVKASEEQVRAMS--R-HEEGG-----IWP--FGGE--------SKG--TINIYQQR-
PT-HSNQYGQLHEVDASQY-R-QLRD--LDLTVSLANITQ-GAMTAPHYNSKATKIALVVDGEG---
YFEMACPHMS------RS-----RGSY--QG------ETR---------------------G-----
RPSYQRVASRLTRGTVVIIPAGHPFVAVASS--NQNLQVLCFEVNANN-----NEKFPLAGR-RNVMNQLER---
```

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--EAKELAFGM-P---AREVEEVSR-S-QQEEFFFKGP---RQQQQ-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------GRADA

Erythranthe guttata                     >TR|A0A022RN45|          M---------
--A-I--------------KFNTKVLSLLLVLIVTFSLLLV----------------------------------
----------------------------------------------------
QSQCHTKYQEEQEEEEEKTAEESLF----------ECFVTCSRHRQNDH-ELTDCEQRCVKQYQETKKQEGQE--
---------------------------------------------------------------------------
--------------------------GSR-------------------RHGGG----------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------GGEGTVENHHREDEPAAQRFKQCQSRCGKQEQG-Q--QRQYCQQKCQWEYEKQK---
REEEQQHGGGRGGGDPTN---AKKESKEEEKQQRQ----------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
NPYFFD-SQ-R-FDS-KYRTEQGHIKI-LERFSKN-SDLLQG-IEN-----------
YRLAILEANPNTFVLPHHCDAESVFLVVGG-RGTISYVWEK-QRKS---YNLKSG-GVL----
WVPAGSIVYLTNND-DN-----ERLYILKLLQP---VNTPGKFKEYF--GVGGENPE-
SFYSSFSNEILEAAFNT---QSEKLQRLFGQQ-------------------------------------------
---------SKGVIIKASKEQIRALSQESESS-----------------PRGRREKESSSWGPIDLLNER-PV-
FSNEFGQYFEASPNHYQ--QLRD--LDVSVLLVNITK-GAMVAPYYNSKSTRLVFVVGGSG---YFEMACPHLA-
-----NAKGKH--GSQGRKERQGEII------------------------T-----
DVHYQKVSARLSVGDAFVVPAGHPIAIVASQ--DSNLQLAGFGIKASH-----NQKYFLAGQ-ENIWNEVQS---
--EAKELAFRV-P---AREVEEIFR-S-QEQSYFMPGPGQ-KGK-------------------------------
------------------------------------------------------------------G--------
---------------------QRH---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------VASILDFVG-F

Sesamum indicum                         >REF|XP_011090693.1|     M---------
--AMI--------------NLNTR-LSLLLLL--TLSLLLL----------------------------------
----------------------------------------------------PSHCYTNPQLQEGEEE--
SAEEGLF----------KCFVSCEKRRENEH-ELSQCEKRCVREYQERKREEREERGGRR---------------
-------------------------------------------------------
GEETVVPKIDEPRKVYEQCLSQCGKTE-GSRQQFDQCRRICERQYEQQQQREKRG--------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------GGEGTIENHHRRDPE--QQYKQCQSRCAREERG-E--QRQYCQQKCQWEYERQK---
REQGREQGGGGGS---TN---PRKEREEEEEQEGK----------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
NPYFFE-SQ-R-FDS-KYRTEEGNVKV-LERFSKK-SELLQG-VDN-----------
YRLAVLEANPNTFVLPHHFDAESVLVVAGG-KGTISYVWQN-RRKS---YNVKLG-DVM----
RVPAGSIVYLVNRD-DN-----EKLYVLKLLQP---VNTPGRFKEYF--GVGGENPE-
SFYRTFSNEILEAAFNV---PSDRLKRLFGQQ-------------------------------------------
---------KKGVIIRASKEQIRALSQESEES-----------------SRGRREE---SWGPFNLLEGR-PL-
FSNRYGQYFEASPNDYQ--QLKD--LDVSVGFMNINK-GGMVAPYYNSRSTKLVLVVGGNG---RFEMACPH-R-
-----SARSK-----QGRKERQGET-------------------------T-----
DVRYQRVSARLSIGDAFIVPAGHPIAMIASQ--DSNLQLVSFGIKGSY-----NQKYFLAGQ-DNIWNQVES---
```

```
--EAKELSFKM-P---AREVEEIFR-R-QEQSYFLPGPGQGEER-------------------------------
------------------------------------------------------------------G--------
---------------------KEH---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----YVASILDFVG-F

Beta vulgaris                           >REF|XP_010679084.1|     M---------
---------------VFFKGKICLVLLLF-SLLVLCASFSVA--KE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELRQCKHQCRHQRQFDSK--QKLGCERSC-
EEYIEEKERREMEE-----------------------------------------------------------
MRTAPRRDPEKAYRECRERCQEVEEG--RREQQVCESECEQRRER------------
IRRDDEIVGRRSVEEEEEEEEEVGGKSG-----------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------------KPYVFE-
DH-H-FST-KFKSKEGRVKV-LKKFNKR-SKLFKG-IQN-----------
YRVIIFEANPQTFVVPNHWDADSVFFVAQG-EGTVSLVYTD-RRDS---FNIKRG-HVM----
VIPAGVTAYLINRG-NN-----DKLVLVKLINP---VSNPGKFESFF--GPGG-
ENPESFFNAFSTDILGAAFKT---SGDKVKRIFSQQ---------------------------------------
-------------HEGAIIRASEEQIRALT----HEKSGH-----WP--FGGK-------GSKESGPFNLL-
KQSPR-ESNEFGTLFEVDSNDY-R-QLRD--LNIALSFANITQ-GSMHTPLYNSRATKIAVVLNGRG---
YFEMACPHVS------KSGHQQHRHRQHGGKSS-RGEEET---------------------T-----
PIHYEKIFSELRQGMVFVVPPGHPFVTLASE--NENLELICFEINAEN-----NHKFPLAGQ-RNIMKNFER---
--EAKELAFAS-S---AEVVDQVFE-N-QEEDFFFKGP---RQQER-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------H--RGYSII

Nelumbo nucifera                        >REF|XP_010256229.1|     MVI-------
------------------KAKLSLLLFLV-SFHLLLSALSLAGEVE-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
------------------------------------------DPELQQCQHQCQHQEHFDEE--KKQYCKEKC-
EKYIIEKHYQQ----------------------------------------------------------------
-------------CQQLCDQ-GRGEQ--EKQLCRQGCEQRHRQQQKEQD------------
ERQREHCAGGSKIDKSKSKGSQEEQEGN-----------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------------------------------------------------------------NPYLFD-EK-S-
FKT-RFQTEEGNIKV-LERFSER-LEFLRG-IES-----------
YRLAIIKASPNTFVTPCHEDADVVFFVTWG-RGVITLVRND-NRES---FKIQKG-DVM----
MIPAGTVVYFINND-NH-----EKLFIAKLLLP---ISTPGHFEAFF--GPGG-
ENPESFYRAFSTEVLEAALNV---RKDKLKRLLGRQ---------------------------------------
-------------DKGVIIKASDEQIKSLS--QHASSRG---GQFWP-----------FDKRETKGPFNLFNKR-
PS-QSNNYGQFYEVKPGEF-K-QLQG--LDIAVSFLNISS-GAMSGPYYNSRATKVAVVIEGNG---
YYEMACPHSS------SSSGGRHGGSEGGSSSRFHHHQDQ---------------------G-----
GVRYRKMSGFLAPESVFLVPAGHPVVTVASS--GQNLQIVCFEIKGEK-----NEKYMVAGE-NNIIKYLEK---
```

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--EAKELSYNI-P---AKEVDEILS-K-QSESLFFPGP---ERRQE------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
--------W--GGRADE

Mcadamia integrifolia                   >SP|Q9SPL5.1|
MAINTSNLCSLLFLLSLFLLSTTVSLA------------------------------------------------
---------------------------------------------------------------------------
------------ESEFDRQEYEECKRQCMQLETSG--QMRRCVSQCDKRFEEDIDWSKYD---------------
-------------------------------------------------------------------
NQEDPQTECQQCQRRCRQQES-GPRQQQYCQRRCKEICEEEEEYN------------------------------
-------------------------------------------------------
RQRDPQQQYEQCQKHCQRRE-TE--PRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEED-----
--------------------------------------NKRDPQQREYEDCRRRCEQQ---E-
PRQQHQCQLRCREQQRQHGRGGDMMN-------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----PQRGGSGRYEEGEEEQSDNPYYFD-ER-S-LST-RFRTEEGHISV-LENFYGR-SKLLR-ALKN-------
----YRLVLLEANPNAFVLPTHLDADAILLVIGG-RGALKMIHHD-NRES---YNLECG-DVI----
RIPAGTTFYLINRD-NN-----ERLHIAKFLQT---ISTPGQYKEFF--PAGG-
QNPEPYLSTFSKEILEAALNT---QTEKLRGVFGQQ---------------------------------------
-------------REGVIIRASQEQIRELTRDDSESRHWHIRR------------------
GGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDY-R-QLQD--MDLSVFIANVTQ-
GSMMGPFFNTRSTKVVVVASGEA---DVEMACPHLS------GRHGGRGGGKRH---------EEEED-------
-------------------VHYEQVRARLSKREAIVVLAGHPVVFV-SS--GNENLLLFAFGINAQ----
NNHENFLAGRERNVLQQIEP--QAMELAFA---------
APRKEVEESFNSQDQSIFFPGPRQHQQQSPRSTKQQQ--------------------------------------
---------------------------------------------------------------------------
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-----------------------------------------------------------------

PLVSILDFVGF

Oryza glaberrima                        >TR|I1PE38|              MATR------
-----------------------ARATILLLLAAVLFAAAAAA--------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------------------------------------------SGED-
---RRRETSLRRCLQRCE---QDRPPYERARCVQECKDQQ--QQQ--QERRREHGGHDDDRRD-RDRRGEGSS--
EEEDEGRERG-SR--------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------RRPYVFG-RR-S-FRQ-VVRSDQGSVRL-
LPPFHQ-ASSLLRG-IKN-----------YRVAVLEANPRSFVMPTHTDAHCICYVAQG-EGVVAII-
ENGEKWS---YAIRQG-DVFVA----PAGTINYLANTD-GR-----RKLIVTKILHT---ISVPGQIQFFF--
APGG-RNPESFLSSFSKGVQRAAFK---ISEEKLEKLL--------------------GK---------------
----------------QDKGV-IIRASEEQVRELRRHAS-EGGHGPHWPLPPF------------
GESSRGPFNILEQRP--RFANRHGRLYEADARSFH--DLAE--HDIRVAVVNITA-
GSMNAPFYNTRSVKVAYVLDGEG---EAEIVCPHLS------RGGRGGESEERRRERGKGKWREEEEEEEEQQK-
--------GQEEEEEEQVGQGYETIRARLSRGTVFVVPSGHPIVVTSSR--DSTLQIVCFDVHANN-----
```

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NERMYLAGM-NSVLKKLDP-----QAKELAFAA-S---AREVDELLNA--QQESAFLAGPEK-
SSRRGEESEDEDRRR------------------------------------------------------------
----RRSHRGRG-------------------------------------------DEA-----------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------VETLLRMAAAAV

Oryza sativa                            >TR|Q75GX9|              MATR------
-----------------------ARATILLLLAAVLFAAAAAA--------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------SGED-
---RRRETSLRRCLQRCE---QDRPPYERARCVQECKDQQ--QQQ--QERRREHGGHDDDRRD-RDRRGEGSS--
EEEDEGRERG-SR--------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------RRPYVFG-RR-S-FRQ-VVRSDQGSVRL-
LPPFHQ-ASSLLRG-IKN-----------YRVAVLEANPRSFVMPTHTDAHCICYVAQG-EGVVAII-
ENGEKWS---YAIRQG-DVFVA----PAGTINYLANTD-GR-----RKLIVTKILHT---ISVPGQIQFFF--
APGG-RNPESFLSSFSKGVQRAAFK---ISEEKLEKLL--------------------GK---------------
----------------QDKGV-IIRASEEQVRELRRHAS-EGGHGPHWPLPPF------------
GESSRGPFNILEQRP--RFANRHGRLYEADARSFH--DLAE--HDIRVAVVNITA-
GSMNAPFYNTRSVKVAYVLDGEG---EAEIVCPHLS------RGGRGGESEERRRERGKGKWREEEEEEEEQQK-
--------GQEEEEEEQVGQGYETIRARLSRGTVFVVPSGHPIVVTSSR--DSTLQIVCFDVHANN-----
NERMYLAGM-NSVLKKLDP-----QAKELAFAA-S---AREVDELLNA--QQESAFLAGPEK-
SGRRGEESEDEDRRR------------------------------------------------------------
----RRSHRGRG-------------------------------------------DEA-----------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------VETLLRMAAAAV

Oryza sativa                            >TR|A2XKC1|              MATR------
-----------------------ARATILLLLAAVLFAAAAAA--------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------------------------------------------SGED-
---RRRETSLRRCLQRCE---QDRPPYERARCVQECKDQQ--QQQ--QERRREHGGHDDDRRD-RDRRGEGSS--
EEEDEGRERG-SR--------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------RRPYVFG-RR-S-FRQ-VVRSDQGSVRL-
LPPFHQ-ASSLLRG-IKN-----------YRVAVLEANPRSFVMPTHTDAHCICYVAQG-EGVVAII-
ENGEKWS---YAIRQG-DVFVA----PAGTINYLANTD-GR-----RKLI-------------------------
--------------------------ISEEKLEKLL--------------------GK-----------------
--------------QDKGV-IIRASEEQVRELRRHAS-EGGHGPHWPLPPF------------
GESSRGPFNILEQRP--RFANRHGRLYEADARSFH--DLAE--HDIRVAVVNITA-
GSMNAPFYNTRSVKVAYVLDGEG---EAEIVCPHLS------RGGRGGESEERRRERGKGKWREEEEEEEEQQK-
--------GQEEEEEEQVGQGYETIRARLSRGTVFVVPSGHPIVVTSSR--DSTLQIVCFDVHANN-----
NERMYLAGM-NSVLKKLDP-----QAKELAFAA-S---AREVDELLNA--QQESAFLAGPEK-
SGRRGEESEDEDRRR------------------------------------------------------------
```

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----RRSHRGRG-------------------------------------------DEA-----------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------VETLLRMAAAAV

Oryza glumipatula                       >TR|A0A0D9ZI03|          MATR------
-----------------------ARATILLLLAAVLFAAAAAA--------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------SGED-
---RRRETSLRRCLQRCE---QDRPPYERARCVQECKDQQ--QQQ--QERRREHGGHDDDRRD-RDRRGEGSS--
EEEDEGRERG-SR--------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------RRPYVFG-RR-S-FRQ-VVRSDQGSVRL-
LPPFHQ-ASSLLRG-IKN-----------YRVAVLEANPRSFVMPTHTDAHCICYVAQG-EGVVAII-
ENGEKWS---YAIRQG-DVFVA----PAGTINYLANTD-GR-----RKLI-------------------------
--------------------------ISEEKLEKLL--------------------GK-----------------
--------------QDKGV-IIRASEEQVRELRRHAS-EGGHGPHWPLPPF------------
GESSRGPFNILEQRP--RFANRHGRLYEADARSFH--DLAE--HDIRVAVVNITA-
GSMNAPFYNTRSVKVAYVLDGEG---EAEIVCPHLS------RGGRGGESEERRRERGKGKWREEEEEEE-QQK-
--------GQEEEEEEQVGQGYETIRARLSRGTVFVVPSGHPIVVTSSR--DSTLQIVCFDVHANN-----
NERMYLAGM-NSVLKKLDP-----QAKELAFAA-S---AREVDELLNA--QQESAFLAGPEK-
SGRRGEESEDEDRRR------------------------------------------------------------
----RRSHRGRG-------------------------------------------DEA-----------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------VETLLRMAAAAV

Oryza meridionalis                      >TR|A0A0E0D4B0|          MATR------
-----------------------ARATILLLLAAVLFAAAAAAAAA-----------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------SGED-
---RRRETSLRRCLQRCE---EDRPLYERARCVQECKDQQ--QQQ--QERRREHGRHDDDRRD-
RDRRGEGSSAEEEEEEGRERG-SR---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------RRPYVFG-RR-S-FRQ-
VVRSDQGSVRL-LPPFHQ-ASSLLRG-IKN-----------YRVAVLEANPRSFVMPTHTDAHCICYVAQG-
EGVVAII-ENGEKRS---YAIRQG-DVFVA----PAGTINYLANTD-GR-----RKLI-----------------
-FFF--APGG-RNPESFLSSFSKGVQRAAFKARIISEEKLEKLL--------------------GK---------
----------------------QDKGV-IIRASEEQVRELRRHAS-EGGHGPHWPLPPF----------------
GESSRGPFNILEQRP--RFANRHGRLYEADARSFH--DLAE--HDIRVAVVNITA-
GSMNAPFYNTRSVKVAYVLDGEG---EAEIVCPHLS------RGGRRGESEEGRRERGKGKWREEEEEEEEQQK-
--------GQEEKEEEQVGQGYETIRARLSRGTVFVVPSGHPIVVTSSR--DSTLQIVCFDVHANN-----
NERMYLAGT-NSVLKKLDP-----QAKELAFAA-S---AREVDELLNA--QQESAFLAGPEQ-
SGRRGEESESEDEGR------------------------------------------------------------
----RRRHRGRG-------------------------------------------DEA-----------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------VETLLRMAAAAV

Oryza sativa                            >TR|A3AR03               MATR------
-----------------------ARATILLLLAAVLFAAAAAA--------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------SGED-
---RRRETSLRRCLQRCE---QDRPPYERARCVQECKDQQ--QQQ--QERRREHGGHDDDRRD-RDRRGEGSS--
EEEDEGRERG-SR--------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------RRPYVFG-RR-S-FRQ-VVRSDQGSVRL-
LPPFST-R-----------------------------RPASCAASRTTASRC----------------------
S---RRTR-------A----PSSCRPTRTRT--------------------------------------------
-------------ASATSPKISEEKLEKLL--------------------GK-----------------------
--------QDKGV-IIRASEEQVRELRRHAS-EGGHGPHWPLPPF------------GESSRGPFNILEQRP--
RFANRHGRLYEADARSFH--DLAE--HDIRVAVVNITA-GSMNAPFYNTRSVKVAYVLDGEG---
EAEIVCPHLS------RGGRGGESEERRRERGKGKWREEEEEEEEQQK---------
GQEEEEEEQVGQGYETIRARLSRGTVFVVPSGHPIVVTSSR--DSTLQIVCFDVHANN-----NERMYLAGM-
NSVLKKLDP-----QAKELAFAA-S---AREVDELLNA--QQESAFLAGPEK-SGRRGEESEDEDRRR-------
---------------------------------------------------------RRSHRGRG----------
---------------------------------DEA---------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------VETLLRMAAAAV

Oryza brachyantha                       >REF|XP_006650381.1|     MATR------
-----------------------ARAMTLVLLAAVLFAAAAAAA-------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------SRED-
---RRGETSLGRCLQRCE---EDRPRYERARCVQECKEQQ--QQQ-EQERRREHGRHDDDRNG-
RDRRGGRSSSEEEEDE-RQQG-RR---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------GRPYVFG-RR-S-FRQ-
VVSSDQGSVRL-LPPFHQ-ASRLLRG-IKN-----------YRVAVLEANPRSFVVPSHTDAHCVCYVAQG-
EGVVAMI-ENGERRS---YAIRQG-DIFVA----PAGTINYLANTD-GR-----RKLIVTKILHT---
ISVPGKIQFFF--GAGG-RNPESFLSSFSKRVQRAAFK---ISDERLEKLL--------------------GK--
-----------------------------QDKGV-IIRASEEQVRELRRHAS-EGGHGSHWPLPPF---------
---GESSRGPFNILEQRP--RFANRHGRLYEADARSFH--DLAE--HDIRVALVNITA-
GSMNAPFYNTRSVKVAYVLDGEG---EAEIVCPHLS------RGG-----EESEGRRGKGKWREEEEEE------
--------GQQQEEEEQVGKGYETIRGRLSRGWVIVAPAGHPIVVSSSR--DSTLQIVCFDVHAEN-----
NERMYLAGT-NSVLKKLDA-----QAKELAFAT-S---AREVDELLNA--QQESAFVAGPEE-SGRRGEQ-
EDEGR---------------------------------------------------------------------
HRGRG-------------------------------------------GEA------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
--------------------------------VETFLRMAAGAV

Leersia perrieri                        >TR|A0A0D9VX50|          MATR------
-----------------------ARATTL-LLAAILFTAAAAAVA------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------SRED-
---RRGETSLGRCMQRCE---EDRPSYERARCLQQCKEQQRQQQQ-EEERRREHGRHDDDRSSSRDRRGEGSS--
EEEDERREQGTSG--------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------RRPYVFG-RR-S-FRQ-VVRSEQGSVEL-
LLPFNQ-ASSLLRG-IKN-----------YRVAVLEANPRSFVVPSHIDAHCICYVAQG-VGVVATI-
ENGEKRS---YTIRQG-DVFVA----PAGTITYLANTD-GR-----RKLIVTKILHT---VSVPGQIQFFF--
GAGG-RNPESFLSSFSKRVQRAAFKAR-ISEERLEKLL--------------------GR---------------
----------------QDKGV-IIRASEEQVSELRRQAS-EGGHGPHWPLPPF------------
GESSRGPFNILEQRP--RFANRHGRLYEADARSFH--DLAE--HDIRVSLVNISA-
GSMNAPFFNTRSVKVAYVLDGEG---EAEIVCPHMS------RG-EGGEREGRRREQGKGRWHEEEEEE------
------------EEEQQVGKGYETIRARLSRGTVFVVPSGHPVVASASR--DATLQIVCFDVHAEN-----
NERMYLAGT-NSVLKKLDP-----QAKELAFAS-S---AREVDEMLNA--
QQEEAFLAGPEQQSGRRGEEEEDEGRRR-----------------------------------------------
-----------------R--HRGRG-------------------------------------------DEA----
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------VETLLRMAVGAA

Zea mays                                >TR|Q03865|              M---------
-----------------------VSARIVVLL-ATLLCAAAAVAS------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------
SWEDDNHHHHGGHKSGQCVRRCE----DRPWHQRPRCLEQCREEEREKRQ-ERS------RHEAD-----
DRSGEGSSE-DEREQEKEK---QK---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------DRRPYVFD-RR-S-FRR-
VVRSEQGSLRV-LRPFDE-VSRLLRG-IRD-----------YRVAVLEANPRSFVVPSHTDAHCICYVAEG-
EGVVTTI-ENGERRS---YTIKQG-HVFVA----PAGAVTYLANTD-GR-----KKLVITKILHT---
ISVPGEFQFFF--GPGG-RNPESFLSSFSKSIQRAAYKT---SSDRLERLF--------------------
GRHG-----------------------------QDKGI-IVRATEEQTRELRRHAS-EGGHGPHWPLPPF-----
-------GES-RGPYSLLDQRP--SIANQHGQLYEADARSFH--DLAE--HDVSVSFANITA-
GSMSAPLFNTRSFKIAYVPNGKG---YAEIVCPH--------RQSQGGESE---RERDKGRR--SEEEEE-----
---------ESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFVAVASR--DSNLQIVCFEVHADR-----
NEKVFLAGA-DNVLQKLDR-----VAKALSFAS-K---AEEVDEVLGS--RREKGFLPGPEE-
SGGHEEREQEEEE-R------------------------------------------------------------
----EERHGGRGERERHGREEREKEEEREGRHGGR-----EEREEEERHG-RGRREEV-----------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------AETLMRMVTARM
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Zea mays                                >TR|C0PGM3|              M---------
-----------------------VSARIVVLL-ATLLCAAAAVAS------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------
SWEDDNHHHHGGHKSGQCVRRCE----DRPWHQRPRCLEQCREEEREKRQ-ERS------RHEAD-----
DRSGEGSSE-DEREQEKEK---QK---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------DRRPYVFD-RR-S-FRR-
VVRSEQGSLRV-LRPFDE-VSRLLRG-IRD-----------YRVAVLEANPRSFVVPSHTDAHCICYVAEG-
EGVVTTI-ENGERRS---YTIKQG-HVFVA----PAGAVTYLANTD-GR-----KKLVIAKILHT---
ISVPGEFQFFF--GPGG-RNPESFLSSFSKSIQRAAYKT---SSDRLERLF--------------------
GRHG-----------------------------QDKGI-IVRATEEQTRELRRHAS-EGGHGPHWPLPPF-----
-------GES-RGPYSLLDQRP--SIANQHGQLYEADARSFH--DLAE--HDVSVSFANITA-
GSMSAPLFNTRSFKIAYVPNGKG---YAEIVCPH--------RQSQGGESE---RERDKGRR--SEEEEE-----
---------ESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFVAVASR--DSNLQIVCFEVHADR-----
NEKVFLAGA-DNVLQKLDR-----VAKALSFAS-K---AEEVDEVLGS--RREKGFLPGPKE-
SGGHEEREQEEEEER------------------------------------------------------------
----EERHGGRGERERHGREEREKEEE----------------EREGRHG-RGRREEV-----------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------AETLMRMVTARM

Zea mays                                >SP|P15590|              M---------
-----------------------VSARIVVLL-AVLLCAAAAVAS------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------------------------------------------
SWEDDNHHHHGGHKSGRCVRRCE----DRPWHQRPRCLEQCREEEREKRQ-ERS------RHEAD-----
DRSGEGSSE-DEREREQEKEEKQK---------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------DRRPYVFD-RR-S-FRR-
VVRSEQGSLRV-LRPFDE-VSRLLRG-IRD-----------YRVAVLEANPRSFVVPSHTDAHCIGYVAEG-
EGVVTTI-ENGERRS---YTIKQG-HVFVA----PAGAVTYLANTD-GR-----KKLVITKILHT---
ISVPGEFQFFF--GPGG-RNPESFLSSFSKSIQRAAYKT---SSDRLERLF--------------------
GRHG-----------------------------QDKGI-IVRATEEQTRELRRHAS-EGGHGPHWPLPPF-----
-------GES-RGPYSLLDQRP--SIANQHGQLYEADARSFH--DLAE--HDVSVSFANITA-
GSMSAPLYNTRSFKIAYVPNGKG---YAEIVCPH--------RQSQGGESE---RERGKGRR--SEEEEE-----
----------SSEEQEEVGQGYHTIRARLSPGTAFVVPAGHPFVAVASR--DSNLQIVCFEVHADR-----
NEKVFLAGA-DNVLQKLDR-----VAKALSFAS-K---AEEVDEVLGS--RREKGFLPGPKE-
SGGHEEREQEEEE-R------------------------------------------------------------
----EERHGGRGERERHGREEREKEEE----------------EREGRHG-RGRREEV-----------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------AETLLRMVTARM

Zea mays                                >TR|Q03866|              M---------
-----------------------VSARIVVLL-AVLLCAAAAVAS------------------------------
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SWEDDNHHHHGGHKSGRCVRRCE----DRPWHQRPRCLEQCREEEREKRQ-ERS------RHEAD-----
DRSGEGSSE-DEREREQEKEEEKQK--------------------------------------------------
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---------------------------------------------------------------------------
-------------------------------------------------------DRRPYVFD-RR-S-FRR-
VVRSEQGSLRV-LRPFDE-VSRLLRG-IRD-----------YRVAVLEANPRSFVVPSHTDAHCICYVAEG-
EGVVTTI-ENGERRS---YTIKQG-HVFVASSSAPAGGTR---NRS-CR-----ASARASRELRT---
RPRATGWRGCS--GGMG-R------TRGSSCVPRRSRPA---SCGATPR--------------------------
-------------------------------------RAATARTGPCRRSAS-RAAPTASWTSGPA---------
---SPT-STGSST---RP--T-------------RAAS--TTSP--
STTSASPSPTSPRGSMSAPLYNTRSFKIAYVPNGKG---YAEIVCPH--------RQSQGGESE---
RERGKGRR--SEEEEE---------------SSEEQEEVGQGYHTIRARLSPGTAFVVPAGHPFVAVASR--
DSNLQIVCFEVHADR-----NEKVFLAGA-DNVLQKLDR-----VAKALSFAS-K---AEEVDEVLGS--
RREKGFLPGPKE-SGGHEEREQEEEE-R-----------------------------------------------
-----------------EERHGGRGERERHGREEREKEEE----------------EREGRHG-RGRREEV----
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----------------------------------------------------AETLLRMVTARM

Sorghum bicolor                         >TR|C5WQD2|
MSANPPHPTQGPHRSTTTHRELYSTHRCHGTRMVSARIVLLLLATLLCAGAAVAS--------------------
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-----SWED-----HDGH---RCARRCE----DRPWHQRARCVEQCREEEERERQ-QQEERGRGDRHE-H-----
DRRGEGSSSGDEREQEQEQ--------------------------------------------------------
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---------------------------------------------------------------------------
-------------------------------------------------------GRRPYVFD-RR-S-FRR-
VVRSEQGSVRA-LRPFHE-ASKLLRG-IRN-----------YRVAVLEANPRSFVVPSHTDAHCIGYVVQG-
EGVVTTI-ENGERRS---YTIKEG-HIFVA----PAGAITYLANTD-GR-----KKLVIAKILHT---
ISVPGEFQFFF--GPGG-RNPESFLSSFSKSIQRAAYKT---SSDRLERLF--------------------
GKRG-----------------------------QDKGV-IVRATEEQIRELRHQASSEGGHGPHWPLPPF-----
-------GES-HGPYSLLDQRP--SIGNQHGQLYEADARSFR--DLAD--HDVSVSFANITA-
GSMSAPLFNTRAFKIAYVARGQG---NAEIVCPH--------QQQQS-QSQ---RG-GKGRRRSEEEEEE-----
---------GGSSEEEEAGQGYRTIRARLSQGTVFVVPVGHPFVAVAAR--DSNLEIVCFELRAEK-----
NEKVFLAGA-DNVLKKLDR-----VAKALSFAA-K---AEEVDEVLGA--
RREKGFLPGPEEESGRREEREREEEE-R-----------------------------------------------
-----------------GGRHGGRGEREK----EEEEEEEREGRHGGRGQRKQEEEEREGRHGGRGRREEA----
---------------------------------------------------------------------------
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----------------------------------------------------AETLLRMVTARM

Setaria italica                         >TR|K4A875|             MATAGAR---
------------------------ATPFLLLFLATLLCAAAA-AS------------------------------
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----------------------------------------------------------------------SWED-
-------REPWRCARRCE----DRPRHERAQCVQECREEERERGR-RDELGRRG-----------
DRRGEGSGDEREREREQEQEQEQ----------------------------------------------------
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---------------------------------------------------------------------------
-------------------------------------------------------SRRPYVFD-RR-S-FRR-
VVRSEQGSVRA-LRPFHE-ASKLLRG-IRN-----------YRVAILEANPRSFIVPSHTDAHSIGYVAQG-
EGVVTTI-ENGERRS---YTVKEG-DVFVAS----AGAVTYLANPD-GR-----RKLVIVKILHT---ISVPGK-
-----------------------------------SSDRLERLF--------------------GK---------
----------------------QDKGI-IVRASEEQVRELRRHAS-EGGHGPHWPLPPF------------GES-
HGPYSLLDQRP--TIANRHGQLYQADARSYR--DLAE--HDVRVSFVNISA-
GSMSAPFYDSRSIKLACVLDGEG---YIEIICPH--------L-AQRHEGR---SERGKGRR--GEEESE-----
---------SEEQEQEEAGQGYHTIRARVSRGTAFVVPVGHPVVEVASR--GSNLQIVYFEIHADK-----
NERVFLAGA-NNVLKKLDN-----TAKELAFAA-R---AREVDEVLDA--QRDQGFLAGPEESS--
REEREEEEE------------------------------------------------------------------
----HEGR-----RGPKEWEKEEEREARRG------REQREKEEERRGHGRREEV--------------------
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---------------------------------------------------------------------------
------------------------------------AETFLRLATGRL

Zea mays                                >GB|ABS89028.1|         M---------
-----------------------VSARIVVLL-ATLLCAAAAVAS------------------------------
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----------------------------------------------------------------------
SWEDDNHHHHGGHKSGRCVRRCE----DRPWHQRPRCLEQCREEEREKRQ-ERS------RHEAD-----
DRSGKGSS---EDEREREQEKEEK---------------------------------------------------
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---------------------------------------------------------------------------
-------------------------------------------------------DRRPYVFD-RR-S-FRR-
VVQSEQGSLRV-LRPFDE-VSRLLRG-IRD-----------YRVAVLEANPRSFVVPSHTDAHCICYVAEG-
EGVVTTI-ENGERRS---YTIKQG-HVFVA----PAGTVTYLANTD-GR-----KKLVITKILHT---
ISVPGEFQFFF--GPGG-RSPESFLSSFSK---------------------------------------------
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Triticum aestivum                       >TR|W5ECA4|              MAIRA---
TIP----------------LLFLLGTS-----------LLFAAAVS-----------------------------
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------------------------------------------------------------------------
ASRDDEEDRRGGHSLQQCVQRCQ---QDRPRYSHARCVQECREDQQQHGRHEQEEQ-----------------
GRGHGRHGEGGREEEQGRGRGRHGQGEREEEEGRGRGRHGEGEREEEEGRGRGRHGEGEREEHGKHEQ-----
GRGRRGEGERDEEHGDS----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------RRPYVFG-PR-N-FRS-
IIRSDHGFVKA-LRPFDE-VSRLLRG-IRN-----------YRVAIMEVNPRSFVVPGLTDADGVGYVAQG-
EGVLTVI-ENGERRS---YSVRQG-DVIVA----PAGSIMHLANTD-GR-----RKLVIAKILHT---
ISVPGKFQYF---------SAKPLLASLSKRVLRAALKT---SDEQLDRLLFGR---------------
RQGQEE-----------------------------EP--ISIVRASEEQLRELRREAS-EGGQGHHWPLPPF---
---------RGDSRDTFNLLEQRP--KIANRHGRLFEADARSFH--ALAQ--HDVRVAVANITP-
GSMTAPYLNTQSFKLAVVLEGEG---EVQIVCPHLG------Q-----DSER-EHEHGKGR-
RSEEEEDDQRQQRRR-GSGSESE----
EEQDQQRYETVRARVSRGSAFVVPPGHPVVEIASSRGSSNLQVVCFEINAER-----NERVWLAGR-
NNVIGKLDN-----PAQELTFGR-P---AREVQEVFRAKDQQDEGFVAGPEQQ------EQERGDR---------
---------------------------------------------------------RRGDRGRG----------
---------------------------------DEA---------------------------------------
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-----------------VEAFLRMATAAL

