Genome-wide analysis of the cupin superfamily in cowpea (*Vigna unguiculata*)

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Abstract

Cowpea [*Vigna unguiculata* (L.)Walp.] is an essential food crop that is cultivated in many important arid and semi-arid regions of the world. In this study the genome-wide database of cowpea genes was accessed in search of genomic sequences coding for globulins, specifically members of the cupin superfamily, a well-documented multigenic family belonging to the globulin protein class. A total of seventy-seven genes belonging to the cupin superfamily were found and divided into six families. We classify *V. unguiculata* genes into two subgroups: classical cupins with one cupin domain (fifty-nine proteins) and bicupins with two cupin domains (eighteen members). In addition, a search for cupin members in other closely related species of the fabaceae family [*V. angularis*, *V. radiatam* and *Phaseolus vulgaris* (common bean)] was performed. Based on those data, a detailed characterization and comparison of the cupin genes on these species was performed with the aim to better understand the connection and functions of cupin proteins from different, but related, plant species. This study was the first attempt to investigate the cupin superfamily in *V. unguiculata*, allowing the identification of six cupins families and better understand the structural features of those proteins, such as number of domains alternative splicing.

Keywords:

Vicilin, Leguminous, aminoacid sequences, protein domain,

1. Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is an important food crop that is cultivated in arid and semi-arid regions of Africa, Asia and Americas. In Brazil, it is mainly found in the northeast region, where it is a source of food for the population of that region (Ehlers *et al.*, 1999).

Cowpea seed storage proteins are classified in four groups based on their solubility: albumins (water-soluble proteins), prolamins (alcohol-soluble), glutelins (acid or alkali-soluble) and globulins (diluted saline solution-soluble) (Osborne 1924). Globulins, in turn, are divided into two subgroups according to their sedimentation coefficients: 7S and 11S globulin-types, respectively known as vicilins and legumins (Ponzoni *et al.*, 2018). Vicilins constitute the major source of nutrients during cowpea seed development (Kriz *et al.*, 1999) and are composed of several isoforms encoded by multigenic families which are categorized based on the occurrence or not of enzymatic activity (Shotwell and Larkins 2012).

Furthermore, the cupin comprises a ubiquitous protein superfamily characterized by the presence of a conserved barrel domain (Dunwell, 1998). This domain has two conserved motifs of β -strands separated by a less conserved region composed by another two β -strands with an intervening variable loop (Dunwell *et al.*, 2000, 2001, 2002, 2003).

Cowpea 7S vicilins were found to contain two cupin_1 domains (bicupins), and β -vignins are the main representative of this protein class (Sales *et al.*, 1992, 2001). Cowpea β -vignins associate in trimers that form a carbohydrate-binding multiprotein. Each monomer possesses an oligosaccharide interacting site that confers specific carbohydrate-binding property to the oligomeric structure (Dunwell *et al.*, 2002, 2003). These binding sites are located at the vertices of the triangle-shaped oligomer and the interaction between β -vignins and oligosaccharides, mainly through hydrogen bond interactions (a typical feature of carbohydrate-protein interaction), was suggested by computational simulations (Rocha *et al.*, 2018).

In this study the genome-wide database of cowpea genes was accessed in search of genomic sequences coding for cupins, given that it represents a well documented multigenic family of globulins. A total of seventy-seven genes belonging to the cupin superfamily were found, which were then classified into six families by phylogenetic reconstruction methods. *V. unguiculata* cupin genes were categorized into two groups: classical cupins (fifty-nine proteins) and bicupins (eighteen members). In addition, a search for cupin members on other related species the fabaceae family (*V. angularis*, *V.*

radiatam and *Phaseolus vulgaris*) was also performed. Based on these data, a detailed characterization and comparison of the cupin genes on the species analyzed was performed with the aim to better understand the connection and functions of cupin proteins from different, but related, plant sources.

2. Methods

2.1 Dataset

The *V. unguiculata* proteome IT97K-499-35 (genome assembly v1.0), available at the Phytozome database (<http://phytozome.jgi.doe.gov/>) (Goodstein et al., 2012), was accessed to search for proteins of the cupin superfamily. Furthermore, Rocha *et al*, 2018 were cloned six sequence denominate IT-81d-1053 (3R) and EPACE-10 3(S). 3 sequences resistance to *C. maculatus* and 3 susceptible to *C. maculatus*,

2.2 Sequences analysis

Analyses of the predicted the cupin superfamily proteins and identification of the cupin domain were performed using five different web servers. Pfam protein Database 2.0 (Finn et al, 2016), HMMER with Biosequence analysis using profile hidden Markov Models (Potter et al, 2018), SMART (Schultz et al, 2000) and Simple Modular Architecture Research Tool from the EMBL server and Conserved Domain tool from NCBI (CDD) (Marchler-Bauer., 2017). When applicable, only the result with the highest e-value was considered for analysis. BioEdit 7.2 software was used for edition (insertion and deletion) of amino acids sequences. The presence or absence of signal peptide was assessed with the SignalP 4,1 server (Petersen et al, 2011). The MEGA 7 (Tamakura *et al*, 2016) software was used for construction of phylogenetic tree using the Neighbor-Joining method (Saitou *et al*, 1987) with bootstrap values (1000 replicates).

323 Protein structural model, docking and dynamic molecular

Proteins structural modeling, docking, and dynamic molecular were performed essentially as described elsewhere (Rocha et al., 2018).

3. Results and discussion

231- Cupin gene identification and analysis

We identified 77 gene sequences encoding proteins containing one or two copies of the cupin superfamily domain in the genome of *V. unguiculata* (Table S1). These

sequences were grouped into six cupin families (cupin-1 to cupin-5 and cupin-8), and no sequences related to cupin-6 and cupin-7 families were found (Table S1).

The cupin-1 domain consists of a conserved barrel structure, and members of the cupin-1 family are represented by 11S and 7S seed storage globulins (termed legumins and vicilins, respectively) and germins (Dunwell et al, 1998). Legumins and vicilins are two-domain proteins (bicupins), whereas germins are single-domain molecules (monocupins) (Rocha et al, 2018) (Figure 1). β -vignins are the most abundant vicilins found in the genome of cowpea comprising 17 sequences (Table S 1 and 3), from which four are devoid of secretion signal peptides sequences: Vigun03g085800.1, Vigun03g085900.1, Vigun05g254700.1, vigun11g151800.1 (Table S2).

In a recent study based on computational simulations, Rocha et al (2018) demonstrated the presence of two cupin-1 domains in the primary structure of several β -vignin isoforms from two *V. unguiculata* genotypes (EPACE-10 and IT81D-1053) differing in the resistance to the bruchid beetle disease (*Callosobruchus maculatus*). In that study, the authors observed by computational simulations that β -vignin sequences presented a unique chitin-binding site (ChBS) in the N-terminal and in C-terminal ends (figure supp. 1). Those findings revealed the presence of three ChBS, which supports the hypothesis of the interaction of *V. unguiculata* β -vignins with the monosaccharide N-Acetyl-D-Glucosamine (GlcNAc) and possibly its oligomeric derivatives, as observed for other bicupins in the present study (figure S1).

Cupin families 2 and 4 were represented by only one sequence with one cupin domain each. Cupin families 3, 5 and 8 were represented, respectively, by 8, 2 and 5 sequences with one cupin domain (Table S1 and 3).

We also identified sequences with 1 or 2 domains not belonging to the cupin-1 domain, such as auxin_BP, ARD, F-box-like, LacAB_rpiB . Some sequences contain one cupin domain and a second one not related to this superfamily. Sequences Vigun06g110700.1 (cupin-2 and LacAB_rpiB domain) and Vigun09g177900.1 (cupin-8 and F-box-like domains). Three sequences with domains Pirin and Pirin C were identified: Vigun03g399100.1, Vigun06g057200.1 and Vigun08g205900.1 (Table S1 and S3).

Other studies screening of the *Capsicum annuum* genome explored different proteins from the vicilin family, with attention to structural and functional features of Vic_capan sequences (vicilin of *C. annuum*) revealing that those vicilins belong to the cupin superfamily. Vic capan are known by their multifunctional enzymatic roles, ranging

from epimerase and transferase in prokaryotes to oxalate oxidase and iron-binding nuclear protein (pirin) in eukaryotes (Dunwell, *et al* 2014). In the genome of pea (*Pisum sativum*), there are at least 18 genes encoding 7S vicilin divided into three small gene families, and 10 genes encoding legumins (Domoney and Casey 1985, Domoney et al. 1986). Furthermore, at least seven 11S globulin genes have been described in soybean (*Glycine max*), and they are arranged in three groups based on amino acid identity (Beilinson et al. 2002). More than 100 cupin sequences have been identified in few plant species, like *Oryza sativa*, *Vitis vinifera* and *Arabidopsis thaliana*. This finding highlights the extent of which cupins have been duplicated and diverged throughout the evolution in genomes of plants to carry out several functions. In addition, Sreedhar et al. (2016) purified a protease from rice (*Oryza sativa* L.), which was further denominated cupincin. This protein was included as a new member of the cupin superfamily.

The *V. unguiculata* cupins were also inspected for the presence of a secretion signal peptide. A total of 52 from the 77 sequences contain a predicted signal peptide sequence, as per the SignalP web server. Several of those sequences share conserved regions (Table S1 and S2).

In addition, the presence of alternative transcripts derived from alternative splicing in the mRNA with primary structure in the cowpea genome was also investigated. Four genes were found (Vigun03g085800, Vigun03g085900, Vigun05g251000 and Vigun07g160600), each one presenting 2 alternative transcripts. Two of these transcripts (Vigun03g085800 and Vigun03g085900) encodes each one polypeptides with identical amino acid sequences, whereas the transcripts of Vigun05g251000 and Vigun07g160600 encodes different proteins. The gene Vigun05g251000.1 encodes a protein with 377 amino acid residues, whereas Vigun05g251000.2 encodes a shorter version (341 amino acid residues) of the same protein, lacking the first 36 N-terminal residues in comparison to the larger isoform. The proteins encoded by Vigun07g160600 were identical, except in one isoform (Vigun07g160600.1; 226 amino acid residues), which was much longer than the other (Vigun07g160600.2; 222 amino acid residues), differing in 4 internal residues our insertion/deletion events.

In addition to *V. unguiculata* proteins, amino acid sequences belonging to other members of the cupin superfamily were also identified in closely related species: *Vigna angularis*, *Vigna radiata* and *Phaseolus vulgaris* (common bean) (Table S4 and S5

Eleven amino acid sequences of 7S vicilins, from which 10 are bicupins and one is a monocupin (ID: XP_017415489.1), were found in the genome of *V. angularis*. The

same distribution pattern was found in *V. radiata* sequences, i.e. 10 sequences corresponding to bicupins and one monocupin, from a total of 11 sequences (Table S4). Regarding to 11S legumins, only 4 amino acid sequences were identified from the databank of cowpea, all sequences being of the bicupin type (Table S4).

Three web servers were used to investigate the *P. vulgaris* genome: NCBI CDD for search for conserved domains, SMART and HMMER (Table S5). Twenty sequences were found with the CDD web server. From these sequences, 12 were monocupins and 3 were bicupins. The remaining 5 sequences were not related to the cupin superfamily; instead, they were identified as proteins associated to the glutelin provisional domain. The SMART web server returned 20 sequences, all of which contain the vicilin-1 domain and 9 of those with the cupin-1 domain. These findings were similar to the HMMER web server results, which led to the identification of 20 sequences (10 bicupins and 10 monocupins) (Table S5).

As discussed before, the high copy number of globulin genes is not exclusive to leguminous plants, being also reported in non-leguminous ones. For example, in *Ficus pumila* (Moraceae family), six 11S globulin isoforms have been reported (Chua et al. 2008). Similarly, also in hemp (*Cannabis sativa* L.), a member of Cannabaceae family that possess seven 11S globulin (called edestin) genes, were identified and arranged into two groups (type1 and type2) based on differences on their primary structures (Docimo et al. 2014). The 11S edestin is the main storage protein representing approximately 80 % of the total seed protein, whereas approximately 13% of the water-soluble protein are 2S albumin.

3.2-Molecular Phylogeny

The phylogenetic classification of the cupin genes was performed initially only with sequences from *V. unguiculata* vicilins (Figure 2). Additionally, we analyzed sequences from 4 leguminous species from fabaceae family (*V. unguiculata*, *V. angularis*, *V. radiata* and *P. vulgaris*) (Figure 3). In the first phylogenetic tree, only 3 clades were identified between the *V. unguiculata* bicupins. The first clade includes 10 vicilin sequences obtained from cowpea database and 6 sequences of vicilins from cowpea with contrasting responses to the bruchid beetle (*Callosobruchus maculatus*) previously cloned by Rocha et al, 2018 (figure 2). In the second and third clades 4 and 5 vicilins are present, respectively, which correspond to the cupin_1 family. Others cupin families,

such as cupin-2, 3, 4, 5, 7 and 8, are also present in this phylogenetic tree, as well as other sequences with non-cupin domain, such as Pirin-C, ARD and Axin_BP.

