

Phosphorylation-dependent sub-functionalization of the calcium-dependent protein kinase CPK28

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ABSTRACT

Calcium (Ca^{2+})-dependent protein kinases (CDPKs or CPKs) are a unique family of Ca^{2+} -sensor/kinase-effector proteins with diverse functions in plants. In *Arabidopsis thaliana*, CPK28 contributes to immune homeostasis by promoting degradation of the key immune signaling receptor-like cytoplasmic kinase BOTRYTIS-INDUCED KINASE 1 (BIK1), and additionally functions in vegetative-to-reproductive stage transition. How CPK28 controls these seemingly disparate pathways is unknown. Here, we identify a single phosphorylation site in the kinase domain of CPK28 (Ser318) that is differentially required for its function in immune homeostasis and stem elongation. We show that CPK28 undergoes intra- and inter-molecular auto-phosphorylation on Ser318 and can additionally be trans-phosphorylated on this residue by BIK1. Analysis of several other phosphorylation sites demonstrates that Ser318 phosphorylation is uniquely required to prime CPK28 for Ca^{2+} activation at physiological concentrations of Ca^{2+} , possibly through stabilization of the Ca^{2+} -bound active state as indicated by intrinsic fluorescence experiments. Together, our data indicate that phosphorylation of Ser318 is required for the activation of CPK28 at low intracellular $[\text{Ca}^{2+}]$ to prevent initiation of an immune response in the absence of infection. By comparison, phosphorylation of Ser318 is not required for stem-elongation, indicating pathway specific requirements for phosphorylation-based Ca^{2+} -sensitivity priming. We additionally provide evidence for a conserved function for Ser318 phosphorylation in related group IV CDPKs which holds promise for biotechnological applications by generating CDPK alleles that enhance resistance to microbial pathogens without consequences to yield.

INTRODUCTION

Protein kinases represent one of the largest eukaryotic protein superfamilies. While roughly 500 protein kinases have been identified in humans (1), the genomes of *Arabidopsis thaliana* (hereafter, *Arabidopsis*) (2) and *Oryza sativa* (3) encode more than 1000 and 1500 protein kinases, respectively, including several families unique to plants. Among these protein kinases are the receptor-like kinases (RLKs), receptor-like cytoplasmic kinases (RLCKs), and calcium-dependent protein kinases (CDPKs or CPKs) that have emerged as key regulators of plant immunity (4–6). Despite encompassing only 2% of most eukaryotic genomes, protein kinases phosphorylate more than 40% of cellular proteins (7, 8), reflecting their diverse roles in coordinating intracellular signaling events. Reversible phosphorylation of serine (Ser), threonine (Thr), and tyrosine (Tyr) residues can serve an array of functions including changes in protein conformation and activation state (9, 10), protein stability and degradation (11, 12), subcellular localization (13–15), and interaction with protein substrates (16–18).

Calcium (Ca^{2+}) is a ubiquitous secondary messenger that acts cooperatively with protein phosphorylation to propagate intracellular signals. Spatial and temporal changes in intracellular Ca^{2+} levels occur in response to environmental and developmental cues (19–23). In plants, Ca^{2+} transients are decoded by four major groups of calcium sensor proteins (CSPs), which possess one or more Ca^{2+} -binding EF-hand motifs (24, 25): calmodulins (CaM), CaM-like proteins (CMLs), calcineurin B-like proteins (CBLs), CDPKs, and Ca^{2+} and Ca^{2+} /CaM-dependent protein kinases (CCaMKs).

At the intersection of phosphorylation cascades and Ca^{2+} signalling are CDPKs, a unique family of Ca^{2+} -sensor/kinase-effector proteins. CDPKs have been identified in all land plants, green algae, as well as certain protozoan ciliates and apicomplexan parasites (26, 27). CDPKs have a conserved domain architecture, consisting of a canonical Ser/Thr protein kinase domain and an EF-hand containing Ca^{2+} -binding CaM-like domain, linked together by an autoinhibitory junction (AIJ) and flanked by variable regions on both the amino (N) and carboxyl (C) termini (28, 29). As their name implies, most CDPKs require Ca^{2+} for their activation (30). Upon Ca^{2+} binding to all EF-hands in the CaM-like domain, a dramatic conformational change occurs, freeing the AIJ from the catalytic site of the kinase, rendering the enzyme active (31–33). CDPKs vary in their sensitivity to Ca^{2+} (30), presumably allowing proteins to perceive distinct stimuli through differences in Ca^{2+} -binding affinity. For example, *Arabidopsis* CPK4 displays half maximal kinase activity in the presence of $\sim 3 \mu\text{M}$ of free Ca^{2+} (30) while CPK5 only requires $\sim 100 \text{ nM}$ (34). Importantly, CDPKs are signaling hubs with documented roles in multiple distinct pathways (4, 24, 35–37) and are therefore likely regulated beyond Ca^{2+} activation.

Sub-functionationization is at least partially mediated by protein localization and interaction with pathway-specific binding partners, as is well-documented for *Arabidopsis* CPK3 which functions in response to biotic and abiotic stimuli in distinct cellular compartments (38). Recent attention has been drawn to site-specific phosphorylation as a way to regulate the activity of multifunctional kinases. For example, phosphorylation sites on the RLK BRASSINOSTEROID INSENSITIVE 1-

ASSOCIATED KINASE 1 (BAK1) are differentially required for its function as a co-receptor with a subset of leucine-rich repeat (LRR)-RLKs (39). Phosphoproteomic analyses indicate that CDPKs are differentially phosphorylated following exposure to distinct stimuli (40–47); however, the biochemical mechanisms by which site-specific phosphorylation regulates multifunctional CDPKs is still poorly understood.