Triticum aestivum                       >TR|W5EAP7|              MATRARV-
TIP----------------LLFLLGTS-----------LLFAAAVS-----------------------------
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------------------------------------------------------------------------
ASHDEEEDRRGGRSLQQCVQRCH---QDRPRYSHARCVQECRDEQQQHGRHEQEEQ-----------------
GHSHGRHGEGGREEEQGRGRGRHG----------------EGEREEEEGRGRGRHGEGEREEHGKHEQ-----
GRGRRGEGERDEEHGDS----------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------------------------RRPYVFG-PR-N-FRS-
IIRSDHGFVKA-LRPFDE-VSRLLRG-IRN-----------YRVAIMEVNPRSFVVPGLTDADGVGYVAQG-
EGVLTVI-ENGERRS---YTVRQG-DVIVA----PAGSIMHLANTD-GR-----RKLVIAKILHT---
ISVPGKFQYF---------SAKPLLASLSKRVLTAALKT---SDEQLGRLLFGR---------------
RQGQEE-----------------------------ES-SISIVRASEEQLRELRRQAS-EGGQGHHWPLPPF---
---------RGDSRDTFNLLEQRP--KIANRHGRLFEADARSFH--ALAQ--HDVRVAVANITP-
GSMTAPYLNTQSFKFAVVLEGEG---EVQIVCPHLA------R-----DSERREHEHGKGR-
RSEEEDDDQRQQRRRRGSGSESESESEEEQDQQRYETVRARVSRGSAFVVPPGHPVVEIASSRGSSNLQVVCFEI
NAER-----NERVWLAGR-NNVIGKLDS-----PAQELTFGR-P---AREVQEVFRAKDQQDEGFVAGPEQQS--
-RHEQEQ-ER-----------------------------------------------------------------
-RRGDRGRG-------------------------------------------DDA--------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------------VGAFLRMATGAF

Triticum aestivum                       >TR|W5EST8|              MATRARV-
TIP----------------LLFLLGTS-----------LLFAAAVS-----------------------------
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ASHDEEDDRRGGHSLQQCVQRCQ---QDRPRYSHARCVQECRDDQQQHGRHEQEEQ-----------------
GRGHGRHGEGGREEEQGRGRGRHGQGEREEEQGRGHGRHGQGEREEEQGRGRGRHGQEEREEHGRREQEEQGQGR
GRRGEGERDEEHGDS------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------RRPYVFG-PR-S-FRS-
IIRSDHGFVKA-LRPFDE-VSRLLRG-IRN-----------YRVAIMEVNPRAFVVPGLTDADGVGYVAQG-
EGVLTVI-ENGEKRS---YTVREG-DVIVA----PAGSIMHLANTD-GR-----RKLIIAKILHT---
ISVPGMFQYF---------SAKPLLASLSKRVLRAALKT---SDERLERLL-DP---------------
RQGQEK-----------------------------TGGSMSIVRASEEQLHELSRQAS-EGSQGHHWPLPPF---
---------RGDSRDTYNLLEQRP--RIANRHGRLYEADARSFH--ALAQ--HDVRVAVANITP-
GSMTAPYLNTQSFKLAVVLEGEG---EVQIVCPHLG------R-----DSERREQ--GKGR-
WSEEEDDDQRQQRRR-
GSGSESESESEEQQDQQRYQTIRARVSRGSAFVVPPGHPVVEIASSQGSSNLQVVCFEINAER-----
NERVWLAGR-NNVIGKLDN-----PAQELTFGR-P---AREVQEVFRAKDQQDEGFVAGPEQQ------
EQERGDR------------------------------------------------------------------
RRGDRGRG-------------------------------------------DEA---------------------
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---------------------------------------------------------------------------
-----------------------------------VEAFLRMATAAL

Triticum aestivum                       >TR|I6QQ39|              MATRGRA-
TIP----------------LLFLLGTS-----------LLFAAAVS-----------------------------
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ASHDEEEDRRGGRSLQRCVQRCQ---QDRPRYSHARCVQECRDDQQQHGRHEQEEQ-----------------
GRGHGRHGEGEREEEQGRGRGRRG----------------QGEREEEQGRGRGR---------------------
--RGEGERDEEHGDG------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------RRPYVFG-PR-S-FRR-
IIRSDHGFVKA-LRPFDE-VSRLLRG-IRN-----------YRVAIMEVNPRAFVVPGLTDADGVGYVAQG-
EGVLTVI-ENGEKRS---YTVRQG-DVIVA----PAGSIMHLANTD-GR-----RKLVIAKILHT---
ISVPGKFQYF---------SAKPLLASLSKRVLTAALKT---SDERLGSLL-GS---------------
RQGKEE-----------------------------EEKSISIVRASEEQLRELRRQAS-EGDQGHHWPLPPF---
---------RGDSRDTFNLLEQRP--KIANRHGRLYEADARSFH--ALAQ--HDVRVAVANITP-
GSMTAPYLNTQSFKLAVVLEGEG---EVEIVCPHLG------R-----
DSERREQEHGKGRWRSEEEEDDRRQQRRR-GSGSESE----
EEQDQQRYETVRARVSRGSAFVVPPGHPVVEIASSRGSSNLQVVCFEINAER-----NERVWLAGR-
NNVIAKLDD-----PAQELAFGR-P---AREVQEVFRAKDQQDEGFVAGPEQQQ-----EHERGDR---------
---------------------------------------------------------RRGDRGRG----------
---------------------------------DEA---------------------------------------
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-----------------VEAFLRMATAAL

Triticum aestivum                       >TR|B7U6L4|              MATRARV-
TIP----------------LLFLLGTS-----------LLFAAAVS-----------------------------
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ASHDEEEDRRGGRSLQQCVQRCQ-Q--DRPRYSHARCVQECRDDQQQHGRHEQEEQ-----------------
GRGHGRHGEGEREEEQGRGRGRHG----------------QGEREEEQGRGRGR---------------------
--RGEGERDEEHGDG------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
-----------------------------------------------------RRPYVFG-PR-S-FRR-
IIRSDHGFVKA-LRPFDE-VSRLLRG-IRN-----------YRVAIMEVNPRAFVVPGLTDADGVGYVAQG-
EGVLTVI-ENGEKRS---YTVRQG-DVIVA----PAGSIMHLANTD-GR-----RKLVIAKILHT---
ISVPGKFQYF---------SAKPLLASLSKRVLTAALKT---SDERLGSLL-GS---------------
RQGKEE-----------------------------EEKSISIVRASEEQLRELRRQAS-EGDQGHHWPLPPF---
---------RGDSRDTFNLLEQRP--KIANRHGRLYEADARSFH--ALAQ--HDVRVAVANITP-
GSMTAPYLNTQSFKLAVVLEGEG---EVEIVCPHLG------R-----
DSERREQEHGKGRWRSEEEEDDRRQQRRR-GSGSESE----
EEQDQQRYETVRARVSRGSAFVVPPGHPVVEIASSRGSSNLQVVCFEINAER-----NERVWLAGR-
NNVIAKLDD-----PAQELTFGR-P---AREVQEVFRAKDQQDEGFVAGPEQQQ-----EHERGDR---------
---------------------------------------------------------RRGDRGRG----------
---------------------------------DEA---------------------------------------
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-----------------VEAFLRMATAAL

Triticum urartu                         >TR|M8A380|              MATRARV-
TIP----------------LLFLLGTS-----------LLFAAAVS-----------------------------
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ASHDEEEDRRGGRSLQQCVQRCQ---QDRPRYSHAR---------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------------------------------------FRR-
IIRSDHGFVKA-LRPFDE-VSRLLRG-IRN-----------YRVAIMEVNPRAFVVPGLTDADGVGYVAQG-
EGVLTVI-ENGEKRS---YTVRQG-DVIVA----PAGSIMHLANTD-GR-----RKLVIAKILHT---
ISLPGKFQYF---------SAKPLLASLSKRVLRAALKT---SDERLGSLL-GS---------------
RQGKEE-----------------------------EEKSISIVRASEEQVRELRREAS-ESGQGHHWPLPPV---
---------RGDSRDTYNLLEQRP--KIANRHGRLYEADARSFH--ALAQ--HDVRVAVANITP-
GSMTAPYLNTQSFKLAVVLEGEG---EVEIVCPHLG------R-----DSERREQEHGKGRW-
GEEEEDDRRQQRRR-
GSGSGSESESEEQQDQQRYETVRARVSRGSAFVVPPGHPVVEIASSRGSSNLQVVCFEINAER-----
NERVWLAGR-NNVIAKLDD-----PAQELTFGR-P---AREVQEVFRAKDQQDEGFVAGPEQQ------
EQERGDR------------------------------------------------------------------
RRGDRGRG-------------------------------------------DDA---------------------
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-----------------------------------VGAFLRMATGAL

Hordeum vulgare                         >TR|Q03678|              MATRAKA-
TIP----------------LLFLLGTS-----------LLFAAAVS-----------------------------
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ASHDDEDDRRGGHSLQQCVQRCR---
QERPRYSHARCVQECRDDQQQHGRHEQEEEQGRGRGWHGEGEREEEHGRGRGRHGEGEREEEHGRGRGRHGEGER
EEERGRGHGRHGEGEREEERGRGRGRHGEGEREE-------EEGRGRGRRGEGERDEEQGDS-------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-------------------------RRPYVFG-PR-S-FRR-IIQSDHGFVRA-LRPFDQ-VSRLLRG-IRD---
--------YRVAIMEVNPRAFVVPGFTDADGVGYVAQG-EGVLTVI-ENGEKRS---YTVKEG-DVIVA----
PAGSIMHLANTD-GR-----RKLVIAKILHT---ISVPGKFQFL---------SVKPLLASLSKRVLRAAFKT--
-SDERLERL-FNQ---------------RQGQEK-----------------------------T-
RSVSIVRASEEQLRELRREAA-EGGQGHRWPLPPF------------RGDSRDTFNLLEQRP--
KIANRHGRLYEADARSFH--ALAN--QDVRVAVANITP-GSMTAPYLNTQSFKLAVVLEGEG---
EVQIVCPHLG------R-----ESE-SEREHGKGR-RREEEEDDQRQQRRR---GSESESE--
EEEEQQRYETVRARVSRGSAFVVPPGHPVVEISSSQGSSNLQVVCFEINAER-----NERVWLAGR-
NNVIGKLGS-----PAQELTFGR-P---AREVQEVFRAQDQ-DEGFVAGPEQQS---REQEQEQERHR-------
---------------------------------------------------------RRGDRGRG----------
---------------------------------DEA---------------------------------------
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-----------------VETFLRMATGAI

Musa acuminata                          >REF|XP_009413945.1|
MATRRVEAFLFPLVLLLLSSSCLLASSSRS---------------------------------------------
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--------------DPEKKR--CAMECRGIPE---QQQRKLCVHRCLDDSSEQESG-------------------
--------------------REH----------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
---------------------------------------------------------NPYYFG-RR-S-YQQ-
WSRTEHG--------------------------------------------------------------------
---------------------------------------------------------------------------
-------------------------------------RRVFRSQ-------------------------------
---------------------RKGEIIKITEDQIRALNESKTESW--PFGL--------------------
SNEPYNLLENS-PS-HSNEHGQLHEATGNDCE--MLQD--LNVDVSIANISE-
RSMMAPNYDTRSTKLAMVVEGRG---YIEMACPHRS------AEQ-------------------RRTQEE-----
-----------TGSQGEQRVRYRTVRSRVSRGSVFVIPAGHPAAVVAAA--NENLQVLCFGTRSEN-----
NRRYYLAGR-NNVLNRLDR-----AAKAMAFGV-P---AEEVEEVLN-A-QPESVFMPGPERRREEEEKWR---
QLIF----------------------------------------------------------------KYAG---
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Musa acuminata                          >REF|XP_009413946.1|
MAIRRVEAFLFPLLLLLLSSSCLLASSSKS---------------------------------------------
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--------------DPEKKR--CVMECRGIPE---QQQRKLC---------------------------------
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-----------------------------------------------------------------------EYH-
-GAAG-RNPQTFYTSFSNEVLEAAFNT---PWDKLGRVFRSQ---------------------------------
-------------------RKGEIIKITEDQIRALNESKTESW--PFGL--------------------
SNEPYNLLENN-PS-HSNEHGQIHEATGNECE--MLQD--LNVDVSIANISE-
RSMMAPNYDTRSTKLAMVVEGRG---YIEMACPHRS------AER-------------------RRTQEE-----
-----------SGSQGEQRVRYRTVRSRVSRGSVFVIPAGHPAAVVAAA--NENLQVLCFGIRSEN-----
NRRYYLAGR-NNVLNRLDR-----AAKAMAFGV-P---AEEVEEVLN-A-QPESVFMPGPERRREEEEKRR---
QLVF----------------------------------------------------------------KYAG---
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Musa acuminata                          >TR|M0TZ68|              MATGTVQV-
GFPLLLLL--SSLLAASSSGS------------------------------------------------------
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-----DPEKTR--CVMECRGTSE---RE------------AGREQEREEEAEG----------------------
---------ETREY-------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------------------------NPYYFG-ER-S-YEH-
WSRSEHGRFKV-LERFSRRSELLI--GIEN-----------YRLAIMEAEPETFIMPSHWDAEEVFYVMEG-
RGTITLLHEE-NRES---HEIKRG-DIM----RIPAGVIVYAINK-AKN-----ERLHIAMLLHP---
ISTPGHFEEFF--GAAG-SNPESFYNSFSNGVLEAAFNT---PRDRLERLFERQ---------------------
-------------------------------KKGEIIKITEEQIRALSQTTGFGGGRHSAR--------------
------SNEPYNLLQKR-PS-HANEYGELYEARSSDYH--RLQD--LDVDVSIANISE-
RSMMAPSYNSRATKLAMVVEGRG---HFEMVCPRRS------GDS-------------------RRSEDA-----
-----------TEPEGQQRVRYRTVRSEVSRGSVFVIPPGHPVTAVAAA--NENLEVLCFGIRAGR-----
NRKCYLAGK-NNVMNLLDR-----EAKQLSFGA-P---AEEVQEVFD-A-
QPESVFLPGPGRRRGEAKRRQPSVESLF-----------------------------------------------
-----------------GFGG------------------------------------------------------
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Musa acuminata                          >TR|M0TZ63|              MATRTVQV-
LFSLLLLL--SSCVLASTYGS------------------------------------------------------
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-----DRAKKR--CHMECRGTPE---GRRRKECVRQCLDHSGREREHGEVAEG----------------------
---------GRRER-------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------------------------NPYFFG-DR-S-YEQ-
WSRSEHGRFEV-LERFARRSELLV--GVEN-----------YRLAVMEAEPETFIMPRHWDAEEVFYVMEG-
RGTITLLHEN-NRET---HDIKRG-DII----WIPAGAIVYAINK-ARN-----EKLRVAILLHP---
ISTPGHVEEFY--GAAG-RNPETFFASFSDEVLEAAFDT---PSEKLERLFEKQ---------------------
-------------------------------RRGEFIKMTEEQMRALSQSTGEGGWP-LAR--------------
------STEPYNLLQNR-PS-HSNEHGQLHEVGANEYQ--QLQD--LDVDVSIANISE-
RSMMAPNYNSLSTKLAMVVQGRG---YIEMACPSRS------GES-------------------RRSEET-----
-----------TESEPQQRVLYRTVRSRVSRGSVFVIPAGHPVAAVAAR--NENLEVLFFGVRAAQ-----
NRNYYLAGR-NNVLNRLDR-----EAKELAFGV-P---AEEVDEVLH-A-
QPESVFLPGPERRREAERGRQPSPESLL-----------------------------------------------
-----------------SFAE------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------S

Elaeis guineensis                       >TR|Q9AU64|              MTIK---
PRAFVPFLLLLSILFVSATLTFSAT---T----------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------------EDP-KQRLERCKQEC-RESRQGER--
QERRCVSQCEERYERERREQEERKG--------------------------------------------------
-QGEER-GRR----EEPEKRLEECRRECREQAE---RRERRECEKRCEEEYKE--
HRGRSKDKEEGEEGRGEKRRESD----------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----PYFFD-EE-S-FLH-RVRTEHGHVRV-LRNFLEK-SKLLLG-VAN-----------
YRVAILETNPNTFVLPSHWDAEALLFVARG-HGHITLQCQD-NKAT---HELRRG-DIM----
RVRAGTIVSFANRGVGN-----EKLVIVILLHP---VATPGMFEAFV--GAGG-
QNPESFYRSFSKRVLSAAFNT---REDKLERLFQKQ---------------------------------------
-------------NKGAIIQASQEQIKEMSR--GSE------GRSWPF-------------GESRRPFNLFHKR-
PA-HSNRHGELREADSDDY--PELRD--LNIHVSYANISK-GSMIAPNYNTEATKISVVVGGNG---
DVQIVCPHIS------RQQEEGRRGREEEEGRGRQEGREEEEEE----------------E--
QQQRGQHYRRVESKVSCGTTFIVPAGHPSVSVSSR--NENLEVLCFEINAKN-----NQRTWLAGR-
NNVLKQMDR-----VTKELAFDL-P---EREVDEVLN-A-PREEVFMAGPEERGRERERGEGRDGPLE-------
---------------------------------------------------------SILEF-------------
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Elaeis guineensis                       >REF|XP_010938152.1|     MTIK---
PRAFVPFLLLLSILFVSATLTFSAT---T----------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------------EDP-KQRLERCKQEC-RESRQGER--
QERRCVSQCEERYERERREQEERKG--------------------------------------------------
-QGEER-GRR----EEPEKRLEECRRECREQAE---RRERRECEKRCEEEYKE--
HRGRSKDKEEGEEGRGEKRRESD----------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----PYFFD-EE-S-FLH-RVRTEHGHVRV-LRNFLEK-SKLLLG-VAN-----------
YRVAILETNPNTFVLPSHWDAEALLFVARG-HGHITLQCQD-NKAT---HELRRG-DIM----
RVRAGTIVSFANSGVGN-----EKLVIVILLHP---VATPGMFEAFV--GAGG-
QNPESFYRSFSKRVLSAAFNT---REDKLERLFQKQ---------------------------------------
-------------NKGAIIQASQEQIKEMSR--GSE------GRSWPF-------------GESRRPFNLFHKR-
PA-HSNRHGELREADSDDY--PELRD--LNIHVSYANISK-GSMIAPNYNTEATKISVVVGGNG---
DVQIVCPHIS------RQQEEGRRGREEEEGRGRQEGREEEEEE----------------
EEEQQQRGQHYRRVESKVSCGTTFIVPAGHPSVSVSSR--NENLEVLCFEINAKN-----NQRTWLAGR-
NNVLKQMDR-----VTKELAFDL-P---EREVDEVLN-A-PREEVFMAGPDERGRERERGEGRDGPLE-------
---------------------------------------------------------SILEF-------------
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Phoenix dactylifera                     >REF|XP_008775109.1|     MTTK---
PRAFIPFLLVLSILLVSATLALS-T---T----------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------------EDP-KRQIERCKQEC-RESRQGEQ--
QERQCVRQCEE--------QEEKRG--------------------------------------------------
-QGDET-GKEGHKGEDPEKRLEECRRECREQAEGRE---QRECEKRCEEECKE--
RRGESKEEEKREEEKGEKRRGSD----------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----PYFFE-EE-S-FLH-RVRTEHGNVRV-LRNFLER-SKLLLG-VAN-----------
YRVAILEANPNTFVLPSHWDAEALLFVARG-NGLITRQCQD-NKET---QELRRG-HII----
RVRAGTIVSFVNKD-RN-----EKLVIVMLFQT---VATPGMLEAFV--GAGG-
RNPESFYRSFSKPVLRAAFNT---GVDKLERLFGRQ---------------------------------------
-------------KKGAMIEASQEQIRELSRRAGSE------GLPWPF-------------GESRRPFNLLDKR-
PS-HSNRHGELREADRDDY--PELRD--LNIQVALARINK-GSMMSPNYNTEATTISIVVGGNG---
QVQIVCPHVS------RQQEEGR-GREGEEGRGQQEGKEEEE---------------------
QQQRGQRYQRVESEVSRGTTYIVPAGHPSVAVSSR--NESLEVLCFEINAMN-----NQRTWLAGS-
NNILKQMDR-----MTKELAFDQ-P---AREVDEVLN-A-PREEVFMAGPQERERESERGEGRDGPLE-------
---------------------------------------------------------SILEF-------------
---------------------------------------------------------------------------
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------------------------AG--F

Elaeis guineensis                       >REF|XP_010938562.1|     MIART-----
------------------RAQVLLPILLFSTLLIIPSFGIPI---------------------------------
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---------------------------------------------------------------------------
-------RKVEECLSKCKESFFYHQDRQLLEKCEQICFDKYDGSH------------------------------
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------------------------------GEGIEKKEGEQQRGEGQNRYCYG-EE-N-FEY-WMKSELGHFKV-
LERFTERF-KLLQG-IGN-----------FRLAILEANPRTFVLPSHMDAEELFYVMEG-RGVLNVL-
EISGRNS---YDIEQG-QIF----SFDAGSQAYLINKD-DN-----KKLRIAMLLHP---VSSPGRFKEFF--
DAGG-RAPESFYRSFSTKVLEAAFNT---TKDRLEKLFGQQ----------------------------------
-------------------RGETINATEEQIKALTEPPTAPGGWFIGP----------------
SKQCRRSGVSLTSRQNRVWYSNEHGELYKIYACDY--SDLCD--LGVEISFANISR-
GSMMAPHYNSMATLAALVVEGEG---YFEMACPHIE------QG-------------------------------
------------------GTHYQAVRSQVSPGSVFMIPAGHPVVAVASR--DENLQVLFLGMNAKH-----
NRVHFLAG-GNNVLNHMER-----VAKELSFNA-P---ARVVDEVFN-A-
QKRAGFLPGPDEIHKEERGTRPWTA--------------------------------------------------
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Amborella trichopoda                    >TR|W1P1Y4|
MASSWILTALLFLFVVVSPLLALSKRDP-----------------------------------------------
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---------------------------------------------------------------------------
--------------ERERQERQCKSECERSREREREVR--QCKQECEERYRRQK---------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-------------------------------GQGRNIEERERESESESEGRRRGVTGNPYAFERDRF----
VRDISTEHGSFRT-LPPFTER-SELFRG-IEN-----------NRICIMELKPNAFVLPHHKDADIIYYVANG-
DARLVTIGE----ERQDSHNLKKG-----DTATIPAGKTTYIINKDSQR-----E-LKIVALLQT---
ISTPGQYEIFFG---ATGQNPPSYLRAFSDEILEASFNV---DRSRLSRLLEQK---------------------
-------------------------------GQGPIVRPSSEQLQGLIHGGSGGGKWPFG---------------
--ESEESERPFNLFSRRP--RISNDHGELYELDETEYS--PLRE--FDIAISFANISR-
GSLEVPFYNSRATEIYVILEGRA---RIEMACPHVSGGREQEGSRRGQGEQEGSRRGQREQEGSRREQEQEER--
------------GKGQGQEIKYHKIRSDLNPEDLFVAPPSHPIAIRASQ--EENLQIICFEINARR-----
NRKYFLAGK-NSILNQIER-----AAKEVSFNV----PSREAEEVLRA--QSDSVFVVGPRQQREGREGEGR---
---------------------------------------------------------------------------
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------------------------------------AVA

Cicer arietinum                         >REF|XP_004496703.1|     MA--------
-TATKARFPL-----LLLLGIIFLASV-CVSYGIV----------------------------------------
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---------------------------------------------------------------------------
--------QGNPCIEKCLQRYNKVHETFKHHECRSHCEKEEEEE-------------------------------
---------------------------------------------------------------------------
--------------------------------------------VEEPLEPREPGR---RERGRQEGEK------
--------EEKRRQL------PPRT--------------------------------------------------
----------------RDEDQ----------------D-------------NDEWRGRRRHQDPEER---
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ARLRRRREE-------KERRQEHQ-------------REEEEETSSESQGRRNPFFFNSN--K-FQTI-
FENEHGHIRL-LQRFDKR-SNL-FENLQN-----------YRLLEYKARPHTLFLPQHTDADFILVVLSG-
KAILTVLNSND-RNS---FNLECG-----DTIKLPAGTIAYLANRDS-N-----EDLRIVDLAIP---
INTPAKF-QAF--FPFANNNQQSYFNGFSKNILEASFN-AKY--EDIERILLEE--PQQ--RRGHRGRQQSQ---
-------------------------------EAEVIVKVSREQIEELSKHAESSS-----------------
RKSISSE---SEPFNLKRRSP--IYSNKFGKFFEITPKK-S-SQLQD--LDILVDYAEINE-
GGLMLPHFNSRATMVVVVNEGKG---NFELVGLRNE-------------------EE------------------
-------------EK---SKQVQRYRANLSPGDVFVIPAGHPVAVNAS----SNLSLLGFGINAQN-----
NQRNFLAGEDDNVISQIER-----PVKELAFP-GS---AQEVDRLI--KNQRQSHFANAQSQ-----GSQRR---
-----------------------------------------------------------------------S---
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LDTFY

Cicer arietinum                         >REF|XP_004496704.1|     MA--------
-TTTKTRFPL-----LLLLGIIFLASV-CVSYGIV----------------------------------------
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-----QYEQGNPCLKKCMQRYNKVNEAFK---------RREEEE-------------------------------
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--------------------------------------------YEERSEHSVPGQ---RERGRQEGEK------
--------EEEHREQRRSRRESERE--------------------------------------------------
----------------REEDEQKQRHPHHEREE----E-------------EDEEFRERRHRGDTEE---
TRFRRRKER-------RQEQQEKKS----------ESKEDEEESSSESQGRRNPFFFRSN--K-FQTI-
FENQHGHIRL-LQNFDKR-SNL-FQNLQN-----------YRFLEYKARPHTLLLPQHIDADFILVVLSG-
KAILTVLNPND-RNS---FNLERG-----DTIKLPAGTTAYLANHDD-E-----EDLRVVELAIP---
VNRPGKF-QSF--FPSSNQNQQSYFNGFSKSILEASFN-TKY--ETIERVLLEEQEPEQ--SRGRRGSEESE---
-------------------------------EGDAIVKVSREQIEELSKHAKSSS-----------------
RKSISSE---SEPFNLRSRNP--IYSNKFGKFFEITPEK-S-PQLQD--LNIFVSCVEINE-
GGLMLPHFNSRAIVVLFINEGKG---HLELVGLRNE------QQEQQQEEDEEQEEE------------------
-------------ER---NNQVQRFRARLSPGDVFIIPAGHPVAVNAS----SDLNFVGFGINAEN-----
NQRNFLAGEDDNVISQIQN-----PVKELTFP-GS---AQEVNRLI--KNQRQSYFANAQPQQREEESQRRR---
-----------------------------------------------------------------------G---
----SLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LGGFY

Lotus japonicus                         >TR|B5U8K3|              MAS-------
-AKIKARLPL-----LLLLGILFLVSVSLA---------------------------------------------
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--------------------------------------------------------------------------
TASRQ----REDPCREQGEDERQPWQPRREREE---HGRER-EE-EDEKESRRPSWE--RKERTR-
EWRRESEERDTPRRPHRQSE-------------------------------------------------------
-------------------------------------------------------------E-------------
---------EESDRPRRPHRESKER--PRR-HQRESEEEEGSSSSS--ESSRRSQRRNPFHFRSS--R-FQT-
HFENEHGHVRV-LQRFDER-SKL-FENLQN-----------YRILEFKAKPQTLVLPHHNDADSIIVILSG-
```

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RAILTIVNPND-RDS---YNLESG-----DALVIPAGATAYLANRDN-D-----ENLRVVKLLIP---
INRPGQY-QPF--FPSSSETQESYLNGFSRNILEASFN-AGY--DEIERVLLQREEQRGEQS-------------
------------------------------QEQGVIVKASQDQIQQLSRHAKSSSR----------------
KRS-SSK---SEPFNLRSSKP--ISSNKFGKLFEITPEK-N-QQLRD--LDILLSEAQIKE-
GSIFLPHYHSTSTLILVVNEGRG---ELELVAQRRQ------QQRG---Q---EEEQEEE---------------
-------------QP---RIEAQRFRARLSPGDVIVIPASHPFAVTAS----SDLNLLAFGINAEN-----
NQRNFLAGRDDNVISQIER-----PVKELAFP-GS---AEEIESLI--KNQRNSCFASAQPQQGEEEGRSGKKD-
-------------------------------------------------------------------QLSSI---
----LGAF-------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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-------------------------------------F-

Lotus japonicus                         >TR|B5U8K8|              MAS-------
-TEMKARFPL-----LLLLGILFLASVSVCY--------------------------------------------
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-------------------------------------------------------------------------
GIVSHD----KED-------DDRRPWWPEPEREEEKHHQRTRGSE-
EGEKEERERHQEPGHRERARQEGEKEEDERQPWWQPGRGEE----------------------------------
---------------------------------------------------------------------------
-------EGEWRGSRRLEDPDER---
ERVRERTERAKKWRRETEERDTPRRPHHRESEEEEGSSSSSSSESSRRSQRRNPFYFRSSSSR-FQT-
RFQNEYGYVRV-LQRFDER-SKL-FENLQN-----------YRIFEFKAKPHTVVLPHHNDADSIVVILSG-
KAIITLVNPND-RES---FNLERG-----DVLVHPAGTIAYVANHDD-N-----ENLRIAKIIIP---
VNRPGEF-QAF--YPSNTEPQESYLNGFSRNILEASFN-AEY--NEIERVLLRG----GEQR-------------
------------------------------QEQGLIVKVSRDLIQQLSRHAKSSSR----------------
KRT-SSE---PEPFNLRSRDP--IYSNEFGKHFEINPNR-N-SQLRD--FDIFLSSTEIRE-
GSIFLPHYNSRSTVILVVNEGRG---EFELVAQRKQ------QQQRRNEE---DEEEEEE---------------
-------------QP---RIEAQRFRARLSPGDVVVIPAGHPVAINAS----SDLNFIAFGINAEN-----
NQRHFLAGGDDNVISQIEK-----VVKEIAFP-GS---AEDIERLI--KNQRNSHFANAQPQQ-REEGGHGRRG-
-------------------------------------------------------------------PLSSI---
----LGAF-------------------------------------------------------------------
---------------------------------------------------------------------------
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-------------------------------------TK

Medicago truncatula                     >TR|A0A072VR24|          MA--------
-TTIKSRFPL-----LLLLGIIFLGSV-CVSYGIVG---------------------------------------
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EQEERHPGQWKPPHEREE----DERRPGEWRPPRGGRQEGQEQRPGQWRPSHEREED-
EEDEHQKRRPGQWRPTRGGRQEGQEQRPGRFPSEREEYDEDDRRERRPGQQRPTREGRW----------------
-----------------------------KGQEQRPEQWRPSRGKEEREKEERQKHPGREREKWEKRE-------
-------DEEWRGRQRHEDPDER---ARLRHREER-------
RQKEEEHQKGDRPSRTPSRRERGEEEEGSSESEGRRNPFLFRSN--R-FQTL-FENENGHIRL-IQRFDKR-
SNL-FQNLKN-----------YRLLEYRAKPHTIFLPHHTDADFILVVLSG-KAILTVLNSNN-RNS---
```

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FNLEQG-----DTIKLPAGSTAYLVNQDN-D-----EDLRVVDLVIP---VNRPGKF-QSF--
DLSGNQNNPSYFRGFSKSILEASFN-TDY--ETIERVLLEEHEHEQQQRRGRKGRQQSQ----------------
------------------EANAIVKVSREQIEELRRHAKSSS-----------------KRSISSE---
SGPFNLRNRNP--LYSNKFGKFFEITPEK-N-PQLQD--LDIFVSSVEINE------------------------
---------------------------------------------------------------------------
------------------------------------------------------------VITYINN-----
KIRQL----------------------------------------------------------------------
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Medicago truncatula                    >TR|A0A072VPD1|          MA--------
-TTIKSRFPL-----LLLLGIIFLGSV-CVSYGIVG---------------------------------------
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EQEERHPGQWKPPHEREE----DERRPGEWRPPRGGRQEGQEQRPGQWRPSHEREED-
EEDEHQKRRPGQWRPTRGGRQEGQEQRPGRFPSEREEYDEDDRRERRPGQQRPTREGRW----------------
-----------------------------KGQEQRPEQWRPSRGKEEREKEERQKHQPGREREKWEKRE------
-------DEEWRGRQRHEDPDER---ARLRHREER-------
RQKEEEHQKGDRPSRTPSRRERGEEEEGSSESEGRRNPFLFRSN--R-FQTL-FENENGHIRL-IQRFDKR-
SNL-FQNLKN-----------YRLLEYRAKPHTIFLPHHTDADFILVVLSG-KAILTVLNSNN-RNS---
FNLEQG-----DTIKLPAGSTAYLVNQDN-D-----EDLRVVDLVIP---VNRPGKF-QSF--
DLSGNQNNPSYFRGFSKSILEASFN-TDY--ETIERVLLEEHEHEQQQRRGRKGRQQSQ----------------
------------------EANAIVKVSREQIEELRRHAKSSS-----------------KRSISSE---
SGPFNLRNRNP--LYSNKFGKFFEITPEK-N-PQLQD--LDIFVSSVEINE-
GALILPHYNSRSTVVLVMNEGKG---HLELVGHKSE------QQEQR----EQDEKE------------------
-------------LR---NPEVQRYNARLSPGDVVIIPAGHPVAINAS----SNLNFLGFGINAEN-----
NQRNFLAGEDDNVISQIER-----PVKEVAFP-GS---AEEVDRLI--KNQRQSYFANAQPQQREEGSQKRK---
-----------------------------------------------------------------------G---
----PLLSI------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LSTLY

Pisum sativum                          >TR|Q9M3X6|              MA--------
-TTIKSRFPL-----LLLLGIIFLASVVCVTYA------------------------------------------
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-------------------------------------------NYDEGSEPRVPAQ---RERGRQEGEK------
--------EEKRH----GEWRPSYEKEEDEEEGQRERGRQEGEKEEKRHGEWRPSYEKQEDEEEK-----
QKYRYQREKEDEEEKQKYQYQREKKEQKEVQPGR--ERWER-------EEDE-EQVDEEWRGSQRREDPEER---
ARLRHR-----------EERTKRDRRHQREG--------EEEERSSESQERRNPFLFKSN--K-FLTL-
FENENGHIRL-LQRFDKR-SDL-FENLQN-----------YRLVEYRAKPHTIFLPQHIDADLILVVLSG-
KAILTVLSPND-RNS---YNLERG-----DTIKLPAGTTSYLVNQDD-E-----EDLRLVDLVIP---
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VNGPGKF-EAF--DLAKNKNQ--YLRGFSKNILEASYN-TRY--ETIEKVLLEEQEK------DRKRRQQGE---
-------------------------------ETDAIVKVSREQIEELKKLAKSSS-----------------
KKSLPSE---FEPINLRSHKP--EYSNKFGKLFEITPEK-KYPQLQD--LDLFVSCVEINE-
GALMLPHYNSRAIVVLLVNEGKG---NLELLGLKNE------QQEREDRK-------------------------
-------------ER---NNEVQRYEARLSPGDVVIIPAGHPVAITAS----SNLNLLGFGINAEN-----
NERNFLSGSDDNVISQIEN-----PVKELTFP-GS---VQEINRLI--KNQKQSHFANAEPEQKEQGSQGKR---
-----------------------------------------------------------------------S---
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LGTFY