With respect to the analysis including the 4 selected plant species, the results showed that 3 clades were classified in accordance with position of the 19 amino acids sequences of bicupins of *V. unguiculata* (Figure 3). Again, clade 1 contains 9 bicupins obtained from the *V. unguiculata* database, as well as the 6 sequences cloned by Rocha et al (2018). Clade 2 contains 5 sequences from *V. unguiculata* bicupins. Clade 3 contains 4 *V. unguiculata* bicupins and other bicupins from *V. angularis*, *V. radiata* and *P. vulgaris* (Figure 3).

All other amino acid sequences from *V. angularis*, *V. radiata* and *Phaseolus vulgaris* are bicupins that were not grouped with *V. unguiculata* bicupins. Moreover, the 34 *V. unguiculata* monocupins identified (non-vicilins) form one large clade. Three pirin domain-containing sequences (pirin and pirin C), which belong to the cupin-2 family were also grouped in this analysis. Other research groups have studied human pirin sequences and have obtained their crystal structure, which is an iron-binding nuclear protein and transcription cofactor (Pang et al. (2004). In accordance with the first phylogenetic tree (Figure 1), in the second tree (Figure 3) also grouped cupin sequences belonging to the same family (1, 2, 3, 4, 5, 7 and 8), as well as sequences with no cupin domain, such as Pirin-C, ARD and Axin_BP.

Conclusion

In this study we identified six cupin families in the *V. unguiculata* genome, followed by the analysis of copy number of 7S vicilins and/or 11S legumin sequences from *V. unguiculata* and other leguminous plants, such as *V. angularis*, *V. radiata*, *P. vulgaris*. This led to the identification of numerous cupin sequences in each species. Furthermore, the kind of and number of domains that are present in each sequence are described; and genes that are originated due to alternative splicing are proposed. In summary, our results represent the first attempt at a thorough characterization of cupin sequences in important leguminous plants. This will support future studies to elucidate their biological role, which are still needed for a complete understanding of the cupin superfamily function, including *V. unguiculata* β -vicilins with two cupin-1 domains that are the major constituent of cowpea vicilins.

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Captions of figures

327 Figure 1- Ribbon diagrams of the β -vignin homotrimer models. Sequences Vicilin-S3-
 328 MG973243.1 (A) and Vicilin-R3-MG973246 (B) are shown. Subunits are colored pink,
 329 green and cyan. Chitooligosaccharide molecules [(GlcNAc) 4] docked in the chitin-
 330 binding sites of each oligomer are also shown as stick models (carbon, nitrogen and
 331 oxygen atoms are colored yellow, blue and red, respectively). For interpretation of the
 332 references to color, the reader is referred to the web version of this article

Figure2- Molecular phylogeny of *V. unguiculata* cupins. The different cupin families are highlighted in several colors and include monocupin and bicupins (vicilins).

Figure 3- Molecular phylogeny of *V. unguiculata*, *V. angularis*, *V. radiata* and *P. vulgaris* cupins. This tree depicts clade 1 with *V. unguiculata* bicupins from the cupin-1 family, as well clades 2 and 3 that were also identified. The largest group in terms of *V. unguiculata* sequences is the one formed with cupin-1 monocupins.

SUPPLEMENTARY MATERIAL

Genome-wide analysis of the cupin superfamily in cowpea (*Vigna unguiculata*)

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Table S1. Cupin superfamily proteins from cowpea (*Vigna unguiculata*)

Gene	Encoded protein	Size (residues)	Molecular mass (Da)	Theoretical pI	Signal peptide (start-end)	Cupin domain(s)				
						PFAM family	Accession	Start-End	Individual E-value	Confidential E-value
Vigun01g148800.1	Protein of unknown function (DUF861)	110	12041.65	8.27	No	Cupin_3	PF05899.11	22-96	4.0e-26	2.4e-30
Vigun01g205600.1	Cupin	217	22824.33	8.52	1-21	Cupin_1	PF00190.21	60-207	7.1e-48	8.5e-52
Vigun02g070100.1	Cupin	216	23407.83	8.49	1-21	Cupin_1	PF00190.21	59-208	1.4e-39	1.7e-43
Vigun02g110000.1	Cupin-like domain	415	47334.28	5.64	1-19	Cupin_8	PF13621.5	100-377	4.4e-76	2.7e-80
Vigun02g134000.1	Cupin	631	73379.36	5.25	1-26	Cupin_1	PF00190.21	238-393	1.8e-32	1.1e-36

Vigun03g085800.1	Cupin Cupin	357	38679.55	5.23	No	Cupin_1 Cupin_1	PF00190.21	5-159	5.5e-21	6.6e-25
							PF00190.21	192-340	6.5e-19	7.8e-23
Vigun03g085900.1	Cupin Cupin	358	38785.50	5.00	No	Cupin_1 Cupin_1	PF00190.21	5-159	7.7e-21	9.2e-25
							PF00190.21	192-341	1.0e-14	1.2e-18
Vigun03g254300.1	Cupin	155	16831.42	9.43	No	Cupin_1	PF00190.21	5-140	2.4e-28	2.8e-32
Vigun03g297500.1	Cupin domain	297	33408.29	5.98	1-19	Cupin_2	PF07883.10	220-289	2.0e-06	2.4e-10
Vigun03g390200.1	Cupin superfamily protein	776	87862.48	8.40	1-17	Cupin_4	PF08007.11	439-575	6.8e-25	4.1e-29
Vigun03g397300.1	Cupin	208	21325.81	7.79	No	Cupin_1	PF00190.21	52-197	2.3e-35	2.8e-39
Vigun03g399100.1	Cupin superfamily (DUF985)	182	21222.94	5.42	No	Cupin_5	PF06172.10	6-166	4.7e-42	2.8e-46
Vigun04g148500.1	Protein of unknown function (DUF861)	98	20202.80	5.09	No	Cupin_3	PF06172.10	6-159	5.2e-41	3.1e-45
Vigun04g167800.1	Cupin superfamily (DUF985)	189	11067.81	7.62	No	Cupin_5	PF05899.11	21-95	1.9e-27	1.1e-31
Vigun04g168100.1	Protein of unknown function (DUF861)	129	14501.24	9.10	1-31	Cupin_3	PF05899.11	51-125	6.6e-24	7.9e-28
Vigun05g001800.1	Pirin Pirin C-terminal cupin domain	322	35815.78	6.31	No	Pirin Pirin_C	PF02678.15	59-354	4.3e-33	5.1e-37
							PF05726.12	207-312	1.3e-31	1.6e-35
Vigun05g152400.1	Protein of unknown function (DUF861)	58	6736.85	9.25	No	Cupin_3	PF05899.11	21-58	4.3e-09	2.6e-13
Vigun05g166300.1	Cupin	222	24032.52	8.51	1-20	Cupin_1	PF00190.21	60-210	2.4e-47	2.9e-51
Vigun05g166800.1	Cupin	222	23998.50	8.51	1-20	Cupin_1	PF00190.21	60-210	3.3e-47	3.9e-51
Vigun05g166900.1	Cupin	222	23983.53	8.51	1-20	Cupin_1	PF00190.21	60-210	6.1e-47	7.2e-51
Vigun05g167000.1	Cupin	222	24051.56	8.51	1-26	Cupin_1	PF00190.21	60-210	6.7e-46	8.0e-50
Vigun05g235200.1	Cupin	204	21833.80	6.26	1-20	Cupin_1	PF00190.21	53-196	5.0e-31	5.9e-35
Vigun05g250800.1	Cupin Cupin	456	50920.54	4.99	1-19	Cupin_1 Cupin_1	PF00190.21	43-192	1.8e-10	2.2e-14
							PF00190.21	292-441	3.8e-27	4.6e-31
Vigun05g250900.1	Cupin Cupin	456	51178.89	5.14	1-19	Cupin_1 Cupin_1	PF00190.21	43-194	6.0e-13	7.2e-17
							PF00190.21	292	3.8e-27	4.6e-31
Vigun05g251000.1	Cupin Cupin	377	42620.97	5.20	1-19	Cupin_1 Cupin_1	PF00190.21	2-113	1.1e-08	6.3e-13
							PF00190.21	213-262	1.8e-25	1.1e-29

Vigun05g254700.1	Cupin Cupin	356	38144.76	5.66	No	Cupin_1 Cupin_1	PF00190.21	6-157	3.6e-27	2.2e-31
							PF00190.21	190-339	1.7e-22	1.0e-26
Vigun06g057200.1	Pirin C- Cupin domain	298	38144.76	5.66	No	Pirin Pirin_C	PF02678.15 PF05726.12	30-126 179-284	1.8e-32 3.7e-31	2.1e-36 4.5e-35
Vigun06g110700.1	Ribose/Galactose Isomerase Cupin domain	302	32834.09	5.09	No	LacAB_rpiB Cupin_2	PF02502.17 PF07883.10	11-139 202-269	3.5e-31 1.1e-07	2.1e-36 4.5e-35
Vigun06g138000.1	Cupin	215	22973.39	6.03	1-19	Cupin_1	PF00190.21	59-209	1.2e-45	1.4e-49
Vigun06g138100.1	Cupin	214	23021.51	6.03	1-20	Cupin_1	PF00190.21	59-209	6.9e-47	8.2e-51
Vigun07g059500.1	Cupin	225	24154.63	6.59	1-23	Cupin_1	PF00190.21	67-213	2.7e-42	3.2e-46
Vigun07g089100.1	Protein of unknown function (DUF861)	104	11564.11	6.71	1-23	Cupin_3	PF05899.11	22-96	3.2e-27	1.9e-31
Vigun07g100400.1	Cupin Cupin	611	69379.61	5.30	1-20	Cupin_1 Cupin_1	PF00190.21	39-192	2.0e-25	1.2e-29
							PF00190.21	443-589	1.0e-30	6.3e-35
Vigun07g106500.1	Cupin-like domain	537	61142.18	5.27	No	Cupin_8	PF13621.5	18-295	1.4e-47	1.7e-51
Vigun07g108200.1	Cupin	510	57790.61	6.00	1-26	Cupin_1	PF00190.21	320-480	7.7e-26	4.6e-30
Vigun07g113800.1	Auxin binding protein	192	21867.96	5.76	1-23	Auxin_BP	PF02041.15	24-192	1.3e-97	1.6e-101
Vigun07g132600.1	Cupin	220	23203.58	6.82	1-22	Cupin_1	PF00190.21	61-209	9.2e-49	1.1e-52
Vigun07g132700.1	Cupin	220	23246.70	7.64	1-22	Cupin_1	PF00190.21	61-209	2.1e-48	2.5e-52
Vigun07g133900.1	Cupin	218	23121.54	8.53	1-22	Cupin_1	PF00190.21	60-208	5.6e-48	6.7e-52
Vigun07g159700.1	Protein of unknown function (DUF861)	115	12642.45	8.91	1-20	Cupin_3	PF05899.11	26-100	7.2e-29	4.3e-33
Vigun07g160600.1	Cupin	226	24302.96	6.81	1-20	Cupin_1	PF00190.21	65-215	9.0e-47	1.1e-50
Vigun07g235300.1	ARD/ARD' family	187	22269.20	5.05	No	ARD	PF03079.13	4-158	2.3e-61	4.0e-65
Vigun07g237100.1	Cupin Cupin	444	51037.19	5.33	1-23	Cupin_1 Cupin_1	PF00190.21	56-206	5.4e-08	3.2e-12
							PF00190.21	258-417	8.6e-27	5.1e-31
Vigun07g237200.1	Cupin Cupin	536	61804.46	5.92	1-23	Cupin_1 Cupin_1	PF00190.21	140-288	0.00011	6.5e-09
							PF00190.21	341-496	8.9e-24	5.3e-28
Vigun07g237300.1	Cupin Cupin	457	52584.93	5.40	1-25	Cupin_1 Cupin_1	PF00190.21	56-206	5.7e-08	3.4e-12
							PF00190.21	258-417	9.1e-27	5.5e-31