Arabidopsis CPK28 is a plasma membrane-localized protein kinase with dual roles in plant immune homeostasis (48–50) and phytohormone-mediated reproductive growth (51, 52). In vegetative plants, CPK28 serves as a negative regulator of immune signal amplitude by phosphorylating and activating two PLANT U-BOX type E3 ubiquitin ligases, PUB25 and PUB26, which target the key immune RLCK BOTRYTIS-INDUCED KINASE 1 (BIK1) for proteasomal degradation (49). Owing to elevated levels of BIK1, CPK28 null plants (*cpk28-1*) have heightened immune responses and enhanced resistance to the bacterial pathogen *Pseudomonas syringae* pv. *tomato* DC3000 (*Pto* DC3000) (50). Upon transition to the reproductive stage, *cpk28-1* plants additionally present shorter leaf petioles, enhanced anthocyanin production, and a reduction in stem elongation (51, 52). The molecular basis for developmental phenotypes in the *cpk28-1* knockout mutant, beyond hormonal imbalance (51, 52), are comparatively unknown.

Our recent work demonstrated that autophosphorylation status dictates Ca^{2+} sensitivity of CPK28 peptide kinase activity *in vitro* (53). While dephosphorylated CPK28 is stimulated by the addition of 100 μM CaCl_2 compared to untreated protein, hyperphosphorylated CPK28 displayed similar levels of activity at basal Ca^{2+} concentrations (53). These results highlight the interesting possibility that

phosphorylation status may control the activation of multifunctional kinases in distinct pathways by allowing CDPKs to respond to stimuli-specific Ca^{2+} signatures.

In the present study, we identify a single autophosphorylation site, Ser318, that decouples the activity of CPK28 in immune signaling from its role in reproductive growth. We show that expression of a non-phosphorylatable Ser-to-Ala variant (CPK28^{S318A}) is unable to complement the immune phenotypes of *cpk28-1* null mutants but is able to complement defects in stem growth. Further, we uncover a functional role for phosphorylation of Ser318 in priming CPK28 for activation at low free $[\text{Ca}^{2+}]$. Together, we demonstrate that site-specific phosphorylation can direct the activity of a multifunctional kinase in distinct pathways and provide evidence for a conserved mechanism in orthologous group IV CDPKs.

RESULTS

Phosphorylation on Ser318 is required for CPK28-mediated immune homeostasis

CPK28 is phosphorylated on multiple sites *in vitro* and *in vivo* (51, 53–55). To determine whether the function of CPK28 in reproductive stage transition and immunity is bifurcated by site-specific phosphorylation, we generated phospho-ablative (Ser-to-Ala) mutations in three known *in vivo* auto-phosphorylation sites conserved in CPK28 orthologs across land plants (Fig S1): Ser228, Ser318, and Ser495 (51) (Fig 1A). When driven by the cauliflower mosaic virus (CaMV) 35S promoter, CPK28^{S228A}, CPK28^{S318A}