Pisum sativum                           >PRF|1713472A|           MA--------
-TTIKSRFPL-----LLLLGIIFLASVVSVTYA------------------------------------------
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-------------------------------------------NYDEGSEPRVPAQ---RERGRQEGEK------
--------EEKRH----GEWRPSYEKEEDEEEGQRERGRQEGEKEEKRHGEWGPSYEKQEDEEEK-----
QKYRYQREKEDEEEKQKYQYQREKKEQKEVQPGR--ERWER-------EEDE-EQVDEEWRGSQRREDPEER---
ARLRHR-----------EERTKRDRRHQREG--------EEEERSSESQERRNPFLFKSN--K-FLTL-
FENENGHIRL-LQRFDKR-SDL-FENLQN-----------YRLVEYRARPHTIFLPQHIDADLILVVLNG-
KAILTVLSPND-RNS---YNLERG-----DTIKLPAGTTSYLVNQDD-E-----EDLRLVDLVIP---
VNGPGKF-EAF--DLAKNKNQ--YLRGFSKNILEASYN-TKY--ETIEKVLLEEQEK------EPQQRR------
----------------------------------AIVKVSREQIEELRKLAKSSS-----------------
KKSLPSE---FEPINLRSHKP--EYSNKFGKLFEITPEK-KYPQLQD--LDLFVSCVEINE-
GALMLPHYNSRAIVVLLVNEGKG---NLELLGLKDE------QQEREDRK-------------------------
-------------ER---NNEVQRYEARLSPGDVVIIPAGHPVAITAS----SNLNLLAFGINAEN-----
NERNFLSGSDDNVISQIEN-----PVKELTFP-RS---VQEINRLI--KNQKQSHFANAEPEQKEQGSQGKR---
-----------------------------------------------------------------------S---
----PLSSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LGTFY

Pisum sativum                           >SP|P13915|              MA--------
-TTVKSRFPL-----LLFLGIIFLASV-CVTYA------------------------------------------
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-------------------------------------------NYDEGSETRVPGQ---RERGRQEGEK------
--------EEKRH----GEWRPSYEKEEHEEE-------------------------------------------
---------KQKYRYQREKKEQKEVQPGR--ERWER-------EEDE-EQVEEEWRGSQRREDPEER---
ARLRHR-----------EERTKRDRRHQREG--------EEEERSSESQEHRNPFLFKSN--K-FLTL-
FENENGHIRR-LQRFDKR-SDL-FENLQN-----------YRLVEYRAKPHTIFLPQHIDADLILVVLNG-
KAILTVLSPND-RNS---YNLERG-----DTIKIPAGTTSYLVNQDD-E-----EDLRVVDFVIP---
VNRPGKF-EAF--GLSENKNQ--YLRGFSKNILEASLN-TKY--ETIEKVLLEEQEKKPQQLRDRKRTQQGE---
-------------------------------ERDAIIKVSREQIEELRKLAKSSS-----------------
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KKSLPSE---FEPFNLRSHKP--EYSNKFGKLFEITPEK-KYPQLQD--LDILVSCVEINK-
GALMLPHYNSRAIVVLLVNEGKG---NLELLGLKNE------QQEREDRK-------------------------
-------------ER---NNEVQRYEARLSPGDVVIIPAGHPVAISAS----SNLNLLGFGINAKN-----
NQRNFLSGSDDNVISQIEN-----PVKELTFP-GS---SQEVNRLI--KNQKQSHFASAEPEQKEEESQRKR---
-----------------------------------------------------------------------S---
----PLSSV------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LDSFY

Vicia narbonensis                       >TR|Q41674|              MA--------
-TAMKSRFPV-----LLLLGIIILASL-CVTYA------------------------------------------
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-------------------------------------------NYDEGTEPRVPGQ---RERGRQEGEK------
--------EEKRH----GEWRPSHE--------------------------------------------------
----------------------KEAQPGR-RERWETS-------EEE-ERVDEEWRGSQRHEDPEER---
ARERYR-----------AE--ERERRRQWEG--------EEKEGSSKSQERRNPFLFKSN--K-FLTL-
FENENGHIRR-LQRFDKR-SDL-FENLQN-----------YRLVEYRAKPHTIFLPQHIDADLILTVLSG-
RAILTVLSPND-RNS---YNLERG-----DTIKLPAGTTSYLLNQDD-E-----EDLRVVDLSIS---
VNRPGKV-ESF--GLSGSKNQ--YLRGFSKNILEASLN-TKY--ETIEKVLLEEPQQSIG----QKRRSQRQ---
-------------------------------ETNALVKVSREQVEELKRLAKSSS-----------------
KKGVSSE---FEPFNLRSQNP--KYSNKFGKLFEITPEK-KYPQLQD--LDIFVSSVEINE-
GGLMLPHYNSRAIVILLVNEGKG---NLELVGLKNE------QQEQRERE-------------------------
-------------D----EQQVQRYEARLSPGDVVIIPAGHPVAVSAS----SNLNLLGFGINAEN-----
NQRNFLTGSDDNVISQIEN-----PVKELTFP-GS---AQEVNRLL--KNQEHSHFANAEPEQKGEESQRKR---
-----------------------------------------------------------------------S---
----PISSI------------------------------------------------------------------
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----------------------------------LGTFN

Lupinus angustifolius                   >TR|F5B8W2|              MIK-------
---MRVRFPTL----VLLLGIVFLMAVSIGIAYG-----------------------------------------
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EKNVIKNHERPQEREQEERDPRQQPRPHHQEEQEREHRREEERDREPSRGRSESEESREEEREQRREPRRERE--
-----------------------------------------------------QEQQPQHGRREEEEE-------
WQPRRQRPQSRREERE----QEQGSSSSSRRQSG------YERRE---EREQ-----------------------
----EQEQGSRSDSRRQRNPYYFSSE--R-FQTL-YRNRNGQIRV-LERFDQR-TD-RLENLQN-----------
YRIVEFQSKPNTLILPKHSDADYILVVLNG-SATITIVNP-DKRQS---YNLENG-----
DALRLPAGTTSYILNPDD-N-----QNLRVVKLAIP---INNPGNFYD-F--
YPSSSKDQQSYFSGFSRNTLEATFN-TRY--EEIQRILLGNEDEQEDD-----EQRHGQEQS-------------
----------------HQDEGVIVRVSKEQVQELRKYAQSSS-----------------RKGKPSK---
SGPFNLRSNKP--IYSNKFGNFYEITPNR-N-PQAQD--LDISLTFIEINE-
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GALLLPHYNSKAIFVVLVDEGEG---NYELVGIRDQ------QRQQDEQE-------------------------
---------------------VRRYSARLSEGDIFVIPAGHPISINAS----SNLRLLGFGINADE-----
NQRNFLAGSEDNVIRQLDT-----EVKGLTFP-GS---TEDVERLI--KNQQQSYFANAQPQQQQQ-R-EREGR-
-------------------------------------------------------------------RGRRGH--
-----ISSI------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LSTLY

Lupinus angustifolius                   >TR|F5B8W4|              MIK-------
---MRVRFPTL----VLLLGIVFLMAVSIGIAYG------------------------------------------
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EKNVIKNHERPQEREQEERDPRQQPRPHHQEEQEREHRREEERDREPSRGRRESEESREEEREQRREPRRERE--
-----------------------------------------------------QEQQPQHGRREEEEE-------
WQPRRQRPQSRREERE----QEQGSSSSSRRQSA------YERREQREEREQ-----------------------
----EQEQGSRSDSRRQRNPYYFSSE--R-FQTL-YRNRNGQIRV-LERFDKR-TD-RLENLQN-----------
YRIVEFQSKPNTLILPKHSDADYILVVLNG-SATITIVNP-DKRQS---YNLENG-----
DALRLPAGTTSYILNPDD-N-----QNLRVVKLAIP---INNPGNFYD-F--
YPSSSKDQQSYFSGFSRNTLEATFN-TRY--EEIQRILLGNEDEQEDD-----EQRHGQEQS-------------
----------------HQDEGVIVRVSKEQVQELRKYAQSSS-----------------RKGKPSK---
SGPFNLRSNKP--IYSNKFGNFYEITPNR-N-PQAQD--LDISLTFIEINE-
GALLLPHYNSKAIFVVLVDEGEG---NYELVGIRDQ------QRQQDEQE-------------------------
---------------------VRRYSARLSEGDIFVIPAGHPISINAS----SNFRLLGFGINADE-----
NQRNFLAGFEDNVIRQLDR-----EVKGLTFP-GF---AEDVERLI--KNQQQSYFANAQPQQQQQ-R-EREGR-
-------------------------------------------------------------------HGRRGH--
-----IFSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LSTLY

Lupinus angustifolius                   >TR|F5B8W1|              MAK-------
---MRVRFPTL----VLLLGIVFLMAVSIGIAYG------------------------------------------
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-----------------------------EKNVLKNHERPQEREQEERDPRQQPRPHHQEEQEREHRRE------
-------SEESQEEEREQRREPRRERE------------------------------------------------
-------QEQQPQHGRREEEEE-------WQPRRQRPQSRREERE----QEQGSSSSSRRQSG------
YERREQREEREQ---------------------------EQEQGSRSDSRRQRNPYYFSSE--R-FQTL-
YRNRNGQIRV-LERFDQR-TN-RLENLQN-----------YRIVEFQSKPNTLILPKHSDADYILVVLNG-
SATITIVNP-DKRQS---YNLENG-----DALRLPAGTTSYILNPDD-N-----QNLRVVKLAIP---
INNPGNFYD-F--YPSSSKDQQSYFSGFSKNTLEATFN-TRY--EEIQSILLGNEDEQEDD-----
EQWHGQEQS-----------------------------HQDEGVIVRVSKEQVQELRKYAQSSS-----------
------RKGKPYE---SGPFNLRSNKP--IYSNKFGNFYEITPDR-N-PQAQD--LDISLTFIEINE-
GALLLPHYNSKAIFVVVVDEGEG---NYELVGIRDQ------QRQQDEQE-------------------------
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---------------------VRRYSARLSEGDIFVIPAGHPISINAS----SNLRLLGFGINADE-----
NQRNFLAGSEDNVIRQLDR-----EVKGLIFP-GS---AEDVERLI--KNQQQSYFANAQPQQQQQ-R-EREGR-
-------------------------------------------------------------------HGRRGH--
-----ISSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LSTLY

Lupinus angustifolius                   >TR|F5B8W0|              MAN-------
---MRVKFPTL----VLLLGIVFLMAVSIGIAYG-----------------------------------------
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EKNAIKNHERPQEREQEERDPRQQPRPRHQEEQEREHGREEERNREPSRGRSESEESREEEREQRREPSRGRE--
-----------------------------------------------------QEQQPQHGRREEEEE-------
WQPRRQRPQSRREERE----QEQGSSSSSGRQSG------YERREQREEREQ-----------------------
----QQEQDSRSESRRQRNPYYFSYE--R-FQTL-YKNRNGQIRV-LERFDQR-TN-RLENLQN-----------
YRIVEFQSKPNTLILPKHSDADYILVVLNG-RATITIVNP-DKRQA---YNLEHG-----
DALRLPAGTTSYILNPDD-N-----QNLRVVKLAIP---INNPGNFYD-F--
YPSSTKDQQSYFNGFSRNTLEATFN-TRY--EEIQRIILGNEDGQEDE-----EQSRGQEQS-------------
----------------HQDQGVIVRVSKEQIQELRKHAQSSS-----------------GKGKPSE---
SGPFNLRSDEP--IYSNKFGNFYEITPDR-N-PQAQD--LDISLTFIEINE-
GGLLLPHYNSKAIFVVVVDEGEG---NYELVGIRDQ------ERQQDEQE------QE-----------------
------------------E--VRRYNAKLSEGDIFVIPAGHPISINAS----SNLRLLGFGINADE-----
NQRNFLAGSEDNVIRQLDK-----EVKQLTFP-GS---VEDVERLI--KNQQQSYFANAQPQQQQQ-R-EKEGR-
-------------------------------------------------------------------
RGRRGLSFPFRSLFTKL----------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
------------------------------------------LSTIM

Lupinus angustifolius                   >TR|F5B8W5|              MAR-------
---MRVRFPTL----VLLLGILFLMAVSIGIAYG-----------------------------------------
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EKDVIKNHERPGEREHEERDPRQQPRPRKQEEQEREHRREEEHDRDPSRGRRESEERQEEERERRREPCRERE--
-----------------------------------------------------QEQQPQHGRREEEEE----
EEEWQPRRLRPQSRKEERE----QEQGSSSSSRKQSG------YERRQYHERREQ--------------------
---RDEKEKEQDSRSDSRRQRNPYHFSSE--R-FQTR-YRNRNGQIRV-LERFDQR-TN-RLENLQN--------
---YRIVEFQSNPNTLILPKHSDADYILVVLNG-RATITIVNP-DKRQA---YNLEYG-----
DALRVPAGTTSYILNPDD-N-----QNLRVVKLAIP---INNPSNFYD-F--
YPSSTKDQQSYFSGFSKNTLEATFN-TRY--EEIQRILLGNEDEQEDE-----EQRRGQEQS-------------
----------------YQDEGVIVRVSKEQIQELRKHAQSSS-----------------RKGKPSE---
SGPFNLRSNES--IYSNKFGNFYEITPER-N-PQVQD--LDISLTFTEINE-
GALLLPHYNSKAIFIVVVDEGEG---NYELVGIRDQ------QRQQDEQE------EE-----------------
```

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------------------EEEVRRYSARLSEGDIFVIPAGYPISVNAS----SNLRLLGFGINANE-----
NQRNFLAGSEDNVISQLDR-----EVKELTFP-GS---AQDVERLI--KNQQQSYFANAQPQQKQQ-R-EKEGR-
-------------------------------------------------------------------RGRRS---
----LISSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LSTLY

Lupinus angustifolius                   >TR|F5B8W3|              MAK-------
---MRVRFPML----VLLLGVVFLLAVSIGIAYG-----------------------------------------
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EKDVIKNPERPEERQEEERDPRQPPRSRQQEEQEREHRREKERDREPSRGRSESKQSQEEERERRKEHDRERE--
-----------------------------------------------------
QEQQPQYGRRHEEEEKGEEEEEGQARRQRPQRRREERE----
QEQGSSSESRRQSGDERRHRHEKREQREEREQEQGSSSGRQSDYGRRQRHEGREQREEREQEQGSSSESHRLRNP
YYFSSE--R-FQTR-YKNKNGQIRV-LERFDQR-TN-RLENLQN-----------
YRIVEFQSRPNTLILPKHSDADYILVVLNG-RATITIVNP-DKRQA---YNLEYG-----
DALRLPAGTTSYILNPDD-N-----QDLRVVKLAIP---INNPGKFYD-F--
YPSRTKDQQSYFSGFSKNTLEATFN-THY--EEIQRILLGYEDEQEDE-----EQRREQEQS-------------
----------------HQDEGVIVRVSKEQIQELRKHAQSSS-----------------RKGKPSE---
SGPFNLRSNEP--IYSNKFGNFYEITPDR-N-PQVQD--LDISLIFTEISE-
GALLLPHYNSKAIFVIVVDEGEG---NYELVGIRNQ------QRQQDEQE------VE-----------------
------------------E--VRSYNARLSEGDILVIPAGHPLSINAS----SNLRLLGFGINADE-----
NQRNFLAGSEDNVIRQLDR-----EVKELIFP-GS---AEDVERLI--RNQQQSYFANAQPQQQQQR-EKEGR-
-------------------------------------------------------------------RGRRG---
----PISSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
----------------------------------LSALY

Lupinus angustifolius                   >TR|F5B8V9|              MAK-------
---MRVRLPML----ILLLGVVFLLAASIGIAYG-----------------------------------------
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-----------------------------EKDFTKNP--
PKEREEEEHEPRQQPRPRQQEEQEREHRREEKHDGEPSRGRSQSEESQEEEHERRREHHRERE------------
-------------------------------------------QEQQPRPQRRQEEEE---
EEEEWQPRRQRPQSRREEREER-EQEQGSSSGSQRGSGDERRQHRERRVHREEREQ-------------------
----------EQDSRSDSRRQRNPYHFSSN--R-FQTY-YRNRNGQIRV-LERFNQR-TN-RLENLQN-------
----YRIIEFQSKPNTLILPKHSDADFILVVLNG-RATITIVNP-DKRQV---YNLEQG-----
DALRLPAGTTSYILNPDD-N-----QNLRVAKLAIP---INNPGKLYD-F--
YPSTTKDQQSYFSGFSKNTLEATFN-TRY--EEIERVLLGDDELQENE-----KQRRGQEQS-------------
----------------HQDEGVIVRVSKKQIQELRKHAQSSS-----------------GEGKPSE---
SGPFNLRSNKP--IYSNKFGNFYEITPDI-N-PQFQD--LNISLTFTEINE-
```

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GALLLPHYNSKAIFIVVVDEGEG---NYELVGIRDQ------QRQQDEQE------EEYE---------------
-------------QG---EEEVRRYSDKLSKGDVFIIPAGHPLSINAS----SNLRLLGFGINANE-----
NQRNFLAGSEDNVIKQLDR-----EVKELTFP-GS---IEDVERLI--KNQQQSYFANAQPQQQQQ-R-EKEGR-
-------------------------------------------------------------------RGRRG---
----PISSI------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
---------------------------------------------------------------------------
----------------------------------LNALY

Lupinus albus                           >TR|Q53HY0|              MGK-------
---MRVRFPTL----VLVLGIVFLMAVSIGIAYG-----------------------------------------
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-----------------------------EKDVLKSHERPEEREQEE----------------------------
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-----------------------------WQPRRQRPQSRREEREQ--
EQEQGSPSYPRRQSGYERRQYHERSEQREEREQ---------------------------
EQQQGSPSYSRRQRNPYHFNSQ--R-FQTL-YKNRNGKIRV-LERFDQR-TN-RLENLQN-----------
YRIVEFQSKPNTLILPKHSDADYVLVVLNG-RATITIVNP-DRRQA---YNLEYG-----
DALRIPAGSTSYILNPDD-N-----QKLRVVKLAIP---INNPGYFYD-F--
YPSSTKDQQSYFSGFSRNTLEATFN-TRY--EEIQRILLGNEDEQEYE-----EQRRGQEQS-------------
----------------HQDEGVIVRVSREQIQELTKYAQSSS-----------------GKDKPSQ---
SGPFNLRSNEP--IYSNKYGNFYEITPDR-N-PQVQD--LDISLTFTEINE-
GALLLPHYNSKAIFIVVVGEGNG---KYELVGIRDQ------QRQQDEQE------EE-----------------
------------------PEEVRRYSARLSEGDIFVIPAGYPISVNAS----SNLRLLGFGINAYE-----
NQRNFLAGSEDNVIRQLDR-----EVKELTFP-GS---AEDIERLI--KNQQQSYFANALPQQQQQ--SEKEGR-
-------------------------------------------------------------------RGRRGP--
---------------------------------------------------------------------------
---------------------------------------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------ISSI

Lupinus albus                           >TR|Q6EBC1|              MGK-------
---MRVRFPTL----VLVLGIVFLMAVSIGIAYG-----------------------------------------
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---------------------------------------------------------------------------
-----------------------------EKDVLKSHERPEEREQEE----------------------------
---------------------------------------------------------------------------
-----------------------------WQPRRQRPQSRREEREQ--
EQEQGSPSYPRRQSGYERRQYHERSEQREEREQ---------------------------
EQQQGSPSYSRRQRNPYHFSSQ--R-FQTL-YKNRNGKIRV-LERFDQR-TN-RLENLQN-----------
YRIVEFQSKPNTLILPKHSDADYVLVVLNG-RATITIVNP-DRRQA---YNLEYG-----
DALRIPAGSTSYILNPDD-N-----QKLRVVKLAIP---INNPGYFYD-F--
YPSSTKDQQSYFSGFSRNTLEATFN-TRY--EEIQRIILGNEDEQEYE-----EQRRGQEQS-------------
----------------DQDEGVIVIVSKKQIQKLTKHAQSSS-----------------GKDKPSD---
SGPFNLRSNEP--IYSNKYGNFYEITPDR-N-PQVQD--LNISLTYIKINE-
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GALLLPHYNSKAIYVVVVDEGEG---NYELVGIRDQ------QRQQDEQE------EK-----------------
------------------EEEVIRYSARLSEGDIFVIPAGYPISINAS----SNLRLLGFGINADE-----
NQRNFLAGSKDNVIRQLDR-----AVNELTFP-GS---AEDIERLI--KNQQQSYFANGQPQQQQQQQSEKEGR-
-------------------------------------------------------------------RGRRGS--
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---------------------------------------------------------------------------
-----------------------------------SLPF

Camelina sativa                         >REF|XP_010467681.1|     M---------
-------SRSTLLPLSVFVYLITLFLCTQSFPDQNGLVSS---SFSSSL--------------------------
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-------------------------------------------------LFKR-DQ----
RMPIVTTEFGEISAVQ-----------------IGDG-------YHLQFITLEPNALLLPLLLHSDMVLFVHTG-
TGTLNWVE----EESERTLELRRG-----DVYRLRSGSVFYVHSNLE--KEKVQEKLRVYAIF-DVG---K--
CLSDPC---LGAYSSIRDLLLGFDDRTLRSAFAV---HGDVLKKIRD----AAKPPLIINALP------------
------------------------RNRTQGSEEDKWQ--SRLVRLFVRVEDVADHLAMKPIGDANKKKT-----
R----TFNVF--ESDPDFENNNGRSIVVDDKDLD--ALKG--SRFGVFMVNLTE-
GSMMAPHWNPSAFEISIVLQGE-GM--IRVVNQRSLSSCKN----------------N-----------------
--------------------SKSE-RFMVEEGDVFVVPKFHPMAQMSFE--NSSFVFMGFSTSVKT-----
NHPQFLVGQ-NSVLKVLDR-----EVLAVSFNL---NNET-IKGLLEA--
QKESVILDCVSCAEGELAKLTREIE----ERERREEEEIERKRKEA--EE-RKR--EEEEKRRREEEE-------
----------------RRREEEEA----------ERRRKEE----EEARKREEERKRE---
EEEAKRREEERKKREEEA--------EEARKREEE----REREEEKAKRQEEERRRR----EEEE----------
-----KEARKREEEREKEEEMAKKRE-QERQQREREEVERKKR-EEEARKRE-EEMAKRRE---------
EQERKRREEE------EMARRREQERQRKEKEEVER-----------------KRREEE---------AMR----
------------------------------REEERKKEE------------------------
EAARRAEEERRKREEE-----------------------------------------------------
EAKRRWPPQ-PRPPFSTVGNMA-GVS

Camelina sativa                         >REF|XP_010414399.1|     M---------
-------SRSTLLPLSVFVYLITLFLCTQSFPDQNGLVSS---SFSSPL--------------------------
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---------------------------------------------------------------------------
-------------------------------------------------LVKR-DQ----
RMPIVTTDFGEISAVQ-----------------IGDG-------YHLQFITLEPNALLLPLLLHSDMVLFVHTG-
SGTLNWVE----EESERRLELRRG-----DVYRLRSGSVFYVHSDLE--RDDVQEKLRVYAIF-DVG---K--
CLNDPC---LGAYSSIRDLLLGFDDRTLRSAFAV---HGDVLSKIRD----AAKPPLIINALP------------
------------------------KNRTQGSEEDKWQ--SRLVRLFVRVEDVADHLAMKPIVDANKKKT-----
R----TFNVF--ESDPDFENNNGRSIVVDDKDLD--ALKG--SRFGFFMVNLTE-
GSMMAPHWNPSACEISIVLQGE-GM--IRVVNQQSLSSCKN----------------N-----------------
```

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--------------------SNSE-RFMVEEGDVFVVPKFHPMAQMSFE--NSSFVFMGFSTSVKA-----
NHPQFLVGQ-SSVLKVLDR-----EVLAVSFNL---NNET-IKGLLEA--
QKESVILDCVSCAEGELAKLTREIE----ERKRREEEEIERKRKEA--EE-
RKRKREEEEKRRREEEEAERRRKEEEARRREEERKREEEKRRREEEEA----------ERRRKEE----
EEARRREEERKRE---EEEAKRREEERKKREEEA--------EEARKREEE----REREKEKAKRQEEERRRR--
--EEEE---------------KEARKREEEREKEEEMAKKRE-EERQQREREEVERKKR-EEEARKRE-
EEMAKRRE---------EQERKRREEE------EMAKRQEEARHRKEKEEVER-----------------
KRREEE---------AMR----------------------------------REEERKKEE--------------
----------EAARRAEEERRKREEE-------------------------------------------------
----EAKRRWPPQ-PQPPFSTMGNMV-GVS

Camelina sativa                         >REF|XP_010489556.1|     M---------
-------SRSTLLPLSVFVYLIT-FLCTQSFPDQNGLVSS---SFSSPL--------------------------
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---------------------------------------------------------------------------
-------------------------------------------------LVKR-DQ----
RTPIVTTEFGEISAVQ-----------------IGDG-------YHLQFITLEPNALLLPLLLHSDMVLFVHTG-
SGTLNWVE----EESERTLELRRG-----DVYRLRSGSVFYVHSDFE--RDEVQEKLTVYAIF-DVG---K--
CLNDLC---LGAYSSIRDLVLGFDDSTLRSAFAV---HGDVLRKIRG----AAKPPLIINALP------------
------------------------KNRTQGSEEDKWK--SRLVRLFVGVEDVADHLAMKPIVDANKKKR-----
R----TFNVF--ESDPDFENNNGRSIVVDDKDLD--ALKG--SRFGVFMVNLTE-
GSMMAPHWNPSACEISIVLQGE-GM--IRVVNQQSLSSCKN----------------N-----------------
--------------------SNSE-RFMVEEGDVFVVPKFHPMAQMSFE--NSSFVFMGFSTSVKT-----
NHPQFLVGQ-SSVLKVLDR-----EILAVSFNL---NNET-IKGLLEA--
QKESVILDCVSCAEGELAKLTREIE----ERERREEEEIERKRKEA--EE-RKR--EEEEKRRREEEE-------
-----------------------------------RRRKEE----EEARRREEERKRE---
EEEAKRREEERKKREEEA--------EEARQREEE----REREEEKAKRQEEERRRR----EEEE----------
-----KEARKREEEREKEEEMAKKRE-EERQQREREEVERKKR-EEEARKRE-EEMAKRRE---------
EQERKRREEE------EMAKRREQERQRKEKEEVER-----------------KRREEE---------AMR----
------------------------------REEERKKEE------------------------
EAARRAEEERRKREEEMGKRREQERQRKEKEEVERKRREEEAMRREEERKKEEEAARRAEEERRKREEEEAKRRW
PPQ-PQPPFSTVGNMA-GVS

Arabidopsis thaliana                    >TR|Q9ZU69|              MQ--------
----QTMSRFRILPLSIFLCFVSLFFCTESFTHQNGVVPSFDPSYSSPL--------------------------
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---------------------------------------------------------------------------
-------------------------------------------------LVKK-DQ----
RTSVVATEFGNISAVQ-----------------IGDG-------YHIQFITLEPNALLLPLLLHSDMVFFVHTG-
TSKHSSTF----VFSKKLLIGPKN-----------------LKPN---------EKLRVYAIF-NVG---K--
CLNDPC---LGAYSSVRDLLLGFDDRTLRSAFAV---PEDILRKIRD----ATKPPLIVNALP------------
------------------------RNRTQGLEEDKWQ--SRLVRLFVSVEDVTDHLAMKPIVDTNKKKS-----
R----TFNVF--EEDPDFENNNGRSIVVDEKDLD--ALKG--SRFGVFMVNLTK-
GSMIGPHWNPSACEISIVLEGE-GM--VRVVNQQSLSSCKN----------------D-----------------
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--------------------RKSE-SFMVEEGDVFVVPKFHPMAQMSFE--NSSFVFMGFSTSAKT-----
NHPQFLVGQ-SSVLKVLDR-----DVVAVSFNL---SNET-IKGLLKA--
QKESVIFECASCAEGELSKLMREIE----ERKRREEEEIERRRKEE--EEARKR----EEAKRREEEEA------
----------------KRREEEET----------ERKKREE----EEARKREEERKRE---
EEEAKRREEERKKREEEA--------EQARKREEE----REKEEEMAKKREEERQRK----
EREEVERKRREEQERKRREEEARKREEERKREEEMAKRRE-QERQRKEREEVERKIR-EEQERKRE-
EEMAKRREQERQKKEREEMERKKREEEARKREEEMAKIREEERQRKEREDVER-----------------
KRREEE---------AMR----------------------------------REEERKREE--------------
----------EAAKRAEEERRKKEEE-------------------------------------------------
----EEKRRWPPQ-PKPPEEI---------

Arabidopsis thaliana                    >TR|F4IQK5|              M---------
-------SRFRILPLSIFLCFVSLFFCTESFTHQNGVVPSFDPSYSSPL--------------------------
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---------------------------------------------------------------------------
-------------------------------------------------LVKK-DQ----
RTSVVATEFGNISAVQ-----------------IGDG-------YHIQFITLEPNALLLPLLLHSDMVFFVHTG-
TGILNWID----EESERKLELRRG-----DVFRLRSGTVFYVHSN---------EKLRVYAIF-NVG---K--
CLNDPC---LGAYSSVRDLLLGFDDRTLRSAFAV---PEDILRKIRD----ATKPPLIVNALP------------
------------------------RNRTQGLEEDKWQ--SRLVRLFVSVEDVTDHLAMKPIVDTNKKKS-----
R----TFNVF--EEDPDFENNNGRSIVVDEKDLD--ALKG--SRFGVFMVNLTK-
GSMIGPHWNPSACEISIVLEGE-GM--VRVVNQQSLSSCKN----------------D-----------------
--------------------RKSE-SFMVEEGDVFVVPKFHPMAQMSFE--NSSFVFMGFSTSAKT-----
NHPQFLVGQ-SSVLKVLDR-----DVVAVSFNL---SNET-IKGLLKA--
QKESVIFECASCAEGELSKLMREIE----ERKRREEEEIERRRKEE--EEARKR----EEAKRREEEEA------
----------------KRREEEET----------ERKKREE----EEARKREEERKRE---
EEEAKRREEERKKREEEA--------EQARKREEE----REKEEEMAKKREEERQRK----
EREEVERKRREEQERKRREEEARKREEERKREEEMAKRRE-QERQRKEREEVERKIR-EEQERKRE-
EEMAKRREQERQKKEREEMERKKREEEARKREEEMAKIREEERQRKEREDVER-----------------
KRREEE---------AMR----------------------------------REEERKREE--------------
----------EAAKRAEEERRKKEEE-------------------------------------------------
----EEKRRWPPQ-PKPPEEI---------

Brassica rapa subsp. pekinensis         >TR|M4E6Q7|              M---------
-------SKFTIIPL----CLLTLFLCTNSFSDQNDGVPSS----QSPL--------------------------
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-------------------------------------------------LVKR-HQ----
RTQLVATEFGEISAVH-----------------IGEE-------YTIQFITLEPNALLLPLLLHSDMVFFVHTG-
SGVLNWVD----EEKERTLELKRG-----DVFRLRYGTVFYLHCNLE--RDEVPEKLRVYAIF-DVG---K--
CLSDQC---LGAYSSIRDLLWGFDEKTLRSAFAV---PKDVFGRLRD----AVKPPLITHAMP------------
------------------------KNRTQGSEEETWG--SRLAKLFVRVED------------------------
-----------------------SIVVDEKDMD--ALKG--SSFGVYMVNLTK-
GSMMGPHWNPNACEISIVLQGE-GM--IRVVNHPSYQS-KN----------------E-----------------
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----------------------SE-RFMVEDGDVFVVPQFYPMAQLSFV--NSSFMFMGFSTSAKT-----
NHPQFLVGQ-NSVLKIFNR-----DVLATSFNM---RYAT-VERLLGA--
QKDGLLLECVSCAEVELSRLMREIE----ERRRREEEEIERRKREE--EEA----------KRQEEER-------
----------------RRREEEEA----------ERKKKAE----EEARKREKERERE---
EEAAKRREEERRRREEEEAERKRKEEEEARKREEE----RKREEEAAKKREEERRKR----EKEE----------
-----EEARKREEAREREEEEAKKRE-EERRKREEEEAERKRRAEEEARERE-EEEAKKRE--------
EEKEAARRREEEREKEEEMAKRREEERQRKEREDVER-----------------KKREEEEERKRREEEAMR---
-------------------------------REEERKREE------------------------
EAAKRAEEERRKREEEA----------------------------------------------------
EHKKRPPPQGPQPPIH---------H

Brassica rapa                           >REF|XP_009150727.1|     M---------
-------SKFTIIPL----CLLTLFLCTNSFSDQNDGVPSS----QSPL--------------------------
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---------------------------------------------------------------------------
-------------------------------------------------LVKR-HQ----
RTQLVATEFGEISAVH-----------------IGEE-------YTIQFITLEPNALLLPLLLHSDMVFFVHTG-
SGVLNWVD----EEKERTLELKRG-----DVFRLRYGTVFYLHCNLE--RDEVPEKLRVYAIF-DVG---K--
CLSDQC---LGAYSSIRDLLWGFDEKTLRSAFAV---PKDVFGRLRD----AVKPPLITHAMP------------
------------------------KNRTQGSEEETWG--SRLAKLFVRVEDVTDHLEMKPVVNKKKKKK-----
KKKSSAYNVF--ESDPDFENDNGQSIVVDEKDMD--ALKG--SSFGVYMVNLTK-
GSMMGPHWNPNACEISIVLQGE-GM--IRVVNHPSYQS-KN----------------E-----------------
----------------------SE-RFMVEDGDVFVVPQFYPMAQLSFV--NSSFMFMGFSTSAKT-----
NHPQFLVGQ-NSVLKIFNR-----DVLATSFNM---RYAT-VERLLGA--
QKDGLLLECVSCAEVELSRLMREIE----ERRRREEEEIERRKREE--EEA----------KRQEEER-------
----------------RRREEEEA----------ERKKKAE----EEARKREKERERE---
EEAAKRREEERRRREEEEAERKRKEEEEARKREEE----RKREEEAAKKREEERRKR----EKEE----------
-----EEARKREEAREREEEEAKKRE-EERRKREEEEAERKRRAEEEARERE-EEEAKKRE--------
EEKEAARRREEEREKEEEMAKRREEERQRKEREDVER-----------------KKREEEEERKRREEEAMR---
-------------------------------REEERKREE------------------------
EAAKRAEEERRKREEEA----------------------------------------------------
EHKKRPPPQGPQPPIH---------H

Brassica oleracea var. oleracea         >TR|A0A0D3BEH9|          M---------
-------SKFTTIPL----CLLTLFLCTNSFSDQNDGVPSS----QSPL--------------------------
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---------------------------------------------------------------------------
-------------------------------------------------LVRR-HQ----
RTQLVATEFGEISAVH-----------------IGEE-------YTIQFITLEPNALLLPLLLHSDMVFFVHTG-
SGVLNWLD----KEKERTLELKRG-----DVFRLRYGTVFYLHCNLE--RDEVPDKLRVYAIF-DVG---K--
CLSDQC---LGAYSSIRDLLWGFDEKTLRSAFAV---PKDVFGRLRD----AVKPPLITHAMP------------
------------------------KNRTQGSEEETWG--SRLAKLFVRVEDVTDHLEMKPVVNKKKKKK------
--SSAYNVF--ESDPDFENDNGQSIVVDEKDMD--ALKG--SSFGVYMVNLTK-
GSMMGPHWNPNACEISIVLQGE-GM--IRVVNHPSYQS-KN----------------E-----------------
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----------------------SE-RFMVEDGDVFVVPQFYPMAQLSFV--NSSFMFMGFSTSAKT-----
NHPQFLVGQ-NSVLKIFNR-----DVLATSFNM---RYET-VERLLGA--
QKHGLMLECVSCAEVELSRLMREIE----ERRRREEEEIERRKRKR--EEA----------RRQEEER-------
----------------RRREEEEA----------ERKRKAE----EEARKREEERERE---
EEAAKRREEERRRREEEEAERKRKEEEEARKREEE----RKREEEAAKKREEERRKR----EKEE----------
-----EEARKREEAREREEEEAKKRDIEERRKREEEEAERKRKAEEEARQRE-EAREREEE--------
EEKEAARKREEEREKEEEMAKRREEERQRKEREEVER-----------------KKREEE---------AMR---
-------------------------------REEERKREE------------------------
EAAKRAEEERRKREEE------------------------------------------------------
HKKRPPPQGPQPPIH---------H

Brassica napus                          >TR|A0A078HFA1|          M---------
-------SKFKIIPL----CLLTLFLCTNSFSDQNDGVPSS----QSPL--------------------------
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---------------------------------------------------------------------------
-------------------------------------------------LVKR-HQ----
RTQLVATEFGEISAVH-----------------IGEE-------YTIQFITLEPNALLLPLLLHSDMVFFVHTG-
TGVLNWLD----KEKERTLELKRG-----DVFRLRYGTVFHLHCNLE--RDEVPDKLRVYAIF-DVG---K--
CLSDQC---LRAYSSIRDLLWGFDEKTLRSAFAV---PEDVFGRLRD----AVKPPLITHAMP------------
------------------------KNRTQGSEEETWG--SRLAKLFVRVED------------------------
-----------------------SIVVDEKDMD--ALKG--SSFGVYMVNLTK-
GSMMGPHWNPNACEISIVLQGE-GM--IRVVNHPSYQS-KN----------------E-----------------
----------------------SE-RFMVEDGDVFVVPQLYPMAQLSFV--NSSFMFMGFSTSAKT-----
NHPQFLVGQ-NSVLKIFNR-----DVLATSFNM---RYET-VERLLGA--
QKHGLMLECVPCAEVELSRLMREIE----ERRRREEEEIERRKREE--EEARKR----EEAKRQEEER-------
----------------RRREEEEA----------ERKRKAE----EEARKREEERERE---
EEAAKRREEERRRREEEEAERKRKEEEEARKREEE----RKREEEAAKKREEERRKR----EKEE----------
-----EEARKREEAREREEEEAKKRE-EERRKREEEEAERKRKAEEEARQRE-EAREREEE--------
EEKEAARKREEEREKEEEMAKRREEERQRKEREEVER-----------------KKREEE---------AMR---
-------------------------------REEERKREE------------------------
EAAKRAEEERRKREEE------------------------------------------------------
HKKRPPPQGPQPPIH---------H

Brassica napus                          >TR|A0A078GRX9|          M---------
-------SRFTIIPL----CLLTLFLCTNSFSEQNDGVPSS----QSPL--------------------------
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---------------------------------------------------------------------------
-------------------------------------------------LVKR-HQ----
RTQLVATEFGEISAVH-----------------IGEE-------YTIQFITLEPNALLLPLLLHSDMVFFVHTG-
SGILNWVD----EEKERTLELKRG-----DVFRLRYGTVFYLHCNLE--RDEVPEKLRVYAIF-DVG---K--
CLSDQC---LGAYSSIRDLLWGFDEKTLRSAFAV---PKDVFGRLRD----AVKPPLITHAMP------------
------------------------KNRTQGSEEETWG--SRLAKLFVRVED------------------------
-----------------------SIVVDEKDMD--ALKG--SNFGVYMVNLTK-
GSMMGPHWNPNACEISIVLQGE-GM--IRVVNHPSYQS-KN----------------E-----------------
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----------------------SE-RFMVEDGDVFVVPQFYPMAQLSFV--NSSFMFMGFSTSAKT-----
NHPQFLVGQ-NSVLKIFNR-----DVLATSFNM---RYAT-VERLLGT--
QKDGLLLECVSCAEVELSRLMREIE----ERRRREEEEIERRKREE--EEA----------KRQEEER-------
----------------RRREEEEA----------ERKKKAE----EEARKREKERERE---
EEAAKRREEERRRREEEEAERKRKEEEEARKREEE----RKREEEAAKKREEERRKR----EKEE----------
-----EEARKREEAREREEEEAKKRE-EERRKREEEEAEQTR-----GREAE-EG--------------------
------------------------ERRCGEK-----------------ETREEE---------AMR---------
-------------------------REEERKREE------------------------
EAAKRAEEERRKREEEA----------------------------------------------------
EHKKRPPPQGPQPPIH---------H

Tarenaya hassleriana                    >REF|XP_010548347.1|     MPNRTK----
-HRAQKMKKFTILPLSV-LLLLTLLISSEA-SVQNDAVACGLP--------------------------------
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---------------------------------------------------------------------------
-------------------------------------------------VVRK-DQ----
RTRIVETEFGEISAVE-----------------ISDGCGI-RGTHSIHFITLEPNSLLLPLLLHSDMVFFVHTG-
SGVLTWVD----EDKETRIEIRRG-----DVYRLRPGTVFYVRSNLER---EIREKLRVYAIFSDTS---
EDDYIYDPC---LGPYSSIRELLLGFDERTLRSAFAV---PEEVIGTIRN----ATKPPLIVHGMP---------
---------------------------KNITHGSDEFLWQIQSRFLRIFVREED-SDEL----IINSRVKKK---
--KTR--TYNVF--EEDPDFENCNGRSITVSKKDLH--ALKG--SSVGVFMVNLTK-
GSMVGPHWNPRACEISIVLRGE-GM--IRVVSSSNEMMKQS----------------K-----------------
--------------------CKSGGRFMVGEGDVFAVPRFHPMAQMSFN--NGSFVFVGFSTSARR-----
NYPRFLAGK-SSVLQVLKR-----EIMAVALNV---SNVT-VDRLLGG--
QEDGVMLECTSCAEEELVKLKEEIQ--------REKEEEERKKREK--EEEAARRREEEEARKREEER-------
----------------QRKEREEA----------ERKRREE----
EEKRRQQEEAERERREEEEMKRREEERERKEREEEERRRQEEMERERREEE----RKREEEAAKREEEERQKK--
--EREEAERQRQEQEEA---ERRRRQQEEERKREEEAAKR---EERERQEQEEAERQRRQEQEAAERQ------
RREQ-------EEEERQRKQEEERKREEEAAKREEAERQRKEREEAER-----------------QRQGQE----
-------------------------------------------EAERQRRQ------------------------
EE----EEEKRRKEEAAA---------------------------------------------------
EREPKPSPMEEQNP------------

Arabidopsis thaliana                    >EMB|CAB80336.1|
MTRFAVLPLSV-----------------LLLVLLFLCTESLAKSEES----------------------------
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-------------------------------------------EEYDVAVPSCCGFSSPLLIKKDQ----
WKPIFETKFGQISTVQ-----------------IGNGCGGM-GPYKIHSITLEPNTILLPLLLHSDMVFFVDSG-
SGILNWVD-----EEAKSTEIRLG-----DVYRLRPGSVFYLQSKPD----------------------------
--PC---FGAYSSITDLMFGFDETILQSAFGV---PEGIIELMRN----RTKPPLIVSETLC-------------
-----------------TPGVA---------NTWQLQPRLLKLFAGSADLVD--NKKKKEKKEKKEK-----
VKKAKTFNVF--ESEPDFESPYGRTITINRKDLK--VLKG--SMVGVSMVNLTQ-
GSMMGPHWNPWACEISIVLKG-AGM--VRVLRSSISSNTSS----------------E-----------------
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--------------------CKN-VRFKVEEGDIFAVPRLHPMAQMSFN--NDSLVFVGFTTSAKN-----
NEPQFLAGE-DSALRMLDR-----QVLAASLNV---SSVT-IDGLLGA--
QKEAVILECHSCAEGEIEKLKVEIE------RKKIDDERKRRHDE----------------RKKEEEEA------
-------------------------------------KREE----
EERRKREEEEEKKRWPPQQPPQEEELRERQLP-------------------------MEKEWEMEGEEES-----
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Eucalyptus grandis                      >REF|XP_010026166.1|     MGSK------
-----P--LAVPF-SVLLLI------AFAVPALRAGGGGARDRDDGVLRG-------------------------
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-------------------------------GGDPDEGGEDVGT-----VVRK-EE----
RTPIAATEYGEITAAR-----------------VADGG---GGVYHLRFVTLEPNALFLPVLLRSDMVLYVHTG-
RGRLNWAD----ENDVKRIDLRRG-----DIYRLRPGTIFYVQSSLEP--ER--EKLRINAIFTNTEEDIYEP--
---S---IGAYSSIGDLLRGFDSKVLQGAFKV---PEEVVEEVIS----ATRPPPIVHAAA--------------
----------------------SEKRTKY----WDWEARFLKTYLSST----GYLA---EGSSSNKK-----TK-
TKTFNVF--DTDHDFENCNGWSLMVTGKDMH--ALKH--SNIGVFMVNLTK-GSMMGPHWNPRATEIAIVLQGQ-
GM--IRVVCSS--TAKES----------------E-------------------------------------
CNN-TRFKVSEGDVFVVPRFHPMAQMSFN--NESLVFMGFSTSTKR-----NYPQFLAGK-SSILRALDR-----
EILAVAFNV---TNTT-IHHILAP--QTDSIILDCTSCAEEEERLMEEEIEK------ERREEE------E----
--EAKRREQEEEAKRREE---------------------EERARQEEEE-------------R---------
EREREEEEEREREEEEERERERKEEEERERE---------------REEEE--------ERERKRQEEEQRR---
-REEEE-------------------------------QEREREE------EEARR--REEEE---------
REREEEQ----RREGGG----GGGAGGGERE-------------QEE-------------------
ARRREEASERWERQRQ--------------------------------------QERRRRQEA------------
-------------AEREQEEARRQEEEMQ---RRH--EEEW---------------------------GGYE---
-------------------GRRAVEEVGIKG

Fragaria vesca subsp. vesca             >REF|XP_004300614.1|     MSNRD-----
--------------------------------------------SNPPFSLTLFIVFFLLLLPASSS--------
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---------------------------------------------------------------------------
------------SAKSLKYDEEDSSGS------------------GSGYLVRR-DQ----
RRALVQTEYGDISSID-----------------VTDGR---RGPYHVQFITMEPNSLFLPVLLHADMVFYVHTG-
SGTLNWAHGE--DDQINKVSIKKG-----DIHRLRPGSLFFIQSDLQT--ER--HKLRINAIFANTEEDVYDP--
---T---IGAYSSVRDLVRGFDTKILRSAFQV---SEEVIQSITN----STDHSAIVHAVP--------------
----------------------PTKKET----FWDLEARFLKTFIGASYDGTALNK---KKDKKHKK-----
KDKSKTYNIF--DTDPDFRNCNGWSTTVNERNSP--LLTG--SNIGLFMVNLTK-
GSMMGPHWNPRATEISVVLHGE-GM--VRVVCSS--TAKRS----------------E-----------------
--------------------CRN-LRFRVKEGDVFAVPMFHPMAQMSYN--NDSLVFMGFSTTTRR-----
```