Vigun07g237400.1	Cupin Cupin	442	50774.80	5.33	1-23	Cupin_1 Cupin_1	PF00190.21	54-204	6.0e-08	3.6e-12
							PF00190.21	256-415	8.5e-27	5.1e-31
Vigun07g237500.1	Cupin Cupin	455	52225.44	5.33	1-23	Cupin_1 Cupin_1	PF00190.21	54-204	5.1e-08	3.1e-12
							PF00190.21	256-415	9.0e-27	5.4e-31
Vigun07g237600.1	Cupin	589	69269.70	6.50	1-24	Cupin_1	PF00190.21	395-551	1.5e-25	8.7e-30
Vigun08g174800.1	Protein of unknown function (DUF861)	143	16551.91	9.18	No	Cupin_3	PF05899.11	61-135	6.9e-20	4.1e-24
Vigun08g205900.1	Pirin Pirin C-terminal cupin domain	301	33819.51	5.95	No	Pirin Pirin_C	PF02678.15	30-126	3.9e-32	4.7e-36
							PF05726.12	179-284	6.7e-34	8.0e-38
Vigun09g037800.1	Cupin	209	21717.89	5.35	1-18	Cupin_1	PF00190.21	53-199	5.9e-36	7.0e-40
Vigun09g089200.1	Cupin-like domain	483	56165.26	5.14	No	Cupin_8	PF13621.5	19-291	2.3e-22	2.8e-26
Vigun09g122200.1	Cupin	231	25405.93	6.74	1-25	Cupin_1	PF00190.21	66-202	1.0e-26	1.2e-30
Vigun09g177900.1	F-box-like Cupin-like domain	962	110138.09	5.42	No	F-box-like Cupin_8	PF12937.6	15-61	5.5e-08	1.3e-11
							PF13621.5	135-367	1.8e-20	4.4e-24
Vigun10g081000.1	Cupin Cupin	457	52757.17	5.31	1-23	Cupin_1 Cupin_1	PF00190.21	51-204	1.8e-06	1.1e-10
							PF00190.21	254-417	6.9e-26	4.2e-30
Vigun10g086400.1	Cupin	220	23724.33	6.06	1-20	Cupin_1	PF00190.21	60-209	4.7e-47	5.6e-51
Vigun10g086500.1	Cupin	220	23700.31	6.06	1-20	Cupin_1	PF00190.21	60-209	3.7e-47	4.4e-51
Vigun10g086600.1	Cupin	220	23679.42	6.90	1-20	Cupin_1	PF00190.21	62-209	2.3e-46	2.8e-50
Vigun10g086700.1	Cupin	220	23682.29	6.06	1-20	Cupin_1	PF00190.21	60-209	6.6e-47	7.9e-51
Vigun10g087300.1	Cupin	220	23655.18	5.77	1-20	Cupin_1	PF00190.21	60-209	6.2e-47	7.5e-51
Vigun10g096400.1	Cupin Cupin	456	52579.95	5.38	1-23	Cupin_1 Cupin_1	PF00190.21	54-204	4.7e-09	2.8e-13
							PF00190.21	256-423	3.2e-25	1.9e-29
Vigun10g096600.1	Cupin Cupin	456	52579.95	5.38	1-23	Cupin_1 Cupin_1	PF00190.21	54-204	4.7e-09	2.8e-13
							PF00190.21	256-423	3.2e-25	1.9e-29
Vigun10g101100.1	Cupin-like domain	516	58866.96	6.51	No	Cupin_8	PF13621.5	214-439	5.1e-22	6.1e-26
Vigun10g164200.1	Cupin	209	22761.19	9.01	1-20	Cupin_1	PF00190.21	57-199	4.5e-15	5.3e-19
Vigun10g164300.1	Cupin	209	21899.21	6.81	1-20	Cupin_1	PF00190.21	54-199	1.9e-34	2.3e-38
Vigun10g164400.1	Cupin	206	21694.07	6.50	1-17	Cupin_1	PF00190.21	51-196	6.0e-34	7.2e-38
Vigun10g164500.1	Cupin	212	22565.74	5.12	1-23	Cupin_1	PF00190.21	60-202	3.0e-22	3.6e-26
Vigun10g164600.1	Cupin	213	22353.56	6.39	1-20	Cupin_1	PF00190.21	54-199	6.8e-35	8.2e-39

Vigun10g164700.1	Cupin	206	21578.92	7.81	1-17	Cupin_1	PF00190.21	52-196	2.6e-31	3.2e-35
Vigun10g164800.1	Cupin	209	21875.32	6.64	1-18	Cupin_1	PF00190.21	53-199	3.3e-29	2.0e-33
Vigun11g024500.1	Cupin	449	51413.94	5.96	1-23	Cupin_1	PF00190.21	44-201	1.8e-06	1.1e-10
	Cupin					Cupin_1	PF00190.21	249-410	7.5e-26	4.5e-30
Vigun11g026700.1	Cupin	228	24995.64	6.06	1-26	Cupin_1	PF00190.21	67-211	1.2e-27	1.4e-31
Vigun11g038900.1	Protein of unknown function (DUF861)	206	23763.62	8.85	1-26	Cupin_3	PF05899.11	169-206	2.8e-07	1.7e-11
Vigun11g098100.1	Cupin	427	49123.27	5.14	1-23	Cupin_1	PF00190.21	51-202	1.5e-07	1.8e-11
	Cupin					Cupin_1	PF00190.21	252-409	6.4e-25	7.6e-29
Vigun11g147100.1	Cupin	444	49794.57	5.21	1-21	Cupin_1	PF00190.21	31-146	1.4e-10	1.6e-14
	Cupin					Cupin_1	PF00190.21	275	1.5e-29	1.8e-33
Vigun11g151800.1	Cupin	356	38458.15	6.38	No	Cupin_1	PF00190.21	5-157	3.1e-29	1.9e-33
	Cupin					Cupin_1	PF00190.21	190-339	2.4e-22	1.5e-26
Vigun11g163100.1	Cupin-like domain	413	46056.06	5.58	No	Cupin_8	PF13621.5	180-410	1.6e-46	2.8e-50

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β-Vignin_EPACE-10	P R G Q N N P F Y F D S D R W F H T L F R N Q Y G H L R V L Q R F D Q R S K Q I Q N L E N Y R V V E F K S K P N T L L L P H H A D A D F L L	84
β-Vignin_IT81D-1053	P R G Q N N P F Y F D S D R W F H T L F R N Q Y G H L R V L Q R F D Q R S K Q I Q N L E N Y R V V E F K S K P N T L L L P H H A D A D F L L	84
Adzuki 7S3	S R G E N N P F Y F S S D R R F H T L F T N Q Y G H L R I L H R F D Q R S K Q I Q N L E N Y R V V E F K S K P N T L L L P H H A D A D F L L	107
V. radiata 8S globulin	S R G Q N N P F Y F N S D R R F H T L F K N Q Y G H L R V I H R F D Q R S K Q I Q N L E N Y R V V E F K S K P N T L L L P H H A D A D F L L	107
β-Conglycinin	R E D E N N P F Y F R S S N S F Q T L F E N Q N V R I R L L Q R F N K R S P Q L E N L R D Y R I V Q F Q S K P N T I L L P H H A D A D F L L	96
Canavalin	S R A Q N N P Y L F R S N - K F L T L F K N Q H G S L R L L Q R F N E D T E K L E N L R D Y R V L E Y C S K P N T L L L P H H S D S D L L V	110

ChBS

β-Vignin_EPACE-10	V V L N G R A I L T L V N P D G R D S Y I L E Q G H A Q K I P A G T T F F L V N P D D N E N L R I V K L A V P V N N P H R F Q D F F L S S T	154
β-Vignin_IT81D-1053	V V L N G R A I L T L V N P D G R D S Y I L E E G H A Q K I P A G T T F F L V N P D D N E N L R I V K L A V S V N N P H R F Q D F F L S S T	154
Adzuki 7S3	V V L N G R A I L T L V N P D S R D S Y I L E Q G H A Q K I P A G T T F F L V N P D D N E N L R I I K L A I P V N N P H R F Q D F F L S S T	177
V. radiata 8S globulin	V V L N G R A I L T L V N P D G R D S Y I L E Q G H A Q K I P A G T T F F L V N P D D N D N L R I I K L A I P V N N P H R F Q N F F L S S T	177
β-Conglycinin	F V L S G R A I L T L V N N D D R D S Y N L H P G D A Q R I P A G T T Y Y L V N P H D H Q N L K I I K L A I P V N K P G R Y D D F F L S S T	166
Canavalin	L V L E G Q A I L V L V N P D G R D T Y K L D Q G D A I K I Q A G T P F Y L I N P D N N Q N L R I L K F A I T F R R P G T V E D F F L S S T	180

Cupin_1 domain

β-Vignin_EPACE-10	E A Q Q S Y L Q G F S K N I L E A S F G S D Y K E I N R V L F G E E E Q Q Q Q D E E S Q Q E G V I V Q L K R E Q I R E L M K H A K S T S K K	224
β-Vignin_IT81D-1053	E A Q Q S Y L Q G F S K N I L E A S F G S D C K E I N R V L F G E E E Q Q Q Q D E E S Q Q E G V I V Q L K R E Q I R E L M K H A K S T S K K	224
Adzuki 7S3	E A Q Q S Y L R G F S K N I L E A S F D S D F K E I N R V L F G E E R Q Q Q Q G E E S R E E G V I V E L K R E Q I Q E L M K H A K S S S R K	247
V. radiata 8S globulin	E A Q Q S Y L R G F S K N I L E A S F D S D F K E I D R V L F G E E R Q Q Q H G E E S Q E E G V I V E L K R E Q I R E L I K H A K S S S R K	247
β-Conglycinin	Q A Q Q S Y L Q G F S H N I L E T S F H S E F E E I N R V L F G E E E E Q R - - - - Q Q E G V I V E L S K E Q I R Q L S R R A K S S S R K	231
Canavalin	K R L P S Y L S A F S K N F L E A S Y D S P Y D E I E Q T L L Q E - - - - - E Q E G V I V K M P K D Q I Q E I S K H A Q S S S R K	240

ChBS

β-Vignin_EPACE-10	S L S S Q N E P F N L R S Q K P I Y S N K F G R L H E I T P E K N P Q L R D L D V F L T S V D M K E G G L M P N Y N S K A I V I L V V N K	294
β-Vignin_IT81D-1053	S L S S Q N E P F N L R S Q K P I Y S N K F G R L H E I T P E K N P Q L R D L D V F L T S V D M K E G G L F M P N Y N S K A I V I L V V N K	294
Adzuki 7S3	E L S S Q D E P F N L R N S K P I Y S N K F G R W Y E M T P E K N P Q L K D L D V F I S S V D M K E G A L L L P H Y N S K A I V I M V I N E	317
V. radiata 8S globulin	E L S S Q D E P F N L R N S N P I Y S N K F G R W Y E I T P E K N P Q L K D L D V F I S S V D M K E G G L L L P H Y N S K A I V I L V I N E	317
β-Conglycinin	T I S S E D E P F N L R S R N P I Y S N N F G K F F E I T P E K N P Q L R D L D I F L S S V D I N E G A L L L P H F N S K A I V I L V I N E	301
Canavalin	T L S S Q D K P F N L R S R D P I Y S N N Y G K L Y E I T P E K N S Q L R D L D I L L N C L Q M N E G A L F V P H Y N S R A T V I L V A N E	310

ChBS

β-Vignin_EPACE-10	G E A N I E L V G Q R E Q Q Q - - Q Q Q E S W E V Q R Y R A E V S E D D V F V I P A S Y P V A I T A T S N L N F I A F G I N A E N N Q R N	362
β-Vignin_IT81D-1053	G E A N I E L V G Q R E Q Q Q - - Q Q Q E S W E V Q R Y R A E V S E D D V F V I P A S Y P V A I T A T S N L N F I A F G I N A E S N Q R N	362
Adzuki 7S3	G E A K I E L V G L S D Q Q Q - Q K Q Q E S L E V Q R Y R A E L S E D D V F V I P A A Y P V A I N A T S N L N F F A F G I N A E N N Q R N	386
V. radiata 8S globulin	G E A K I E L V G P S D Q Q Q - - - Q D E S L E V Q R Y R A E L S E D D V F V I P A A Y P V A I N A T S N L N F F A F G I N A E N N Q R N	383
β-Conglycinin	G D A N I E L V G I K E Q Q Q K Q K Q E E P L E V Q R Y R A E L S E D D V F V I P A A Y P F V V N A T S N L N F L A F G I N A E N N Q R N	371
Canavalin	G R A E V E L V G L E Q Q Q Q - - - Q G L E S M Q L R R Y A A T L S E G D I I V I P S S F P V A L K A A S D L N M V G I G V N A E N N E R N	377

ChBS

Cupin_1 domain

β-Vignin_EPACE-10	F L A G E E G N V M S E I P T E A L D V T F P A S G E K V E K L I N K Q S D S H F T D A Q P E Q Q Q R E E D R K G R K G P L S S I L G T F Y	432
β-Vignin_IT81D-1053	F L A G E E D N V M S E I P T E V L D V T F P A S G E K V E K L I N K Q S D S H F T D A Q P E Q Q Q R E E D R K G R K G P L S S I L D S L Y	432
Adzuki 7S3	F L A G G K D N V M S E I P T E V L E V S F P A S G K K V E K L I K K Q S E S H F V D A Q P E Q Q Q R E E G H K G R K G S L S S I L G S L Y	456
V. radiata 8S globulin	F L A G E K D N V M S E I P T E V L D V S F P A S G N K V E K L I K K Q S E S H F V D A Q P E Q Q Q R E E G H K G R K G S L S S I L G S L Y	453
β-Conglycinin	F L A G E K D N V R Q I E R Q V Q E L A F P G S A Q D V E R L L K K Q R E S Y F V D A Q P Q - - Q K E E G S K G R K G P F P S I L G A L Y	439
Canavalin	F L A G H K E N V I R Q I P R Q V S D L T F P G S G E E V E E L L E N Q K E S Y F V D G Q P R - - H I D A G G K A R R A H L P N L F R T F Y	445

368 **Fig. S1. Multiple sequence alignment of the amino acid sequences of β -vignin with the primary structures of representative vicilin-like 7S globulins.**
369 **Amino acid sequences of β -vignin obtained from *V. unguiculata* genotypes EPACE-10 (sequence S2) and IT81D-1053 (sequence R2) were aligned**
370 **with those of *V. angularis* (adzuki bean) 7S globulin-3 (Adzuki 7S3; UniProtKB accession number: A0A0S3SX36), *V. radiata* 8S globulin (UniProtKB**
371 **accession number: Q198W3), β -conglycinin (from Glycine max; UniProtKB accession number: P25974) and canavalin (from *Canavalia ensiformis*;**
372 **UniProtKB accession number: P50477). Segments in the primary structures of β -vignin that were shown to contribute to their chitin-binding site**
373 **(ChBS), as evidenced by computational simulations, are indicated. The alignment was edited using the program ALINE.**