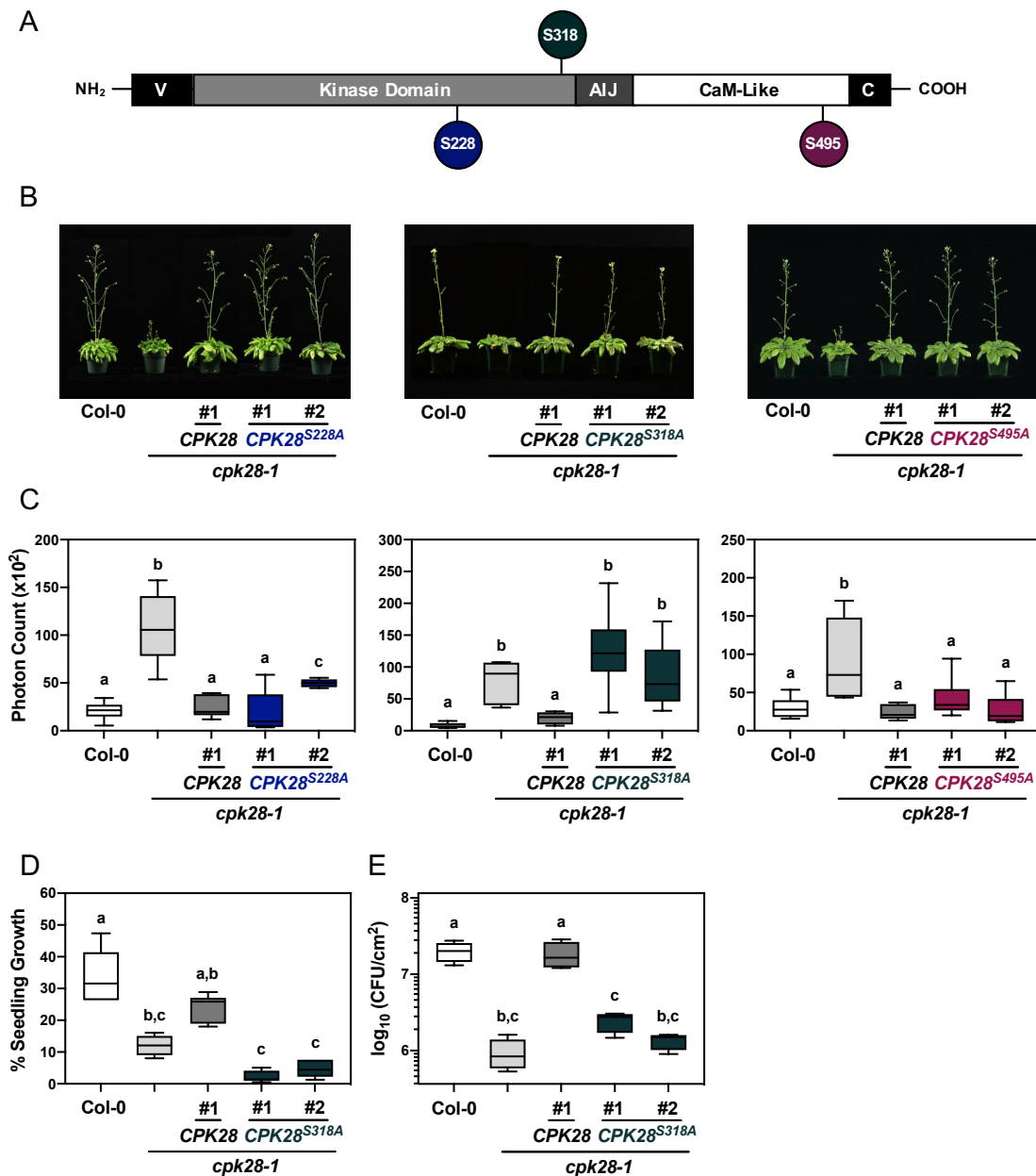


Figure 1. Ser318 phosphorylation differentially regulates CPK28 function in immune homeostasis.

(A) Domain structure of CPK28 and position of tested autophosphorylation sites. V= amino-terminal variable domain; AIJ= autoinhibitory junction; C= carboxyl-terminal variable domain. (B) Stem elongation of six-week-old *Arabidopsis* plants and (C) AtPep1 (500 nM) triggered oxidative burst in 5-week-old plants (n=6) in the indicated genotypes. Data are presented as boxplots indicating first and third quartiles, split by a median line. Whiskers represent maximum and minimum values. (D) Seedling growth inhibition of Col-0, *cpk28-1*, *cpk28-1/pCPK28:CPK28-FLAG*, and *cpk28-1/pCPK28:CPK28^{S318A}-FLAG* lines (n=6) resulting from continual growth in AtPep1 (500 nM) for 12 days. Values are normalized to untreated seedlings and presented as boxplots indicating first and third quartiles, split by a median line. Whiskers represent maximum and minimum values. (E) Growth of virulent *Pseudomonas syringae* pv. *tomato* (DC3000) in Col-0, *cpk28-1*, *cpk28-1/pCPK28:CPK28-FLAG*, and *cpk28-1/pCPK28:CPK28^{S318A}-FLAG* lines (n=4). Samples were collected 3 days post infection and serially diluted. Values are presented as log transformed colony forming units (CFU) per cm² and displayed as boxplots indicating first and third quartiles, split by a median line. Whiskers represent maximum and minimum values. At least three independent biological replicates were conducted for all experiments with similar results. Statistically different groups (p<0.005) are indicated with lowercase letters, as determined by ANOVA analysis followed by Tukey's posthoc test.

and CPK28^{S495A} functionally complement the stem elongation phenotype observed in *cpk28-1* (51); however, it is unknown if these phosphosites regulate CPK28 function in immune homeostasis. To mitigate the possible effects of ectopic overexpression, we chose to stably express CPK28 mutants under the control of the native *pCPK28* promoter in the *cpk28-1* background and assessed functional complementation of defects in both stem elongation and immune signaling. Interestingly, we found that while all three mutations were able to complement the stem elongation phenotype of *cpk28-1* (Fig 1B), only CPK28^{S228A} and CPK28^{S495A} complemented the enhanced oxidative burst in *cpk28-1* following treatment with the endogenous immune elicitor peptide AtPep1 (Fig 1C). In addition, *cpk28-1/pCPK28:CPK28^{S318A}-FLAG* lines did not complement *cpk28-1* in oxidative burst assays following treatment with the bacterial elicitor peptide elf18 (Fig S2), remained hyper-responsive to AtPep1 in seedling growth inhibition assays (Fig 1D), and more resistant than Col-0 to infection with the virulent bacterial pathogen *Pto* DC3000 (Fig 1E). Together, these results suggest that phosphorylation of Ser318 is uniquely required for CPK28 function in immune signaling.

Confocal imaging confirmed that CPK28^{S318A}-YFP localizes to the plasma membrane in Arabidopsis stably expressing *35S:CPK28^{S318A}-YFP* (Fig S3A), suggesting that phosphorylation of Ser318 does not affect the subcellular localization of CPK28. Catalytically inactive CPK28^{D188A}-YFP was also observed at the plasma membrane (Fig S3A), indicating that CPK28 autophosphorylation is not required for appropriate localization. Furthermore, ablation of Ser318 phosphorylation did not compromise catalytic activity toward biological substrates PUB25 and PUB26 in *in vitro*

kinase assays (Fig S3B), leading us to conclude that Ser318 phosphorylation does not regulate the function of CPK28 in immunity through altered subcellular localization or substrate specificity.

CPK28-Ser318 undergoes intra- and inter-molecular autophosphorylation

Most protein kinases autophosphorylate *in vitro* (56). CPK28 peptides containing a phosphorylated Ser318 have been observed in mass spectra from several studies (51, 53–55). We validated that Ser318 is a Ca²⁺-dependent autophosphorylation site by conducting autophosphorylation assays with increasing levels of CaCl₂ (Fig 2A) and probing with a phosphorylation and site-specific antibody raised against phosphorylated Ser318 (Fig S4). We also used the pIMAGO phospho-protein detection reagent to observe total autophosphorylation levels of CPK28. To determine if CPK28 autophosphorylates Ser318 *in cis* or *in trans*, we additionally conducted *in vitro* kinase assays using recombinantly produced MBP-His₆-CPK28^{D188A} as a substrate for His₆-CPK28 (Fig 2B). His₆-CPK28 could trans-phosphorylate MBP-His₆-CPK28^{D188A}, indicating that Ser318 autophosphorylation can occur in both *cis* and *trans* (Fig 2B). Importantly, these results indicate that CPK28 autophosphorylation, including on Ser318, can occur at levels of free Ca²⁺ expected to occur under resting conditions *in vivo*.