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NYPQFLAGK-YSVLQTLNR-----QILAVSLNV---TNTT-VDQLLAA--
QVESIILDCTSCAEEEEKIMLEEIEK------EREEEEARKREE----------------QRKREEEQRQR-E--
------------EEARKREEEQ--------------RKREE----
EQRQREEEEARKREKEEEKRKREEEEEERRREEQ--------------------------------EEEERRQ--
--REEEEEERRKREGEE-----------------EQERERQQEEEQ------ERKR--REEQERQRQ------
QEEEER----RREEAA----AAAR--------REQEEEAARAREEQ-----------------EEARRQQQE---
--------------------------------------------EYSRRREE-----------------------
--EAQTEQEEARRQQEEIE---RR---TRPEEQ-------------------ETEGDQGFDGEAGRR--------
-------------------EI

Morus notabilis                         >TR|W9RZX9|              MAKK------
---------------------------------------------------ALTLLIFFFFSLSLLH--------
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------------LALHAQAKAKHFGDDEDVWGYHDFR-----------PLVRK-TQ----
RKSLVDNEYGQISAVN-----------------ISDGI---RGPYHIQFFTLEPNSLFLPVLLHADMVLFVHTG-
SGRLSYAD----EEETRSVHLRSA-----DIFRLQTGSVFFVQSDLQP--ER--ESLRIYAMFSNTDDELFEP--
---A---IGAYSGFRNLVRGFDKVTLKQAFKV---PDEVIESITS----ATDAEAIVHAIPS-------------
-----------------SKKEKKEKKEKKKKALWEMETRFLKAFL-EDEESAAY----------NKK-----
KKSGEGYNLF--DAEPDFENCNGWSLTVNRKQAAH-ILKD--TNVGLFMVNLTK-
GSMMGPHWNPKSTEIAIVLQGQ-GM--VRVVCSSGPNKSKQ----------------E-----------------
--------------------CKN-MRFRVKEGDVFAVPRFHPMAQISFN--NDSLVFMGFTTTGVE-----
NHPQFLAGK-QSILQTLDR-----DILALSFNV---SNTT-IDQLLAP--
QADSIILDCTSCAEKEERIMEEEIEK------EKEEEEARKRE-------------------KQEEERRKRE---
------------EEERKREEEE--------------KRREE----EERKREEEEERSREEEE----
RKREEEERKREE-----------------------------ERKREEEEARK----REEEEREKQREEEEE----
-------------------------------EERR--REEEKQ--------RQKEEER----ERQRRE----EE-
-----------EEERESQREEE---------------------RRREEE--------------------------
------------------------RQRQE-----------------------EEEREQEQEEVRRQEDERE----
-------RER-------------------QQKEEEGGGGGEGENHLKM----------------------WTV

Cucurbita maxima                        >TR|Q8W3X8|              MKKCTAIS--
GSPFSLSFLFTVFFLFLSLPSNADDKWWEAAC-------------------------------------------
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------------------------------------------------PV-KRANE----
RKSLLKTEYGEISAVD-----------------LHDASQF--GPYHLQFITMEPNSLFLPVLLHADMVLYMHTG-
SGRLNWFD----DDDLREVDLRRG-----DIFRLQPGAIFYIHSSLETER----EKLRMYALFSSTDEDPFE---
--PA---IGAYSRVTDHVRGFDKEILCKAFMV---PEEVIEEIMD----AKRPPLIVHAATT-------------
-----------------LSTLSK-KQRSSLSMSLELEARFLKSFIGGGGIGMDF---------KKKK-----
KKKKGLYNVF--EADPDFENCNGWSLTVTKKV-SH-QLKG--SNIGFFVVNLTA-
GSMMGPHWNPRAWEIGIVTSEEAGV--VRVGCSSMT-NSSK----------------------------------
--------------------CKK-WSFVVGKGDVFVVPRFHPMAQMSFN--NGSFAFVGFSTTNRN-----
NLPQFLAGR-SSVLQTVER-----QVLAWSFDV----NVTTIDRLLEA--
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RVESVILECTSCAEEEVMKMEEEAE------RERQEEEERRREEEER-E------REEEEARKREEEER-ER---
----------EEEEARKREEEE--------------REREE----EEARKREEEERER--
EEEEARKREEEEREREEEEE----------RRREEEE---REREEEEARKREEEEARK----REEEE--------
-------REREEEEARKREEEEARKREEEEARKREEEEARK--REKEEARKRE-EEEREREEEA-----------
---ERERREEEEEARRREEAERGEREAER-----------------EAEEARESEEAHRRE--------------
--------------------------RGRRRREAE--------------------------
REAEERQRRRREEEEEPTLR-------------------------------------------------------
------------ILRQRT

Cucumis sativus                         >TR|A0A0A0KGF2|
MKKHSAVSVSGSSFSPSILIPIFFLFLSLPAYADDGWWEGDT---------------------------------
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---------------------------------------------------------------------------
----------------------------------------------------------PVVKRANE----
RIPILKTEYGEISAVD-----------------FDDGTRF--GRYHLQFITLEPNSLFLPVLLHSDMVFYVHTG-
SGRLNWFD----DNDLKEVDLRRG-----DLYRLHPGSIFYLQSSLETER----EKLRIYALFSSTDEDSFN---
--PS---IGAYSRVTDLVRGFGKEVLRKAFMA---PDEVIEEIMN----AKRPPLIVHAAAP-------------
-----------------TPSIKA-KSSSPW----EFEARLLKSFLGGDASAIEF---------NKKK-----
KKK-GIYNVY--EVDPDFENCNGWSLTVTKKN-SH-QLKG--SNIGFLVVNLTA-
GSMMGPHWNPRAWEIGIVTSDEPGV--IRVGCSSTSANSSK----------------------------------
--------------------CKN-WSFVVEKGDVFVVPRFHPMAQMSFN--NGTFVFVGFSTTNGH-----
NMPQFFAGS-SSVLKIVDR-----EVLAWSFDV----NVTTIDRLLKA--
RVESIVLECTSCAEEEVRKMEEEAE------REREEEEERKREEEERRK------REEEEERKREEEERRKR---
----------EEEEERKREEEE--------------REEE--------RKREEEE------
EEEERKREEEEEKKREEE-----------E--EEEE---RKREEEEEKKREEEE--------EEEE---------
------RKREEEEEKKREEEE---EEEERKRKRKRGGGEK--RKREKERKRR-ERERKREE--------------
-----RRNRGGEKKKRKKKKRG-RQRER-----------------RRKLGKERKNIKEREG--------------
-------------------------RGGERGRKD--------------------------
KEDGGRKRKKKVEERS---R-------------------------------------------------------
------------SCHSQY

Glycine max                             >TR|I1LHP6|              M---------
-------------------------------------------EPRK---ASPLSWVLIFFLTISLW--------
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------------GVKVSSEE-H-----------------HHHGKSKEGPVVER-DQ----
RRTLLVTEFGEITAID-----------------IKEGQKEL--PYHLQFITLEPNSLFLPVLLQADMVFYVHTG-
SGKLTWAN----DDGTSTIRLREG-----DVCSLNEGSVFYIQSNLEAER----RKLRIYAMFTNTDDNTY----
-DPS---IGAYSRINELVKGFDKKIMQAALKV---PEDLIEAIIN----KTETPAIVHAVP--------------
--------------------------EKR-NIVQELEASFLKNFLGVG-------------SNSKKL--------
-ETYNIF--EHDPDFKNPIGWSTAVTKKQLK--SLKR--TNIGFLMVNLNM-GSILGPHWNAKATELTVGVDGE-
GM--VRVVCGSG-NENET----------------E-------------------------------------
CQN-MRFKVKEGDAFLVPRFHPMAQMSFN--NGPFVFLGFSTSAKK-----NHPQFLAGK-GSVLHILDK-----
KILARSLGV---SNRT-IDELLRS--PEDSIIFRCSSCAEEEEKIMKEEEE---
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EEESKKEEEERKKKEEEEEEEE-----KKKKEERKREEEEAKRQ-------------QEEREKKRGEEEA-----
------KREREEE----KARMEKE----RERKGEEEAEREEEEARREQEWRRK----
KEEAAAKREQEKRERRRQEEEAK-KWAEEKAER----EQEQ-----------------
ATREAEEAQREQEQAKR-EA---AQREQERAKREQERR--RREEV-
AGKGEEEEEHAGRGHERRKEEEETARREQEQEQAERQQQKREKRRQKEEQGEGEEEEEEDEEEPTWWERRERRKQ
K------------------------------------------GKSPEEGVEWEQE-------------------
-----EA-RTASREGEKK-------------TPRE----------------------------------------
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Glycine soja                            >TR|A0A0B2RSR0|          M---------
-------------------------------------------EPRK---ASPLSWVLIFFLSISLS--------
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---------------------------------------------------------------------------
------------GVKVLSEE-Q-----------------HH-AKSQEGPVVER-DQ----
RRTLLVTEFGEITAID-----------------IKEGQKEL--PYHLRFITLEPNSLFLPVLLHADMVFYVHTG-
SGKLTWAN----DDGTSTIRLREG-----DVCSLKEGSVFYIQSNLEAER----RKLRIYAMFTNTDDNTY----
-DPS---IGAYSRINELVKGFDTKIMQAALKV---PEDLIEAIIN----KTETPAIVHAVP--------------
--------------------------EKR-NILQELEASFLKNFLGIG-------------SNSKKL--------
-KTYNIF--DHDPDFKNPNGWSTAVTKKQLK--SLKR--TNIGFLMVNLAM-GSILGPHWNPKATELVVGVDGG-
GM--VRVVCGSS-NEDET----------------E-------------------------------------
CQN-MRFKVKEGDAFLVPRFHPMAQMSFN--DGPFVFLGFSTSAKK-----NHPQFLAGK-GSVLHILDK-----
RILATSFGV---SNRT-IDQLLRS--PEDSIIFGCSSCAEEEEKIMKDEEE---NR--
KREEEEKEKKKEEEEEK------------RKREEEEERKR-------------EEEEERKR-EEEE---------
--ERKREEE--------EDE----KKRRREEE---EEEKKKEEEEEKRK----
REEEEAKRQQEEREKKREEEEAR-R---EK-ER----ERE-----------------------
EEAEREQEQAKR-EAEAAAQREQEQAKREQERR------------------------------------------
-------ERRRQ----------EEEDEEEPTRWERRGRR-EK---------------------------------
---------GKSPE-GVEWEQE------------------------EA-RRQQAESDRQ-------------
VEEQSHRNSFEGRRALKI-RNV-----------------------------------------------

Phaseolus vulgaris                      >TR|V7CFI9|              M---------
-------------------------------------------EPRKK--ALPLSWFLIFFVIVSLW--------
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------------GVKAS--------------------------KSQEGPVVEK-DQ----
RRTLLATEFGQITALD-----------------IKEEPEKQ--PYHLQFITLEPNSLFLPVLLHADMVFYVHTG-
SGKLTWAN----DDGTGTIPLREG-----DLCNLNEETVFYIQSDLEAER----RKLRIYAMFTNTEDNTF----
-NPS---IGAYSRIDELVKGFDKKIMQAALKV---PDDLIEEIIN----KKNTPTIVHADS--------------
--------------------------KKI-NIVQKLEASFLKNFLGVG-------------SNSNKL--------
-ETYNIF--DHDPDFKNRNGWSVAVSKTQLK--SLKQ--TNIGFLMVHLTK-GSILGPHWNPKATELAVAVEGR-
GM--VRVVCGSS-NEDET----------------E-------------------------------------
SLN-MRFKVNPGDAFVVPRFHSMAQMSFN--DEPFVFLGFSTSAKN-----NHPHFLAGK-GSVLYNLNR-----
QILATSFGV---SDRT-IDELLHS--PRDSIIFGCSSCAEEEEKIMKEEEE---
EEERERKREEEETKREEEEEDR-----KKERE-RKREEEEAKRQ-------------
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QEEREKKREEEEEREQQEGTGGEKEREREEE----
IEKEQEEAGREKEREREEEIEKEQEEAGREKEREREEEIEKEEEEAGRQQEKREKKREKEKGEGKEAEEEGRR--
--EAE--------------------KEAEEASAKREQEKRRKKEEAAAKEEAAAKREQEKREMRRQEE-
AEKEQEED----------KREGESEVAQKEQAEAKREHEKREKKRQEEGQREG----
EEEEEDQAWGESVRREKGK------------------------------------------RSEEEEVAQGEQE-
-----------------------QA-KRQQEEREKRRDEDGDHDHIESEAEENSYKSSFEGRRALKV-RNL----
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Medicago truncatula                     >TR|G7ZW34|              M---------
----------IVTTALYIIDTFAKCKTTSIVLSNFSTLTLLMMETQKSFLASKFSSLLIFFLIIT-S--------
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------------LCELNALSSD-----------------EHSVKAHKGPVVER-GQ----
RKTLFETEYGEISATD-----------------VKDGHNTQ--HYHIEFFTLEPNSVFLPVLLHAAMLFYVHTG-
SGKLSWAN----EDGTSTIDIREG-----DVGSLTEGSVFYIHNNLDDQR----KKLRIYAMFTNTDDSTF----
-DPS---IGAYSRINELVKGFDKKIIQAAFKV---PEDLIEAITN----KTETPPIVHAVS--------------
--------------------------EKKHSTVLELEASFLKYFTGIE-------------YNSKNL--------
-KTYNIF--DSDHDFENCYGWTSTVTKKQLK--RLKS--NNIGFLMVNLTR-ASMLGPHWNPMATEVAVVLEGE-
GM--VRVVCGSN-NDDK-------------------------------------------------------
CKN-KRFRVQQGDVFVVPRFHPMAQMSFV--NQPLVFMGFSTAAKK-----NHPQFLAGK-ESVLQILDR-----
EIVATSLGV---SNTT-IDKLLEK--
PDDSIIFECNSCAEEEERLMEEEKETGKEEEDEKREKEEREREREEEEEV-----RRREEERKREEEAARRQ---
----------QEERERRRREEEQ----------EEREREKE---------------GEKEREEE--
EEEAAARRQQEERERK---EEAARREREREK-EEARREMERERKRREKEVER----EKE----------------
----RKRQEAESEEEAARRQQE----ERERKREEKEARRRKERGQEG-RSKEEEEEEEA---------
EGEEEAARRQQEKRERRREEGEARTEEERREEGREEEGETESETGGGWRQPKRGDT-------------------
-----------------------GRRSRGGTEWEEE------------------------
AAARRQQEERERRRKQGG--------------WSSYEGRRVLKMRRNV---------------------------
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Cicer arietinum                         >REF|XP_004512222.1|
MHLPNCHLFKQLTCLKTRHAALKNALYIVTPLLRAKS---
LLSNFCFVTLLIMEPRKSFLASQFSSLLIFFLVITIS--------------------------------------
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---------------------------------------------------------LCE-GKESSE--------
---------EHSVKPHKGPVVER-DE----RRTLFDTEYGEISAID-----------------VKDGNKTL--
PYHLQFFTLEPNSVFLPVLLHAAMVFYVHTG-SGKLSWAN----EDETGTTEICEG-----
DVGSLREGSVFYIHSNLEAQR----KKLRIYAMFTNTDDSTF-----DPS---
IGAYSRINELVKGFDKKIIQAAFKV---PEDLVEAITN----KKETPAIVHAPS---------------------
-------------------KRKHNSVLELEPSFLKYFIGIE-------------SNSKKL---------
QTYNIF--DNDPDFKNSHGWTLTVTKKQLK--PLKQ--HNIGFLMVNLTM-ESMLGPHWNPLATEIAVVLEGE-
GM--VRVVCGSN-NVDE-------------------------------------------------------
CQN-KRFRVKQGDVFLVPRFHPMAHMSFD--KEPLVFMGFSTAAKK-----NHPQFLAGK-GSVLQILDK-----
QIVATSLCV---SKRT-IDQLLDS--PDDSIIFGCNSCAEEEEKLMEEEKEKEKEEE-EKRKREEEE----
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EEEKG-----REKEEAKKREEE------------------EKERERRRKEEEE----------EEVRRREE----
------------ERKREEE--E----AKRQQEERERKREEKEARRREEARRKQEEIRRQKERERE--EKKAEK--
--GKE--------------------RRTEEAESEEEAARRQQE----KRERKREERE------------------
QEEES---------EGE-----------------GEAKTEEE--------EEETESE--GGRRQRRRS-------
---------------------------------------REEETTEWEEE------------------------
VA-KRQQEERERRREHGSDN----KSMKGKSNESSFDGRRVLKIPRNV---------------------------
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Jatropha curcas                         >TR|A0A067KHS0|          MKS-------
----------------------------------------------------LLLLLFLSLPFCFSL--------
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------------EAKDV------SSAG------------------MRPSLVKR-ED----
RKSLIVTEYGQISAVD-----------------ISTGT---IGDYHLEFITLEPNSLFLPVILHSDMVFYVNTG-
SGRLSWAEG---GKELKRMDIKKG-----DVYRLHPGSVFFMQSNLET--ER--KKLRIYAIFSNADEGTYEP--
---H---IGAYSSINDLVLGFDTKLLQSAFKV---PEEVIEEMKS----AMRPPDIVHAAP--------------
----------------------Q-KKSI----LLEIEDRLLQAFVG-NKDGTLYSS---NGGHK----------
KTKKVNLL--DGKPDFENCNGWSVTVDKKDLK--RLKG--SGISVFMVNLTK-
GSMMGPHWNPMANEIAVVLQGL-GM--VRVVCSS--NVNET----------------E-----------------
--------------------CKN-MRFRVQEGDVFAIPRFHPMAQMAFN--NESLVFMGFSTSTSK-----
NDPQFLAGK-RSVFQTLNK-----EILALSFNV---PNTT-VDKLLNP--
QEEEIILECISCAEEEERKMEEEMER------EREREE----EE----------------ARKREEEERKRKE--
------------EEARKREEEEA-------------RKREE----EERRREEEEAREREEEEEERKREEE---
RRREE-----------------------------------EEARE----REEEEEERKR----E-----------
------EEEREKR--EMK------ERKK--RERKEAERR------QREERR----RRE-------SEAR------
--REQEQ--ARKEEEE-----------------RQRRQRQRE---------------------------------
--------------EEAKERER-------------------------EREVQPEEEIKRSEESE---
EEKEGTRKQER-------------------EYQGDSGPGKRALRKV-------------------------WKL

Populus trichocarpa                     >TR|U5GAT4|              MLQK------
-----------------------------------------------VPLLSLLFLGLLLCL-------------
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-------------SIHVEAF------------------SEDVSAWERPYLVRR-GH----
RRSLVVTEYGEISAAE-----------------ISSGT---KGPYHIQFITLEPNSLLLPVLLHADMVFYVHTG-
NGKLSWTD----GREMKRMNLRRG-----DVYRLQAGSVFFVRSNLDS--ER--QKMRIHAIFSNTDEDIYEP--
---S---IGAYSSVSDLVLGFDRKVLQEAFKV---PEEVLEELTS----ATKPPAVVHAVT--------------
----------------------KDQKSVN----WELEDRMLDFLIGN----------------KHKK-----
TKETKTFNIL--DAKPDFENCNGWSLTVDKHSLK--SLSD--SNIGIFMVNLTK-
GSMMGPHWNPMATEIAIVLHGR-GM--VRVICHS--TANES----------------E-----------------
--------------------CKN-MRFKVKEGDVFAVPRFHPMAQISFN--NDSFVFMGFSTSTKR-----
NHPQFLTGK-SSILQILDR-----GILAVSFNV---TNTT-MDQLLNA--
QEEALILDCTSCAEIEENKMKEEFEK------EKQEEEARKREEE------EARKKEEEEARKREEE--------
-------------EEREREEEEA-------------RKREE----
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AERERQEEEEKQRREEEEEEARKREEEEREREEEE---------ARKREEEER-REQEEAERERQEEEEKQRR--
--EEEEEEARKREEAE-------------RERQEEEEKQRREEEE------EEARK--REEEQ---------
REREEEE----RREQEE----EERERQEEEEKQRREEEE----QQEE-------------------
ARRREEKKKRQEKQRQ-------------------------------------------REET------------
-------------PRREHEEARRQEEERQ---KRRWKEEERAK-------------------
ERERREGGGEQPEEQEVEARKEDQERKGDEGKGRRALRNPW-KL

Solanum bulbocastanum                   >TR|A9XLG8|              MSVKNC----
-FS--IQCCKMLFKFLLFMIII-SYVSVDVRAKRE----------------------------------------
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-----------------------------------NEG----WEWGLDPLVKR-AE----
RKTIISTENGQVSSVT-----------------IADGT---TGSYHLQFITLEPNSLFLPVVLHSDMVFYVHTG-
SGKLTWMH----ENEEKSVDLRIG-----DVFRLPFGSIFFLESNLDPI--R--QKLRVYSIFPNSGDDFRESL-
---N----GPYSSIRKMVLGFDKKVLQAAFHV---PEDVIEQVLA----GTEVPAIVHGVP--------------
----------------------KSTKKK--NNLWEMEAQFMKTVLRRG----SYSF---FDNQKNKK-----K-
SSKLFNVF--QEKPDFENCNGWSTVIDRKKLP--ALKG--SQIGIYVVNLTK-
GSMMGPHWNPMATEIGIAIQGE-GM--VRVVCSN--SGTGQ----------------G-----------------
--------------------CKN-MRFKMEEGDVFVVPRFHPMAQMAFN--NNSFVFVGFSTTTKK-----
HHPQYLTGR-ASVLQTLDR-----HILEASFNV---ANTT-MHQILEA--QGDSVILECTSCAEEEKRLMEEER-
-------RREEEEAKKKEEEER-------RKEEEEARKAEEERREKEA--------------EEARKREEEEE--
-----------RKRQE----EEAKRQEEEIRRRQEEEEA-RKRQEEEERERQEA-----------RKRQEE----
-KEEEAAQR--EAEQARR------EEEEAEKRRHEEE---------EARRQEEEKEEARRRQQEEETE----
EARR--REEEEAVKR------KQEEEA----QRE-------EEAETR------
RKQEEEEARRQEEEKEEARRRQQEEET---TEEARRREEEEARRREEEA------------
ETTRKQEEEESWRREEEEEESRSSEEDAESERQE-------------------------VAERQ-
EEARRQEEETE---KRHQ----QE--------------------TEEDEPG----RHERILL-------------
--KVAMSTYHHHN

Solanum tuberosum                       >REF|XP_006363154.1|     MSVKNC----
--------CKILFKFLLFMIII-SYVSVDVRAKRE----------------------------------------
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-----------------------------------NEG----WEY---PLVKR-AE----
RKTIISTENGEVSSVT-----------------VADGT---TGSYHLQFITLEPNSLFLPVVLHSDMVFYVHTG-
SGKLTWMN----ENEEKSVDLRIG-----DVFRLPFGSIFYLESNLDPI--R--QKLRVYSIFPNSGDDLRESL-
---N----GPYSSIRKMVLGFDKKVLQAAFHV---PEDVIEEVLA----GTEVPAIVHGVP--------------
----------------------KSTKKKK-NNLWEMEAQFKKTVLGRG----SYSF---FDNQRNKK-----K-
SSKLFNVF--QEKPDFENCNGWSTVINRKKLP--ALKG--SQIGIYVVNLTK-
GSMMGPHWNPMATEIGIAIQGE-GM--VRVVCSN--SGTGQ----------------G-----------------
--------------------CKN-MRFKVEEGDVFVVPRFHPMAQMAFN--NNSFVFVGFSTTTKK-----
HHPQYLTGR-ASVLRTLDR-----HILEASFNV---ANTT-MHQILEA--QGDSVILECTSCAEEEKRLMEEER-
-------RREEEEAKKKEEEER-------RKEEEEARKAEEEKREKEA---RKREEEEAKEKEEERKRQEEEA--
-----------RKREE----EEAKRQEEEIRRRQEEEEA-RKRQEEQERERQEAEE--------ARKREEE----
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-KEEEAAQR--EAEQARR------EEEEAEKRRQEEE---------EAKR----
REEARRRQQEEEAEREAEEARR--RGEEEAAKR------QQEEES----QRE--A----EEAETR------
RKQEEEESRKQEEE-------------------SRRREEEAAR--------------------------------
------------EAERGRQE-------------------------EAERQ-EE--EAEEETE---KRQE----
EE--------------------TEEEEPG----RHERILL---------------KVA--------