374

375 **Table S2- the 77 cupins sequences of the *V. unguiculata* showed the absence or presence of signal peptides and positions of cleavage sites.**

376 **Signal peptides**

377

378 # Measure Position Value Cutoff signal peptide?
379 max. C 27 0.110
380 max. Y 27 0.109
381 max. S 22 0.134
382 mean S 1-26 0.108
383 D 1-26 0.108 0.450 NO

384 Name=**Vigun01g148800.1** SP='NO' D=0.108 D-cutoff=0.450 Networks=SignalP-noTM

385

386

387 # Measure Position Value Cutoff signal peptide?
388 max. C 22 0.439
389 max. Y 22 0.637
390 max. S 12 0.974
391 mean S 1-21 0.922
392 D 1-21 0.791 0.450 YES

393 Name=Vigun01g205600.1 SP='YES' Cleavage site between pos. 21 and 22: ITA-SD D=0.791 D-cutoff=0.450

394 Networks=SignalP-noTM

395

396 # Measure Position Value Cutoff signal peptide?
397 max. C 22 0.712
398 max. Y 22 0.790
399 max. S 13 0.959


```

400     mean S      1-21      0.878
401         D      1-21      0.838      0.450      YES
402 Name=Vigun02g070100.1   SP='YES' Cleavage site between pos. 21 and 22: SRP-DP D=0.838 D-cutoff=0.450 Netw
403
404 # Measure  Position  Value      Cutoff      signal peptide?
405     max. C      20      0.471
406     max. Y      20      0.503
407     max. S       1      0.743
408     mean S      1-19      0.505
409         D      1-19      0.504      0.450      YES
410 Name=Vigun02g110000.1   SP='YES' Cleavage site between pos. 19 and 20: CLT-FP D=0.504 D-cutoff=0.450
411 Networks=SignalP-noTM
412
413 # Measure  Position  Value      Cutoff      signal peptide?
414     max. C      27      0.707
415     max. Y      27      0.770
416     max. S      17      0.914
417     mean S      1-26      0.831
418         D      1-26      0.803      0.450      YES
419 Name=Vigun02g134000.1   SP='YES' Cleavage site between pos. 26 and 27: VKA-SS D=0.803 D-cutoff=0.450
420 Networks=SignalP-noTM
421 # data
422
423 # Measure  Position  Value      Cutoff      signal peptide?
424     max. C      41      0.110
425     max. Y      41      0.107
426     max. S      25      0.121
427     mean S      1-40      0.099
428         D      1-40      0.103      0.450      NO
429 Name=Vigun03g085800.1   SP='NO' D=0.103 D-cutoff=0.450 Networks=SignalP-noTM
430
431 # Measure  Position  Value      Cutoff      signal peptide?
432     max. C      41      0.110
433     max. Y      41      0.107
434     max. S      25      0.121
435     mean S      1-40      0.099
436         D      1-40      0.103      0.450      NO

```

437 Name=Vigun03g085800.2 SP='NO' D=0.103 D-cutoff=0.450 Networks=SignalP-noTM

438

#	Measure	Position	Value	Cutoff	signal peptide?

440	max. C	13	0.123		

441	max. Y	58	0.107		

442	max. S	13	0.140		

443	mean S	1-57	0.101		

444	D	1-57	0.104	0.450	NO

445 Name=Vigun03g085900.1 SP='NO' D=0.104 D-cutoff=0.450 Networks=SignalP-noTM

446

#	Measure	Position	Value	Cutoff	signal peptide?

448	max. C	13	0.123		

449	max. Y	58	0.107		

450	max. S	13	0.140		

451	mean S	1-57	0.101		

452	D	1-57	0.104	0.450	NO

453 Name=Vigun03g085900.2 SP='NO' D=0.104 D-cutoff=0.450 Networks=SignalP-noTM

454

#	Measure	Position	Value	Cutoff	signal peptide?

456	max. C	24	0.140		

457	max. Y	12	0.159		

458	max. S	1	0.327		

459	mean S	1-11	0.217		

460	D	1-11	0.182	0.500	NO

461 Name=Vigun03g254300.1 SP='NO' D=0.182 D-cutoff=0.500 Networks=SignalP-TM

462

#	Measure	Position	Value	Cutoff	signal peptide?

464	max. C	20	0.835		

465	max. Y	20	0.862		

466	max. S	12	0.935		

467	mean S	1-19	0.891		

468	D	1-19	0.877	0.450	YES

469 Name=Vigun03g297500.1 SP='YES' Cleavage site between pos. 19 and 20: AFS-EE D=0.877 D-cutoff=0.450

470 Networks=SignalP-noTM

471

#	Measure	Position	Value	Cutoff	signal peptide?

473	max. C	48	0.127		

```

474     max. Y      48      0.155
475     max. S      43      0.336
476     mean S      1-47    0.151
477     D          1-47    0.153    0.450    NO
478 Name=Vigun03g390200.1   SP='NO' D=0.153 D-cutoff=0.450 Networks=SignalP-noTM
479
480 # Measure  Position  Value    Cutoff    signal peptide?
481     max. C      18      0.816
482     max. Y      18      0.880
483     max. S      10      0.979
484     mean S      1-17    0.952
485     D          1-17    0.919    0.450    YES
486 Name=Vigun03g397300.1   SP='YES' Cleavage site between pos. 17 and 18: SHA-SV D=0.919 D-cutoff=0.450
487 Networks=SignalP-noTM
488
489 # Measure  Position  Value    Cutoff    signal peptide?
490     max. C      68      0.110
491     max. Y      57      0.103
492     max. S      20      0.107
493     mean S      1-56    0.095
494     D          1-56    0.099    0.450    NO
495 Name=Vigun03g399100.1   SP='NO' D=0.099 D-cutoff=0.450 Networks=SignalP-noTM
496
497 # Measure  Position  Value    Cutoff    signal peptide?
498     max. C      59      0.110
499     max. Y      59      0.105
500     max. S      53      0.122
501     mean S      1-58    0.098
502     D          1-58    0.101    0.450    NO
503 Name=Vigun04g148500.1   SP='NO' D=0.101 D-cutoff=0.450 Networks=SignalP-noTM
504
505 # Measure  Position  Value    Cutoff    signal peptide?
506     max. C      45      0.115
507     max. Y      45      0.107
508     max. S      22      0.114
509     mean S      1-44    0.097
510     D          1-44    0.102    0.450    NO

```

511 Name=Vigun04g167800.1 SP='NO' D=0.102 D-cutoff=0.450 Networks=SignalP-noTM

512

#	Measure	Position	Value	Cutoff	signal peptide?

514	max. C	45	0.115		

515	max. Y	45	0.107		

516	max. S	22	0.114		

517	mean S	1-44	0.097		

518	D	1-44	0.102	0.450	NO

519 Name=Vigun04g167800.1 SP='NO' D=0.102 D-cutoff=0.450 Networks=SignalP-noTM

520

#	Measure	Position	Value	Cutoff	signal peptide?

522	max. C	32	0.432		

523	max. Y	32	0.611		

524	max. S	16	0.995		

525	mean S	1-31	0.895		

526	D	1-31	0.764	0.450	YES

527 Name=Vigun04g168100.1 SP='YES' Cleavage site between pos. 31 and 32: ETA-MK D=0.764 D-cutoff=0.450

528 Networks=SignalP-noTM

529

#	Measure	Position	Value	Cutoff	signal peptide?

531	max. C	32	0.165		

532	max. Y	32	0.181		

533	max. S	27	0.500		

534	mean S	1-31	0.193		

535	D	1-31	0.188	0.450	NO

536 Name=Vigun05g001800.1 SP='NO' D=0.188 D-cutoff=0.450 Networks=SignalP-noTM

537

#	Measure	Position	Value	Cutoff	signal peptide?

539	max. C	28	0.156		

540	max. Y	28	0.230		

541	max. S	26	0.704		

542	mean S	1-27	0.342		

543	D	1-27	0.291	0.450	NO

544 Name=Vigun05g152400.1 SP='NO' D=0.291 D-cutoff=0.450 Networks=SignalP-noTM

#	Measure	Position	Value	Cutoff	signal peptide?

546	max. C	21	0.717		

547	max. Y	21	0.780		

```

548     max. S      16      0.903
549     mean S      1-20    0.851
550     D          1-20    0.818    0.450    YES
551 Name=Vigun05g166300.1   SP='YES' Cleavage site between pos. 20 and 21: ASA-YD D=0.818 D-cutoff=0.450
552 Networks=SignalP-noTM
553
554 # Measure  Position  Value    Cutoff    signal peptide?
555     max. C      21      0.721
556     max. Y      21      0.797
557     max. S      12      0.932
558     mean S      1-20    0.881
559     D          1-20    0.842    0.450    YES
560 Name=Vigun05g166800.1   SP='YES' Cleavage site between pos. 20 and 21: ASA-YD D=0.842 D-cutoff=0.450
561 Networks=SignalP-noTM
562
563 # Measure  Position  Value    Cutoff    signal peptide?
564     max. C      21      0.721
565     max. Y      21      0.797
566     max. S      12      0.932
567     mean S      1-20    0.881
568     D          1-20    0.842    0.450    YES
569 Name=Vigun05g166900.1   SP='YES' Cleavage site between pos. 20 and 21: ASA-YD D=0.842 D-cutoff=0.450
570 Networks=SignalP-noTM
571
572 # Measure  Position  Value    Cutoff    signal peptide?
573     max. C      21      0.717
574     max. Y      21      0.780
575     max. S      16      0.903
576     mean S      1-20    0.851
577     D          1-20    0.818    0.450    YES
578 Name=Vigun05g167000.1   SP='YES' Cleavage site between pos. 20 and 21: ASA-YD D=0.818 D-cutoff=0.450
579 Networks=SignalP-noTM
580
581 # Measure  Position  Value    Cutoff    signal peptide?
582     max. C      26      0.408
583     max. Y      26      0.560
584     max. S      17      0.859

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585     mean S      1-25      0.759
586         D      1-25      0.667      0.450      YES
587 Name=Vigun05g235200.1   SP='YES' Cleavage site between pos. 25 and 26: CGG-DP D=0.667 D-cutoff=0.450
588 Networks=SignalP-noTM
589
590 # Measure  Position  Value      Cutoff      signal peptide?
591   max. C      24      0.547
592   max. Y      20      0.703
593   max. S       3      0.961
594   mean S      1-19      0.920
595         D      1-19      0.820      0.450      YES
596 Name=Vigun05g250800.1   SP='YES' Cleavage site between pos. 19 and 20: GVA-VT D=0.820 D-cutoff=0.450
597 Networks=SignalP-noTM
598
599 # Measure  Position  Value      Cutoff      signal peptide?
600   max. C      20      0.561
601   max. Y      20      0.721
602   max. S       3      0.964
603   mean S      1-19      0.926
604         D      1-19      0.832      0.450      YES
605 Name=Vigun05g250900.1   SP='YES' Cleavage site between pos. 19 and 20: GVA-VT D=0.832 D-cutoff=0.450
606 Networks=SignalP-noTM
607
608 # Measure  Position  Value      Cutoff      signal peptide?
609   max. C      23      0.229
610   max. Y      23      0.216
611   max. S       3      0.291
612   mean S      1-22      0.204
613         D      1-22      0.210      0.450      NO
614 Name=Vigun05g251000.1   SP='NO' D=0.210 D-cutoff=0.450 Networks=SignalP-noTM
615
616 # Measure  Position  Value      Cutoff      signal peptide?
617   max. C      39      0.109
618   max. Y      12      0.108
619   max. S       1      0.131
620   mean S      1-11      0.094
621         D      1-11      0.101      0.450      NO