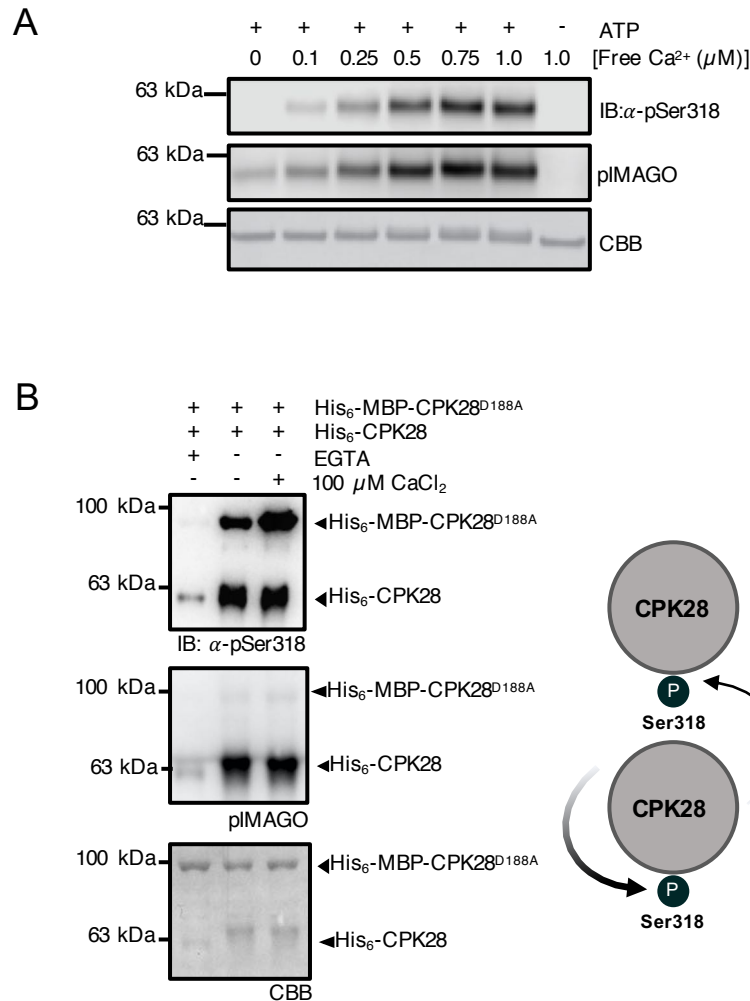


Figure 2. CPK28 undergoes intra- and inter-molecular autophosphorylation at Ser318. (A) His₆-CPK28 autophosphorylation under increasing Ca²⁺ concentrations. (B) *In vitro* kinase assays using recombinant His₆-CPK28, His₆-CPK28^{S318A}, or His₆-CPK28^{D188A} and His₆-MBP-CPK28^{D188A}. Blots were probed with pIMAGO for the detection of phosphoproteins or α-pSer318 (1:5,000) antibody. Nylons were stained with Coomassie brilliant blue (CBB) to assess protein loading. Experiments were conducted three times with similar results.

BIK1 can phosphorylate CPK28 on Ser318

CPK28 is a highly active kinase even at basal cellular levels of Ca^{2+} (49, 53). Increasing $[\text{Ca}^{2+}]$, either by adding CaCl_2 to *in vitro* kinase assays (53), or via immune treatment *in vivo* (49), increases overall phosphorylation on CPK28, including on Ser318 (Fig 2A). Although CPK28 can autophosphorylate on Ser318, it is possible that this site is phosphorylated by additional protein kinases. BIK1 is a critical convergent substrate of multiple immune receptors whose activity and abundance is tightly regulated by layers of dynamic post-translational modifications including phosphorylation/dephosphorylation (57–61) and mono- (62) and poly-ubiquitination (49, 50, 63). CPK28 phosphorylates both BIK1 (50) and the E3 ubiquitin ligases PUB25 and PUB26 (49). A recent study demonstrated reciprocal phosphorylation between the rice orthologs of CPK28 and BIK1, OsCPK4 and OsRLCK176 (64), leading us to hypothesize that a similar mechanism may exist in Arabidopsis. To test if CPK28 is a substrate of BIK1, we conducted *in vitro* kinase assays using recombinantly produced GST-BIK1 and catalytically inactive His₆-CPK28^{D188A}. Phospho-tag gel stain for the detection of phosphorylated proteins indicated that BIK1 is indeed able to phosphorylate CPK28 *in vitro* (Fig 3A). Next, we tested if BIK1 can phosphorylate Ser318 by conducting *in vitro* kinase assays between GST-BIK1 and His₆-CPK28^{D188A/S318A} compared to His₆-CPK28^{D188A}. We observed comparably less phosphorylation when CPK28^{D188A/S318A} was used as a substrate (Fig 3A), suggesting that Ser318 can be phosphorylated by BIK1. Furthermore, immunoblot analysis using anti-pSer318 confirmed that BIK1 is capable of phosphorylating Ser318 *in vitro* (Fig 3B). As we still observed some level of