Solanum lycopersicum                    >TR|K4BB70|              MSVKNC----
-MS--IQCCKILFKFLLFMIIIISSVFIDVRAKRE----------------------------------------
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-----------------------------------NEG----WEWGLGPLIKR-AE----
RKTVISTENGEVSSVT-----------------VADGT---T--YHLQFITLEPNSLFLPVVLHTDMVFYVHTG-
SGKLTWMN----ENEEKSVDLRIG-----DVFRLPFGSIFFLESDLDPI--R--HKLRLYSIFPNSG---RESL-
---S----EPYSSIRKMVLGFDKKVLQAAFHV---PEDVIEEVLA----GTEVPAIVHGVP--------------
----------------------KSTKKKK-N-LWEMEAQFMKTVLGRG----SYSF---FDNRRNKK-----K-
SSQLFNVF--QEKPDFENCNGWSTVINRKKLP--ALKG--SQIGIYVVNLTK-
GSMMGPHWNPMATEIGIAIQGE-GM--VRVVCSK--SGTG-----------------------------------
--------------------CKN-MRFKVEEGDVFVVPRFDPMAQMAFN--NNSFVFVGFSTTTKK-----
HHPQYLTGK-ASVLRTLDR-----QILEASFNV---GNTT-MHQILEA--QGDSVILECTSCAEEEKRLMEEEM-
-------RKEEEEAKKKEE----------------ARKAEEERREKEA--------------EEERKRQEEEA--
-----------RKREE----EE-------IRRRQEEEEA-RRRQEEEEEER-ERQE--------ARKKQEE----
---EEAAQR--EAEQARR------EEEEAEKRRQEEE---------ESRR----EEKARRRQQEE--------
ARR--REEEEAAKR------QHEEEA----ERE--A----EEA---------RRIEEEEAQREAEEA----
RRIQQEEE---AERARRREEEAETRRKEEE------------EEESRRQEEESRRSEEE------
AAREAERERQE-------------------------EAERQ-EEARRREEETE---ERHQ----QEE--------
-----------TEEEEPG----QPEM-----------------------NGYSSN

Nicotiana sylvestris                    >REF|XP_009803271.1|     MSDQKS----
-VSTPFQCCRILFKFLLFMVII-SNVAISVTALTE----------------------------------------
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-----------------------------------QEG-TPGREWGLGPLVKR-GE----
RKSVVSTENGEVSSVR-----------------VADGI---TGSYHLQFITLEPNSLFLPVVLHADMVFYVHTG-
SGRLTWMD----ETEQKSVDLRIG-----DVFRLPYGTIFFIESNLEPA--R--QKLRVYSIFANSGDDLREPL-
---S----GPYSNIRDMILGFDRKVLQAAFHV---PEDVIDEVLN----GTEVPAIIHGVP--------------
----------------------KTTKKT----LWEMEAEFMKSLLGRG----GHSF---FDSQSNKK-----K--
TELFNIF--KEKPDFENCNGWSTVITRKKLP--ALKG--SHIGIYVVNLTK-GSMMGPHWNPTATEIGIALQGE-
GM--VRVVCSS--TGTEQ----------------G-------------------------------------
CKN-MRFKVEEGDVFAVPRFHPMAQMAFN--NNSFVFVGFSTTTKR-----HHPQYLTGK-ASVLRTLDR-----
QILAASFNV---TNTT-MDRILEA--
QGESVILECTSCAEEEVRLMEEERRRAEEEARRREEEEARQREEERRREEEEARRKEEEEARKAEEERREREA--
------------EEARRR-EEEA-------------AKEKE----EQRRRQEEEARRK--EEEE-
ARRQEEEIRRRQEE------EE--ARKREEEEAAKRQQEESAER--EAEAARR----R-EEEEAARRQQEEEA--
--QKEAEEARRR-EEEAERRR--EEQAQREAEEARR--REEEAAARR-----RQEQEEA----ERERQA----
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EEARR--EEKETRRHEEE---EEEEEARRGERGEEEEEE------G-RREEEEAR--------------------
------------------------EAERRRQE-------------------------EAERQEEAARRQEEEME-
--RRHQ---EEEE-------------------TEEEEQGPYTRRRKRTFL---------------KTA-------
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Nicotiana tomentosiformis               >REF|XP_009590474.1|     MSDKKS----
-VSTPFECCRILFKFLLFMVII-SNVAIHVTALSG----------------------------------------
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-----------------------------------REGITPSTEWGLGPLVKR-GE----
RKLVVSTENGEVSSVR-----------------VADGI---TGSYHLQFITLEPNSLFLPVVLHADMVFYVHTG-
SGRLTWMD----ETEQKSVDLRIG-----DVFRLPFGTIFFIESNLEPA--R--QKLRVYSIFTNSGDDLREPL-
---S----GPYSSIRDMVLGFDRKVLQAAFHV---PEDVIDEVLN----GTEVPAIIHGVP--------------
----------------------KTTKKT----LWEMEAQFMKSLLGKG----GHGF---FDSQSNKK-----K--
TELFNIF--KEKPDFENCNGWSTVITRKKLP--ALKG--SHIGIYVVNLTK-GSMMAPHWNPTATEIGIALQGE-
GM--VRVVCSS--TGTKQ----------------G-------------------------------------
CQN-MRFKVEEGDVFAVPRFRPMAQMAFN--NNSFVFVGFSTTTKR-----HHPQYLTGK-ASVLRTLDR-----
QILAASFNV---TNTT-IDRILEA--
QGESVILECTSCAEEEVRLMEEERRRAEEEERRREEEEARQREEERRREEEEARRKEEEEARKAEEERRKREA--
------------EEARRR-EEEA-------------TREKE----EQRRRQEEEARRR--EEEE-
ARRQEEEIRRRQEE------EE--ARKREEEEAARRQQEEEAER--EAEEART----R-EEEEAAR-QQGEEA--
--QREAEEARRR-EEEAARRR--EEQAQREAEEASR--REEEAAARR-----RQEREEA----ERERQA----
EEARR--EGEETRRHEEE---EEEEETRRGERGEEEEEE------GGRKEEEAAR--------------------
------------------------EAEKRRQE-------------------------EAQRQQEAARRQEEEME-
--RRHQ---EEE--------------------TEEEEQGPYARR-KRTFL---------------KTA-------
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Petunia integrifolia subsp. inflata     >TR|A9XLF3|              MSENKY----
--------CRILLKFLL-LVLI-SNVVINVTALRE----------------------------------------
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-----------------------------------NEGV-PSWGWGSGPLVKR-GE----
RKSVVTTENGEVSSVR-----------------IADGV---TGSYHLQFITLEPNSLFLPVLLHADMVFYVHTG-
SGRLTWMG----EDELKSEDLRIG-----DVFRLPFGTIFFLESNLEPA--R--QKLRVYSIFANSGDDLREPL-
---S---TGPYSSIRDIILGFDRKVLQAAFNV---PESVIDEVLN----GTEVPAIIHGVP--------------
----------------------KTSKKT----LWEMEAQFMKSLLGRG----SYGF---FETQSNKK-----K--
TKLFNVF--NEKPDFQNCNGWSTVITRKKLP--ALKG--SRIGIFVVNLTK-GSMMGPHWNPMATEIGIALQGE-
GM--VRLVCSN--TGTDQ----------------Q-------------------------------------
CKN-MRFKVEEGDVFSIPRFHPMAQMAFN--NNSFVFVGFSTTAKK-----HHPQYLAGK-ASVLRTLDR-----
QILAASLNV---TNTT-MDRILES--
QGESVILECTSCAEEEARLMEEEMRREEEEARRREEEEERKREEERRRKEEEARKKEEEQARKAEEERRQREE--
------------EEARRKQEEEA-------------RRREE----EEARKQEEEARRRQEEEEE-
ARRKEEEAAKRREEQAQREAEE--ARRREEEAAARRQQEEEAARRQEEEERER----Q-
AAEEATRRQQEEEEARRRQQEEEETRKRQEEEAARRQQEEEEAQREAEEARR--SEEEAARRR--------
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EEQA----QRE--A----EEARRREEEAEARRKEEEAAQREEEQGRRRERGEEEEETEGGGGGGGRSEEEEAR--
------------------------------------------EAERRRQE-------------------------
EAERQEAAARRQEE-ME---RRHEQGREEEE-------------------SREEKQGTYEQR-RRTFL-------
--------TAA--------

Sesamum indicum                         >REF|XP_011100121.1|     MLKQRA----
-AAAAGFRLQA----------------------------------------------------------------
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--------------------------------------------------VKR-EE----
RRALVSTEYGQISAVR-----------------VRDDV---SGSHLLHFITLEPNSLFLPVVLHADMVFYVHTG-
SGRVSWTE----EDDLKNADLRRG-----DVYRLPQGSVFFIQSNLETETER--
QKLRIHAIFANSDNGLTVQSFWEQA---NGPYSSIRDMVLGFDRKVLQAAFKV---PEEVIDELFN----
GTQQPTIIHRVP-------------------------------------ATKRT----AWETEVEFVRGLLASR-
---SYNI---FELNRKKR-----KESARLFNLF--KEDKDFENCNGWSTTVTRKKLS--ALKG--
SNVGLFMVNLTA-GSMMGPHWNPRAAEIAVVLWGR-GM--VRVVCSG--ISNET----------------G----
---------------------------------CRN-MRFEVEEGDVFVVPRFHPMAQMSFN--
NGTLVFMGFSTSTKK-----NHPQFLAGQ-ASVLRTLDK-----DVLAMSFNV---TNTT-LDQLLAQ--
QHDSVILGCISCAEEELRIMEEEIERERQEAREREEEEARKREEERRREEEEARKREEEEARRQEEEKRKREQ--
------------EEERRRQEEEA-------------RKREE----
EEARRQEEEKRKREEEEEEEERRRQEEEARKREEEEAAKREEEEE---RRRREEEAAKREEEEERREEQARQEEEAR--
--KREEEEAAKR-EEEERREEEERQEEEARKREEEEEAAKREEEERRQQEEEEEEAAE--RREEEARQRE-
EAARREQEEA----RRE--E----
EAARREEEDRRQREEEEEARQREEEEASRKREEEEAARQREEEQEGRQREEEHQRGRSEDER-------------
----------------------AAEEERRRQE-------------------------
ETQREEEAARQWERQHEGGTEEKEQEWGETE-------------------LEGRNQGDKKWR-------------
----------AILNKRWTV

Beta vulgaris subsp. vulgaris           >REF|XP_010680893.1|     MGKNSG----
-DMKSFWC--VFFFFSLQLVILMKCVSGSLNFHEDTSVSSGSTGTV-----------------------------
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-----------------------------------------------GKLVKK-EE----
RIPVVATEYGEISAVD-----------------IDDGTGTGRHNYHLQFITLEPNSIFLPVLLNADMVFYVQTG-
SGKISWAN----SDELYKVSLQRG-----DVYRLRSGTLFYIHSSLEA--ER--PRLRIIAIFANPE----
EEQLQGPS---IGPYSNINDLVRGFDKRVLQAAFQV---SEEVIEELTS----ATDTPAIVHAEP----------
--------------------------------KRKNFWQQELLYVNAFLG------IKRY---SKQVSENK----
-KKHTKTFNFF--KEDPDFKSCNGWSTLVTKHNLD--ALHG--SHIGVFMVNLTK-
GSMMGPHWNPMATEVSVVLEGE-GM--VRVVCPS--TLTNK----------------E-----------------
--------------------CKN-SRFKIEEGDVFTVPRFHPMAQTSFN--NGSLVFMGFSTSTKN-----
NHPQFLIGK-ASVLQTLSK-----PILGASFNV---SGTT-IEQLLGA--
QEKAIILDCTSCAEEQEMLMEDEIEK------ERQEEEERREEEE------EARRREEEERRKQEEEEQRRE---
------------EEERRKHEEEE-------------RRREE----EQRKREEEEEEEERQREEE--
RRKREEEEERRREEEEEE--------RQREEEEQEERRRKEEEEEERRQEEEERQ----REEEEE--
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RRQEEEERHREEEQRKHEEERRREEEEQRRQEEEEK--KEQEEEQR--RQEEERREQE-EQQRRQEEER----
QRQEDERGEREEQQRREEEKRQRQEQEEEAARQKEE--------------------RRREEEEWRRREEEKGRG-
----------------------------------EEEETEQEI-------------------------
ARREEEERRREWERQAEEAARRRQERYERE-------------------RYESESGGSREEGRRFLRHTT-----
----------------KV

Nelumbo nucifera                        >REF|XP_010254919.1|
MLKRALTWQFFFLLFCSSTVIALEDDVLAMR--------------------------------------------
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----------------------------------------------------------PLFTKY-S----
RRSITSTEFGEITAVE-----------------ISDGSTG--GTYQLQFITLEPNSLFLPVLLHEDMMFYVLTG-
SGSLNWVDE---EGVTNQIDVKRG-----DVFRIPSASFFFAKSSLESTR----ERLRIFAIFDNANN------
AHELS---VGAYSRLSDLVLGFDWKILQSAFKV---SPEMIEEIKS----AAKLPAILHVPS-------------
--------------------------KNETEQTKWQ--ARIIKALMGSG-------------SYELNK-----
KKKTKIFNFL--KAKRDVENANGWSVTVNKKD-----LKG--SSFGAFMVNLSK-
DSMMAPHWNPMATEIAIVTHGE-GI--VSIVCSSSTYESSS----------------D-----------------
--------------------CKN-MRFKVQEGDVFVVPQFHPMAQMSFS--NDSLVFMGFSTMAKK-----
NYPQFLAGK-NSVLQTLDR-----DILALSMNV---SNKT-IDRLLSS--
QSESFILSCPSCAEEEEAAMQEEIERERQEEEQRRREEEEARREEEREAREREEERKKEEAKRRQEEERKRQEEE
QRRREEREAREKEEERKKEEAKRRQEEEKRQQEEARRRQEEAAKREEQRREEEEAWRKEEKEAREREEKEKQEQE
ARRRQEEEKRQQEEARKRQEEAA---
KREQEEARRQEEERQKKQKQQEKEEEEWQEQEEEVRRQEEEARRRQREEAKWEEKEASRQEEERQKKQRQEEEEA
RRQQEEEARGQEGKRQERQKEEEAGRWHEGQQEEMKAKRQERERQERQRQEEEEEASRRQRQEEDARRQQEQQEE
ETRRQEGKKQERQKQEEEEEEEEEASARRQQGQQEEEAAKRQEGERQEKHRKEDEEEEEQQQEEEARRQERHRKE
DEEEEEEDRRQHEEEVRKEESEEAQRPRGKEEQEARKAEDEDRGRREQPETEEEAARRQEEERQRKQRREEEGDQ
GYGGGGEGRRALRNIKR----------------IGHYF

Brachypodium distachyon                 >TR|I1H8K5|
MATATARWLVLLLFVSAA---SAAAYGEEKWNGGATV--------------------------------------
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---------------------------------------------------------GGMVVEKER----
RRVVAASEAGTVTAAD-----------------VADDAAGTV--YRLQFVTMEPGSLFLPVELHADMVFYVHSG-
RGKVTYIQEG--GSEASALEVERG-----DVYNLEQGTILYIQSYPNATR----ERLRIYAIFSSSAISSDDP--
SHPT---SEAYSNVSNLLKGFEVEILRRGFGV---PTEVVEPIKS----APSPPLIIPYNP--------------
------------------------KGKEQESSNWA--EEIFDAFWGIRDPQFLNKKKKKS---KDKKDK-
DKKSKDKTFNFY--SGEPDVKNCHGWSKTMTNEDLQN--LRE--SNIGMFMVNLTT-
GSMMGPHWNPKATEIAIVTHGS-GI--VQTVCPSSPSGEGKRGPHEKGG--------EE----------------
------------------IKCKNSL-FRVKEGDVFVVPRFHPMAQMSFN--NDSFVFVGFSTHMGQ-----
NHPQFLAGK-LSALQVIGK-----EILALSLGQ---DNSTAVEKLLSA--
QSDSTILTCVSCAEELEKKVEQEEQEREKEKREREEEERRKKEEE-------------EERKRKEEEEEKAR---
-----------KEEEERRKEEE-------------KARREE----
EERRRREEEEEKRRKEEERGREEEEEKRRKEEE------------RARQEEEERRRREEEERARREEEERKR---
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--------------------------EEEKAKKEEEERARREQKQE---
EEERARREQEAQEEAKREQEEIARREQEERA------------------------
RREQEEEERRRREQEGGGGGGG--DEPSEEEE--GRRKQEEGGRGRE----------------------------
-------------DEPRKEDEGGDWGDL-----------------QNH--TAKKLRKRYSL-RKGA---------
------------------------------------------------------------VLQSA

Triticum urartu                         >TR|M7YE46|              MATP--
RWLVLSLLVSAAWASAAAAAHEKKWKAGAAV--------------------------------------------
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---------------------------------------------------GGQVVEKER----
RRVVAEGEAGTVTATD-----------------VAD-AAGTV--YRLQFITMDPGALFLPVQLHADAVFYVHSG-
RGKVTYIQEG--GSETSSLEVQRG-----DVYNLEQGSILYIQSYPNATR----ERLRIYAIFTSNAINSDDP--
SHPT---SEAYSSVSNLLRGFDVKILRQGFGV---SAEVVEAIRS----AKSPQSIITYNP--------------
------------------------DQKKEEKSNWT--EEIFDALWGDESP--
LNKKKKKKDKHKKKKDKKDDKSKSETFNFY--SGKPDVKNCFGWSKTMTNKDLQN--LRG--SNIGMFMVNLTT-
GSMMGPHWNPKATEIAIVTHGS-GI--VQV----GGRRVGDHGHHDAGGRRGGDHGQEG----------------
------------------VECKNSV-FRVKEGDVFVVPRFHPMAQLSFN--NGSFVFVGFSTHMGQ-----
NNPQFLAGE-HSVLQVIGK-----EIVALALGQ---KNTTAVEKLLSA--
KSGSTIMACVSCAEELERKAEQEEQEGGKGEREREREE----EEE-------------RERKQREEEERK-----
----------------KREEEE-------------RARREE----EERARREEKERKKR----------------
-------------------EEEEQRRREEEERQRREEKERKQ---------------------------------
--REEEEAARREQEEE---EERRGREE----EEGGGGQGGGGGGGDDPR--------------------------
--EEEERRRREEEEGGGGQGGRGDDPREEEERRGRREEEEGGRGGRGG---------------------------
------------DDPWEEEEG-DWGDS-----------------SRYRAAATNLKKRYHRGRKGA----------
-----------------------------------------------------------VFQSA

Musa acuminata subsp. malaccensis       >REF|XP_009396731.1|
MDSKVAVFVVGMILLCSLSSVNGEEWPS-----------------------------------------------
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----------------------------------------------------------PLVTR-ES----
RRTLVLTESGRITAVD-----------------VHDG---YGGSYHLQFITLEPVSLFLPVLLHTDMVFYVHTG-
RGTVTYVNED--KDETDEMDVGHG-----DVYRLEQGTVFFVRSHPDPTR----
EKLRIHAIFDTAGIDHPLGCA-------VRAYSNISDLVQGFDERVLQMGFGA---SLESIRGIKW----
APSPPSIVPFG---------------------------------------QKDARVKSKWK--
EGVFEALMGVRGPTGIV--------NKKRK------TKSKTFNFF--RAKPDVENCNGWSTAVTHKDLK--
ALKG--SNLAAFMVNLAT-GSMMGPHWNPRATEIATVIQGQ-GM--VQVICPSDPSGKVG---------------
-DV----------------------------------SKCQNK-KFKVQEGDVFVVPRFHPMAQVSYN--
NDTLVFVGFSSMAGK-----NHPQFLAGK-RSVLRTIDR-----DVLAASFNA---PNASAIGDLLVS--
QGESVMLACTSCAEEMERKMTEEIE-----RQKQEEE--RKKEEE--------------E-RKKEEEEAKKR---
-------------------EEET------------RRREEE----EAKKREEEEAKRREEE--
AAKRREEEEARRREEEEERREEEEARRR----EEEEAKKREEEEAKRREEEEGRK----
REGEEEARKREEEETK------RREEEEARREAEEARRREEEEGRKTEGEEE--ARREAEEARRRE-
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EEEEGRREEE--------------EARRREEEEEGRRPEEEEARRREEEEAE----------
RREQEEAARRREEEEARRRQG-----------------------------------------GRRKKRE------
------------------GQRKGKEQGEKKKR----GDGRNKRRLPREVERNSLWWTGNDEDKHESRQ-------
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Phoenix dactylifera                     >REF|XP_008798757.1|     M-
GKMTSTLLAAIFLWSLVTINGEGFPKF------------------------------------------------
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-------------------------------------------------------GRLVPM-ES----
RRTLVTTDSGLITAAD-----------------VHDG---YRGLYHLQFITMEPSSLFLPVLLHTDMLFYVQTG-
SGTVSYTTED--G--TTRVDVERG-----DIYRLEEGTVFYVRSHPSPMR----
EKLRINAIFDTNNMENPSESF-------VGAYSNISDLVRGFDDKVLEMGFGV---SKEIIRSIEG----V-
KPPSIIPFTP--------------------------------------KKNESKKHNWK--EGIFEALLG--
SPTDII--------NKKKK-----KTKTKTFNIY--STSPDVENCNGWSIAVTKKEFR--SLKG--
SHFGVFMVNLTE-GSMMGPHWNPTATEIAVVIEGQ-GM--VQVVCPSKPSGEGG----------------DT---
-------------------------------FRCQNT-RFRVKEGDLFVVPRYHPMVQISFN--
NNSFVFVGFSTMVKK-----NYPQFLVGE-RSVLQTIER-----GILEVSFNS---SNTT-IETLLTS--
QRESIMLSCTSCAEELEREVEEEIE-----RQKKEEEEARKREEE--------------EARKREEEEEARR---
------------------EEEEA------------RRREEE----EARKREEEEARRREEE-EAKK-
REEEEARRREEEEEATR------------EQEEARRREEEEAKKKEEEEARR----REEE-EAKKKEEEATR----
--EEEEETERREEEEAREREEKEAKRTEEEE--ARR--KEEARMRE-EEEAKKREEE--------------
TRRREEEETKKR--EEEEAKRREEEEAPT-------TREREQTT----EEEQEA---------------------
-------------------------ARRREEE------------------------EVGKREEEEEVRKREEL-
GSGRRERKSQLKGK-------GR-KNKL--------GD-------------------------------------
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Elaeis guineensis                       >REF|XP_010905079.1|     M-
GKMASTLLAAIFLWSLVAINGEEFPSF------------------------------------------------
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-------------------------------------------------------GPLVTR-ES----
RRTLVTTDSGMITAVD-----------------VHDG---YKGLYHLQFITMEPSSLFLPVLLHTDMLFYVQTG-
RGTVSYTTED--G--TTQVDVKRG-----DIYRLEEGTVFYVRSHPDPMR----
EKLRIHAIFDTNNMENPSESF-------VGAYSNISDLVRGFDEKVLEMSFAV---SEEIIRSIEW----V-
KPPSIIPFTP--------------------------------------KKNESRKHNWK--
EGIFEALVGFQGPTDII--------NKKKK------TKTKTFNIY--TATPDVENCNGWSIAVTKKEFR--
SLKG--SQFGVFMVNLTK-GSMMGPHWNPTATEIAVVIEGQ-GM--VQVVCPSKPSGEGG---------------
-DT----------------------------------FRCRNT-KFRVKEGDLFVVPRYHPMVQISFN--
NNSFVFVGFSTMVKK-----NYPQFLVGE-RSVLQTIER-----EILEVSFNS---SNTT-IETLLTS--
QRESIMLACTSCAEELERQMEEEIE-----RQKREEEEARKREEE--------------EARKREEEEEARR---
---------RQEEEEARREEEEA------------RREKEE----
EARKREEEEARRREEEAEARRWQEEEEARRREEEETRKKAEEETRRREEEEEEEEARRREEEETRKKEEEEARR--
--REEEAEARRRQEEEAK------REQEEARRREEEEARKREEEETRKREEEEEEEARRREKEEARKRE-
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EEEAKKREEE--------------EARKAEKETERR--
EEEEVREREEKEAKEEVRKKEETREKEEEEAKMREEEEEAERREE------------------------------
----------EARRREKE------------------------RAQKREEEEEAKKREEEEGGGTREEKEPTNGK-
------WRGKTSLEIRKIKGRNI---------------------------------------

Amborella trichopoda                    >REF|XP_011627755.1|
MHSTFSLLSSLVVCLLLALPTDGYD--------------------------------------------------
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----------------------------------------------------------PLITR-DN----
RKPIVSTEFGRVESVE-----------------VYDGSEKE--PLNLQFFTLEPSSLLLPLLVEADMVFFVQTG-
SGRVSWVE----KGDITHMDIARG-----DVYRLRSGSVFYVQSKTTAT----GEKLRLNALFTRRDYEDT----
LDEF---IGTYANLSDVVLGFDNKVLQASFKI---SEELIKEIKS----RKKPQMIVPAVL--------------
------------------------KEKTEEDSNWKL--GILEALVGGGS----------HEERSNKKR-------
-KPFNVY--KKEPDFKNPNGWTLTVTRKDFP--PLKG--TNVGVFMVNLTK-GSMVGPHWNPRATEIAIVTHGQ-
GM--VNIVCPSKKSQCPRT--------------------------------------------------------
--SFKVKEGDIFMVPKFHPMSQMSFS--NESLSFMGFTTMAKK-----NHPQFIAGK-LSVLNTLDP-----
DIVAEALNL---PKSS-VQELLSC--QRDAIILPCTYCAEEEERAMEEEV-------RKREEEEREAAAAA----
-----------ARKREEER--------------------KERERREEA--------------RRREE--------
--EEVRERERQEEEEARQREEEAARERE------------------------RQEEEEAKQKEEEAVR-------
-------------------------ERERQEEEGRQREDEEARQREREKEDARKREEEAARERE-----------
---------------------------RQEEEVRQTEEEQRER--------------------------------
-----------------------------------------------------------------------
AAMREEEGGRPH---------------------------------------------------------------
-------------MILRSF

Camelina sativa                         >REF|XP_010488296.1|     MTMT--
KKLVITFLLLI-SIAFAHCLAF----HV-----------------------------------------------
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----DLEEFEP-PQQEEQDVPRR--------GSGGR----SGEGWQEESTEFPYHFGK---RSFKNWFQSNE-
GFVKM-LPKFTKRAPNLFRG-IEN-----------YRFAVFEMEPNTFLVPHHLDADSVVLVLQG-
HGVVEFVTDKTKES----FQVTKG-----DVVRLPSGITHFATNTNQ-T-----VPLRFVKIIVP---
VNNPGRFKDYF---PARSQFQQSYFTGFSKEVLSASFNI---PEELVGRLFSG-SQQT-----------------
-------------------------------GQGIMRRVSPDQIKKLTKH--ATSPSNKH----KES---KSKH-
-KDISTKLRPFNLFTQDSVSTYTNDFGHFHEAHPESFD--QLQD--LRIAVAWTNMSQ-
GSLFLPHYNSKTTFVTFVENG---CARYEMASPY--SFQGEQQQK--QWW----PEQGGEEE--E-D--------
-----------------MSGQVHKIVSRVCKGDVFIIPAGHPVTLVSH---NENFVSVGFGIHASN-----
CTRTFLAGQ-ENVLSNLDT-----VATRVTFGVG----SKVAEKLFTS--
QNHSYFAPTTRSHQQTQEKREPSFQSIF-----------------------------------------------
-----------------SF--------------------------------------------------------
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-------------------------------------------------------------AGF

Camelina sativa                         >REF|XP_010466550.1|     MTMT--
KKLVITLLLLI-SIAFVHCLAF----HV-----------------------------------------------
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----ELEEFEP-PQQEEQDVPRR--------GPGGRPGGRSGEGWQEESTEFPYHFGK---RSFKNWFQSNE-
GFVKM-LPKFTKRAPNLFRG-IEN-----------YRFALFEMEPNTFLVPHHLDADSVVLVLQG-
HGVVEFVTDKTKES----FHVTKG-----DVVRLPSGVTHYATNTNQ-T-----VPLRFVKIIVP---
VNNPGQFKDYF---PARSQFQQSYFTGFSKEVLSASFNI---PEELVGRLFSG-SQQT-----------------
-------------------------------GQGIMRRVSPDQIKELTKH--ATSPSNKH----KET---KSKH-
-KDTSTKLRPFNLFTQDSVSTYTNDFGHFHEARPESFD--QLQD--LRIAVAWTNMSQ-
GSLFLPHYNSKTTFVTFVENG---CARYEMASPY--SFQGEQQQQ--QWW----PEQGGEEE--EED--------
-----------------MSGQVHKIVSRVCKGDVFIIPAGHPVTLVSH---NENFVSVGFGIHASN-----
CTRTFLAGQ-ENVLSNLDT-----VATRVTFGVG----SKVAEKLFTS--
QNYSYFAPTTRSHQQTQEKREPSFQSIF-----------------------------------------------
-----------------SF--------------------------------------------------------
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-------------------------------------------------------------AGF

Camelina sativa                         >REF|XP_010511540.1|     MTMT--
KKLVITLLLLI-SIAFVHCLAF----HV-----------------------------------------------
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----DLEEFEP-PQQEEQDVPRR--------GPGGR----SSEGWEEESTEFPYHFRK---RSFKNWFQSNE-
GFVKM-LPKFTKRARNLFRG-IEN-----------YRFALFEMEPNTFLVPHHLDADSVVLVLQG-
HGVVEFVTDKTKES----FHVTKG-----DVVRLPSGVTHFATNTNQ-T-----VPLRFVKIIVP---
VNNPGQFKDYF---PARSQFQQSYFTGFSKEVLSASFNI---PEELVGRLFSG-SQQT-----------------
-------------------------------GQGIMRRVSPDQIKELTKH--ATSPSNKH----KET---KSKH-
-KDISTKLRPFNLFTQDSVSSYTNDFGHFHEAHPESFD--QLQD--LRIAVAWTNMSQ-
GSLFLPHYNSKTTFITFVENG---CARYEMASPY--SFQGEQQQQEQQWW----PQQGGEEE--E-D--------
-----------------MSGQVHKIVSRVCKGDVFIIPAGHPFTLVSH---DENFVSVGFGIHASN-----
CTRTFLAGQ-ENVLSNLDT-----VATRVTFGVG----SKVAEKLFTS--
QNHSYFAPTTRSHQQTREKREPSFQSIF-----------------------------------------------
-----------------SF--------------------------------------------------------
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-------------------------------------------------------------AGF
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Capsella rubella                        >TR|R0I7W9|              MTMT--
KKLIITLLLLI-SIAFVHCLAF----HV-----------------------------------------------
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----EFEEFEP-PQQEEQDVPRRILAVVLAVVPGAA---QARDGRKSQRPRF-----L---TSFKNWFQSNE-
GFVKI-LPKFTKRAPNLFRG-IGN-----------YRFALFEMEPNTFLVPHHLDADFVVIILQG-
QGVVEYVTDKTKES----FQVTKG-----DVVRLPSGVTHFATNTNQ-T-----VPLRFAKIMVP---
VNNPGQFKDYF---PARSQFQQSYFTGFSKEVLSASFNI---PEELVGRVFFG-SQQM-----------------
-------------------------------GQGIMRRISPDQIKELTEG--ATSPSNKH----KEK---KSKH-
-KDTNTKWNPFNIFKHDSVETYTNDFGHFHEAHPESFD--QLQD--LHISVAWVNMKQ-
GSLFLPHYNSRTTFVTFVENG---CARYEMASPY--TSQGEKQQQ-QQLW----PEQGGEEQ--EED--------
-----------------MSGQVHKIVSRVCKGDVFIIPAGHPVTLVSH---DENFVSVGFGIHASN-----
CTRTFLAGE-ENMLSNLDT-----VATKVTFSVG----SKMAEKLFTS--
QNYSYFAPTTRSHQQTQEKREPSFQSIF-----------------------------------------------
-----------------SF--------------------------------------------------------
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-------------------------------------------------------------AGF