```


622 Name=Vigun05g251000.2 SP='NO' D=0.101 D-cutoff=0.450 Networks=SignalP-noTM

623

#	Measure	Position	Value	Cutoff	signal peptide?

625	max. C	16	0.129		

626	max. Y	37	0.105		

627	max. S	25	0.111		

628	mean S	1-36	0.093		

629	D	1-36	0.099	0.450	NO

630 Name=Vigun05g254700.1 SP='NO' D=0.099 D-cutoff=0.450 Networks=SignalP-noTM

631

#	Measure	Position	Value	Cutoff	signal peptide?

633	max. C	23	0.109		

634	max. Y	11	0.138		

635	max. S	2	0.243		

636	mean S	1-10	0.144		

637	D	1-10	0.141	0.450	NO

638 Name=Vigun06g057200.1 SP='NO' D=0.141 D-cutoff=0.450 Networks=SignalP-noTM

639

#	Measure	Position	Value	Cutoff	signal peptide?

641	max. C	66	0.110		

642	max. Y	11	0.119		

643	max. S	2	0.205		

644	mean S	1-10	0.128		

645	D	1-10	0.124	0.450	NO

646 Name=Vigun06g110700.1 SP='NO' D=0.124 D-cutoff=0.450 Networks=SignalP-noTM

647

#	Measure	Position	Value	Cutoff	signal peptide?

649	max. C	23	0.717		

650	max. Y	23	0.833		

651	max. S	16	0.994		

652	mean S	1-22	0.967		

653	D	1-22	0.905	0.450	YES

654 Name=Vigun06g138000.1 SP='YES' Cleavage site between pos. 22 and 23: AAA-TS D=0.905 D-cutoff=0.450

655 Networks=SignalP-noTM

656

#	Measure	Position	Value	Cutoff	signal peptide?

658	max. C	21	0.870		

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659     max. Y      21      0.921
660     max. S      13      0.994
661     mean S      1-20     0.976
662     D          1-20     0.950    0.450    YES
663 Name=Vigun06g138100.1   SP='YES' Cleavage site between pos. 20 and 21: ALA-AD D=0.950 D-cutoff=0.450
664 Networks=SignalP-noTM
665
666 # Measure  Position  Value      Cutoff    signal peptide?
667     max. C      24      0.848
668     max. Y      24      0.893
669     max. S      15      0.980
670     mean S      1-23     0.940
671     D          1-23     0.918    0.450    YES
672 Name=Vigun07g059500.1   SP='YES' Cleavage site between pos. 23 and 24: TLA-SD D=0.918 D-cutoff=0.450
673 Networks=SignalP-noTM
674
675 # Measure  Position  Value      Cutoff    signal peptide?
676     max. C      27      0.110
677     max. Y      27      0.108
678     max. S      22      0.143
679     mean S      1-26     0.105
680     D          1-26     0.106    0.450    NO
681 Name=Vigun07g089100.1   SP='NO' D=0.106 D-cutoff=0.450 Networks=SignalP-noTM
682
683 # Measure  Position  Value      Cutoff    signal peptide?
684     max. C      21      0.326
685     max. Y      21      0.556
686     max. S      15      0.982
687     mean S      1-20     0.950
688     D          1-20     0.769    0.450    YES
689 Name=Vigun07g100400.1   SP='YES' Cleavage site between pos. 20 and 21: ASA-CF D=0.769 D-cutoff=0.450
690 Networks=SignalP-noTM
691
692 # Measure  Position  Value      Cutoff    signal peptide?
693     max. C      46      0.111
694     max. Y      11      0.113
695     max. S      1       0.128