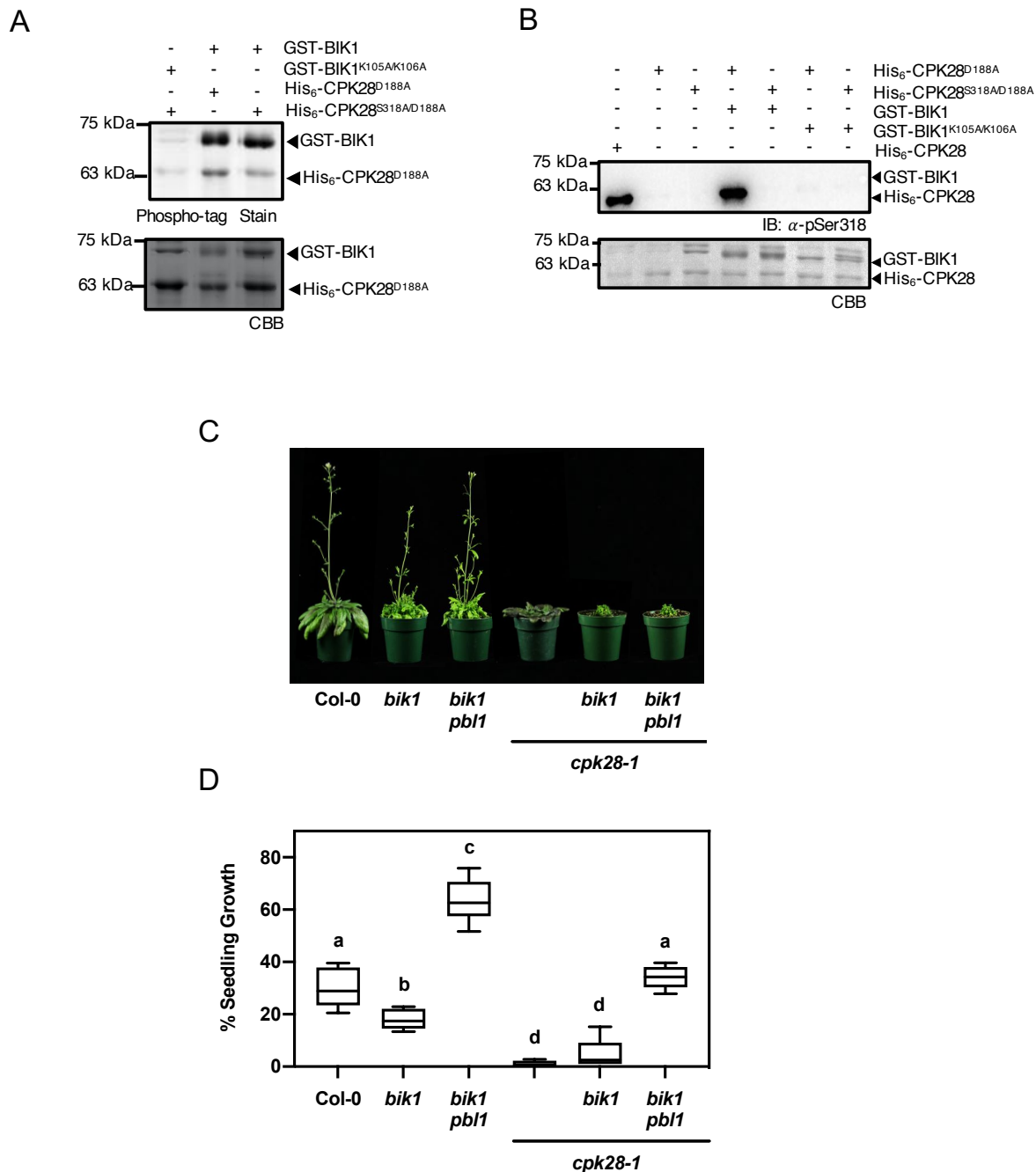


Figure 3. BIK1 transphosphorylates CPK28 at Ser318 and is required for CPK28-dependent immune signaling. (A) Phospho-tag gel stain and (B) Western blot analysis (α -pSer318) of *in vitro* kinase assay using recombinant GST-BIK1 or GST-BIK1^{K105A/K106A} and His₆-CPK28^{D188A} or His₆-CPK28^{S318A/D188A}. In order to visualize both Ser318 autophosphorylation and GST-BIK1 transphosphorylation, 500 ng of His₆-CPK28 and 2 μ g of His₆-CPK28^{D188A} were loaded for auto- and trans-phosphorylation reactions, respectively. Gels and nylons were stained with Coomassie Brilliant Blue (CBB) to assess protein loading. (C) Stem-elongation of six week old plants and (D) seedling growth following continual treatment with 500 nM AtPep1 for 12 days (n=6). Values were compared to plants grown without AtPep1 and presented as boxplots indicating first and third quartiles, median values, and whiskers representing maximum and minimum values. Statistically different (p<0.005) values are denoted by lowercase letters according to an ANOVA analysis followed by Tukey's posthoc test. All experiments were conducted at least three times with similar results.

transphosphorylation by BIK1 on CPK28^{D188A/S318A} (Fig 3A), Ser318 is likely not the only site BIK1 phosphorylates on CPK28. Additional BIK1-mediated phosphorylation sites on CPK28 await to be discovered.

BIK1 is part of a large gene family in Arabidopsis, and shares biological function with its closest homolog PBL1 (57, 65–67). To investigate the genetic requirement of BIK1 and PBL1 on CPK28-mediated signaling, we generated both *bik1 cpk28-1* double and *bik1 pbl1 cpk28-1* triple mutants and assessed whether loss of BIK1/PBL1 was able to suppress *cpk28-1* phenotypes. In congruence with our finding that Ser318 differentially regulates CPK28 function in immune homeostasis, we found that delayed stem elongation was not suppressed in *bik1 cpk28-1* or *bik1 pbl1 cpk28-1* (Fig 3C), but that AtPep1-triggered seedling growth inhibition was partially or fully restored in *bik1 cpk28-1* and *bik1 pbl1 cpk28-1*, respectively (Fig 3D). These data suggest that the function of CPK28 in immune signaling, but not in stem elongation, is dependent on BIK1/PBL1, and provides further evidence for complex regulatory feedback between BIK1/PBL1 and CPK28.