Camelina sativa                         >REF|XP_010466552.1|     MAMT--
KKLIITLLLLI-SIAFVHCLAF----HV-----------------------------------------------
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----ELEEFKP-PQQEEQDV----------HGGGG-----SSKGWQEELSEFPYHFKK---QSFKNWFQSKE-
GFVKM-LPKFTKRAPNLFRG-IEN-----------YRFSLYEMEPNTFLVPLHLDADSVVIILQG-
QGVAEFVTAKTKEL----FHLTKG-----DVVRLPSGITHFAINTNQ-T-----VPLRFAKITIP---
VNIPGQFQNYF---SAPSQFQQSYFTGFSKEVLSASFNI---PEELVGRIFFG-SQQM-----------------
-------------------------------GQGILRRITPEQIKEITEN--STSRSNKD----K----------
--DKSTKFSPFNLFTHDSVSSYTNDFGHFHEAQPDSFD--QIQD--LQIAVTWTNMTQ-
GSVFLPQYNSKATFVTFVENG---CARYEMASPY--SFQREQQQQ--QWW----PEQGGEEE--E-D--------
-----------------MSGQVHKIVSRVCKGDVFIIPAGHPFTIVSH---DENFVSVGFGIYASN-----
SIRTFLAGQ-GNVLSNLDT-----VATRVAFGVR----SKVAEKLFTS--QNYSYFAPTTRSHQQT---------
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Arabidopsis lyrata subsp. lyrata        >TR|D7L1S0|              MAIT--
NKLIITLLLLI-SIAFVHCLAF----HV-----------------------------------------------
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----DIEKFEP-PQQEEQE------------GPGRRPGGGSGEGWEEESTNHPYHFRK---RSFKNWFQSKE-
GFVKL-LPKFTKRAPALFRG-IEN-----------YRFSLVEMEPTTFFVPHHWDADSVVIVLQG-
KGVIEFVTDNTKEA----FHINKG-----DVVRVPSGVTHFLTNTNQ-T-----VPLRLAKFIVP---
VNNPGQFKDYF---PSPSQFQQSYFSGLSKEVLSTSFNV---PEELLERLVTR-SKER-----------------
-------------------------------GQGIIRRISPDQIKELAEH--ATSPSNKH----KAK---
KEKEEDKDLRTMWTPFNLFAIDPI--YSNDFGHFHEAHPKSFD--QLQD--LHIATAWASMRQ-
GSLFLPHFNSKTTFVTFVENG---CARFEMATPY--KSQEEQQQ-----W----PGQGQEQE--EED--------
-----------------LSEDVHKVVSRVCKGEVFIVPAGHPFTILSQ---DQDFVAVGFGIYATN-----
NKRTFLAGE-ENMLSNLNP-----AATRVTFGVG----SKLAEKLFTS--
QNYSYFAPTSRSQQQIPEKHKPSFQSIL-----------------------------------------------
-----------------DF--------------------------------------------------------
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Arabidopsis thaliana                    >TR|Q9LUJ7|              MAIT--
NKLIITLLLLI-SIAVVHCLSF----RV-----------------------------------------------
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----EIDEFEP-PQQGEQE------------GPRRRPGGGSGEGWEEESTNHPYHFRK---RSFSDWFQSKE-
GFVRV-LPKFTKHAPALFRG-IEN-----------YRFSLVEMEPTTFFVPHHLDADAVFIVLQG-
KGVIEFVTDKTKES----FHITKG-----DVVRIPSGVTNFITNTNQ-T-----VPLRLAQITVP---
VNNPGNYKDYF---PAASQFQQSYFNGFTKEVLSTSFNV---PEELLGRLVTR-SKEI-----------------
-------------------------------GQGIIRRISPDQIKELAEH--ATSPSNKH----KAK---
KEKEEDKDLRTLWTPFNLFAIDPI--YSNDFGHFHEAHPKNYN--QLQD--LHIAAAWANMTQ-
GSLFLPHFNSKTTFVTFVENG---CARFEMATPY--KFQRGQQQ-----W----PGQGQE-E--EED--------
-----------------MSENVHKVVSRVCKGEVFIVPAGHPFTILSQ---DQDFIAVGFGIYATN-----
SKRTFLAGE-ENLLSNLNP-----AATRVTFGVG----SKVAEKLFTS--
QNYSYFAPTSRSQQQIPEKHKPSFQSIL-----------------------------------------------
-----------------DF--------------------------------------------------------
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Brassica napus                          >TR|A0A078H9R3|          MAI---
NKLTITLFLLI-SFAVFHCLAF----RV-----------------------------------------------
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----EVQEFEP-PRQEGQEGP------------G----GGSGEGWDEEATKNPYHFGQ---WSFKNFFQSKD-
GFVKM-LPKFTKRSSTLFRG-IEN-----------YRFLFQEMEPNTFLVPHHLDADYVFLVVQG-
KGVIGFVTDTANES----FQITKG-----DVVRVPSSVTHFFANTNG-T-----VPLRLAKIAVP---
ANVPGHFQVFF---PAHSGFHQSYFTGFSKDVLTASFNI---PEELLGRLIRGPQQQV-----------------
-------------------------------GQGIIRRVSPEQIKELTEHEHATSPSNKH----KDK---
KDKHKDKDRSTFGSPFNLLTQDAI--YSNKFGRYHEAHPKRFS--QLQD--LDIAVGWVNMTQ-
GSLFLPQYNSETTFVTFVENG---CARYEMASPY--TFQGEQQQ----PWF----GPGQEEE-VEEE--------
-----------------MSGQVHKIVSRVCKGEVFILPAGHPFAILSQ---DENFVAVGFGIHASN-----
STRTFLAGQ-DNMLSNINT-----VATRLSFGLG----SKMAEKLFTS--QNYSHFAPTTPSHQFPE-
KPKPSFQSIF----------------------------------------------------------------
NL-------------------------------------------------------------------------
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--------------------------------------------AGF

Brassica rapa subsp. pekinensis         >TR|M4E4V9|             MAI---
NKLTITLFLLI-SFAVFHCLAF----RV-----------------------------------------------
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----EVQEFEP-PRQEGQEGP------------G----GGSGEGWDEEATKNPYHFGQ---WSFKNFFQSKD-
GFVKM-LPKFTKRSSTLFRG-IEN-----------YRFLFQEMEPNTFLVPHHLDADYVFLVVQG-
KGVIGFVTDTANES----FQITKG-----DVVRVPSSVTHFFANTNG-T-----VPLRLAKIAVP---
ANVPGHFQVFF---PAHSGFHQSYFTGFSKDVLTASFNI---PEELLGRLIRGPQQQV-----------------
-------------------------------GQGIIRRVSPEQIKELTEHEHATSPSNKH----KDK---
KDKHKDKDRSTFGSPFNLLAQDAI--YSNKFGRYHEAHPKRFS--QLQD--LDIAVGWVNMTQ-
GSLFLPQYNSETTFVTFVENG---CARYEMASPY--TFQAEQQQ----PWF----GPGQEEE-VEEE--------
-----------------MSGQVHKIVSRVCKGEVFILPAGHPFAILSQ---DENFVAVGFGIHASN-----
STRTFLAGQ-DNMLSNINT-----VATRLSFGLG----SKLAEKLFTS--QNYSHFAPTTPSHQFPE-
KPKPSFQSIF----------------------------------------------------------------
NL-------------------------------------------------------------------------
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Brassica napus                          >TR|A0A078J095|         MAI---
NKLTITLFLLI-SLAVFHCLAF----RV-----------------------------------------------
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----EVQEFEP-PQQEGQEGH------------G----GGSGEGWDEEATKNPYHFGR---WSFKNFFQSQE-
GFVKM-LPKFTKRSSTLFRG-IEN-----------YRFFFQEMQPNTFLVPHHLDADYVFLVVQG-
KGVIGFVTDTENES----FQITKG-----DVVRVPSSVTHFFANTNG-T-----VPLRLAKIAVP---
ANVPGHFQVFF---PSHSGFHQSYFTGFSKDVLTASFNV---PEELLGRLIRRPQQQV-----------------
-------------------------------GQGIIRRVSPDQIKELTEH--AISPSNKH----KNK---
KDKHKDKDRSTFGSPFNLLTQDAI--YSNDFGRYHEAHPKKFS--QLQD--LDIAVGWVNMTQ-
GSLFLPQYNSETTFVTFVENG---CARYEMASPY--TFQGEQQQ----PWF----GPGQEEE-VEEE--------
-----------------MSGQVHKIVSRVCKGEVFILPAGHPFAILSQ---DENFVAVGFGIHASN-----
STRTFLAGQ-DNMLSNINT-----VATRLSFGLG----SKMAEKLFTS--QNYSHFAPTTPRHQFPE-
KPKPSFQSIF----------------------------------------------------------------
NL-------------------------------------------------------------------------
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--------------------------------------------AGF

Brassica oleracea var. oleracea         >TR|A0A0D3ABI5|          MAI---
NKLTITLFLLI-SLAVFHCLAF----RV-----------------------------------------------
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----EVQEFEP-PQQEGQEGH------------G----GGSGEGWDEEATKNPYHFGR---WSFKNFFQSQE-
GFVKM-LPKFTKRSSTLFRG-IEN-----------YRFLFQEMQPNTFLVPHHLDADYVFLVVQG-
KGVIGFVTDTENES----FQITKG-----DVVRVPSSVTHFFANTNG-T-----VPLRLAKIAVP---
ANVPGHFQVFF---PSHSGFHQSYFTGFSKDVLTASFNV---PEELLGRLIRRPQQQV-----------------
-------------------------------GQGIIRRVSPDQIKELTEH--AISPSNKH----KNK---
KDKHKDKDRSTFGSPFNLLTQDAI--YSNDFGRYHEAHPKKFS--QLQD--LDIAVGWVNMTQ-
GSLFLPQYNSETTFVTFVENG---CARYEMASPC--TFQGEQQQ----PWF----GPGQEEE-V-----------
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Eutrema salsugineum                     >TR|V4LB10|              MAMT--
NKLTITLVLLI-SIAFFHCLAF----RL-----------------------------------------------
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----EFEEFEPRQQQEEQEGP------------GAGHGGSSGRGWEEEATNNPYHFKE---
RSFKSWFQSKEVGYMKM-LPKFTKRSSTLFRG-IEN-----------
HRFMFMEMEPNTFLVPHHVDADFVFIVLQG-KGMIGFVTDKTKES----FEIKKG-----
DVVRVPSGVTHFFTNTNE-T-----VPLRLAKIAVP---VNTPGHFQANF---
PSRSKFQQSYFSGFSNDVLSASFNI---PEELVGSLIRG-SQQM-------------------------------
-----------------GQGIIRRVSPEQIKELTEH--ATSPSNKH----KEKGKGK----
EKDTSTMWNPFNIFKEDPI--YSNDFGHLHEAHPKKFS--QLQD--LDISVSWINMTQ-
GSLFLPHYNSKTTFVVFVENG---CARFEMASPY--TFQGEQQQQQ-KPWFEQEQGEEQEQE--EEE--------
-----------------MSGQVHKFVSRVCKGEVFIIPAGHPFAVLAQ---DQNYVAVGFGINAFN-----
SKRTFLAGQ-ENMLNNLDK-----VATRLSFGVG----SKMAEKLFTS--QNYSYFAPTDRSRQFPE-
KRKPSFQSIF----------------------------------------------------------------
NI-------------------------------------------------------------------------
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--------------------------------------------AGF

Eutrema salsugineum                     >TR|V4LUV6|              MAMT--
NKLTITLLLLI-SIAFFHCLAF----HL-----------------------------------------------
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----EFEEFEPRQQQEEQEGP------------G----GSSGRGWEEEETNNPYHFKE---
RSFKSWFRSKEVGFMKM-LPKFTKRSSTLFRG-IEN-----------
HRFMFMEMEPNTFLVPHHLDADFVLIVLQ----------------------------------------------
--------------------------------------------------------------------
ELVGSLIRG-SQQM------------------------------------------------
GQGLIRRVSPEQIKELAEH--ATSPSNKH----KEKGKGKGKGKDKDTSTMWNPFNLLTQDPI--
YSNDFGHFHEAHPKKFS--QLQD--LDIAVSWVNMTQ-GSVFLPQFNSKATFVTFVENG---CARYEMASPY--
TFQGEQQQQQQKPWFEQ--GEEQEQE--EEE-------------------------
MSGQVHKFVSRVCKGEVFIIPAGHPTAVLAQ---DQNFVAVGFGIHAFN-----SKRTFLAGQ-ENMLKNLDK--
---VATKLSFGVG----SKMAEKLFTS--QNYSYFAPTDRSHQFPE-KRKPSFQSIF------------------
----------------------------------------------NI---------------------------
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---------------AGF

Arabis alpina                           >TR|A0A087HEI1|          MAMI--
NKLTITLLLLI-SIAFFHCFAF----RV-----------------------------------------------
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----EFEEFEP-PQQEEQEGPE-------FRPGGGPSGGGSGKGFEEESTENPFHFAK---RSFENVFKSNE-
GFVKL-LPKFTKRSSTLFRG-IEN-----------YRFSFMEMEPSTFLVPHHWDADSVFLVLQG-
KGVIAFVTDSTKES----FHIRRG-----DVLRVPSGVTHFLTNTND-T-----VPLRIAKILVP---
VNIPGRFQDFF---PARSQFHQSYFTGFSKQVLSASFNI---PEELLERLISR-SQQM-----------------
-------------------------------GQGIIRRVSPDQIKELAEQ--ATSPSNKH----K----------
DSDMSKFWTPFSIFKQDPV--YSNDFGHFHEVDPTSFS--QLQD--LHIAVAWVNMTQ-
GSLFLPQFNSKTTFVTFVENG---CAHFEMASPY--KFQSKQQQ-----WF----GPREEEE-EEEE--------
-----------------IGGQVQKIVSRVCKGDAFVIPAGHPFTILSQ---DQNFVGIGFGIFASN-----
NIRTFLAGQ-ENMLNNLDT-----VATRLSFGVG----SKMAEKLFTS--
QNYSYFAPSNPSRQFPEEKRTPSFQSIF-----------------------------------------------
-----------------NF--------------------------------------------------------
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Tarenaya hassleriana                    >REF|XP_010551719.1|
MAMTRNNLLTITIALLFFSLASGHSHRVVPPETV-----------------------------------------
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----------AEDEFPPQPHA-----------------------GGVG-GWE-----HPFYFGQ---
RSFQTLLRSKE-GFMKL-LPSFTSRS-WLFRG-IEN-----------
YRFAFLKMAPRTFVQPHHPDADVVFVVLQG-KGVAMFLTQEEKET----FHIEKG-----
HVVRMPAGTTHYVANTGD-D-----EPLRLAAIFVP---VNIPGSFQVFF---
PAAAEFQQSYFDGFSSKVLSASFNV---SEELLGRFLRGP--QT-------------------------------
-----------------GRKAIQTISPEEIKELRKHV----SSEKH----KHQGR------------
LWSPFDIHSQEPV--YSNEFGRFYEAHPERFR--QLRD--LGISVTCINMTQ-GSIFVPHFSSKATFIVFVESG-
--CARFEMAKPHIGSGQWQQQQQEGPQW----GGQGQEQQWGEQE-------------------------
MTGKIHRVVSQVCKGELFVIPASHPVAIITQ---DQNFTAVGFGINAHN-----SSRTFLAGQ-GNILSKLDT--
---AEKRLTFGVG----KEVSERVFTS--QDYSYFVPTHQRRQQ-----KPSFQSIF------------------
----------------------------------------------NY---------------------------
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Arabidopsis thaliana                    >TR|Q9SK09|
MEKNKRAIGFLLLVVLI-------NGVMMTR--------------------------------------------
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SNGYEGEEEWGGAGGGEWGGAEGGGAWGGGGGGGGAWGGEGEGGGEWGGGGE----GGGGGRRGWFMMRESR---
-Q--VIKSEGGEMRVVLSPRGR-IIEKP-----------------
MHIGFLTMEPKTLFVPQYLDSSLLIFIRQG-EATLGVIC----KDEFGERKLKAG-----
DIYWIPAGSVFYLHNTGL------GQRLHVICSIDPTQS-LGFETFQPFY---IGGG--
PSSVLAGFDPHTLTSAFNV---SLPELQQMMMSQFRG---PIVYVTE-----
GPQPQPQSTVWTQFLGLRGEEKHKQLKKLLETKQGSPQDQQ------YSSGWSWRNIVRSIL-------
DLTEEKNKGSGSSECE-DSYNIYDKKDKPSFDNKYGWSIALDYDDYK--PLKH--SGIGVYLVNLTA-
GAMMAPHMNPTATEYGIVLAGS-GE--IQVVFPNGTSAMNT----------------------------------
---------------------------RVSVGDVFWIPRYFAFCQIASR--TGPFEFVGFTTSAHK-----
NRPQFLVGS-NSLLRTLNL-----TSLSIAFGV---DEET-MRRFIEA--QREAVILPTPAAAP-----------
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----------------PHVGEMVSDRFV-----------------------------------------------
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Gossypium arboreum                      >TR|A0A0B0PUP3|          MGK-------
GVSFLLLALV--LCYGV-TVT------------------------------------------------------
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-----------------------------------------------------------MGY-
RGEKQWRKERERR------------------------EEEMEPEEEEQ----EESESRKSWFLMPKSR----P--
VMTTDAGEMRMVRSPGGR-IVDKP-----------------LHMGFITMEPQSLFIPQYLDSSLILFVRTG-
EARVGCIY----KDEMVERRLKIG-----DVYHIPAGSTFYILNPGE------GQRLHIICSIDPSES-
LNLDTFQSFF---IGGGTHPTSVLAGFGPETLSTAFNV---SMSKLEEIMRGQQEG---PIVHVTK---------
SHAPSIWTKLSQLQEQDRLKQVKRMVQGEADEEEKE-----------WSWWKLFGIFSG------NERRIFGDK-
----AP-DSYNIYK-R-KADFKNDYGWSVAVDGSVYK--PFKH--SGTGVYLVNLTA-
GSMMAPHVNPRATEYGIVLRGT-GR--IQIVYPNGTLAMDA----------------------------------
---------------------------RVREGDVFWVPRYFAFCQIASR--SSPFEFFGFTTTSDK-----
NRPQFLVGA-NSLLHTFNT-----PELAAAFGV---TEER-MRRFINA--
QKEAVILPSASAAPPDEDLKGREEK--------------------------------------------------
------------------------------------SEDEGPKVIRNFGDQMIM-GF------------------
---D-----------------------------------------------------------------------
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Morus notabilis                         >TR|W9SCA8|
MGRRRSSRSRALSLLVLGLL--LCHGLLGMA--------------------------------------------
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VGYDEEEEDWRRERERE------------------------EKRREREEERG----EDFEP----FLLKDSK---
-H--VVKTDAGEMRVVKSFGGR-FVQGP-----------------
MRIGFIMMEPKTLFVPQYLDSSLIIFIRRG-EAKLGFIY----KDQLAERRLKIG-----
DVYRIPAGSAFYLVNTGE------GQRLHIICSIDTSES-LTFGSFQSFF---
VGGGINPTSVLSGFDSEILENAFNV---THAELKEFLTSQQEG---PIVYISD---------
SRSPKLWSKFLELKESEKLEHLKKMVGFDDEEEEEEYSGGEKKEEEIWSWRKLLGSVFS------
NREKRPEDVKGKGKSP-DSYNLYD-R-KPDFKNNYGWSVALDETSYS--PLRK--SGFGVYLVNLTA-
GSMMAPHINPRATEFGIVLRGS-GN--IQIVYPNGSLAMNT----------------------------------
---------------------------DVKEGDVFWVPRYFPFCQIASR--TGPMEFFGFSTSARK-----
NRPQFLVGA-SSILRSMRG-----PELAAAFGL---TEDR-LRNITDA--QREAVILPSPMAAPP--------
IQ-------------------------------------------------------------------------
-------------AEKI-PELIKTFGSD-----L-----------------------------------------
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Glycine max                             >TR|I1NGF4|              M---------
---MRVRFPLL-----VLLGTVFLASV-CVS--------------------------------------------
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LKV--REDE------------------------------------------------------------------
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----------------------------------------------NNPFYLRSSN-S-FQTL-FENQNGRIRL-
LQRFNKR-SP-QLENLRD-----------YRIVQFQSKPNTILLPHHADADFLLFVLSG-RAILTLVNNDD-
RDS---YNLHPG-----DAQRIPAGTTYYLVNPHD-H-----QNLKIIKLAIP---VNKPGRY-DDF--
FLSSTQAQQSYLQGFSHNILETSFH-SEF--EEINRVLFGEE-E----------------EQ-------------
----------------RQQEGVIVELSKEQIRQLSRRAKSSS-----------------RKTISSE---
DEPFNLRSRNP--IYSNNFGKFFEITPEK-N-PQLRD--LDIFLSSVDINE-
GALLLPHFNSKAIVILVINEGDA---NIELVGIKEQ------QQKQKQ-----------E---------------
-------------EE---PLEVQRYRAELSEDDVFVIPAAYPFVVNAT----SNLNFLAFGINAEN-----
NQRNFLAGEKDNVVRQIER-----QVQELAFP-GS---AQDVERLL--KKQRESYFVDAQP--QQKEEGSKGR--
-------------------------------------------------------------------KG------
----PFPSI------------------------------------------------------------------
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----------------------------------LGALY

Glycine soja                            >TR|A0A0B2QNP6|          MGSR------
-MSLLMLFLV--LCHGV-ALT------------------------------------------------------
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---------------------------------------------------------------------------
-----------------------------------------------------------MGL------WRTEVE-
-----------------------------EREEGHP----RPDKL----FMMLKSK----R--
VAQTDAGEMRVLESYGGR-ILERR-----------------LNIGFINMEPRSLFIPQYIDSTLIIFLRSG-
EAKLGFIY----KDKLAERHLKMG-----DVYQIPAGSAFYLVNIEE------AQKLHIICSIDPSES-
LGIDIFQSFY---LGGGAHPASVLSGFEPQILETAFNA---SGEELRKMFTRQHEG---PIVHVGD---------
SHATSIWTKFLQLKEEDKLQHLREMVQQEQEEEEEEFVAEEEKQTS-WSWRKLLESVFG------
DEIKNTREKVTK-KSP-HSCNLYD-R-KPDFKNSYGWSVALDGSEYS--PLKS--SGVGIYHVNLSA-
GSMMAPHVNPRATEYGIVLKGS-GR--IQIVFPNGSNAMDA----------------------------------
---------------------------HIKEGDVFFIPRYFAFCQIASR--GEPLEFFGFTTSAQK-----
NRPQFLVGA-TSLMRTMVG-----PELAAAFGV---SEET-MNRVARA--QHEAVILPTPWAAHAHDHK----
VK-------------------------------------------------------------------------
-------------EEVV-VDIFQKLARNEIM-GF-----------------------------------------
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Glycine soja                            >TR|A0A0B2QQS2|          MGNKT-----
--TLLLLLFV--LCHGVATTT------------------------------------------------------
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-----------------------------------------------------------MAFHD-----------
-----------------------------DEGGDKK----SPKSL----FLMSNST----R--
VFKTDAGEMRVLKSHGGR-IFYRH-----------------MHIGFISMEPKSLFVPQYLDSNLIIFIRRG-
EAKLGFIY----DDELAERRLKTG-----DLYMIPSGSAFYLVNIGE------GQRLHVICSIDPSTS-
LGLETFQSFY---IGGGANSHSVLSGFEPAILETAFNE---SRTVVEEIFSKELDG---PIMFVDD---------
SHAPSLWTKFLQLKKDDKEQQLKKMMQDQEEDEEE-------KQTSR-SWRKLLETVFG------
KVNEKIENKDTAG-SP-ASYNLYDDK-KADFKNAYGWSKALHGGEYP--PLSE--PDIGVLLVKLSA-
GSMLAPHVNPISDEYTIVLSGY-GE--LHIGYPNGSKAMKT----------------------------------
---------------------------KIKQGDVFVVPRYFPFCQVASR--DGPLEFFGFSTSARK-----
NKPQFLAGA-ASLLRTLMG-----PELSAAFGV---SEDT-LRRAVDA--QHEAVILPSAWAAPPENAGK---
LK-------------------------------------------------------------------------
-------------MEEE-PNAIRSFANDVVMDGFLFEHLIWNRGYLVVLVPSGILC-------------------
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Phaseolus vulgaris                      >GB|AAC23610.1|          M---------
---MRARVPL------LLLGILFLASL-SASFATSL---------------------------------------
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---------------------------------------REEEESQDNPFYFNSDN-S-WNTL-FKNQYGHIRV-
LQRFDQQ-SK-RLQNLED-----------YRLVEFRSKPETLLLPQQADAELLLVVRSG-SAILVLVKPDDRRE-
--YFFLTSDNPIFSDHQKIPAGTIFYLVNPDP-K-----EDLRIIQLAMP---VNNPQ--IHEF--
FLSSTEAQQSYLQEFSKHILEASFN-SKF--EEINRVLFEEE---------------GQQEE-------------
----------------GQQEGVIVNIDSEQIKELSKHAKSSS-----------------RKSLSKQ---DNTI--
---------GNEFGNLTERTDN--------S--LNVLISSIEMEE-GALFVPHYYSKAIVILVVNEGEA---
HVELVGPKGN------KE-------------------------------------------------
TLEYESYRAELSKDDVFVIPAAYPVAIKAT----SNVNFTGFGINANN-----
NNRNLLAGKTDNVISSIGRALDGKDVLGLTF-SGS---GDEVMKLI--NKQSGSYFVDAHHHQQEQQKGSHQQE-
-------------------------------------------------------------------QQKGR---
----KGAFV------------------------------------------------------------------
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Vigna radiata                           >TR|Q198W3|              M---------
---VRARVQLL-----L--GILFLASL-SVSFGI-----------------------------------------
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----------------------------VHREHQESQEE-SDSRGQNNPFYFNSDR-R-FHTL-FKNQYGHLRV-
IHRFDQR-SK-QIQNLEN-----------YRVVEFKSKPNTLLLPHHADADFLLVVLNG-RAILTLVNPDG-
RDS---YILEQG-----HAQKIPAGTTFFLVNPND-N-----DNLRIIKLAIP---VNNPHRF-QNF--
FLSSTEAQQSYLRGFSKNILEASFD-SDF--KEIDRVLFGEE-R-----------QQQHGEE-------------
----------------SQEEGVIVELKREQIRELIKHAKSSS-----------------RKELSSQ---
DEPFNLRNSNP--IYSNKFGRWYEITPEK-N-PQLKD--LDVFISSVDMKE-
GGLLLPHYNSKAIVILVINEGEA---KIELVGPSDQ------Q-QQ-----------------------------
-------------DE---SLEVQRYRAELSEDDVFVIPAAYPVAINAT----SNLNFFAFGINAEN-----
NQRNFLAGEKDNVMSEIPT-----EVLDVSFP-AS---GNKVEKLI--KKQSESHFVDAQPEQQQREEGHKGR--
-------------------------------------------------------------------KGS-----
-----LSSI------------------------------------------------------------------
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----------------------------------LGSLY

Vigna luteola                           >TR|A5WYF9|              M---------
---LSARVSLL-----L--GILFLASL-SVSLGI-----------------------------------------
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----------------------------SHRGHQESQEE-SDSSGRNNPFYFSSDR-S-FNTL-FKNQYGHIRV-
LQRFDQR-SK-QIQNLEN-----------YRVVEFKSKPNTLLLPHHADADFLLVVLNG-RALLTLVNPDG-
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RDS---YILEQG-----HAQRIPAGTTFFLVNPND-N-----DNLRIIKLAIP---VNNPHRF-QDF--
FLSSTEAQQSYLQGFSKNVLEASFD-SDF--NEINKVLFGEE----------------QGEE-------------
----------------SEQEGVIVELKREQIQELMRHAKSSS-----------------RKTLSSE---
DEPFNLRNQKP--IYSNKFGRWYEITPEK-N-PQLKD--LDVFLSSVDMKE-
GSLLMPHYNSKAIVIMVINEGEA---NIELVGPREQ------Q-QQ-Q-----------Q---------------
-------------EE---SWQVQRYAAELSEDDVFVIPAAYPVAINAT----SNLNFFVFGINGEN-----
NQRNFLAGEKDNVMSEIPT-----EVLDVTFP-AS---GEKVEKLI--KKQSQSHFVDAQPDEQE-----KGR--
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------------------------------------FVY

Vigna radiata                           >TR|Q198W5|              M---------
---VRARIPLL-----LLLGILFLASL-SVSFGI-----------------------------------------
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----------------------------VHRENIDGAE-VSVSRGKNNPFYFNSDR-W-FHTL-FRNQFGHLRV-
LQRFDQR-SK-QMQNLEN-----------YRVVEFMSKPNTLLLPHHADADFLLVVLNG-RAVTLTVNPDG-
RDS---NILEQG-----HAQKIPAGTTFFLVNPDD-N-----ENLRIIKLAVP---VNNPHRF-QDF--
FLSSTEAQQSYLQGFSKNILEASFD-SDI--KEISRVLFGEEGQ-----------QQQQGQE-------------
----------------SQQEGVIVELKREQIRELTKHAKSSS-----------------KKSLSSE---
DQPFNLRNQKP--IYSNKLGRWFEITPEK-N-PQLRD--LDMFIRSVDMKE-
GSLLLPHYNSKAIVILVINEGKA---NIELVGQREQ------QKQQEE-----------Q---------------
-------------EE---SWEVQRYRAELSEDDVFIIPATYPVAINAT----SNLNFFAFGINAEN-----
NQRNFLAGEKDNVISEIPT-----EVLDVTFP-AS---GEKVKKLI--KKQSESQFVDAQPEQQEREEARKGG--
-------------------------------------------------------------------KGP-----
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------------------------------------FVY

Vigna radiata                           >TR|Q198W4|              M---------
----SARVPLL-----LLLGILFLASL-SVSFGI-----------------------------------------
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----------------------------VHRENHDAAE-VSVSRGKNNPFYFNSDR-W-FRTL-FRNEFGHLRV-
LQRFDQR-SK-QMQNLEN-----------YRVVEFQSKPNTLLLPHHADADFLLVVLNG-
RAVTLTVNPDGGRDS---HILEQG-----HAQKIPAGTIFFLVNPDD-N-----ENLRIIKLAVP---
VNNPHRF-QDF--FLSSTEAQQSYLQGFSKNILEASFD-SDI--KEINRVLFGEEGQ-----------
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QQQQGQE-----------------------------SQQEGVIVELKREQIRELTKHAKSSS-------------
----KKSLSSE---DQPFNLRNQKP--IYSNKFGEFYEITPKK-N-PQLKD--LDVFISSVDMKE-
GSLLLPHYNSKAIVILVINEGEA---NIELVGLREE------Q-QQQQ-----------Q---------------
-------------DE---RLEVQRYRAEVSEDDVFVIPAAYPVAINAT----SNLNFFAFGINAEN-----
NQRNFLAGEKDNVISEIPT-----EVLDLAFP-AP---GEKVEKLV--QKQSTSHFVDAQPEEQQREEGPKGR--
-------------------------------------------------------------------KGH-----
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------------------------------------FVY

Canavalia gladiata                      >EMB|CAA33172.1|         MA--------
---FSARFPLW-----LLLGVVLLASVSA----------------------------------------------
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------------------------SFAHSGHSGGEAEDESEESRAQNNPYLFRSN--K-FLTL-FKNQHGSLRL-
LQRFNED-TE-KLENLRD-----------YRVLEYCSKPNTLLLPHHSDSDLLVLVLEG-QAILVLVNP-
DGRDT---YKLDQG-----DAIKIQAGTPFYLINPDN-N-----QNLRILKFAIT---FRRPGTV-EDF--
FLSSTKRLPSYLSAFSKNFLEASYD-SPY--DEIEQTLLQEE---------------------------------
------------------QEGVIVKMPKDQIQEISKHAQSSS-----------------RKTLSSQ---
DKPFNLRSRDP--IYSNNYGKLYEITPEK-N-SQLRD--LDILLNCLQMNE-
GALFVPHYNSRATVILVANEGRA---EVELVGLEQQ------QQQGLE---------------------------
------------------SMQLRRYAATLSEGDILVIPSSFPVALKAA----SDLNMVGIGVNAEN-----
NERNFLAGNKENVIRQIPR-----QVSDLTFP-GS---GEEVEELL--ENQKESYFVDGQPRHID----------
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AGGKARRAHLPNL--------------------------------------------------------------
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--------------------------------------FRTFY

Canavalia ensiformis                    >SP|P50477|              MA--------
---FSARFPLW-----LLLGVVLLASVSA----------------------------------------------
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------------------------SFAHSGHSGGEAEDESEESRAQNNPYLFRSN--K-FLTL-FKNQHGSLRL-
LQRFNED-TE-KLENLRD-----------YRVLEYCSKPNTLLLPHHSDSDLLVLVLEG-QAILVLVNP-
DGRDT---YKLDQG-----DAIKIQAGTPFYLINPDN-N-----QNLRILKFAIT---FRRPGTV-EDF--
FLSSTKRLPSYLSAFSKNFLEASYD-SPY--DEIEQTLLQEE---------------------------------
------------------QEGVIVKMPKDQIQEISKHAQSSS-----------------RKTLSSQ---
DKPFNLRSRDP--IYSNNYGKLYEITPEK-N-SQLRD--LDILLNCLQMNE-
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GALFVPHYNSRATVILVANEGRA---EVELVGLEQQ------QQQGLE---------------------------
------------------SMQLRRYAATLSEGDIIVIPSSFPVALKAA----SDLNMVGIGVNAEN-----
NERNFLAGHKENVIRQIPR-----QVSDLTFP-GS---GEEVEELL--ENQKESYFVDGQPRHID----------
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AGGKARRAHLPNL--------------------------------------------------------------
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--------------------------------------FRTFY