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696     mean S      1-10      0.112
697         D      1-10      0.112    0.450    NO
698 Name=Vigun07g106500.1   SP='NO' D=0.112 D-cutoff=0.450 Networks=SignalP-noTM
699
700 # Measure  Position  Value    Cutoff    signal peptide?
701   max. C     27       0.769
702   max. Y     27       0.858
703   max. S     16       0.993
704   mean S     1-26     0.952
705         D     1-26     0.909    0.450    YES
706 Name=Vigun07g108200.1   SP='YES' Cleavage site between pos. 26 and 27: ACA-KK D=0.909 D-cutoff=0.450
707 Networks=SignalP-noTM
708
709 # Measure  Position  Value    Cutoff    signal peptide?
710   max. C     24       0.839
711   max. Y     24       0.873
712   max. S     18       0.966
713   mean S     1-23     0.905
714         D     1-23     0.890    0.450    YES
715 Name=Vigun07g113800.1   SP='YES' Cleavage site between pos. 23 and 24: VLA-SS D=0.890 D-cutoff=0.450
716 Networks=SignalP-noTM
717
718 # Measure  Position  Value    Cutoff    signal peptide?
719   max. C     23       0.857
720   max. Y     23       0.868
721   max. S     13       0.938
722   mean S     1-22     0.879
723         D     1-22     0.874    0.450    YES
724 Name=Vigun07g132600.1   SP='YES' Cleavage site between pos. 22 and 23: AFA-SD D=0.874 D-cutoff=0.450
725 Networks=SignalP-noTM
726
727 # Measure  Position  Value    Cutoff    signal peptide?
728   max. C     23       0.833
729   max. Y     23       0.837
730   max. S     16       0.894
731   mean S     1-22     0.842
732         D     1-22     0.840    0.450    YES

```

733 Name=Vigun07g132700.1 SP='YES' Cleavage site between pos. 22 and 23: AFA-SD D=0.840 D-cutoff=0.450
 734 Networks=SignalP-noTM
 735
 736 # Measure Position Value Cutoff signal peptide?
 737 max. C 23 0.610
 738 max. Y 23 0.734
 739 max. S 11 0.980
 740 mean S 1-22 0.882
 741 D 1-22 0.814 0.450 YES
 742 Name=Vigun07g133900.1 SP='YES' Cleavage site between pos. 22 and 23: VSS-DP D=0.814 D-cutoff=0.450
 743 Networks=SignalP-noTM
 744
 745 # Measure Position Value Cutoff signal peptide?
 746 max. C 49 0.112
 747 max. Y 49 0.108
 748 max. S 38 0.117
 749 mean S 1-48 0.100
 750 D 1-48 0.104 0.450 NO
 751 Name=Vigun07g159700.1 SP='NO' D=0.104 D-cutoff=0.450 Networks=SignalP-noTM
 752
 753 # Measure Position Value Cutoff signal peptide?
 754 max. C 21 0.736
 755 max. Y 21 0.831
 756 max. S 11 0.985
 757 mean S 1-20 0.937
 758 D 1-20 0.888 0.450 YES
 759 Name=Vigun07g160600.1 SP='YES' Cleavage site between pos. 20 and 21: AFA-YD D=0.888 D-cutoff=0.450
 760 Networks=SignalP-noTM
 761
 762 # Measure Position Value Cutoff signal peptide?
 763 max. C 21 0.735
 764 max. Y 21 0.830
 765 max. S 11 0.985
 766 mean S 1-20 0.936
 767 D 1-20 0.887 0.450 YES
 768 Name=Vigun07g160600.2 SP='YES' Cleavage site between pos. 20 and 21: AFA-YD D=0.887 D-cutoff=0.450
 769 Networks=SignalP-noTM

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770
771 # Measure Position Value Cutoff signal peptide?
772 max. C 58 0.110
773 max. Y 32 0.112
774 max. S 13 0.141
775 mean S 1-31 0.113
776 D 1-31 0.113 0.450 NO
777 Name=Vigun07g235300.1 SP='NO' D=0.113 D-cutoff=0.450 Networks=SignalP-noTM
778
779 # Measure Position Value Cutoff signal peptide?
780 max. C 26 0.502
781 max. Y 24 0.692
782 max. S 16 0.992
783 mean S 1-23 0.957
784 D 1-23 0.835 0.450 YES
785 Name=Vigun07g237100.1 SP='YES' Cleavage site between pos. 23 and 24: SVS-FG D=0.835 D-cutoff=0.450
786 Networks=SignalP-noTM
787
788 # Measure Position Value Cutoff signal peptide?
789 max. C 26 0.487
790 max. Y 26 0.670
791 max. S 15 0.993
792 mean S 1-25 0.924
793 D 1-25 0.808 0.450 YES
794 Name=Vigun07g237200.1 SP='YES' Cleavage site between pos. 25 and 26: SFG-IA D=0.808 D-cutoff=0.450
795 Networks=SignalP-noTM
796
797 # Measure Position Value Cutoff signal peptide?
798 max. C 26 0.607
799 max. Y 26 0.750
800 max. S 17 0.989
801 mean S 1-25 0.926
802 D 1-25 0.845 0.450 YES
803 Name=Vigun07g237300.1 SP='YES' Cleavage site between pos. 25 and 26: SFG-IV D=0.845 D-cutoff=0.450
804 Networks=SignalP-noTM
805
806 # Measure Position Value Cutoff signal peptide?

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807 max. C 24 0.521
808 max. Y 24 0.697
809 max. S 14 0.988
810 mean S 1-23 0.932
811 D 1-23 0.824 0.450 YES
812 Name=Vigun07g237400.1 SP='YES' Cleavage site between pos. 23 and 24: SFG-IV D=0.824 D-cutoff=0.450
813 Networks=SignalP-noTM
814
815 # Measure Position Value Cutoff signal peptide?
816 max. C 24 0.520
817 max. Y 24 0.695
818 max. S 14 0.985
819 mean S 1-23 0.928
820 D 1-23 0.821 0.450 YES
821 Name=Vigun07g237500.1 SP='YES' Cleavage site between pos. 23 and 24: SFG-IV D=0.821 D-cutoff=0.450
822 Networks=SignalP-noTM
823
824 # Measure Position Value Cutoff signal peptide?
825 max. C 25 0.701
826 max. Y 25 0.796
827 max. S 16 0.979
828 mean S 1-24 0.904
829 D 1-24 0.854 0.450 YES
830 Name=Vigun07g237600.1 SP='YES' Cleavage site between pos. 24 and 25: SLS-EK D=0.854 D-cutoff=0.450
831 Networks=SignalP-noTM
832
833 # Measure Position Value Cutoff signal peptide?
834 max. C 19 0.126
835 max. Y 19 0.142
836 max. S 17 0.246
837 mean S 1-18 0.155
838 D 1-18 0.149 0.450 NO
839 Name=Vigun08g174800.1 SP='NO' D=0.149 D-cutoff=0.450 Networks=SignalP-noTM
840
841 # Measure Position Value Cutoff signal peptide?
842 max. C 24 0.111
843 max. Y 15 0.111

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844 max. S      2      0.130
845 mean S     1-14    0.103
846 D         1-14    0.107    0.450    NO
847 Name=Vigun08g205900.1 SP='NO' D=0.107 D-cutoff=0.450 Networks=SignalP-noTM
848
849 # Measure  Position  Value    Cutoff    signal peptide?
850 max. C     19        0.857
851 max. Y     19        0.906
852 max. S     13        0.985
853 mean S     1-18      0.960
854 D         1-18      0.935    0.450    YES
855 Name=Vigun09g037800.1 SP='YES' Cleavage site between pos. 18 and 19: SHA-SV D=0.935 D-cutoff=0.450
856 Networks=SignalP-noTM
857
858 # Measure  Position  Value    Cutoff    signal peptide?
859 max. C     47        0.133
860 max. Y     47        0.117
861 max. S     44        0.139
862 mean S     1-46      0.096
863 D         1-46      0.106    0.450    NO
864 Name=Vigun09g089200.1 SP='NO' D=0.106 D-cutoff=0.450 Networks=SignalP-noTM
865
866 # Measure  Position  Value    Cutoff    signal peptide?
867 max. C     26        0.782
868 max. Y     26        0.844
869 max. S     15        0.973
870 mean S     1-25      0.905
871 D         1-25      0.877    0.450    YES
872 Name=Vigun09gl22200.1 SP='YES' Cleavage site between pos. 25 and 26: CLA-EC D=0.877 D-cutoff=0.450
873 Networks=SignalP-noTM
874
875 # Measure  Position  Value    Cutoff    signal peptide?
876 max. C     25        0.131
877 max. Y     25        0.129
878 max. S     7         0.227
879 mean S     1-24      0.129
880 D         1-24      0.129    0.450    NO

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881 Name=Vigun09g177900.1 SP='NO' D=0.129 D-cutoff=0.450 Networks=SignalP-noTM
882
883 # Measure Position Value Cutoff signal peptide?
884 max. C 24 0.511
885 max. Y 24 0.689
886 max. S 15 0.986
887 mean S 1-23 0.927
888 D 1-23 0.817 0.450 YES
889 Name=Vigun10g081000.1 SP='YES' Cleavage site between pos. 23 and 24: SFG-IV D=0.817 D-cutoff=0.450
890 Networks=SignalP-noTM
891
892 # Measure Position Value Cutoff signal peptide?
893 max. C 21 0.828
894 max. Y 21 0.868
895 max. S 11 0.951
896 mean S 1-20 0.908
897 D 1-20 0.889 0.450 YES
898 Name=Vigun10g086400.1 SP='YES' Cleavage site between pos. 20 and 21: VSA-YD D=0.889 D-cutoff=0.450
899 Networks=SignalP-noTM
900
901 # Measure Position Value Cutoff signal peptide?
902 max. C 21 0.816
903 max. Y 21 0.852
904 max. S 11 0.944
905 mean S 1-20 0.887
906 D 1-20 0.871 0.450 YES
907 Name=Vigun10g086500.1 SP='YES' Cleavage site between pos. 20 and 21: VSA-YD D=0.871 D-cutoff=0.450
908 Networks=SignalP-noTM
909
910 # Measure Position Value Cutoff signal peptide?
911 max. C 21 0.828
912 max. Y 21 0.866
913 max. S 11 0.951
914 mean S 1-20 0.904
915 D 1-20 0.887 0.450 YES
916 Name=Vigun10g086600.1 SP='YES' Cleavage site between pos. 20 and 21: VSA-YD D=0.887 D-cutoff=0.450
917 Networks=SignalP-noTM

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918
919 # Measure Position Value Cutoff signal peptide?
920 max. C 21 0.828
921 max. Y 21 0.868
922 max. S 11 0.951
923 mean S 1-20 0.908
924 D 1-20 0.889 0.450 YES
925 Name=Vigun10g086700.1 SP='YES' Cleavage site between pos. 20 and 21: VSA-YD D=0.889 D-cutoff=0.450
926 Networks=SignalP-noTM
927
928 # Measure Position Value Cutoff signal peptide?
929 max. C 21 0.645
930 max. Y 21 0.751
931 max. S 11 0.931
932 mean S 1-20 0.870
933 D 1-20 0.815 0.450 YES
934 Name=Vigun10g087300.1 SP='YES' Cleavage site between pos. 20 and 21: VSS-YD D=0.815 D-cutoff=0.450
935 Networks=SignalP-noTM
936
937 # Measure Position Value Cutoff signal peptide?
938 max. C 24 0.533
939 max. Y 24 0.715
940 max. S 15 0.990
941 mean S 1-23 0.955
942 D 1-23 0.845 0.450 YES
943 Name=Vigun10g096400.1 SP='YES' Cleavage site between pos. 23 and 24: SVS-FG D=0.845 D-cutoff=0.450
944 Networks=SignalP-noTM
945
946 # Measure Position Value Cutoff signal peptide?
947 max. C 24 0.533
948 max. Y 24 0.715
949 max. S 15 0.990
950 mean S 1-23 0.955
951 D 1-23 0.845 0.450 YES
952 Name=Vigun10g096600.1 SP='YES' Cleavage site between pos. 23 and 24: SVS-FG D=0.845 D-cutoff=0.450
953 Networks=SignalP-noTM
954

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955
956
957 # Measure Position Value Cutoff signal peptide?
958 max. C 60 0.111
959 max. Y 11 0.107
960 max. S 1 0.128
961 mean S 1-10 0.097
962 D 1-10 0.102 0.450 NO
963 Name=Vigun10g101100.1 SP='NO' D=0.102 D-cutoff=0.450 Networks=SignalP-noTM
964
965 # Measure Position Value Cutoff signal peptide?
966 max. C 21 0.743
967 max. Y 21 0.704
968 max. S 12 0.817
969 mean S 1-20 0.653
970 D 1-20 0.676 0.450 YES
971 Name=Vigun10g164200.1 SP='YES' Cleavage site between pos. 20 and 21: CHG-DS D=0.676 D-cutoff=0.450
972 Networks=SignalP-noTM
973
974 # Measure Position Value Cutoff signal peptide?
975 max. C 21 0.471
976 max. Y 21 0.633
977 max. S 15 0.919
978 mean S 1-20 0.854
979 D 1-20 0.753 0.450 YES
980 Name=Vigun10g164300.1 SP='YES' Cleavage site between pos. 20 and 21: SYA-AV D=0.753 D-cutoff=0.450
981 Networks=SignalP-noTM
982
983 # Measure Position Value Cutoff signal peptide?
984 max. C 18 0.510
985 max. Y 18 0.696
986 max. S 9 0.983
987 mean S 1-17 0.948
988 D 1-17 0.832 0.450 YES
989 Name=Vigun10g164400.1 SP='YES' Cleavage site between pos. 17 and 18: SDA-AV D=0.832 D-cutoff=0.450
990 Networks=SignalP-noTM
991

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992 # Measure Position Value Cutoff signal peptide?
993 max. C 24 0.516
994 max. Y 24 0.646
995 max. S 17 0.913
996 mean S 1-23 0.811
997 D 1-23 0.735 0.450 YES
998 Name=Vigun10g164500.1 SP='YES' Cleavage site between pos. 23 and 24: SHA-SP D=0.735 D-cutoff=0.450
999 Networks=SignalP-noTM
1000
1001 # Measure Position Value Cutoff signal peptide?
1002 max. C 21 0.517
1003 max. Y 21 0.676
1004 max. S 14 0.926
1005 mean S 1-20 0.887
1006 D 1-20 0.790 0.450 YES
1007 Name=Vigun10g164600.1 SP='YES' Cleavage site between pos. 20 and 21: SNA-AV D=0.790 D-cutoff=0.450
1008 Networks=SignalP-noTM
1009
1010 # Measure Position Value Cutoff signal peptide?
1011 max. C 18 0.830
1012 max. Y 18 0.874
1013 max. S 11 0.956
1014 mean S 1-17 0.920
1015 D 1-17 0.898 0.450 YES
1016 Name=Vigun10g164700.1 SP='YES' Cleavage site between pos. 17 and 18: SHA-FV D=0.898 D-cutoff=0.450
1017 Networks=SignalP-noTM
1018
1019 # Measure Position Value Cutoff signal peptide?
1020 max. C 19 0.839
1021 max. Y 19 0.892
1022 max. S 11 0.976
1023 mean S 1-18 0.947
1024 D 1-18 0.922 0.450 YES
1025 Name=Vigun10g164800.1 SP='YES' Cleavage site between pos. 18 and 19: SHA-TV D=0.922 D-cutoff=0.450
1026 Networks=SignalP-noTM
1027