Phosphorylation of Ser318 primes CPK28 Ca²⁺-responsiveness

We previously reported on the phosphorylation-dependent Ca²⁺-sensitivity priming of CPK28 peptide kinase activity (53), and were interested to understand which phosphorylation site or sites mediated this priming function. We suspected that a phosphorylation site in either the protein kinase domain, the AIJ, or the CLD would be responsible for Ca²⁺-priming and therefore generated individual phospho-null (Ser/Thr-

to-Ala) mutants for autophosphorylation sites within these domains of CPK28 that we identified from *in situ* phosphorylated recombinant protein (Fig S5A) (53). Wild-type hyperphosphorylated CPK28 is insensitive to the addition of excess Ca^{2+} in peptide kinase assays (Fig S5B) (53). We thus hypothesized that phospho-null mutation of the phosphorylation site(s) responsible for Ca^{2+} -sensitivity priming would restore CPK28 activation by excess Ca^{2+} . To test this hypothesis, we expressed hyperphosphorylated forms of each phospho-null mutant and compared peptide kinase activity in untreated samples versus samples supplemented with 100 μM CaCl_2 . Much to our surprise, our biochemical analysis converged on Ser318 as a critical regulatory phosphorylation site of CPK28. Of all the phospho-null mutants tested, only the S318A mutant had enhanced peptide kinase activity upon addition of excess Ca^{2+} . We therefore further characterized the CPK28^{S318A} mutant for Ca^{2+} -dependent autophosphorylation and for peptide kinase activity at different concentrations of Ca^{2+} .

To confirm that phosphorylation of Ser318 plays a role in Ca^{2+} -responsiveness, we used *Escherichia coli* Lambda phosphatase (LamP)-expressing cells to produce dephosphorylated His₆-CPK28 and His₆-CPK28^{S318A} and conducted comparative *in vitro* autophosphorylation assays either in the complete absence of Ca^{2+} (+ 10 mM EGTA), in the presence of background Ca^{2+} (no treatment), or with the addition of excess Ca^{2+} (+ 100 μM CaCl_2). Autophosphorylation levels were detected using pIMAGO. Both His₆-CPK28 and His₆-CPK28^{S318A} showed low levels of autophosphorylation in chelation experiments (Fig 4A), confirming their Ca^{2+} -dependence. His₆-CPK28 was highly active