Pisum sativum                           >TR|Q43626|              MAA-------
-TPIKP---------LMLLAIAFLASV-CVS--------------------------------------------
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---------------------------------------------------------------------------
--------------------------------------SRSD---QENPFIFKSN--R-FQTL-YENENGHIRL-
LQKFDKR-SKI-FENLQN-----------YRLLEYKSKPHTLFLPQYTDADFILVVLSG-KATLTVLKSND-
RNS---FNLERG-----DAIKLPAGTIAYLANRDD-N-----EDLRVLDLAIP---VNKPGQL-QSF--
LLSGTQNQPSLLSGFSKNILEAAFN-TNY--EEIEKVLLEQQEQEPQHRRSLKD--RRQEI--------------
-----------------NEENVIVKVSREQIEELSKNAKSSS-----------------KKSVSSE---
SGPFNLRSRNP--IYSNKFGKFFEITPEK-N-QQLQD--LDIFVNSVDIKE-
GSLLLPNYNSRAIVIVTVTEGKG---DFELVGQRNE------NQG---KENDKEEEQ-EE---------------
-------------ET---SKQVQLYRAKLSPGDVFVIPAGHPVAINAS----SDLNLIGFGINAEN-----
NERNFLAGEEDNVISQVER-----PVKELAFP-GS---SHEVDRLL--KNQKQSYFANAQPLQRE----------
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Pisum sativum                           >TR|D3VNE1|              MAA-------
-TPIKP---------LMLLAIAFLASV-CVS--------------------------------------------
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--------------------------------------SRSD---QENPFIFKSN--R-FQTL-YENENGHIRL-
LQKFDKR-SKI-FENLQN-----------YRLLEYKSKPRTLFLPQYTDADFILVVLSG-KATLTVLKSND-
RNS---FNLERG-----DTIKLPAGTIAYLANRDD-N-----EDLRVLDLTIP---VNKPGQL-QSF--
LLSGTQNQPSLLSGFSKNILEAAFN-TNY--EEIEKVLLEQQEQEPQHRRSLKD--RRQEI--------------
-----------------NEENVIVKVSREQIEELSKNAKSSS-----------------KKSVSSE---
SGPFNLRSRNP--IYSNKFGKFFEITPEK-N-QQLQD--LDIFVNSVDIKE-
GSLLLPNYNSRAIVIVTVTEGKG---DFELVGQRNE------NQG---KENDKEEEQ-EE---------------
-------------ET---SKQVQLYRAKLSPGDVFVIPAGHPVAINAS----SDLNLIGFGINAEN-----
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NERNFLAGEEDNVISQVER-----PVKELAFP-GS---SHEVDRLL--KNQKQSYFANAQPLQRE----------
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Pisum sativum                           >TR|D3VNE0|              MAA-------
-TPMKASFPL-----LMLMGISFLASV-CVS--------------------------------------------
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--------------------------------------SRSD---PQNPFIFKSN--K-FQTL-FENENGHIRL-
LQKFDQR-SKI-FENLQN-----------YRLLEYKSKPRTLFLPQYTDADFILVVLSG-KATLTVLKSND-
RNS---FNLERG-----DTIKLPAGTIAYLANRDD-N-----EDLRVLDLAIP---VNKPGQL-QSF--
LLSGTQNQPSLLSGFSKNILEAAFN-TNY--EEIEKVLLEQQEQEPQHR-SLKD--RRQEI--------------
-----------------NEENVIVKVSREQIEELSKNAKSSS-----------------KKSVSSE---
SGPFNLRSRNP--IYSNKFGKFFEITPEK-N-QQLQD--LDIFVNSVDIKE-
GSLLLPNYNSRAIVIVTVTEGKG---DFELVGQRNE------NQG---KENDKEEEQ-EE---------------
-------------ET---SKQVQLYRAKLSPGDVFVIPAGHPVAINAS----SDLNLIGFGINAEN-----
NERNFLAGEEDNVISQVER-----PVKELAFP-GS---SHEVDRLL--KNQKQSYFANAQPLQRE----------
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Pisum sativum                           >TR|D3VND7|              MAA-------
-TPIKP---------LMLLAIAFLASV-CVS--------------------------------------------
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--------------------------------------SRSD---QENPFIFKSN--R-FQTL-YENENGHIRL-
LQKFDKR-SKI-FENLQN-----------YRLLEYKSKPHTLFLPQYTDADFILVVLSG-KATLTVLKSND-
RNS---FNLERG-----DAIKLPAGTIAYLANRDD-N-----EDLRVLDLAIP---VNKPGQL-QSF--
LLSGTQNQPSLLSGFSKNILEAAFN-TDY--EEIEKVLLEEHEKETQHRRSLKD--KRQQS--------------
-----------------QEENVIVKLSRGQIEELSKNAKSTS-----------------KKGVSSE---
SEPFNLRSRGP--IYSNEFGKFFEITPGK-N-QQLQD--LDIFVNSVDIKE-
GSLLLPNYNSRAIVIVTVTEGKG---DFELVGQRNE------NQG---KENDKEEEQ-EE---------------
-------------ET---SKQVQLYRAKLSPGDVFVIPAGHPVAINAS----SDLNLIGFGINAEN-----
NERNFLAGEEDNVISQVER-----PVKELAFP-GS---SHEVDRLL--KNQKQSYFANAQPLQRE----------
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Pisum sativum                         >SP|P13918|             MAA-------
-TTMKASFPL-----LMLMGISFLASV-CVS--------------------------------------------
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--------------------------------------SRSD---PQNPFIFKSN--K-FQTL-FENENGHIRL-
LQKFDQR-SKI-FENLQN-----------YRLLEYKSKPHTIFLPQHTDADYILVVLSG-KAILTVLKPDD-
RNS---FNLERG-----DTIKLPAGTIAYLVNRDD-N-----EELRVLDLAIP---VNRPGQL-QSF--
LLSGNQNQQNYLSGFSKNILEASFN-TDY--EEIEKVLLEEHEKETQHRRSLKD--KRQQS--------------
-----------------QEENVIVKLSRGQIEELSKNAKSTS-----------------KKSVSSE---
SEPFNLRSRGP--IYSNEFGKFFEITPEK-N-PQLQD--LDIFVNSVEIKE-
GSLLLPHYNSRAIVIVTVNEGKG---DFELVGQRNE------NQQEQRKEDDEEEEQGEE---------------
-------------EI---NKQVQNYKAKLSSGDVFVIPAGHPVAVKAS----SNLDLLGFGINAEN-----
NQRNFLAGDEDNVISQIQR-----PVKELAFP-GS---AQEVDRIL--ENQKQSHFADAQPQQRERG---SRET-
-------------------------------------------------------------------RDR-----
------LSS------------------------------------------------------------------
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Vicia narbonensis                     >TR|Q41677|             MAA-------
-ITMKVSFPL-----LMLLGISFLASV-CVS--------------------------------------------
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--------------------------------------SRSD---QENPFIFKSN--K-FQTL-FENDNGHIRL-
LQKFDER-SKI-LENLQN-----------YRLLEYKSKPRTIFLPQQTNADFILVVLSG-KAILTVLKPDD-
RNS---FNLERG-----DTIKLPAGTIAYLVNKDD-N-----EDLRVLDLAIP---VNGPDQL-QSF--
LLSGSENQQSILSGFSKSVLEASFN-TGY--EEIEKVLLEEREKETQHRRSLRD--KRQHS--------------
-----------------QDEDVIVKLSRGQIEELSRNAKSSS-----------------KKSVSSE---
SEPFNLRSRNP--IYSNKFGKFFEITPEK-N-PQLQD--LDVLVNSVEIKE-
GSLLLPHYNSRAIVIVTVNDGKG---DFEIVGQRNE------NRQGQRKEDDEEEEQGDE---------------
-------------NT---NTQVQNYKAKLSRGDVFVIPAGHPVSIKAS----SNLDLLGFGINAKN-----
NQRNFLAGEEDNVISQIDR-----PVKELAFP-GS---AQEVDRLL--ENQKQSHFANAQPQQRERG---SHET-
-------------------------------------------------------------------RDH-----
------LSS------------------------------------------------------------------
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----------------------------------ILDAF

Vicia faba                              >TR|I0B569|              MAA-------
-TTLKDSFPL-----LTLLGIAFLASV-CLS--------------------------------------------
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--------------------------------------SRSD---QDNPFVFESN--R-FQTL-FENENGHIRL-
LQKFDQH-SKL-LENLQN-----------YRLLEYKSKPHTIFLPQQTDADFILVVLSG-KAILTVLLPND-
RNS---FSLERG-----DTIKLPAGTIGYLVNRDD-E-----EDLRVLDLVIP---VNRPGEP-QSF--
LLSGNQNQPSILSGFSKNILEASFN-TDY--KEIEKVLLEEHGKEKYHRRGLKD--RRQRG--------------
-----------------QEENVIVKISRKQIEELNKNAKSSS-----------------KKSTSSE---
SEPFNLRSREP--IYSNKFGKFFEITPKR-N-PQLQD--LNIFVNYVEINE-
GSLLLPHYNSRAIVIVTVNEGKG---DFELVGQRNE------NQQGLREEYDEEKEQGEE---------------
-------------EI---RKQVQNYKAKLSPGDVLVIPAGYPVAIKAS----SNLNLVGFGINAEN-----
NQRYFLAGEEDNVISQIHK-----PVKELAFP-GS---AQEVDTLL--ENQKQSHFANAQPRERERG---SQEI-
-------------------------------------------------------------------KDH-----
------LYS------------------------------------------------------------------
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----------------------------------ILGSF

Vicia faba var. minor                   >EMB|CAA68525.1|         MAA-------
-TTLKDSFPL-----LTLLGIAFLASV-CLS--------------------------------------------
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--------------------------------------SRSD---QDNPFVFESN--R-FQTL-FENENGHIRL-
LQKFDQH-SKL-LENLQN-----------YRLLEYKSKPHTIFLPQQTDADFILVVLSG-KAILTVLLPND-
RNS---FSLERG-----DTIKLPAGTIGYLVNRDD-E-----EDLRVLDLVIP---VNRPGEP-QSF--
LLSGNQNQPSILSGFSKNILEASFN-TDY--KEIEKVLLEEHGKEKYHRRGLKD--RRQRG--------------
-----------------QEENVIVKISRKQIEELNKNAKSSS-----------------KKSTSSE---
SEPFNLKSREP--IYSNKFGKFFEITPKR-N-PQLQD--LNIFVNYVEINE-
GSLLLPHYNSRAIVIVTVNEGKG---DFELVGQRNE------NQQGLREEYDEEKEQGEE---------------
-------------EI---RKQVQNYKAKLSPGDVLVIPAGYPVAIKAS----SNLNLVGFGINAEN-----
NQRYFLAGEEDNVISQIHK-----PVKELAFP-GS---AQEVDTLL--ENQKQSHFANAQPQERERG---SQEI-
-------------------------------------------------------------------KDH-----
------LYS------------------------------------------------------------------
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----------------------------------ILGSF

Vicia faba                              >PRF|1502201A|           MAA-------
-TTLKDSFPL-----LTLLGIAFLASV-CLS--------------------------------------------
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--------------------------------------SRSD---QDNPFVFESN--R-FQTL-FENENGHIRL-
LQKFDQH-SKL-LENLQN-----------YRLLEYKSKPHTIFLPQQTDADFILVVLSG-KAILTVLLPND-
RNS---FSLERG-----DTIKLPAGTIGYLVNRDD-E-----EDLRVLDLVIP---VNRPGEP-Q----------
--------------------TDY--KEIEKVLLEEHGKEKYHRRGLKD--RRQRG--------------------
-----------QEENVIVKISRKQIEELNKNAKSSS-----------------KKSTSSE---SEPFNLRSREP-
-IYSNKFGKFFEITPKR-N-PQLQD--LNIFVNYVEINE-GSLLLPHYNSRAIVIVTVNEGKG---
DFELVGQRNE------NQQGLREEYDEEKEQGEE----------------------------EI---
RKQVQNYKAKLSPGDVLVIPAGYPVAIKAS----SNLNLVGFGINAEN-----NQRYFLAGEEDNVISQIHK---
--PVKELAFP-GS---AQEVDTLL--ENQKQSHFANAQPRERERG---SQEI-----------------------
---------------------------------------------KDH-----------LYS-------------
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Medicago truncatula                     >TR|Q2HW19|              MA--------
---IKAPFQL-----LMLLGIFFLASV-CVS--------------------------------------------
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--------------------------------------SRDDRHDQENPFFFNAN--H-FQTL-FENENGHIRL-
LQRFDKR-SKI-FENLQN-----------YRLLEYHSKPHTLFLPQHNDADFILAVLSG-KAILTVLNPDN-
RNS---FNLERG-----DTIKLPAGSIAYLANRDD-N-----EDLRVLDLAIP---VNRPGKF-QSF--
SLSGSQNQQSFFSGFSKNILEAAFN-ANY--EEIERVLIEEHEQEPQHRRGLRKD-RRQQS--------------
-----------------QDSNVIVKVSREQIEELSRHAKSSS-----------------RRSGSSE---
SAPFNLRSREP--IYSNEFGNFFEITPEK-N-PQLKD--LDILVNYAEIRE-
GSLLLPHFNSRATVIVVVDEGKG---EFELVGQRNE------NQQ---EQRE-EDEQQEE---------------
-------------ER---SQQVQRYRARLSPGDVYVIPAGHPTVVSAS----SDLSLLGFGINAEN-----
NERNFLAGEEDNVISQIER-----PVKEVAFP-GS---AQDVESLL--KNQRQSYFANAQPQQREREEGRSQRQ-
-------------------------------------------------------------------REL-----
------ISS------------------------------------------------------------------
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----------------------------------ILGVF
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Medicago truncatula                     >TR|Q2HW18|              MA--------
---IKAPFQL-----FMLLGIFFLASV-CVS--------------------------------------------
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--------------------------------------SKDDQHDQENPFFFNAN--R-FQTL-FENENGHIRL-
LQRFDKR-SKI-FENLQN-----------YRLLEYHSKPHTLFLPQHNDADFILAVLSG-KAILTVLNPNN-
RNS---FNLERG-----DTIKLPAGSIAYLANRDD-N-----QDLRVLDLAIP---VNRPGQF-QSF--
SLSGSQNQQSFFSGFSKNILEAAFN-ANY--EEIERVLIEEQEQDP-HRRGLRDR-RHKQS--------------
-----------------QEANVIVKVSREQIEELSRHAKSSSS----------------RRSASSE---
SAPFNLRSRKP--IYSNEFGNFFEITPEK-N-QQLQD--LDILVTNAEIRE-
GSLLLPHFNSRATVIVVVDEGKG---EFELVGQRNE------NQQ---EQREYEEDEQEE---------------
-------------ER---SQQVQRYRARLTPGDVYVIPAGYPNVVKAS----SDLSLLGFGINAEN-----
NQRSFLAGEEDNVISQIQR-----PVKELAFP-GS---AQDVESLL--KNQRQSYFANAQPQQREREEGRSQRQ-
-------------------------------------------------------------------REP-----
------ISS------------------------------------------------------------------
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----------------------------------ILGAF

Medicago truncatula                     >TR|Q2HW22|              MA--------
---IKAPCSL-----LMLLGIVFLASI-CVS--------------------------------------------
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--------------------------------------SRSDQ-DQENPFIFNSN--R-FQTL-FENENGHIRL-
LQRFDKR-SKI-FENLQN-----------YRLLEYHSKPHTLFLPQHNDADFILVVVSG-KAILTVLNPNN-
RNS---FNLERG-----DTIKLPAGTLGYLANRDD-N-----KDLRVLDLAIP---VNRPGQF-QSF--
SLSESENQQSFLSGFSKNILEAAFN-SNY--EEIERVLIEENEQEPQHRRGLRKDERRQQS--------------
-----------------QEANVIVKVSREQIEELSKNAKSSS-----------------RRSESSE---
SEPINLRNQKP--IYSNKFGNFFEITPEK-N-PQLKD--LDILVNYAEIRE-
GSLLLPHFNSRATVIVAVEEGKG---EFELVGQRNE------NQQ---EQREYEEDEQQQ---------------
-------------ER---SQQVQRYRARLSPGDVYVIPAGHPIVVTAS----SDLSLLGFGINAEN-----
NQRNFLAGEEDNVISQIER-----PVKEVAFP-GS---AQDVESLL--KNQRQSYFANAQPQQREREEGRSQRQ-
-------------------------------------------------------------------REP-----
------ISS------------------------------------------------------------------
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----------------------------------ILGAF

Cicer arietinum                         >REF|XP_004493035.1|     MA--------
---IKARFPL-----LVLLGIVFLASV-CAK--------------------------------------------
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--------------------------------------S-----DKENPFFFKSN--N-FQTL-FKNENGHVRL-
LQRFDKR-SQL-FENLQN-----------YRLVEYNSKPHTLFLPQHNDADFILVVLSG-RAILTVLNPND-
RNT---FKLERG-----DTIKLPAGTIAYLANRDD-N-----EDLRVLDLAIP---VNRPGQF-QSF--
SLSGSENQQSYFQGFSKKILEASFN-SDY--EEIERVLLEEQEQKPKQRRGHKDRQQSQ----------------
----------------RQEADVIVKISREQIEELSKNAKSSS-----------------KRSVSSE---
SEPFNLRSRNP--IYSNKYGNFFEITPEK-N-PQLQD--LDISLNSVEINE-
GSLLLPHFNSRATVILVVNEGKG---EVELVGLRNE------NEQ----ENKKEDEEEEE---------------
-------------DR---NVQVQRFQSKLSSGDVVVIPASHPFSINAS----SDLFLLGFGINAQN-----
NQRNFLAGEEDNVISQIQR-----PVKEVAFP-GS---AEEVDRLL--KNQRQSHFANAQPQQKDEG---SQKI-
-------------------------------------------------------------------R-------
----IPLSS------------------------------------------------------------------
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----------------------------------ILGGF

Cicer arietinum                         >REF|XP_004493034.1|     MA--------
---IKARFPL-----LVLLGIVFLASV-CAK--------------------------------------------
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--------------------------------------S-----NKENPFFFKSN--N-FQTL-FKNENGHVRL-
LQRFDKR-SQL-FENLQN-----------YRLVEYNSKPHTLFLPQHNDADFILVVLSG-RAILTVLNPND-
RNT---FNLERG-----DTIKLPAGTIAYLANRDD-N-----EDLRVLDLAIP---VNRPGQF-QSF--
SLSGSENQQSYFQGFSKKILEASFN-SDY--EEIERVLLEEQEQKPKQRRGHKDRQQSQSQS-------------
----------------QQEADVIVKISREQIEELSKNAKSSS-----------------KKSVSSE---
SEPFNLRSRNP--IYSNKYGNFFEITPEK-N-PQLQD--LDISLNSVEINE-
GSLLLPHFNSRATVILVVNEGKG---EVELVGLRNE------NEQ----ENKKEDEEEEE---------------
-------------DR---NVQVQRFQSRLSSGDVVVIPASHPFSINAS----SDLFLLGFGINAQN-----
NQRNFLAGEEDNVISQIQR-----PVKEVAFP-GS---AEEVDRLL--KNQRQSHFANAQPQQKDEG---SQKK-
-------------------------------------------------------------------RGHFI---
----FQARA------------------------------------------------------------------
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----------------------------------REKGF

Cicer arietinum                         >REF|XP_004492829.1|     MA--------
---IKARFPL-----LVLLGIVFLASV-CAK--------------------------------------------
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--------------------------------------S-----DKENPFFFKSN--N-CQTL-FENENGHVRL-
LQRFDKR-SQL-FENLQN-----------YRLMEYNSKPHTLFLPQHNDADFILVVLRG-RAILTVLNPND-
RNT---FKLERG-----DTIKLPAGTIAYLANRDD-N-----EDLRVLDLAIP---VNRPGQF-QSF--
SLSGNENQQSYFQGFSKKILEASFN-SDY--EEIERVLLEEQEQKPEQRRGHKGRQQSQ----------------
------------------ETDVIVKISREQIEELSKNAKSNC-----------------KKSVSSE---
SEPFNLRSRSP--IYSNRFGNFFEITPEK-N-PQLKD--LDIFVNSVEIKE-
GSLLLPHFNSRATVILVVNEGKG---EVELVGLRNE------NEQ----ENKKEDEEEEE---------------
-------------DR---NVQVQRFQSKLSSGDVVVIPASHPFSINAS----SDLFLLGFGINAQN-----
NQRNFLAGEEDNVISQIQR-----PVKEVAFP-GS---AEEVDRLL--KNQRQSHFANAQPQQKRKG---SQRI-
-------------------------------------------------------------------R-------
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------------------------------------SPF

Cicer arietinum                         >TR|Q304D4|
MIVRFSLPDNENDLKLTRSINRDGEILIPKIFIIISV-SQI----------------------------------
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------------------------------------------------SNGASREFDGISSLKVE--V-
FLSLGFNTVSIALHLGLQDGSRH-HCV-VEE-RG-----------CEVLSY-------FLQT-----VVLEVL--
-KLLRTFVEPLE-KTNVTVFVLEKSL----KVVRL--------------------KEKRILLIGIS----
HKLRPR-KQF--LSSTKSGNRALIAILMIEFL-LSFR-ID---DEIERVLLEEQEQKPKQRRGHKDRQQSQSQS-
----------------------------QQEADVIVKISREQIEELSKNAKSSS-----------------
KKSVSSE---SEPFNLRSRNP--IYSNKYGNFFEITPEK-N-PQLQD--LDISLNSVEINE-
GSLLLPHFNSRATVILVVNEGKG---EVELVGLRNE------NEQ----ENKKEDEEEEE---------------
-------------DR---KVQVQRFQSRLSSGDVVVIPATHPFSINAS----SDLFLLGFGINAQN-----
NQRNFLAGEEDNVISQIQR-----PVKEVAFP-GS---AEEVDRLL--KNQRQSHFANAQPQQKDE---ESQKI-
-------------------------------------------------------------------R-------
----IPLSS------------------------------------------------------------------
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----------------------------------ILGGF

Jatropha curcas                         >TR|A0A067L245|         MSIK------
-------------------ANPSSLLFLPILSLLFLSSALPSLGYG-----------------------------
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-----------------------------------------------RRQQQCRR--------------------
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---------------------------------------------------------D-----------------
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-----------------------RETRSRELE-----------EQRDIPYYFS-AE-R-FEY-LQKTQEGNIRA-
LEKFS---SEHLRG-IEN-----------YRLLTLEANPSTFVVPQHNNAKSIVVVLRG-KATITYVLGE-
KRQS---YNLEKG-----DVIEIPAGAVIYLINPD-KN-----EKLNMIILTQP---VTSPGNLANYF--VAGG-
--V-SFYEVFSNDVLEAALNI---TREKLDQLFAEQ---------------------------------------
-------------RQGVILKAPQEQLMALNSNIS--------------------ATKQKGQK-SAGPFNILDQL-
PL-YYNQFGHFLQAS--------LKG--EDISVSYAEIKS-GALMVPFYNSKATAIIFVVEGDG---
YFEMVSPCVS------SQAMEGKGEETE---------------------------------G-----
NEPYQQINSNVSAGDVIVLPAGSPFAILASG--NQNLIAASFTVNDKH-----NQRNFLAG-AGNVMTQLDR---
--EAIKLCFTG-S---AESIESLFR-N-QQEAHFVSMQR------------------------------------
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Vitis vinifera                          >TR|F6GTY5|              MW--------
---------C--AVGGVLGHL------------------------------------------------------
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-----------------------------------------------------------EGGGE-----------
-----------------------------ERQESEG----GEHEL----FLMHDSK----Q--
MVKTDAGEMRVVRSAAGRSIVEKP-----------------MHIGFITMEPKSLFVPQYLDSSLILFIRRG-
EAKVGSIY----NDELVEKQLKIG-----DLYTIPAGSAFYLVNTGE------GQRLHIICSIDMSES-
LKMDTFQSFF---LGGGTHPTSILTGFAPETLSTAFNI---SMSELEEIMTRQEGG---PIIYIKD---------
SQQPSTWAKFLEMKTQDKVKHLKRIMGFDVETEQ--------KHGTWWSWRKLLNSVIG------
NENKKQPVEPTE------PYNLYD-R-KPDFKNSYGWSIALDESDYS--ALAD--SGVGIYSVNLTA-
GSMMAPHLNPTATEIGIVLKGS-GT--VKVVFPNGTSAMDA----------------------------------
---------------------------KVREGDVFWVPRYFPFCQIASR--TGPFEFFGFTTSARR-----
NRPQFLAGA-NSLLKSMRG-----SEFAMAFGV---SEDK-YDHMVNS--
QREAVILPSADVSPPDERKKETGTE--------------------------------------------------
------------------------------------TERV-LKLIKGFGNDVMM-GF------------------
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Nicotiana tomentosiformis               >REF|XP_009605859.1|
MSFHHSSIFITMAIF--------------TK-PKLLFLFF---LILSIFLYSQCD--------------------
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-----------------------------------------------------EEENNPYLFE-SQ-R-FRS-
RFKSKHGEFRV-LEKFTER-SELLGG-LEK-----------YGVAVLEFEPLSFMFPHHCDAEIILFVVRG-
RGTISIAEQE-EKNS---FNLENG-----DVIRVNAGSTIYMINRN-NN-----ERFFVYVLAKT---
VNIPGQFQEYF--SGGGENPE-SFYRAFSSEILETAFNI---PRDTIEGLFGQQ---------------------
-------------------------------RKGIFVKASEEQIRAISEHASRS-----------------
TKQQTRG------PFNLLNER-PL-LGNRFGQYFEATPERFE--QLRD--LDAAAGIMNINQ-
GGMLLPVYCTRTTWFVMVVEGNG---RFEMACPH-L------GSQSQ----RQGR--------------------
--------------------HYQKVQGSLSVGDVLIIRAGHPITVVATG--DSDLRMVGIGFNAHN-----
NRMNFLAGR-QSIWRNIDR-----EAKEVSFNM-P---ASEVEEILQ-K-QDQSYFVAGPEQRQQQMREEATR--
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----------ER---------------------------------Q-----------------------------
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---------------------------YVSSSLDFV--F

Nicotiana sylvestris                    >REF|XP_009771135.1|     M---------
--AIF--------------SK-PKLLFLFF---LILSIFLASQCD------------------------------
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-------------------------------------------EAENNPYLFK-SH-R-FRS-RFTSKHGEFRV-
LEKFTER-SELLGG-LEK-----------YRVAVLEFEPLSFMLPHHCDAEVIFFVVRG-RGTISIAEQD-
EQNS---FNLEHG-----DVIRVNAGSTIYMINRD-NN-----ERFFVYVLAKT---VNIPGQFQEYF--
SGGGENPE-SFYRAFSSEILETAFNT---SIDTIEGLLGQQ----------------------------------
------------------RKGIFVKASEEQIRAISEHASLS-----------------TKQQTRG------
PFNLLNER-PL-LGNKFGHYFEATPERFE--QLRD--LDAAAGIMNINQ-GGMLLPVYCTRTTWFVMVVEGNG--
-RFEMACPH-L------SSQSQSQ--RQGR----------------------------------------
HYQKVQGSLSVGDVMIIRAGHPITVIATG--DSELRMVGIGFNAHN-----NRMNFLAGR-QSIWRNVDR-----
EAKEVSFNM-P---AREVEEILQ-K-QDQSYFVAGPEQRQQQMREERTR--------------------------
-------------------------------------------------------------GQ------------
---------------------Q-----------------------------------------------------
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---YVSSSLDFV--F

Solanum lycopersicum                    >TR|K4CVL0|              M---------
--AIF--------------TKLPKFLFLFFYLLILISMFIACQCEC-----------------------------
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-----------------------------DRE-----------KENNNPYLFE-SH-M-FKS-RFESKHGEFRV-
LDKFTQ----LLLG-IEN-----------YRIGVLEFEPRSFLLPHHFDAQLLLLIVRG-RGSISIAEED-
EKNS---FNLEYG-----DVLSVSAGSTIYFTNTD-NK-----EKFSVYVLAKA---INVPGQFQEFF--
SAGSENPE-TFYRAFSSDILETAFNT---PRSRLERLFGLQ----------------------------------
------------------KQGIIIKASEEKIRAISQHASRS-----------------TRGETRG------
PFNVLNQR-PL-IGNRFGQYFEAAPESFQ--HLMD--LDVAVGIMNINQ-GGMILPVYSTRTTWLVMVAQGNG--
-RFEM-----V------SSQSQER--RG------------------------------------------
HRKAVRDCLSVGDFFVIPAGHPITVIANA--DSNLSMVGFGINGHN-----SMLNFLAGQ-ESIWRNVNR-----
ETKELSFNM-P---AREVEEILQ-N-QNESYFVAAPN----------EE--------------------------
-------------------------------------------------------------GKKM----------
-------------------GQQ-----------------------------------------------------
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---YESLILDLV--F

Aegilops tauschii                       >TR|M8BGV8|
MEVNPRAFVVPGFTDADGVGYVAQGEGVLTVIESGEKRSYTVRQGDVIVAPAGS-
IMHLANTDARRKLVIAKILHTISVPGRFQYFSAKPLLASLSKRVLRAALKKK-L---------------------
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----------------------------------------------GTYIHGHGRERADLRRAAGEAARQAPR-
QGGGVQVHLFG--------S-IIRTDHGFVKA-LRPFDE-VSRLLRG-IRN---------
YRVAIMEVNPRAFVVPGLTDADGVGYVAQG-EGVLTVI--ENGEKRS--YTVREG-----
DVIVAPAGSIMHLANTD-GR-----RKLIIAKILHT---ISVPGMFQYF---------
SAKPLLASLSKRVLRAALKT---SDERLERLL-DP---------------RQGQEK-------------------
----------TGGSMSIVRASEEQLHELSRQAS-EGSQGHHWPLPPF------------RGDSRDTYNLLEQRP-
-KIANRHGRLYEADARSFH--ALAQ--HDVRVAVANITP-GSMTAPYLNTQSFKLAVVLEGEG---E--------
---------------------QGKGRW-SEEEDDDQRQQRRR-
GSGSESESESEEQQDQQRYQTIRARVSRGSAFVVPPGHPVVEIASSQGSSNLQVVCFEINAER-----
NERVWLAGR-NNVIGKLDN-----PAQELTFGR-P---AREVQEVFRAKDQQDEGFVAGPEQDQ-----------
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ERGERGRG-------------------------------------------DDA---------------------
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-----------------------------------VGAFLRMATGAF

Oryza sativa subsp. indica              >TR|B8AL97|              MA--------
--KKKTSSS--MARSQ---LAALLI-SLCFLS-L-----------------------------------------
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-----------ASNAVGWSRRGERE-EEDERRR----HGG----EGGRPYHFGEESFRHWTRT----RHGRFSV-
LERFPDE--QVVGAAVGG-----------YRVAVLEAAPRAFLQPSHYDADEVFYVKEG-EGVIVLLR-EGR-
KES--FCVREG-----DAMVIPAGAIVYSANTH-SS-----KWFRVVMLLNPV---STPGHFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERQRE---------------------------------------
-----------G-GEITTAPEEQIRELSKSCSR-------G-------GGGGSGS----EWEIKPSSLTGKSP--
YFSNNHGKLFELTGDEC--RHLKK--LDLQIGLANITR-GSMIAPNYNTRATKLAVVLQ-G-SG-
YFEMACPHVSGG---GSSERRE----REREHG----RRRE---E--EQGEEE--------
HGERGEKARRYHKVRAQVREGSVIVIPASHPATIVASE--GESLAVVCFFVGANH-----DEKVFLAGR-
NSPLRQL---DD--PAKKLVFGGS--AARE-ADRVLAA--QPEQILLRGPHGRGS--------------------
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-------------------------VSDM

Oryza nivara                            >TR|A0A0E0GUU5|          MA--------
--KKKTSSS--MARSQ---LAALLI-SLCFLS-L-----------------------------------------
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-----------ASNAVGWSRRGERE-EEDERRR----HGG----EGGRPYHFGEESFRHWTRT----RHGRFSV-
LERFPDE--QVVGAAVGG-----------YRVAVLEAAPRAFLQPSHYDADEVFYVKEG-EGVIVLLR-EGR-
RES--FCVREG-----DAMVIPAGAIVYSANTH-SS-----KWFRVVMLLNPV---STPGHFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERQRE---------------------------------------
-----------G-GEITTAPEEQIRELSKSCSR-------G-------GGGGSGS----EWEIKPSSLTGKSP--
YFSNNHGKLFELTGDEC--RHLKK--LDLQIGLANITR-GSMIAPNYNTRATKLAVVLQ-G-SG-
YFEMACPHVSGG---GSSERRE----REREHG----RRRE---E--EQGEEE--------
HGERGEKARRYHKVRAQVREGSVIVIPASHPATIVASE--GESLAVVCFFVGANH-----DEKVFLAGR-
NSPLRQL---DD--PAKKLVFGGS--AARE-ADRVLAA--QPEQILLRGPHGRGS--------------------
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-------------------------VSDM

Oryza sativa subsp. japonica            >TR|Q852L2|              MA--------
--KKKTSSS--MARSQ---LAALLI-SLCFLS-L-----------------------------------------
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-----------ASNAVGWSRRGERE-EEDERRR----HGG----EGGRPYHLGEESFRHWTRT----RHGRFSV-
LERFPDE--QVVGAAVGG-----------YRVAVLEAAPRAFLQPSHYDADEVFYVKEG-EGVIVLLR-EGR-
RES--FCVREG-----DAMVIPAGAIVYSANTH-SS-----KWFRVVMLLNPV---STPGHFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERQRE---------------------------------------
-----------G-GEITTAPEEQIRELSKSCSR-------G-------GGGGSGS----EWEIKPSSLTGKSP--
YFSNNHGKLFELTGDEC--RHLKK--LDLQIGLANITR-GSMIAPNYNTRATKLAVVLQ-G-SG-
YFEMACPHVSGG---GSSERRE----REREHG----RRRE---E--EQGEEE--------
HGERGEKARRYHKVRAQVREESVIVIPASHPATIVASE--GESLAVVCFFVGANH-----DEKVFLAGR-
NSPLRQL---DD--PAKKLVFGGS--AARE-ADRVLAA--QPEQILLRGPHGRGS--------------------
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-------------------------VSDM

Oryza sativa subsp. japonica            >TR|Q8L8I0|              MA--------
--KKKTSSS--MARSQ---LAALLI-SLCFLS-L-----------------------------------------
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-----------ASNAVGWSRRGEQE-EEDERRR----HGG----EGGRPYHLGEESFRHWTRT----RHGRFSV-
LERFPDE--QVVGAAVGG-----------YRVAVLEAAPRAFLQPSHYDADEVFYVKEG-EGVIVLLR-EGR-
RES--FCVREG-----DAMVIPAGAIVYSANTH-SS-----KWFRVVMLLNPV---STPGHFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERQRE---------------------------------------
-----------G-GEITTAPEEQIRELSKSCSR-------G-------GGGGSGS----EWEIKPPSLTGKSP--
YFSNNHGKLFELTGDEC--RHLKK--LDLQIGLANITR-GSMIAPNYNTRATKLAVVLQ-G-SG-
YFEMACPHVSGG---GSSERRE----REREHG----RRRE---E--EQGEEE--------
HGERGEKARRYHKVRAQVREGSVIVIPASHPATIVASE--GESLAVVCFFVGANH-----DEKVFLAGR-
NSPLRQL---DD--PAKKLVFGGS--AARE-ADRVLAA--QPEQILLRSPHGRGS--------------------
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-------------------------VSDM

Oryza glumipatula                       >TR|A0A0D9ZEA9|          MA--------
--KKKTSSS--MARSQ---LAALLI-SLCFLS-L-----------------------------------------
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-----------ASNAVGWSRRGERE-EEDERRR----HGG----EGGRPYHFGEESFRHWTRT----RHGRFSV-
LERFPDE--QVVGAAVGG-----------YRVAVLEAAPRAFLQPSHYDADEVFYVKEG-EGVIVLLR-EGR-
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RES--FCVREG-----DAMVIPAGAIVYSANTH-SS-----KWFRVVMLLNPV---STPGHFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERQRE---------------------------------------
-----------G-GEITTAPEEQIRELSKSCSR-------G-------GGGGSGS----EWEIKPSSLTGKRP--
YFSNNHGKLFELTGDEC--RHLKK--LDLMVGLANITR-GSMIAPNYNTRATKLAVVLQ-G-SG-
YFEMACPHVSGG---GSSERRE----REREHG----RRRE---E--EQGEEE--------
HGERGEKARRYHKVRAQVREGSVIVIPASHPATIVAGE--GESLAVVCFFVGANH-----DEKVFLAGR-
NSPLRQL---DD--PAKKLVFGGS--AARE-ADRVLAA--QPEQILLRGPHGRGS--------------------
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-------------------------VSDV

Oryza meridionalis                      >TR|A0A0E0D840|          MA--------
--KKKTSSSSSMARS----LAALLL-SLCFLS-L-----------------------------------------
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-----------ASNAVGWSRRGEREREEEDERR----HGGGRGGEGGRPYHFGEESFRHWTRT----RHGRFSV-
LERFSDE--QVVGAAVGG-----------YRVAVLEAAPRAFLQPSHYDADEVFYVKEG-EGVIVLLR-EGR-
RES--FCVREG-----DAMVIPAGAIVYSANTH-SS-----KWFRVVMLLNPV---STPGHFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERQRE---------------------------------------
-----------G-GEITTAPEEQIRELSKSCSRRG-----G-------GGGGSGS----EWEIKPSSLTGKRP--
YFSNNHGKLFELTGDEC--RHLKK--LDLLIGLANITR-GSMIAPNYNTRATKLAVVLK-G-SG-
YFEMACPHVSGG---GSSERRE----REREHG----RR-E---E--EQGEE---------
HGERGEKARRYHKVRAQVREGSVIVIPASHPATIVAGE--GESLAVVCFFVGANH-----DERVFLAGR-
NSLLRQL---DD--PAKKLVFGGS--AARE-ADRVLAA--QPEQILLRGPPGRGS--------------------
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-------------------------VSDM