1028 # Measure Position Value Cutoff signal peptide?

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1029 max. C 24 0.522
1030 max. Y 24 0.695
1031 max. S 15 0.986
1032 mean S 1-23 0.926
1033 D 1-23 0.820 0.450 YES
1034 Name=Vigun11g024500.1 SP='YES' Cleavage site between pos. 23 and 24: SFG-IS D=0.820 D-cutoff=0.450
1035 Networks=SignalP-noTM
1036
1037 # Measure Position Value Cutoff signal peptide?
1038 max. C 27 0.781
1039 max. Y 27 0.828
1040 max. S 15 0.981
1041 mean S 1-26 0.882
1042 D 1-26 0.857 0.450 YES
1043 Name=Vigun11g026700.1 SP='YES' Cleavage site between pos. 26 and 27: CLG-DC D=0.857 D-cutoff=0.450
1044 Networks=SignalP-noTM
1045
1046 # Measure Position Value Cutoff signal peptide?
1047 max. C 50 0.125
1048 max. Y 11 0.182
1049 max. S 1 0.368
1050 mean S 1-10 0.318
1051 D 1-10 0.237 0.500 NO
1052 Name=Vigun11g038900.1 SP='NO' D=0.237 D-cutoff=0.500 Networks=SignalP-TM
1053
1054 # Measure Position Value Cutoff signal peptide?
1055 max. C 24 0.518
1056 max. Y 24 0.704
1057 max. S 17 0.993
1058 mean S 1-23 0.956
1059 D 1-23 0.840 0.450 YES
1060 Name=Vigun11g098100.1 SP='YES' Cleavage site between pos. 23 and 24: SVS-FG D=0.840 D-cutoff=0.450
1061 Networks=SignalP-noTM
1062
1063 # Measure Position Value Cutoff signal peptide?
1064 max. C 22 0.860
1065 max. Y 22 0.872

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1066 max. S 4 0.936
 1067 mean S 1-21 0.884
 1068 D 1-21 0.878 0.450 YES
 1069 Name=Vigun11g147100.1 SP='YES' Cleavage site between pos. 21 and 22: AMA-IP D=0.878 D-cutoff=0.450
 1070 Networks=SignalP-noTM
 1071
 1072 # Measure Position Value Cutoff signal peptide?
 1073 max. C 51 0.126
 1074 max. Y 51 0.119
 1075 max. S 50 0.167
 1076 mean S 1-50 0.103
 1077 D 1-50 0.111 0.450 NO
 1078 Name=Vigun11g151800.1 SP='NO' D=0.111 D-cutoff=0.450 Networks=SignalP-noTM
 1079
 1080
 1081 # Measure Position Value Cutoff signal peptide?
 1082 max. C 58 0.187
 1083 max. Y 58 0.143
 1084 max. S 1 0.162
 1085 mean S 1-57 0.104
 1086 D 1-57 0.122 0.450 NO
 1087 Name=Vigun11g163100.1 SP='NO' D=0.122 D-cutoff=0.450 Networks=SignalP-noTM
 1088

1089

1090 Supplementary material

Suence Number	Query Name	Hits Found	Identifier	Accession	Clan	Description	Protein size (aa)	Signal
1	Vigun01g148800.1	1	Cupin_3	PF05899.11	CL0029	Protein of unknown function (DUF861)	110	
2	Vigun01g205600.1	2	Cupin_1	PF00190.21	CL0029	Cupin	217	1
3	Vigun02g070100.1	2	Cupin_1	PF00190.21	CL0029	Cupin	216	1
4	Vigun02g110000.1	1	Cupin_8	PF13621.5	CL0029	Cupin-like domain	415	1
5	Vigun02g134000.1	1	Cupin_1	PF00190.21	CL0029	Cupin	631	1
6	Vigun03g085800.1	2	Cupin_1	PF00190.21	CL0029	Cupin	357	

7	Vigun03g085800.2	2	Cupin_1	PF00190.21	CL0029	Cupin	357	
			Cupin_1	PF00190.21	CL0029	Cupin		
			Cupin_1	PF00190.21	CL0029	Cupin		
8	Vigun03g085900.1	2	Cupin_1	PF00190.21	CL0029	Cupin	358	
			Cupin_1	PF00190.21	CL0029	Cupin		
9	Vigun03g085900.2	2	Cupin_1	PF00190.21	CL0029	Cupin	258	
			Cupin_1	PF00190.21	CL0029	Cupin		
10	Vigun03g254300.1	2	Cupin_1	PF00190.21	CL0029	Cupin	155	
11	Vigun03g297500.1	2	Cupin_2	PF07883.10	CL0029	Cupin domain	297	1
12	Vigun03g390200.1	1	Cupin_4	PF08007.11	CL0029	Cupin superfamily protein	776	1
13	Vigun03g397300.1	2	Cupin_1	PF00190.21	CL0029	Cupin	208	
14	Vigun03g399100.1	1	Cupin_5	PF06172.10	CL0029	Cupin superfamily (DUF985)	189	
15	Vigun04g148500.1	1	Cupin_5	PF06172.10	CL0029	Cupin superfamily (DUF985)	182	
16	Vigun04g167800.1	1	Cupin_3	PF05899.11	CL0029	Protein of unknown function (DUF861)	98	
17	Vigun04g168100.1	2	Cupin_3	PF05899.11	CL0029	Protein of unknown function (DUF861)	129	1
18	Vigun05g001800.1	2	Pirin	PF02678.15	CL0029	Pirin	322	
			Pirin_C	PF05726.12	CL0029	Pirin C-terminal cupin domain		
19	Vigun05g152400.1	1	Cupin_3	PF05899.11	CL0029	Protein of unknown function (DUF861)	58	
20	Vigun05g166300.1	2	Cupin_1	PF00190.21	CL0029	Cupin	222	1
21	Vigun05g166800.1	2	Cupin_1	PF00190.21	CL0029	Cupin	222	1
22	Vigun05g166900.1	2	Cupin_1	PF00190.21	CL0029	Cupin	222	1
23	Vigun05g167000.1	2	Cupin_1	PF00190.21	CL0029	Cupin	222	1
24	Vigun05g235200.1	2	Cupin_1	PF00190.21	CL0029	Cupin	204	1
25	Vigun05g250800.1	2	Cupin_1	PF00190.21	CL0029	Cupin	456	1
			Cupin_1	PF00190.21	CL0029	Cupin		
26	Vigun05g250900.1	2	Cupin_1	PF00190.21	CL0029	Cupin	456	1
			Cupin_1	PF00190.21	CL0029	Cupin		
27	Vigun05g251000.1	1	Cupin_1	PF00190.21	CL0029	Cupin	377	1
			Cupin_1	PF00190.21	CL0029	Cupin		

28	Vigun05g251000.2	1	Cupin_1	PF00190.21	CL0029	Cupin	341	
29	Vigun05g254700.1	1	Cupin_1	PF00190.21	CL0029	Cupin	356	
			Cupin_1	PF00190.21	CL0029	Cupin		
30	Vigun06g057200.1	2	Pirin	PF02678.15	CL0029	Pirin	298	
			Pirin_C	PF05726.12	CL0029	Pirin C-terminal cupin domain		
31	Vigun06g110700.1	3	LacAB_rpiB	PF02502.17	n/a	Ribose/Galactose Isomerase	302	
			Cupin_2	PF07883.10	CL0029	Cupin domain		
32	Vigun06g138000.1	2	Cupin_1	PF00190.21	CL0029	Cupin	215	1
33	Vigun06g138100.1	2	Cupin_1	PF00190.21	CL0029	Cupin	214	1
34	Vigun07g059500.1	2	Cupin_1	PF00190.21	CL0029	Cupin	225	1
35	Vigun07g089100.1	1	Cupin_3	PF05899.11	CL0029	Protein of unknown function (DUF861)	104	1
36	Vigun07g100400.1	1	Cupin_1	PF00190.21	CL0029	Cupin	611	1
			Cupin_1	PF00190.21	CL0029	Cupin		
37	Vigun07g106500.1	2	Cupin_8	PF13621.5	CL0029	Cupin-like domain	537	
38	Vigun07g108200.1	1	Cupin_1	PF00190.21	CL0029	Cupin	510	1
39	Vigun07g113800.1	2	Auxin_BP	PF02041.15	CL0029	Auxin binding protein	192	1
40	Vigun07g132600.1	2	Cupin_1	PF00190.21	CL0029	Cupin	220	1
41	Vigun07g132700.1	2	Cupin_1	PF00190.21	CL0029	Cupin	220	1
42	Vigun07g133900.1	2	Cupin_1	PF00190.21	CL0029	Cupin	218	1
43	Vigun07g159700.1	1	Cupin_3	PF05899.11	CL0029	Protein of unknown function (DUF861)	115	1
44	Vigun07g160600.1	2	Cupin_1	PF00190.21	CL0029	Cupin	226	1
45	Vigun07g160600.2	2	Cupin_1	PF00190.21	CL0029	Cupin	222	1
46	Vigun07g235300.1	3	ARD	PF03079.13	CL0029	ARD/ARD' family	187	
47	Vigun07g237100.1	1	Cupin_1	PF00190.21	CL0029	Cupin	444	1
			Cupin_1	PF00190.21	CL0029	Cupin		
48	Vigun07g237200.1	1	Cupin_1	PF00190.21	CL0029	Cupin	536	1
			Cupin_1	PF00190.21	CL0029	Cupin		
49	Vigun07g237300.1	1	Cupin_1	PF00190.21	CL0029	Cupin	457	1
			Cupin_1	PF00190.21	CL0029	Cupin		

50	Vigun07g237400.1	1	Cupin_1	PF00190.21	CL0029	Cupin	442	1
			Cupin_1	PF00190.21	CL0029	Cupin		
51	Vigun07g237500.1	1	Cupin_1	PF00190.21	CL0029	Cupin	455	1
			Cupin_1	PF00190.21	CL0029	Cupin		
52	Vigun07g237600.1	1	Cupin_1	PF00190.21	CL0029	Cupin	589	1
53	Vigun08g174800.1	1	Cupin_3	PF05899.11	CL0029	Protein of unknown function (DUF861)	143	
54	Vigun08g205900.1	2	Pirin	PF02678.15	CL0029	Pirin	301	
			Pirin_C	PF05726.12	CL0029	Pirin C-terminal cupin domain		
55	Vigun09g037800.1	2	Cupin_1	PF00190.21	CL0029	Cupin	209	1
56	Vigun09g089200.1	2	Cupin_8	PF13621.5	CL0029	Cupin-like domain	483	
57	Vigun09g122200.1	2	Cupin_1	PF00190.21	CL0029	Cupin	231	1
58	Vigun09g177900.1	4	F-box-like	PF12937.6	CL0271	F-box-like	962	
			Cupin_8	PF13621.5	CL0029	Cupin-like domain		
59	Vigun10g081000.1	1	Cupin_1	PF00190.21	CL0029	Cupin	457	1
			Cupin_1	PF00190.21	CL0029	Cupin		
60	Vigun10g086400.1	2	Cupin_1	PF00190.21	CL0029	Cupin	220	1
61	Vigun10g086500.1	2	Cupin_1	PF00190.21	CL0029	Cupin	220	1
62	Vigun10g086600.1	2	Cupin_1	PF00190.21	CL0029	Cupin	220	1
63	Vigun10g086700.1	2	Cupin_1	PF00190.21	CL0029	Cupin	220	1
64	Vigun10g087300.1	2	Cupin_1	PF00190.21	CL0029	Cupin	220	1
65	Vigun10g096400.1	1	Cupin_1	PF00190.21	CL0029	Cupin	456	1
			Cupin_1	PF00190.21	CL0029	Cupin		
66	Vigun10g096600.1	1	Cupin_1	PF00190.21	CL0029	Cupin	456	1
			Cupin_1	PF00190.21	CL0029	Cupin		
67	Vigun10g101100.1	2	Cupin_8	PF13621.5	CL0029	Cupin-like domain	516	
68	Vigun10g164200.1	2	Cupin_1	PF00190.21	CL0029	Cupin	209	1
69	Vigun10g164300.1	2	Cupin_1	PF00190.21	CL0029	Cupin	209	1
70	Vigun10g164400.1	2	Cupin_1	PF00190.21	CL0029	Cupin	206	1
71	Vigun10g164500.1	2	Cupin_1	PF00190.21	CL0029	Cupin	212	1

72	Vigun10g164600.1	2	Cupin_1	PF00190.21	CL0029	Cupin	213	1
73	Vigun10g164700.1	2	Cupin_1	PF00190.21	CL0029	Cupin	206	1
74	Vigun10g164800.1	1	Cupin_1	PF00190.21	CL0029	Cupin	209	1
75	Vigun11g024500.1	1	Cupin_1	PF00190.21	CL0029	Cupin	449	1
			Cupin_1	PF00190.21	CL0029	Cupin		
76	Vigun11g026700.1	2	Cupin_1	PF00190.21	CL0029	Cupin	228	
77	Vigun11g038900.1	1	Cupin_3	PF05899.11	CL0029	Protein of unknown function (DUF861)	206	1
78	Vigun11g098100.1	2	Cupin_1	PF00190.21	CL0029	Cupin	427	1
			Cupin_1	PF00190.21	CL0029	Cupin		
79	Vigun11g147100.1	2	Cupin_1	PF00190.21	CL0029	Cupin	444	1
			Cupin_1	PF00190.21	CL0029	Cupin		
80	Vigun11g151800.1	1	Cupin_1	PF00190.21	CL0029	Cupin	356	
			Cupin_1	PF00190.21	CL0029	Cupin		
81	Vigun11g163100.1	3	Cupin_8	PF13621.5	CL0029	Cupin-like domain	413	

1091

Query Name	CDD	SMART	PFAM (HMMER)
Vigun01g148800.1	monocupin (22-96)	monocupin (22-96)	monocupin (22-96)
Vigun01g205600.1	monocupin (61-207)	monocupin (58-207)	monocupin (60-207)
Vigun02g070100.1	monocupin (61-208)	monocupin (59-208)	monocupin (59-208)
Vigun02g110000.1	monocupin (100-377)	monocupin (100-377)	monocupin (100-377)
Vigun02g134000.1	monocupin (244-393)	monocupin (238-393)	monocupin (238-393)
Vigun03g085800.1	bicupin (12-159)	bicupin (3-159)	bicupin (5-159)
	bicupin (35-323)	bicupin (194-240)	bicupin (192-240)
Vigun03g085900.1	monocupin (41-324)	bicupin (3-159)	bicupin (5-159)
	no cupin (41-324)	bicupin (192-341)	bicupin (192-341)
Vigun03g254300.1	monocupin (11-140)	monocupin (8-140)	monocupin (5-140)

Vigun03g297500.1	AlIE super family(58-297)	monocupin (220-289)	monocupin (220-289)
Vigun03g390200.1	cupin-like(442-605)	JmjC (434-573)	cupin-like (439-575)
Vigun03g397300.1	monocupin (52-198)	monocupin (52-198)	monocupin (52-197)
Vigun03g399100.1	monocupin (7-165)	monocupin (6-166)	monocupin (6-166)
Vigun04g148500.1	monocupin (7-158)	monocupin (6-159)	monocupin (6-159)
Vigun04g167800.1	monocupin (21-95)	monocupin (21-95)	monocupin (21-95)
Vigun04g168100.1	monocupin (51-125)	monocupin (51-125)	monocupin (51-125)
Vigun05g001800.1	pirin (57-310)	Pirin (59-154)	Pirin (59-154)
	Pirin C (57-310)	pirin C (207-312)	Pirin C (207-312)
Vigun05g152400.1	monocupin (25-55)	monocupin (21-58)	monocupin (21-58)
Vigun05g166300.1	monocupin (63-210)	monocupin (59-210)	monocupin (60-210)
Vigun05g166800.1	monocupin (63-210)	monocupin (59-210)	monocupin (60-210)
Vigun05g166900.1	monocupin (63-210)	monocupin (59-210)	monocupin (60-210)
Vigun05g167000.1	monocupin (63-210)	monocupin (59-210)	monocupin (60-210)
Vigun05g235200.1	monocupin (52-196)	monocupin (52-196)	monocupin (53-196)
Vigun05g250800.1	bicupin (76-192)	bicupin (40-193)	bicupin (43-192)
	bicupin (296-441)	bicupin(292-441)	bicupin(292-441)
Vigun05g250900.1	bicupin (74-193)	bicupin (58-194)	bicupin (43-194)
	bicupin (296-441)	bicupin(292-441)	bicupin(292-441)
Vigun05g251000.1	bicupin (2-113)	bicupin (2-114)	bicupin (2-113)
	bicupin (216-362)	bicupin(213-362)	bicupin(213-362)
Vigun05g254700.1	monocupin (48-354)	bicupin (3-157)	bicupin (6-157)
	No cupin (48-354)	bicupin (195-339)	bicupin (190-339)
Vigun06g057200.1	pirin C (24-279)	Pirin (30-126)	Pirin (30-126)
	No cupin domain	Pirin C (179-284)	Pirin C (179-284)
Vigun06g110700.1	LacAB_rpiB (11-131)	LacAB_rpiB (11-139)	LacAB_rpiB (11-139)
	cupin-like (159-268)	bicupin (202-269)	bicupin (202-269)
Vigun06g138000.1	monocupin (59-208)	monocupin (59-209)	monocupin (59-209)
Vigun06g138100.1	monocupin (59-209)	monocupin (59-209)	monocupin (59-209)

Vigun07g059500.1	monocupin (70-212)	monocupin (68-213)	monocupin (67-213)
Vigun07g089100.1	monocupin (22-96)	monocupin (22-96)	monocupin (22-96)
Vigun07g100400.1	monocupin (25-594)	bicupin (39-234)	bicupin (39-192)
	No cupin (25-594)	bicupin (443-589)	bicupin (443-589)
Vigun07g106500.1	monocupin (18-292)	monocupin (146-303)	monocupin (18-2953)
Vigun07g108200.1	monocupin (323-481)	monocupin (320-484)	monocupin (320-480)
Vigun07g113800.1	monocupin (27-192)	monocupin (70-150)	monocupin (70-150)
Vigun07g132600.1	monocupin (62-209)	monocupin (61-209)	monocupin (61-209)
Vigun07g132700.1	monocupin (62-209)	monocupin (61-209)	monocupin (61-209)