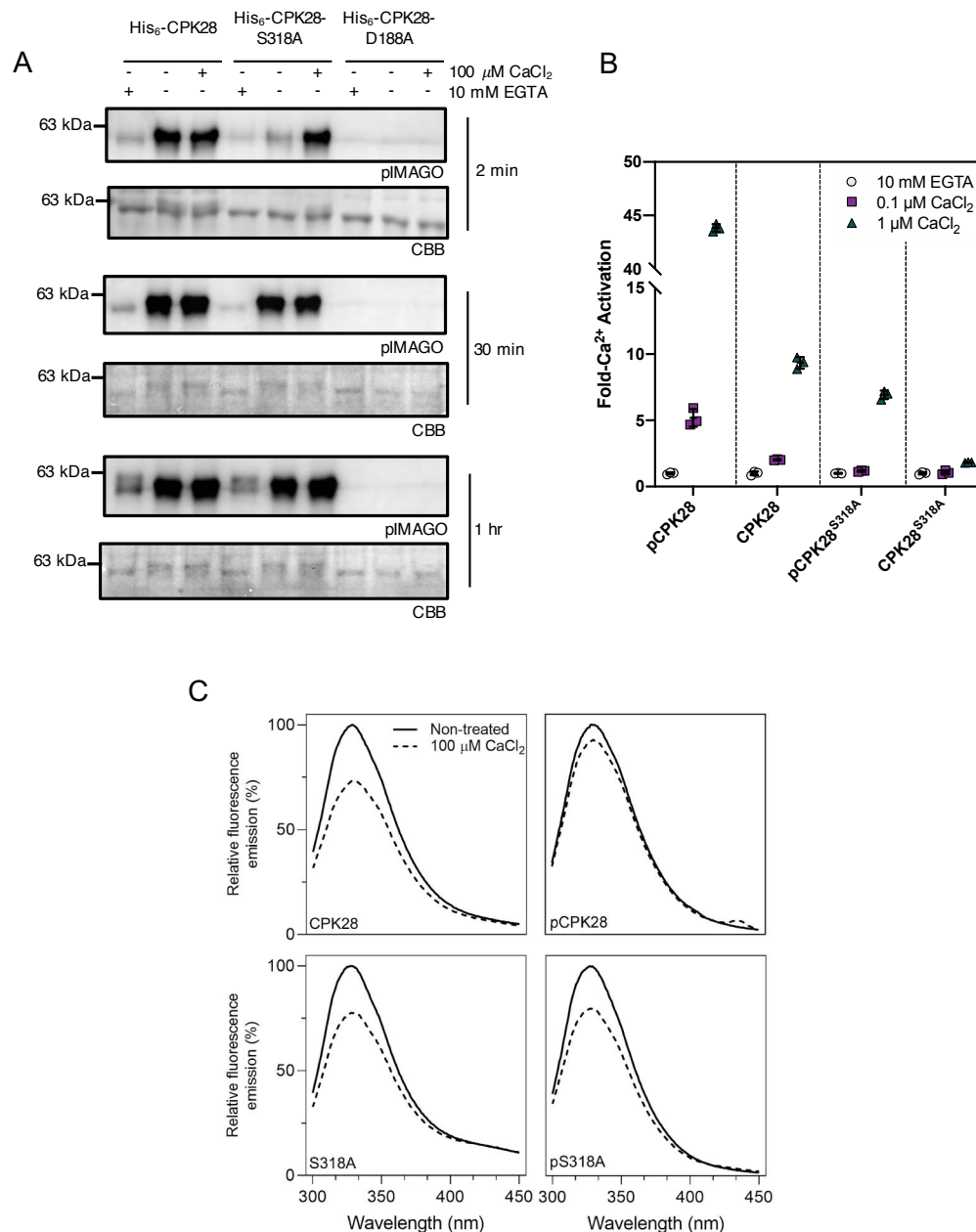


Figure 4. Phosphorylation at Ser318 primes CPK28 Ca^{2+} -responsiveness. (A) Autophosphorylation of recombinant His₆-CPK28 or His₆-CPK28^{S318A} without Ca^{2+} (+10 mM EGTA), at background Ca^{2+} (-EGTA, - CaCl_2), or with the addition of 100 μ M CaCl_2 for 1-30 min as indicated. Kinase dead His₆-CPK28^{D188A} was used as a negative control. Phosphorylated proteins were detected using pIMAGO and nylons were stained using Coomassie Brilliant Blue (CBB) to assess protein loading. (B) Peptide kinase activity of phosphorylated (pCPK28, pS318A) and dephosphorylated (CPK28, S318A) purified recombinant proteins at physiological Ca^{2+} concentrations. Free Ca^{2+} concentrations were established as described in the Experimental Procedures. Mean with standard deviation of three replicate reactions as well as individual values are shown. The experiment was repeated twice with independent preparations of all recombinant proteins with similar results observed each time. (C) Intrinsic Trp fluorescence of dephosphorylated (CPK28, S318A) or hyperphosphorylated (pCPK28, pS318A) His-tagged recombinant proteins before ('non-treated', solid line) or after (dashed line) the addition of 100 μ M CaCl_2 . Curves are averages of two scans following appropriate background subtraction. Experiments were performed twice using independent preparations of recombinant proteins with similar results observed in both experiments.

at background Ca^{2+} and was not substantially stimulated by additional CaCl_2 (Fig 4A). In contrast, at background Ca^{2+} levels, His₆-CPK28^{S318A} displayed dramatically reduced autophosphorylation activity compared to wild-type protein (Fig 4A). However, when assays were conducted in the presence of excess Ca^{2+} , His₆-CPK28 and His₆-CPK28^{S318A} exhibited comparable levels of autophosphorylation (Fig 4A). Together, these data suggest that phosphorylation of Ser318 is required for full activity when Ca^{2+} levels are not saturating. Interestingly, when autophosphorylation assays were allowed to proceed for longer time intervals (30 min and 1 hr), His₆-CPK28^{S318A} displayed similar levels of activity as wild-type protein at basal [Ca^{2+}] (Fig 4A). Collectively, these data suggest that phosphorylation of Ser318 is important for the rapid autophosphorylation of CPK28 under limiting [Ca^{2+}].

To better understand how phosphorylation of Ser318 affects activation of CPK28 by Ca^{2+} , we assessed CPK28 peptide kinase activity using the ACSM+1 synthetic peptide as substrate (53) at Ca^{2+} concentrations that would be expected at the lower (0.1 μM) and upper (1.0 μM) range of intracellular physiological conditions. Phosphorylated and dephosphorylated forms of both His₆-CPK28 and His-CPK28^{S318A} were used to determine if overall phosphorylation status could supersede the requirement for site-specific phosphorylation at Ser318. At free Ca^{2+} concentrations of 0.1 and 1.0 μM , dephosphorylated His₆-CPK28 (Fig 4B) displayed ~2- and 9-fold activation by Ca^{2+} relative to EGTA-treated protein, respectively (Fig 4B). Similarly, phosphorylated CPK28 (Fig 4B) had ~5-fold activation with the addition of 0.1 μM free Ca^{2+} and ~43-fold activation with 1.0 μM free Ca^{2+} (Fig 4B), indicating that

phosphorylation enhances CPK28 peptide kinase activity at physiological Ca^{2+} . By comparison, His₆-CPK38^{S318A} was substantially less active at physiological Ca^{2+} , having negligible activity at 0.1 μM Ca^{2+} (relative to EGTA-treated protein) regardless of its overall phosphorylation status and only ~2 and 7-fold activation for dephosphorylated and phosphorylated His₆-CPK28^{S318A}, respectively, at 1.0 μM Ca^{2+} . Collectively, these results indicate that phosphorylation of Ser318 is prerequisite for substrate phosphorylation by CPK28 at low free Ca^{2+} , and that phosphorylation of Ser318 is required for full responsiveness to Ca^{2+} elevations within the physiological range. Taken together, these data support the hypothesis that phosphorylation of Ser318 is uniquely important in priming CPK28 for activation by Ca^{2+} at concentrations that would be expected under cellular conditions.

Ser318 phosphorylation promotes a Ca^{2+} -bound conformation

Ser318 is located at the C-terminal end of the canonical protein kinase domain of CPK28, very close to the autoinhibitory junction (AIJ) (Fig 1A), suggesting that phosphorylation of Ser318 might affect Ca^{2+} -dependent conformational changes of the AIJ-CAD fragment of CPK28. To better understand the biochemical function of Ser318 phosphorylation, we measured Ca^{2+} -induced conformational changes in hyper- and hypo-phosphorylated CPK28 and CPK28^{S318A} by intrinsic Trp fluorescence. Trp fluorescence emission properties depend on the local environment of Trp residues, and can thus be used to assess protein conformational changes (68). For dephosphorylated His₆-CPK28 and His₆-CPK28^{S318A} (Fig 4C), Trp fluorescence emission decreased

following the addition of 100 μ M CaCl_2 (relative to non-treated protein), indicating that CPK28 undergoes a Ca^{2+} -dependent conformational change. By comparison, Trp fluorescence of hyper-phosphorylated His₆-CPK28 showed only a marginal decrease after addition of excess Ca^{2+} (Fig 4C), suggesting that CPK28 phosphorylation promotes a Ca^{2+} -bound conformation at low levels of Ca^{2+} . In agreement with our activity assays, Trp fluorescence of hyper-phosphorylated His₆-CPK28^{S318A} decreased similar to the wild-type dephosphorylated protein, suggesting that phosphorylation of Ser318 is responsible for the effect observed with hyperphosphorylated CPK28.