Oryza barthii                           >TR|A0A0D3FQ29|          MA--------
--KKKTSSS--MARSQ---MAALLI-SLCFLS-L-----------------------------------------
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-----------ASNAVGWSRRGERE-EDDE----------------------GVKWLKHY---------------
----------------------------------------AFLQPSHYDADEVFYVKEG-EGVIVLLR-EGR-
RES--FCVREG-----DAMVIPAGAIVYSANTH-SS-----KWFRVVMLLNPV---STPGHFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERHRE---------------------------------------
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-----------G-GEITTAPEEQIRELSKSCSRGG-----G-------GGGGSGS----EWEIKPSSLTGKSP--
YFSNNHGKLFELTGDEC--RHLKK--LDLQIGLANITR-GSMIAPNYNTRATKLAVVLQ-G-SG-
YFEMACPHVSGG---GSSERRE----REREHG----RRRE---E--EQGEEE--------
HGERGEKARRYHKVRAQVREGSVIVIPASHPATIVASE--GESLAVVCFFVGANH-----DEKVFLAGR-
NSPLRQL---DD--PAKKLVFGGS--AARE-ADRVLAA--QPEQILLRGPHGRGS--------------------
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-------------------------VSDM

Oryza punctata                          >TR|A0A0E0KK37|          MV--------
--KKTTTSSS-MARSPSPLLTALLL-SLCFLS-L-----------------------------------------
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-----------ASTAVGWSRRGEREEDE----R----HGGGRG-EGGRPYHFGEESFRHWTRT----RHGRFSV-
LERFSDE--PVVGA-VGD-----------YRVAVLEAAPRAFLQPSHYDADEVFYVKEG-EGVIVLLR-DGK-
RES--FCVREG-----DAMVIPAGAIVYSANTH-SN-----KWFRVVMLLNPV---STPGHFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERKRE---------------------------------------
-----------G-GEISTAPEEQIRELSKSCSR---------------GGGGSGS----EWEIKPSSLTGKRP--
SFSNNHGKLFELTGDEC--RHLKK--LDMLIGLANITR-GSMMAPSYSTRATKVAVVLQ-G-NG-
YFEMACPHVSGG---RSSERRE----REREHG----RRRE---EWGREEEQE--------
EEERGEKARRYKKVRAQVREGSVIVIPASHPATIVAGE--GENLAVLCFAVGANH-----DEKVFLAGR-
NSLLKQL---DD--PAKKLVFGGS--AARE-ADRVLAA--QPEQIFLRGPHGDRS--------------------
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-------------------------VSDM

Oryza brachyantha                       >TR|J3LTM2|              MV--------
--N--TTSS--MARSP--LVVALLL-SLFLLSSL-----------------------------------------
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-----------ASSAVGWSRRGEEEEGDDERRRGR--HG-----EGGRPYHFGEESFRHWTRT----RHGRFSV-
LERFSDE--PLVGA-VWD-----------YRVAVLEAAPRAFLQPSHYDADEVFYVKEG-EGVIVLLR-EGR-
RES--FCVREG-----DAMVIPAGAIVYSANTH-SS-----KWFRVVMLLNPV---STPGRFEEYFPVG-GDR--
PESFFSAFSDDVLQAAFNTR---REELEKVFERQRE---------------------------------------
-----------G-GEITTAPEEQVRELSKSCSR----------------GGGSGS----EWEIKPSSLTGKRP--
TYSNNHGKMFEIDGDEC--RHLRK--LDMLVGLANITR-GSMMAPSYSTRATKVAMVLH-G-SG-
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YFEMACPHVSGG---RSSERRE----REREQG----RREEWGREEEEQEEEQ--------
HGGRQQKARRYHKVRAQVREGSVIVIPAAHPATFVAGD--DENLSVLCFGVGANY-----DDKVFLAGR-
NSLLRQL---DD--PAKALVFGGS--AAREMVDRVLAA--QPEQIFLRGPHGRGG--------------------
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-------------------------VSDA

Leersia perrieri                        >TR|A0A0D9W021|          MA--------
--S--------MATSPLLATALLLFFSLCIILSH-----------------------------------------
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-----------ADADAG----------------------------GGRPYHFGEESFRHWTRT----RHGRFSV-
LERFSGE--AIDGA-VGD-----------YRLAVLEAAPRAFLQPSHYDADEVFFVKEG-EGVIVLLRGNGR-
RES--FCVKEG-----DAMVIPAGAIVYSANTH-DS-----KWFRVVMLLNPV---ATPGHFEEYFPVG-VGR--
PESYFDAFSEDVLQAAFNTP---REEWEKVFERKQE---------------------------------------
-----------R-GEITTAPEEQIRELTKSCSR-S-----G-------YSGRSGS----DWEIKPISLTGKRP--
SFSNSHGKMFDIDGDDS--RHLRK--LDML------------------------------G-RG-
IFEMACPHKSGE---EKSER----------HG----RRRE---EWGRGEEEE--------E----
EKARRYKKVRAEIREGSVVVIPAAHPATLVAGE--GENLAVLCFGVGANY-----DEKVFLAGR-NSLLRQI---
DD--AAKALVFGGGSPAAARDVDRLLAA--QPEQVFLRGPHGRGH------------------------------
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---------------VSDM

Zea mays                                >TR|B6UGJ0|              M---------
----------------KVPVLLLLVSL-CFSLAL-----------------------------------------
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-----------A-----WQTDTE---------------SGSG-----RPYHYGEESFRHWTRS----RQGRFRV-
LERFTHE--LLEDA-VGN-----------YRVAELEAAPRTFLQPSHYDADEVMFVKEG-EGVIVLLRG-GK-
RES--FCVREG-----DVMVIPAGAVVYSANTH-QS-----EWFRVVMLLSPV--VSTSGRFEEFFPIG-GES--
PESFLSVFSDDVIQASFNTR---REEWEKVFEKQSK---------------------------------------
-------------GEITTASEEQIRELSRSCSRGG-RGSRG-------EGGDSGSSSSSKWEIKPSSLTDKKP--
THSNSHGRHYEITGDEC--PHLRL--LDMDVGLANIAR-GSMMAPSYNTRANKIAIVLK-G-QG-
YFEMACPHVSGG---RSSP-R-----RERGHG----REEEEERE----EEQG--------GGG-
GQKARSYRQVKSRIREGSVIVIPAGHPTALVAGE--DKNLAVLCFEVNASF-----DDKVFLAGT-NSALQKM--
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-DR--PAKLLAFGADE---EQQVDRVIGA--QKDAVFLRGPQSH-R-----------------------------
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----------------VSSV

Zea mays                                >TR|Q7M1Z8|              M---------
----------------KVPVLLLLVSL-CFSLAL-----------------------------------------
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-----------A-----WQTDTE---------------SGSG-----RPYHYGEESFRHWTRS----RQGRFRV-
LERFTHE--LLEDA-VGN-----------YRVAELEAAPRAFLQPSHYDADEVMFVKEG-EGVIVLLRG-GK-
RES--FCVREG-----DVMVIPAGAVVYSANTH-QS-----EWFRVVMLLSPV--VSTSGRFEEFFPIG-GES--
PESFLSVFSDDVIQASFNTR---REEWEKVFEKQSK---------------------------------------
-------------GEITTASEEQIRELSRSCSRGG-RSSRS-------EGGDSGSSSS-KWEIKPSSLTDKKP--
THSNSHGRHYEITGDEC--PHLRL--LDMDVGLANIAR-GSMMAPSYNTRANKIAIVLK-G-QG-
YFEMACPHVSGG---RSSP-R-----RERGHG----REEEEERE----EEQG--------GGG-
GQKSRSYRQVKSRIREGSVIVIPAGHPTALVAGE--DKNLAVLCFEVNASF-----DDKVFLAGT-NSALQKM--
-DR--PAKLLAFGADE---EQQVDRVIGA--QKDAVFLRGPQSH-R-----------------------------
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----------------VSSV

Sorghum bicolor                         >TR|C5WY16|              MP--------
--H-------TGAMKTKVLVLLLLLSV-CSSLAL-----------------------------------------
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-----------E-----WQTDTG---------------SGSG-SGSGRPYHFGEESFRHWTRS----RQGRFRV-
LEQFTHE--LLEDA-VGN-----------YRVAELEAAPRAFLQPSHYDADEVMFVKEG-EGVVVLLRG-ER-
KES--FCVREG-----DVLVIPAGAVVYSANTH-HS-----EWFRVVMLLSPV---STSGHFEEFYPIG-GES--
PESFLSVFSDDVIQASFNTR---REEWEKVFEKQSK---------------------------------------
-------------GEITTASEEQIRELSRSCSRGGGRSSRE-------EGGDTGSRSSSKWEIKPSSLTGKRP--
THSNSHGKHYEITGDEC--PHLRV--LDMKVGLANISR-GSMMALSYSTRAHKIAIVVD-GGEG-
YFEMACPHVSGG---RSSSQR-----REREHG----RREWGGRE----EEEE--------
EGGRGHKSRSYRQVKSRVREGSVIVIPAGHPTALVAGE--NSNLAVLCFEVNANF-----DEKVFLAGR-
NSALKQM---DG--PAKLLAFGADE---EEVVDRVIGA--QKDAVFLRGPQSR-R--------------------
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-------------------------VSSA

Setaria italica                         >TR|K4A9S8|              M---------
-----------GAMKRSPLVLLLLLSLLCSSLAL-----------------------------------------
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-----------AS----YSYGDA---------------GGEGRSGSGRPYHFGEERFRQWAQS----RQGRFRV-
LERFTHE--LLEDA-VGN-----------YRVAELEAAPRAFLQPSHYDADEVMFVKEG-EGVVALLAR-GK-
RES--FCVKEG-----DVLVIPAGAVVYSANTH-GS-----KWFRVVMLLNPV---STKGRFEEFFPIG-GES--
PESFFSVFSDDVLQAAFNTR---REEWEQVFEKQSK---------------------------------------
-------------GEITTASEEQIRELSRSCSRTG----RS-------HGG-----GESMWDIKLCSLTSKRP--
LHSNNHGRHYEITGDDC--PQLRA--LDIEVGLTNLSR-GSMTAPSYSTHADKLFVVLD-G-SG-
YFEMACPHLSSG---RSSSPR-----RERGHG----SREWGKEE----EEEA--------
EQEGGQKSRGYKQVKSRIREGSVIVIPAGHPMTLVAGE--DNNLAVLYFSVNARH-----DEKVFLVGS-
NGLLRQM---DE--AAKALAFGAEK---EK-VDRVIGA--QSDAVFLRGPNSR-R--------------------
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-------------------------VSSA

Brachypodium distachyon                 >TR|I1GMC8|              M---------
---------KLTARSRLLLVLALAILSLCLSVSS-----------------------------------------
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-----------ASD---WDTEREERGGQSAGRQGEGEQEQGRYSSSGRPYHYGEESFKYRTTT----RHGRFRV-
LERFTHE--LLRDSPVGD-----------RRVAVLEAAPRAFLQPSHYDADEVFYVREG-EGVVVML-WKGK-
RQS--FCVREG-----DVMVIPAGATVYSANTH-DS-----RWFRVVMLLNPV---STPGRFGEFFPVGSGER--
QESFFGAFSDDILQASFNAR---KEEVEKVFEESSE---------------------------------------
-------------GEITQAPEEQIRALSKSCS----------------SSRGSGSGSRSEQDFKPTSIASKKP--
RYSNNHGRLSEITGDEC--PHLRR--LDMEVGLANITR-GSMMAMSYSTRATKIAVVVE-G-NG-
YFEMACPHMSGSSSRRSERRRE----
REQEHGSEQERRERQEREHEQSSEEERRREREQGQREGGQKSRGYRQVGANIKEGSVIVLPAAHPATFVAGG--
DGNLAVLCFGVGAER-----DEKVFLTGK-NSPLRQLVEEDE--AARKLVFGER----AQEAEKLVRG--
QSDDVFVRGPRQRQSG-----------------------------------------------------------
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------------------------------------------------------------VADM

Triticum urartu                         >TR|M7ZQM3|              M---------
----------KSAV-RSPWLVLAIVLSLCLSLSF-----------------------------------------
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-----------AS----WDAEDVGRGS----RRWQEGGDEGRSGGSGRPYHFGQESYREWAKS----RHGHFKV-
LERFDHE--LLRGS-IGD-----------YRVAYLDAAPRAFLQPSHHDADEIAFVREG-EGVLVLLR-NGK-
RES--FCIREG-----DVIVIPAGSIVYSANTH-RS-----KWLRVVMLINPV---STPGRFQEFFLIGSGDER-
PQSFLSVFSDEVIQAALNTR---REDVDRVFESKSK---------------------------------------
-----------GEGEIYEASEEQIRELSRSCSRGGRGGGG------------SGS---EKEDIQPRSLTGEKP--
RYSNKHGRFHQITGDQC--HHLRK--LDMDVTLVNITR-GSMTALKYTTRSTRIYVVVE-GRDG-
YFEMACPHISSS---GRSERREHEQEREREHG--
QGRRSEEREREQGRGRRSEEREQEQGHGREQEKSRGYRQVRAQIKVGSVIVLPAGHPATFVAGN--
DGNLALLSFGVGANN-----DEEVFVTGG-NSVLKQL---DE--AAKALAFPQQ---ARELADRVIRA--
QPESVFVAGPQQQ-RR-----------------------------------------------------------
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------------------------------------------------------------VADM

Aegilops tauschii                       >TR|M8B8C6|              M---------
----------KSTVVRSPWLALALVLSLCLSLSF-----------------------------------------
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-----------AS----WDAEDEGRGS----RRWQEGGDERRSGESGRPYHFGEESFREWAKS----RHGHFK--
--------------------------------------------PSHYDADEIAFVREG-EGVLVLLR-NGK-
RES--FCVREG-----DVFVIPAGSIVYSANTH-RS-----KWFRVVMLLNPV---STPGSFQEFSPIGFGGEQ-
PQSFFSVFSDEVIRAAFNTRQ--REDVDRVFETKSR---------------------------------------
-----------GEGQISEGSEEQIRELSRSCSRGGRGGGGG-----------SGS---EKEDIQPRSLTGEKP--
RYSNKHGRFHQITGDQC--HHLRK--LDMDVTLVNITR-GSMTALRYTTRSTRIYIVVE-GRDG-
YFEMACPHVSSS---GRSERREHEQEREREHG--HGRRSEERGQEHGR--RSEE--
EEHGHGGEQEKSRGYRQVRAQIKVGSVIVLPAGHPATFVAGN--EGNLALLSFGVGANN-----DEEVFVTGG-
NSVLKQL---DE--AAKALAFPQQ---ARELADRVIRA--QPESVFVPGPQQQ-RR-------------------
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-------------------------VADM

Hordeum vulgare var. distichum          >TR|M0XUU4|
MITNSSDQCTRQRAPTSITMKPAAARSPWLALAIVLSLCLSLSF-------------------------------
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---------------------AS----WDAEDEGRGS----RRWQEGGDEGRSGESGRPYHFGEESYREWAKS--
--RHGHFKV-LKRFDHE--LIRGS-IGD-----------YRVACLDAAPRAFLQPSHYDADEIAYVREG-
EGVVVLLR-NGK-RES--LCVREG-----DVFVIPAGSIVYSANTH-RS-----KWFRVVMLLNPV---
STPGSFQEFFPIGYGGEQQPESFFSVFSDEVIRAAFNTRR--REDVDRVFKRNSR--------------------
------------------------------GEGEISEASEEQIRELSRSCSRGGRGGGGG-------GGGGSGS-
--EKEDIRPRSLTGEKP--RYSNKHGRLHQITGDQC--PHLRN--LDLDVNLVNITR-
GSMTALRYTTRATKIVVVVEAGNDGNYFEMACPHLSSS---GRSERRE------------RGRSEEQGGQE----
-------EEKGHGGEQEKSRGYRQVRAEIKVGSVIVLPAGHPATFVAGN--EGNLAL------------------
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Brachypodium distachyon                 >TR|I1GMD1|              M---------
---------KPAARRSPLLVLALVLLSL---SSF-----------------------------------------
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-----------ASLITGSHAEAVRRPDAAE----------------GRPYIFGEESFRDWTPTGKQPQGGRFRV-
LDRFTDE--LLRDTPAGA-----------RRVAMLELAPRAVLLPSHKDADEAFYVKEG-
EGVAVLLRTNGTTRES--FCVREG-----DVMVIPAGAIA------------------------PV--
STPPGRF--------GSR----SIFGGFSEDVLQAAFNVNA--GDVLR--IQAEMD-------------------
-------------------------------ARGVIVRVPAGLIRAL----------------------------
--------------GKKP--LYSNDHGRLFEITGDEF--PDLLN--IDVELGLANITR-
GSMMAPSFRTRAATIALVLE--GNGQVEVVGGPGVSA--PGGRSE-------RQQEQG-----------------
------------AQKAERSNMQQGVRADIKEGPVVVLPAGHPATLVAG---------------------------
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Aegilops tauschii                       >TR|M8C814|              M--------
APLLVLLLLLSGWSAMGTPRLR-----------------------------------------------------
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------------------------------------------------------------ERWEEGEGEWRPE--
------------------------------EEAKGGG----GGGGTGKGLFLLDKVE----K--
VVESEGGSVHVVRGLPASGVPEAPWQHGGWSAGCGACREGLMHIGFITMEPKTLFVPQYIDSNLILFVQRG-
DVKVGWIH----KGGLVEKQLKMG-----DVLQIDAGSTFYMVNTGK------GQRLHIICSIDASDSA-
GFAPYQSFY---LGGGGKRTSVLAGFEPKILVTALNT---TFDELERILPVKPLG---PFVSYTTESG--
GKEHGQGDKR-DVG---ENGRESEPWRPVGRGNDDERGSGQSTWT------WSWRKLMSRFIG--------
GELNKKSDKTVRAP-EPYNLFD-H-EPSFRNTYGWSISVDKHDYH--PLDH--SDIGVYLVNLTA-
GSMMAPHVNPRATEYGVVLAGE-GV--IQVVFPNGSLAMSA----------------------------------
---------------------------EARAGDVFWIPRHFPFVQVASR--GGPFVFFGFTTSARR-----
NKPQFLTGP-TSVLRMMLG-----PELAAGLGV---PEKE-LKDVMEA--QKVAVIEPP---------
LPEKEKG--------------------------------------------------------------------
------------------GKEREPFVMKQVAME------------------------------------------
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Brachypodium distachyon                 >REF|XP_003557965.1|
MDRCGVVVMTPLLTLLLLLSGRSAMGAPRYR--------------------------------------------
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ERWEQEGPEWRPD--------------------------------EEGKGG-----------KGLFLLDNVE---
-K--VVDSEGGQVHVVRG---PFVPEQPWQQ------
YGACREGLMHIGFITMEPKTLFVPQYIDSNLILFVQRG-EVKIGWIH----NDELVQKQLKMG-----
DVLHIEAGATFYMVNTGK------GQRLQIICSIDASDSPIGLGPYQSFF---
LTGGGNPTSVLAGFDPKMLVTAFNT---TYDEVARLFRPETRG---
PFVSFGTEPGSGGKERGQREEEGDAGNKEEASRKAGPWRPVGRGDDEERDDEQSS-T------
WSWRKLMGSFIGFGGASNDAAQLENKKDKTVRAP-EPYNLFD-H-EPGFRNAYGWSVSVDKHAYE--PLDH--
SDIGVYLVNLTA-GSMMAPHVNPRATEYGVVLGGE-GE--VQVVFPNGSLAMSA---------------------
----------------------------------------RVRPGDVFWIPRYFPFAQVASR--
SGPFEFFGFTTSARR-----NKPQFLVGA-NSLLRTMLG-----PELAAGFGV---PEKE-LGELMRA--
QKEAVILSS---------LPEKEE---------------------------------------------------
-------------------------------------KGREQSVIKQVAKE------------------------
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Musa acuminata subsp. malaccensis       >TR|M0TXJ0|              MGRRSEVTL-
-LLLQLLAVASCCAMAVTGYR------------------------------------------------------
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-----------------------------------------------------------ER------EIGGE---
-----------------------------EEVRG----------TTASPFKLEKSE----Q--
VVKTEGGEVRVVRGFGSS----SKWGGGGPVSP--------MHIGFIFMEPKTLFIPQYLDSSLILFVHRG-
DVRVGWIY----KDGLAERQLKMG-----DIIHIPAGSTFYMVNAGE------GQRLQIICSIDTSDS-
MDFSPYQSFF---IGGGMYPTSVVAGFDMGTLSTAFNV---TEEEVQAILGSQTGG---PIVLLT----------
GEAAERID-----RRRRKG-----LLEFHDEEEEDGW----------WTWRKLLTGILGGG-----
FGDRNRGKKRPVRSP-DPYNVYD-R-DPDFRNDYGWSLALDEHDYH--PLKH--SDIGVYVVNLTA-
GSMMAPHVNPRATEYGVVLGGS-GE--VHVVSPNGTGAMKA----------------------------------
---------------------------EVAEGDVFWIPRYFPFCQVASR--SGPLEFFGFTTSARR-----
NRPQFLVGA-SSILTAMMG-----PELAAGFGV---SEEQ-LRDVVDA--QREATILPS---------
RPWPPVR--------------------------------------------------------------------
------------------REGKTP------VNR------------------------------------------
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Musa acuminata subsp. malaccensis       >TR|M0SMF3|
MAVAVGDRAVVALLTLLLLFSVPASG-------------------------------------------------
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---------------------------------HQERGTEREEAEKVRECGEDATGRGRFILGRTR----R--
AVRTEAGQVRVVSG------------------DRWKGHPSTMHIGFLRLEPNSLFLPQYVDANLIQFVREG-
EVEAGWIH----KDELVQRKLKRG-----DINVIPAGSPFYIANTN-------SERSHMVCGIDTSQS-
LTYNSQQSFF---IGGGTNPTSVLAGFDVNTLANAFNI---TSDQLRPMMRRQSGG---PIVHFS----------
------------------GQQEEELDPNNDDEEAA----------TTWTRKNLLDYLFGRS------
GREKARSTESHHAP-YAFNLYNN--EPSFQNSYGWSTAIDEHDYS--LLSS--CGVGVYLVNLTA-
GSMMAPHFNPVATEYGVILSGS-GS--IEVVYPNGSTAMNA----------------------------------
---------------------------EVSEGDVFWIPRYHPFCQVASR--GGPMEFFGFTTSSKR-----
NHPQFLAGA-SSVLRSMSG-----PELATAFGV---SEEQ-LGRLVKA--QRESVILPAS-----
NNWDGGRETA-----------------------------------------------------------------
---------------------DERKKEKMVEEL----------------------LVIKRGFLA-----------
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Araucaria angustifolia                  >TR|Q8LKI7|              M--
ANGRFPLLYLVLVLGFVCAIRC-----------------------------------------------------
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-------------------------------------NEVDHYKVHRHGEEEGRNPYVFKEEE----
QERRLATDAGEIRAVPLFREFSTL--------------VRDLENYELNFFHMKPDAFMRHHYSGADHLSFVLQG-
KARIQCVR----KEKSMEENLDRG-----NLLFIPRGSMLSIVNNDPR------EELIMVNLLYNPNPYR-
QRHHESFY---------PVDMLNAFRRESLEAAFKVRS---EDIERMFSRQ------------------------
----------------------------DQRVFRFLSREEREKIMGRDDSQLSSFWPL----------
KTRKGEAEEEHNKPFNLEKKD--AKYSNKNGKYMEVDSEDYRPLKRQEDRNSMGVGYTRIEP-
GKITVPYWHSHAFTICVVVRGPG---MLQM-HPRGGKQQTEAAKGKGEENQNGNARRREEGEGE-FRV-------
--------------------SYRRVESELRVGDVFVMPAGHASVQM-A-SS-ERLEFLTFFVNFDR-----
DSGNFLAGN-NSVLKQLRE-----EQLAADFGV---ERKE-MQRMIGS--QDKAVFVDGPRGSR-----------
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---------------------------------SLWSIV

Picea sitchensis                        >TR|A9NW52|
MIMAFRKFSLLCLVVFLSLVVSVIQC-------------------------------------------------
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----------------------------------------NAIRHDRSYSEEGEEGENQFIFKREN----W-
KIIDAEAGHIRVAPSFRENARS--------------APQLHNFEVNSFEMDPNSLMLPRYITASWYMYAYEG-
KGRIGWVH----NQKSIEQDIEAG-----QVYYVPKGAPFYVINTDKN------
QSLHLINLMHNENPGSPDRHHESYY---VGGGQDPPTVFSGFRRETLAAGFGIGI---REVEKVLSKQ-------
---------------------------------------------VRGSIVSLNKEQT------NDEFLP--
WPW----------SSKKHEGSEEEEKPFNLQKKE--LVFSNDHGEYIKADGESFRPLERLD----
MAMGLTTIKE-ESMLALHWSSRTTAVSMILKGRG---RVEIVTP-----------------GRSESKREVE----
-------------------------------SYKRVEAELTAGDLWVVPAGLPNAEINP-
YSDQPLVILTFHINNED-----NEFYYLTGQ-HSVASLIKD-----EVMAISMN----EKQQALEKVIDA--
QKDEMFLRGPKEDE-------------------------------------------------------------
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----------------------------------------------------------G-WSIV

Picea sitchensis                        >TR|B8LLB1|
MIMAFRKFSLLCLVVFLSLVVSVIQC-------------------------------------------------
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----------------------------------------NAIRHDRSYSEEGEEGENQFIFKREN----W-
KIIDAEAGHIRVAPSFRENARS--------------APQLHSFEVNSFEMDPNSLMLPRYITASWYMYAYEG-
KGRIGWVH----NQKSIEQDIEAG-----QVYYVPKGAPFYVINTDKN------
QSLHLINLMHNENPGSPDRHHESYY---VGGGQDPPTVFSGFRRETLAAGFGIGI---REVEKVLSKQ-------
---------------------------------------------VRGSIVSLNKEQT------NYQFLP--
WPW----------SSKKHEGSEEEEKPFNLQKKK--LVFSNDHGDYIKADGESFRPLERLD----
MAMGLTTIKE-ESMLALHWSSRTTAVSMILKGRG---RVEIVTP-----------------GRSESKREVE----
-------------------------------SYKRVEAELTAGDLWVVPAGLPNAEINP-
YSDQPLVILTFHINNED-----NEFYYLTGQ-HSVASLIKD-----EVMAISMN----EKQQALEKVIDA--
QKDEMFLRGPKEDE-------------------------------------------------------------
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----------------------------------------------------------G-WSIV

Picea glauca                            >TR|Q40873|              MA-
LASLLIIILLAISSSS-AALTEPLASTA-----------------------------------------------
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------------------NPEVFPEYLGRG--------------RGRREEEREENPYVFHSDSFR----
TRASSEAGEIRA-LPNF--GEVSELLEGIRK-----------FRVTCIEMKPNTVMLPHYIDATWILYVTRG-
RGYIAYVHQN----ELVKRKLEEG-----DVFGVPSGHTFYLVNNDDHN-----T-LRIASLVRPVSTVR--
GEYQPFY---VAGGRNPQTVYSAFSDDVLEAAFNTNV---QQLE-RIFGGH------------------------
---------------------------KSGVIIHANEEQIREMMRKR--GFSAGS-----------------
MSAPEHPKPFNLRNQKPD--FENENGRFTIAGPKN--YPFLDA--LDVSVGLADLNP-
GSMTAPSLNSKSTSIGIVTNGEG---RIEMACPHLGQ-HGWSSPR------------------------------
-------------ERGDQDITYQRVWAKLRTGSVYIVPAGHPITEIAS--TNSRLQILWFDLNTRG-----
NERQFLAGK-NNVLNTLER-----EIRQLSFNV---PRGEEIEEVLQA--QKDQVILRGPQRRSRDEAR------
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------------------------------------SSS

Picea glauca                            >TR|Q40844|
MPKLTRSSIILLAISSSSSAALTEPLASTA---------------------------------------------
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---------------------NPEVFPEYLGRG--------------RGRREEEREENPYVFHSDSFR----
TRASSEAGEIRA-LPNF--GEVSELLGGIRK-----------FRVTFIEMKPKTVMLPHYIDATWILYVTRG-
RGYITYVHQN----ELVKRKLEEG-----DVFGVPSGHTFYLVNSDDHN-----T-LRIASLLRPVSTVR--
GEYQPFY---VAGGRNPQTVYSAFSDDVLEAAFNTNV---QQLE-RIFGGH------------------------
---------------------------KSGVIIHPNEEQIREMIRKR--GFSAGS-----------------
MSAPEHPKPFNLRNQKPD--FENENGRFTIAGPQN--YPFLDA--LDVSVGLADLNP-
GSMTAPSLNSKSTSIGIVTNGEG---RIEMACPHLGQ-HGWSSPR------------------------------
-------------ERGDQDITYQRVWSKLRTGSVYIVPAGHPITEIAS--TNSRLQILWFDLNTRG-----
NERQFLAGK-NNVLNTLER-----EIRQLSFNV---PRGEEIEEVLQA--QKDQVILRGPQRRSRDEAR------
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------------------------------------SSS

Pinus koraiensis                        >TR|V9VGU0|                MA-
FVSLLTILLAISSSS-VALTEPVASMA------------------------------------------------
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------------------DQGVFPEQHGRGHHGVFPEEHGRGHHRGGREEEREENPYVFHSDRFR----
IRASSEAGEIRA-LPNF--GEVSELLEGISR-----------YRVTCIEMKPNTVMLPHYIDAKWILYVTGG-
RGYIAYVQQN----ELVKRKLEEG-----DVFGVPSGHTFYLVNNDDHN-----S-LRIASLLRTESTMR--
GEYEPFY---VAGGRNPETVYSAFSDDVLEAAFNTDV---QKLE-HIFGAH------------------------
---------------------------RRGVIFYANEEQIREMMRRG--GFSAES-----------------
TSASEQPKPFNLRNQKPD--FENDNGRFTRAGPKD--NPFLDS--VDVTVGFGVLNP-
GTMTAPSHNTKATSIAIVMEGEG---RIEMACPHLGQEHGWSSPR------------------------------
-------------ERGHQDINYERVRARLRTGTVYVVPAGHPITEIAS--TNGRLEILWFDINTSG-----
NEREFLAGK-NNVLQTLEK-----EVRHLSFNI---PRGEEIEEVLQA--QKDQVILRGPQRQRRDEPR------
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------------------------------------SSS

Zamia furfuracea                        >TR|Q41727|
MAHLCSLPLMAVLMLLLASACF-----------------------------------------------------
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---------------------------------------------------SELEIEDPYVFDQRSFV----
TTVQCKAGQIRA-LPNFSAGGRCELPRGLGD-----------YSVAQISLEPRSVLLPHYIEADLALYVTGG-
RGRVAFVHEE----RLVERQLRDG-----DVYAIAAGIPFYILNTDDSR-----R-LFIHCLLRTQCSTT--
GLYESFY---VVGGRNPQNVLSQFSEDVLQAAFNSSK---AVLDPMLVSGF------------------------
---------------------------NRGAIIRVSREQMERLSRGRIKGFGG----------------------
SEEPQPFNLLYRNPD--FSNNNGEIFTADAAD--HRVLRR--LNVGVQLLNLKP-
RSMTAPHYDTRSTRIGIVRNGRG---ILELVRP---QEQEQQQQ-------------------------------
-------------QQGP---TYQKLRANLNPGTVFLTRPGYPSTVIAS--GNEALQILYLDNYSQG-----
SRRQFLAGR-SNVLRYLPR-----EIKRLVFP----SSAEEIEATLEA--QEDEVLLNAQQ------GR------
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------------------------------------ADQ

Selaginella moellendorffii              >TR|D8RUY4|              MARKSL----
---ILCALALLIVSSSAS---------------------------------------------------------
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------------EHDRHERH-----DRGDEEG-------DHHK-QATSPFVLKEPV----Q--
VVSTEAGDIQVLPGPKE-LGA---LA------------ENHIGLSIITIEPKGLLLPQYLDASCVLYVHKG-
KLSFSLLS----FGF--RFDLETG-----DIYALPGGFVFYVLNTDE------GQRLRLYGMCDTSES-
LDAGHFQSFF---VGGGVDPRTILSGFHKEAVAAALKV---APEDVSEILGSQTEG---PIVYTSR---------
-------------------AGY-DFLKGDSAASNA----------------------------------------
-RRDAP-KPFNLL--KKAPDFKNENGWTIAVHGAEFS--PLKE--ADVGVFAVSLKP-
GAMLAPHWNPRAAEVAFITKGN-GR--IQVSYPNGTNALDK----------------------------------
---------------------------ELDESKVVFVPRYFPMCQIASR--NGDFEFVGFSTSSRR-----
NRPQFLAGS-NSVFKAFSK-----DIMSKTFNV---DAKR-LEAVLDN--QRDAVILPG-------------
FIE------------------------------------------------------------------------
--------------EDGKRSSAM----------------------------------------------------
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Selaginella moellendorffii              >TR|D8T005|              MARKSL----
---ILCALALLIVSSSAS---------------------------------------------------------
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------------EHDRHERH-----DRGDEEG-------DHHK-QATSPFVLKEPV----Q--
VVSTEAGDIQVLPGPKE-LGA---LA------------ENHIGLSIITIEPKGLLLPQYLDASCVLYVHKG-
RMTLGWAE----QDYLNRQDLETG-----DIYALPGGFVFYVLNTDE------GQRLRLYGMCDTSES-
LDAGHFQSFF---VGGGVDPRTILSGFRKEAVAAALKV---APEDVSEILGSQTEG---PIVYTSR---------
-------------------AGY-DFLKGDSAASNA----------------------------------------
-RGDAP-KPFNLL--KKAPDFKNENGWTIAVHGAEFS--PLKE--ADVGVFAVSLKP-
GAMLAPHWNPRAAEVAFITKGN-GR--IQVSYPNGTNALDK----------------------------------
---------------------------ELDESKVVFVPRYFPMCQIASR--NGDFEFVGFSTSSRR-----
NRPQFLAGS-NSVFKAFSK-----DIMSKTFNV---DAKR-LEAVLDN--QRDAVILPG-------------
FIE------------------------------------------------------------------------
--------------EDGKRSSAM----------------------------------------------------
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Matteuccia struthiopteris               >TR|Q40371|
MGTYTLRYKSCWWVVAALLLCIGCRTSLSTRWPQYPHDHALPSIPALIGQMVAEPLHVLDKQLQLKPLFSEDGQ-
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-------------AVSGYDGGRQEEEHEREREHEHERHQKEEEEHEHHHHHEKTQRQESFVLEKPI----K--
VIKTEAGELRMLP----QAGINSELV------------RQRLGLGFLSLEPKALLIPQYIDADCLFLVHEG-
RGQLSWVE----EGDVQEVDVEEG-----DVFEIESGTVFYMLNQDE------GQRLSIFSIYDTATV-
FNDQMFHSFF---VAGGQKPKTILSGFDEDVLATVFKA---HADEVGDMLSSQTQG---PIIYFSG---------
--------------------------RNESKRGDAAG-------------LGLGKSLTD---------
MLDRYIGLPTDSGKKPYNLF--KEKADFGNDYGSTTTIHGKDFK--LLKA--LNKGVFLVRLKA-
GAVLAPHWNPRATEIALVTKGE-GE--TQIVYPNGSAAATQ----------------------------------
---------------------------RVSEGSVFFVPQNFPMCQIASQ--SGSFEFMGFTTSSRP-----
NRPQFLAGS-NSVLKGIEA-----EVLASSFNI---PVEH-LQHFLHL--QPEAVILPG-------------
QPT------------------------------------------------------------------------
--------------KPNL-DTII----------------------------------------------------
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