Vigun07g133900.1	monocupin (62-208)	monocupin (59-208)	monocupin (60-208)
Vigun07g159700.1	monocupin (26-100)	monocupin (26-100)	monocupin (26-100)
Vigun07g160600.1	monocupin (67-215)	monocupin (67-215)	monocupin (65-215)
Vigun07g235300.1	ARD (4-158)-No cupin	monocupin (83-143)	monocupin (83-149)
Vigun07g237100.1	bicupin (59-205)	bicupin (56-206)	bicupin (56-206)
	bicupin (261-417)	bicupin (258-417)	bicupin (258-417)
Vigun07g237200.1	bicupin (140-281)	bicupin (138-288)	bicupin (140-288)
	bicupin (344-495)	bicupin (341-497)	bicupin (341-496)
Vigun07g237300.1	bicupin (59-205)	bicupin (56-206)	bicupin (56-206)
	bicupin (261-417)	bicupin (258-417)	bicupin (258-417)
Vigun07g237400.1	bicupin(57-203)	bicupin(54-204)	bicupin(54-204)
	bicupin (259-415)	bicupin (256-415)	bicupin (256-415)
Vigun07g237500.1	bicupin (57-203)	bicupin (54-204)	bicupin (54-204)
	bicupin (259-415)	bicupin (256-415)	bicupin (256-415)
Vigun07g237600.1	bicupin(196-346)	bicupin (188-347)	no domain cupin
	bicupin(398-551)	bicupin 395-341	monocupin (395-551)
Vigun08g174800.1	monocupin (61-135)	monocupin (61-135)	monocupin (61-135)
Vigun08g205900.1	Pirin C (14-279)	Pirin (61-135)	Pirin (30-126)
	No domain	Pirin C	Pirin C (179-284)
Vigun09g037800.1	monocupin (53-199)	monocupin (53-199)	monocupin (53-199)

Vigun09g089200.1	cupin like (20-289)	JmjC (122-302)	Cupin_8 (19-291)
	No domain	No domain	JmjC (179-285)
Vigun09g122200.1	monocupin (78-181)	monocupin (66-208)	monocupin (66-202)
Vigun09g177900.1	F-box-like (15-59)	F-box-like (18-58)	F-box-like (18-58)
	cupin-like (135-367)	JmjC (210-337)	cupin_8 (135-367)
Vigun10g081000.1	bicupin (57-203)	bicupin (46-204)	bicupin (51-204)
	bicupin (257-417)	bicupin (254-417)	bicupin (254-417)
Vigun10g086400.1	monocupin (62-209)	monocupin (60-209)	monocupin (60-209)
Vigun10g086500.1	monocupin (62-209)	monocupin (60-209)	monocupin (60-209)
Vigun10g086600.1	monocupin (64-209)	monocupin (61-209)	monocupin (62-209)
Vigun10g086700.1	monocupin (62-209)	monocupin (60-209)	monocupin (60-209)
Vigun10g087300.1	monocupin (62-209)	monocupin (60-209)	monocupin (60-209)
Vigun10g096400.1	bicupin (57-203)	bicupin (54-204)	bicupin (54-204)
	bicupin (259-423)	bicupin (256-423)	bicupin (256-423)
Vigun10g096600.1	bicupin (259-423)	bicupin (54-204)	bicupin (54-204)
	bicupin (259-423)	bicupin (256-423)	bicupin (256-423)
Vigun10g101100.1	F-box-like (100-139)	F-box-like (98-138)	JmjC (323-434)
	cupin-like (215-434)	JmjC (282-451)	Cupin_8 (2014-439)
Vigun10g164200.1	monocupin (66-199)	monocupin (55-199)	monocupin (57-199)
Vigun10g164300.1	monocupin (60-199)	monocupin (55-199)	monocupin (54-199)
Vigun10g164400.1	monocupin (54-196)	monocupin (52-196)	monocupin (51-196)
Vigun10g164500.1	monocupin (69-202)	monocupin (58-202)	monocupin (60-202)
Vigun10g164600.1	monocupin (60-199)	monocupin (55-199)	monocupin (54-199)
Vigun10g164700.1	monocupin (54-196)	monocupin (52-196)	monocupin (52-196)
Vigun10g164800.1	monocupin (54-199)	monocupin (53-199)	monocupin (53-199)
Vigun11g024500.1	bicupin (54-200)	bicupin (51-201)	bicupin (44-201)
	bicupin (252-410)	bicupin (249-411)	bicupin (249-410)
Vigun11g026700.1	monocupin (78-188)	monocupin (66-201)	monocupin (67-201)
Vigun11g038900.1	monocupin (173-203)	monocupin (169-206)	monocupin (169-206)

Vigun11g098100.1	bicupin (55-201)	bicupin (52-202)	bicupin (51-202)
	bicupin (256-408)	bicupin (252-409)	bicupin (252-409)
Vigun11g147100.1	bicupin (35-187)	bicupin (28-187)	bicupin (31-146)
	bicupin (278-424)	bicupin (275-424)	bicupin (275-424)
Vigun11g151800.1	No cupin (48-354)	bicupin (3-157)	bicupin (5-157)
	No cupin (48-354)	bicupin (195-339)	bicupin (190-339)

1092

1093 Vigna algalares

Query Name	Hits Found	Identifier	Accession	Clan	Description	Domain E-values			
						Start	End	Individual	Conditional
BAT97405.1		Cupin_1	PF00190.21	CL0029	Cupin	51	204	1,30E-07	7,60E-12
						256	416	3,30E-27	2,00E-31
KOM36077.1		Cupin_1	PF00190.21	CL0029	Cupin	56	207	2,20E-06	1,30E-10
						259	378	8,00E-13	4,80E-17
KOM36078.1		Cupin_1	PF00190.21	CL0029	Cupin	120	269	0,00026	1,50E-08
						321	476	1,90E-24	1,10E-28
XP_017411733.1		Cupin_1	PF00190.21	CL0029	Cupin	79	194	1,10E-12	1,30E-16
						322	471	1,00E-25	1,20E-29
XP_017413272.1		Cupin_1	PF00190.21	CL0029	Cupin	57	207	1,20E-07	7,10E-12
						259	417	1,70E-25	1,00E-29
XP_017413273.1		Cupin_1	PF00190.21	CL0029	Cupin	56	207	3,40E-08	2,00E-12
						259	421	8,70E-27	5,20E-31
XP_017413275.1		Cupin_1	PF00190.21	CL0029	Cupin	193	347	3,40E-05	2,00E-09
						397	553	2,50E-25	1,50E-29
XP_017414388.1		Cupin_1	PF00190.21	CL0029	Cupin	120	269	0,00018	1,10E-08

XP_017414389.1	Cupin_1	PF00190.21	CL0029	Cupin	321	476	1,30E-24	7,70E-29
					56	207	3,00E-06	1,80E-10
					259	420	1,30E-26	7,60E-31
XP_017415489.1	Cupin_1	PF00190.21	CL0029	Cupin	320	480	2,10E-27	1,30E-31
Hits Found					49	205	1,40E-08	8,20E-13
					257	420	2,80E-26	1,70E-30
					Start	End	Individual	Conditional
					10	131	6,30E-16	3,80E-20
					5	159	4,10E-20	4,90E-24
					192	341	5,20E-18	6,30E-22
					39	192	1,20E-25	7,50E-30
					450	596	6,30E-30	3,80E-34
					5	157	5,60E-28	3,30E-32
					190	339	9,40E-23	5,60E-27
XP_017433627.1	Cupin_1	PF00190.21	CL0029	Cupin				

1094 Vigna rariata

NP_001304202	Cupin_1	PF00190.21	CL0029	Cupin	56	206	8,00E-08	4,80E-12
					259	420	1,70E-26	1,00E-30
NP_001304231.1	Cupin_1	PF00190.21	CL0029	Cupin	47	204	3,00E-08	1,80E-12
					256	413	8,90E-29	5,30E-33
XP_014492536.1	Cupin_1	PF00190.21	CL0029	Cupin	49	205	3,10E-08	3,70E-12
					257	413	3,50E-26	4,10E-30
XP_014493578.1	Cupin_1	PF00190.21	CL0029	Cupin	83	196	1,10E-10	1,30E-14
					323	472	5,30E-25	6,30E-29
XP_014512682.1	Cupin_1	PF00190.21	CL0029	Cupin	318	479	1,80E-28	1,10E-32
XP_014507363.1	Cupin_1	PF00190.21	CL0029	Cupin	58	206	6,20E-08	3,70E-12

1095	Vigna radiata legumins	XP_014523923.1	Cupin_1	PF00190.21	CL0029	Cupin	259	413	1,70E-29	9,90E-34
							57	206	4,20E-08	2,50E-12
		XP_014523928.1	Cupin_1	PF00190.21	CL0029	Cupin	206	339	7,10E-18	4,20E-22
							200	353	5,50E-05	3,30E-09
		XP_014523936.1	Cupin_1	PF00190.21	CL0029	Cupin	403	560	2,60E-25	1,60E-29
							129	278	7,60E-05	4,50E-09
		XP_014523938.1	Cupin_1	PF00190.21	CL0029	Cupin	329	485	2,30E-25	1,40E-29
							58	206	6,90E-08	4,10E-12
		XP_014524354.1	Cupin_1	PF00190.21	CL0029	Cupin	259	420	9,70E-27	5,80E-31
							57	206	1,30E-08	8,10E-13
							259	419	8,90E-27	5,40E-31

1095 Vigna radiata legumins

1096		XP_014506003.1	Cupin_1	PF00190.21	CL0029	Cupin	25	179	9,20E-22	1,10E-25
							212	361	1,60E-15	1,90E-19
		XP_014508262.1	Cupin_1	PF00190.21	CL0029	Cupin	5	159	4,60E-21	5,50E-25
							192	321	6,80E-14	8,10E-18
		XP_014508263.1	Cupin_1	PF00190.21	CL0029	Cupin	5	159	4,30E-21	5,10E-25
							192	314	6,50E-14	7,70E-18
		XP_014521758.1	Cupin_1	PF00190.21	CL0029	Cupin	39	192	9,40E-26	1,10E-29
							445	591	3,10E-31	3,70E-35

1096

Phvul.002G239800	Cupin_1	smart00835	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.002G239900	No cupin	cl28274	glutelin; Provisional, No vicilin domain
Phvul.002G239900	No cupin	cl28274	glutelin; Provisional, No vicilin domain
Phvul.002G249800	Cupin_1	smart00835	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...

Phvul.003G131400	Cupin_1	pfam00190	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.005G137200	Cupin_1	smart00835	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
	Cupin_1	smart00835	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.007G173600	Cupin_1	smart00835	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
	cupin_like super family	cl21464	onserved domain found in cupin and related proteins; A diverse protein domains superfamily ..
Phvul.007G192800	No cupin	cl28274	glutelin; Provisional, No vicilin domain
Phvul.007G206600	Cupin_1	pfam00190	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.007G207800	Cupin_1	pfam00190	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.007G229500	Cupin_1	pfam00190	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.009G227800	Cupin_1	pfam00190	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.010G129800	Cupin_1	pfam00190	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.011G067800	No cupin	cl28274	glutelin; Provisional, No vicilin domain
Phvul.011G072800	Cupin_1	smart00835	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
	Cupin_1	smart00835	Cupin; This family represents the conserved barrel domain of the 'cupin' superfamily ('cupa' ...
Phvul.L001743	No cupin	cl28274	glutelin; Provisional, No vicilin domain

1097

Phvul.003G131400	Cupin_1	PF00190.21	CL0029	Cupin	52	197	2,20E-33	2,60E-37
Phvul.005G137200	Cupin_1	PF00190.21	CL0029	Cupin	43	198	5,40E-09	6,40E-13
					297	446	1,40E-32	1,60E-36
Phvul.007G173600	Cupin_1	PF00190.21	CL0029	Cupin	121	260	7,00E-05	4,20E-09
					314	475	1,60E-29	9,80E-34
Phvul.007G192800.1	Cupin_1	PF00190.21	CL0029	Cupin	36	188	3,70E-26	2,20E-30
					458	604	9,80E-32	5,90E-36
Phvul.007G206600	Cupin_1	PF00190.21	CL0029	Cupin	65	213	7,70E-48	9,30E-52
Phvul.007G207800	Cupin_1	PF00190.21	CL0029	Cupin	61	209	2,30E-48	2,70E-52
Phvul.007G229500	Cupin_1	PF00190.21	CL0029	Cupin	67	213	7,40E-43	8,90E-47
Phvul.009G227800	Cupin_1	PF00190.21	CL0029	Cupin	54	200	5,80E-35	7,00E-39
Phvul.010G129800	Cupin_1	PF00190.21	CL0029	Cupin	53	198	1,10E-29	1,40E-33

Phvul.011G067800.1	Cupin_1	PF00190.21	CL0029	Cupin	5	157	7,80E-29	4,70E-33
					190	339	9,00E-22	5,40E-26
Phvul.011G072800.2	Cupin_1	PF00190.21	CL0029	Cupin	32	148	2,10E-10	2,50E-14
					273	422	5,40E-31	6,50E-35
Phvul.L001743	Cupin_1	PF00190.21	CL0029	Cupin	5	157	4,30E-29	2,60E-33
					190	339	6,10E-22	3,70E-26
Phvul.003G131400	Cupin_1	PF00190.21	CL0029	Cupin	52	197	2,20E-33	2,60E-37
Phvul.005G137200	Cupin_1	PF00190.21	CL0029	Cupin	43	198	5,40E-09	6,40E-13
					297	446	1,40E-32	1,60E-36
Phvul.007G173600	Cupin_1	PF00190.21	CL0029	Cupin	121	260	7,00E-05	4,20E-09
					314	475	1,60E-29	9,80E-34
Phvul.007G192800.1	Cupin_1	PF00190.21	CL0029	Cupin	36	188	3,70E-26	2,20E-30
					458	604	9,80E-32	5,90E-36
Phvul.007G206600	Cupin_1	PF00190.21	CL0029	Cupin	65	213	7,70E-48	9,30E-52
Phvul.007G207800	Cupin_1	PF00190.21	CL0029	Cupin	61	209	2,30E-48	2,70E-52
Phvul.007G229500	Cupin_1	PF00190.21	CL0029	Cupin	67	213	7,40E-43	8,90E-47
Phvul.009G227800	Cupin_1	PF00190.21	CL0029	Cupin	54	200	5,80E-35	7,00E-39
Phvul.010G129800	Cupin_1	PF00190.21	CL0029	Cupin	53	198	1,10E-29	1,40E-33
Phvul.011G067800.1	Cupin_1	PF00190.21	CL0029	Cupin	5	157	7,80E-29	4,70E-33
					190	339	9,00E-22	5,40E-26
Phvul.011G072800.2	Cupin_1	PF00190.21	CL0029	Cupin	32	148	2,10E-10	2,50E-14
					273	422	5,40E-31	6,50E-35
Phvul.L001743	Cupin_1	PF00190.21	CL0029	Cupin	5	157	4,30E-29	2,60E-33
					190	339	6,10E-22	3,70E-26

1098

Gene	Signal peptide	Name	Start	End	E-value
Phvul.001G221200.1	1-22	Cupin_1	59	208	1.9e-34
Phvul.002G027900.1	1-17	Cupin_1	233	388	5,85E-44

Phvul.002G027900.2	N/A	Cupin_1	90	245	5,85E-44
Phvul.002G077300	1-21	Cupin_1	59	208	8,29E-35
Phvul.002G239800	N/A	Pfam:Cupin_1	1	87	0,0000019
	N/A	Cupin_1	120	228	0,00812
Phvul.002G239900.1	N/A	Cupin_1	3	159	2,11E-27
		Cupin_1	192	341	2,10E-13
Phvul.002G239900.2	N/A	Pfam:Cupin_1	1	87	0,0000065
		Cupin_1	120	269	2,10E-13
Phvul.002G249800	N/A	Cupin_1	3	159	7,75E-26
		Cupin_1	192	341	1,68E-12
Phvul.003G131400	1-17	Cupin_1	52	198	1,62E-37
Phvul.005G137200	1-23	Cupin_1	55	198	5,09E-12
		Cupin_1	297	446	5,21E-50
Phvul.007G173600.1	1-24	Cupin_1	115	274	0,431
		Cupin_1	314	478	6,27E-44
Phvul.007G192800.1	1-23	Cupin_1	36	228	3,93E-27
		Cupin_1	458	604	9,08E-41
Phvul.007G206600.1	1-27	Cupin_1	64	213	8,42E-36
Phvul.007G207800.1	1-22	Cupin_1	61	209	5,73E-38
Phvul.007G229500	1-23	Cupin_1	67	213	5,94E-45
Phvul.009G227800	1-19	Cupin_1	54	200	8,60E-42
Phvul.010G129800	1-19	Cupin_1	54	198	1,24E-33
Phvul.011G067800	N/A	Cupin_1	3	157	5,07E-30
		Cupin_1	195	339	3,23E-14
Phvul.011G072800	1-21	Cupin_1	31	187	1,04E-17
		Cupin_1	237	422	1,65E-52
Phvul.L001743	N/A	Cupin_1	3	157	6,10E-33
		Cupin_1	195	339	6,21E-16