Ser318 is a conserved and unique feature of subgroup IV CDPKs

CDPK gene families are highly conserved across land plants and form four major subgroups (26, 27). To determine the level of conservation of Ser318, the amino acid sequences of CPK28 and other subgroup IV orthologs from all genomes available on Phytozome were compared. Amongst the 114 sequences included in our analysis, a Ser residue was strictly conserved at the position orthologous to Ser318 of AtCPK28 (Fig 5A and Fig S1). Comparison of all subgroup I-III CDPKs from 12 representative species spanning all major taxonomic groups indicated that although several flanking residues are highly conserved in all subgroups, conservation of Ser318 is a unique and specific feature of subgroup IV CDPKs (Fig 5A).

To determine if the Ca^{2+} -priming function of Ser318 autophosphorylation is conserved, we generated a phospho-ablative variant of the rice CPK28 ortholog (OsCPK4^{S315A}). Short 1 min autophosphorylation assays were conducted using

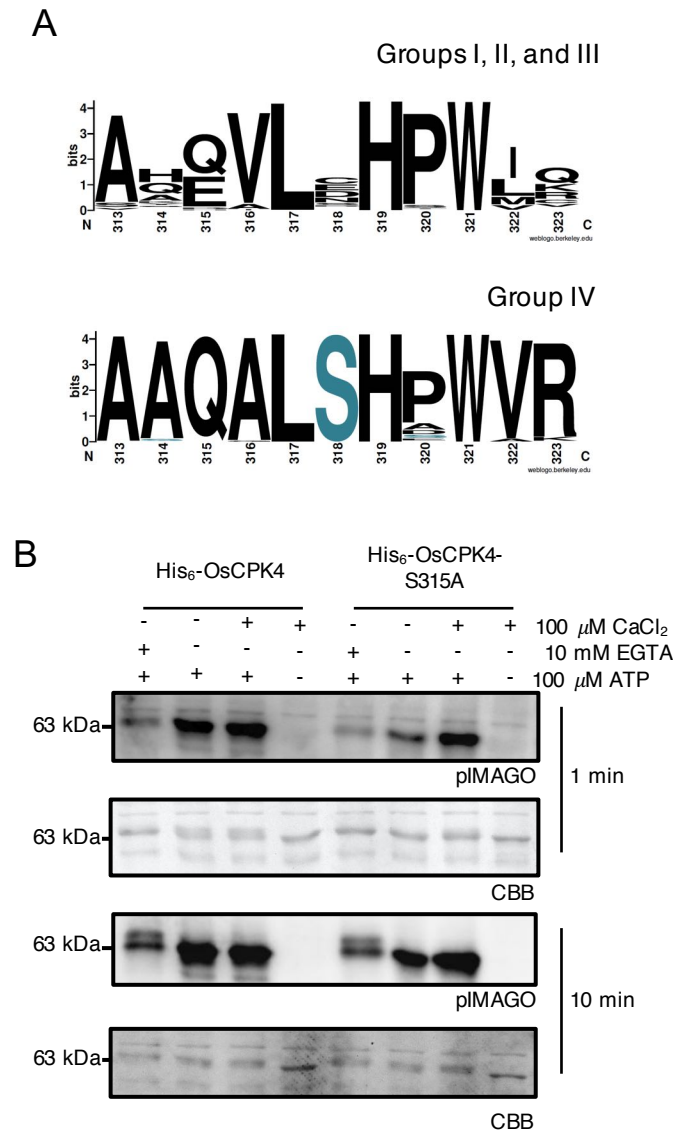


Figure 5. Ser318 is a conserved feature of group IV CDPKs. (A) Amino acid consensus at position 318 (AtCPK28) across CDPK subgroups. Sequences were retrieved from Phytozome and aligned as described in the Experimental Procedures. Logos were generated using WebLogo (97). (B) Autophosphorylation of recombinant His₆-OsCPK4 and His₆-OsCPK4^{S315A}. Reactions were carried out in the absence of Ca²⁺ (+10 mM EGTA), in the presence of background Ca²⁺ (-EGTA, -CaCl₂), or with the addition of 100 μ M CaCl₂ for 1 or 10 min as indicated in figures. Phosphorylation was detected using pIMAGO. Nylons were stained with Coomassie Brilliant Blue (CBB) to assess protein loading. All experiments were conducted at least three times with similar results.

recombinant His₆-OsCPK4 and His₆-OsCPK4^{S315A} produced in LamP-expressing *E. coli* cells, as described above. His₆-OsCPK4 displayed a clear requirement for Ca²⁺ with a marked decrease in overall phosphorylation in the presence of 10 mM EGTA (Fig 5B). While wild-type His₆-OsCPK4 displayed high levels of autophosphorylation at basal [Ca²⁺], His₆-OsCPK4^{S315A} was comparatively less active (Fig 5B). The addition of 100 μM CaCl₂ did not further activate His₆-OsCPK4 but did restore His₆-OsCPK4^{S315A} autophosphorylation levels to that observed with wild-type protein (Fig 5B). Together, these data provide evidence of a conserved biochemical function for phosphorylation of this residue in orthologous CDPKs across the plant lineage.

DISCUSSION

Expansion of CDPKs in plants is predicted to have occurred under selective adaptation for kinases with varying Ca²⁺ sensitivities (27), however the biophysical properties underlying Ca²⁺ sensitivity are not fully understood. Analysis of protein sequences from Arabidopsis indicates that CDPKs with little or no requirement for Ca²⁺ possess one or more degenerated EF-hand motifs (37, 69). However, some CDPKs with the ability to bind Ca²⁺ do not require it for their activation (30, 70–72) pointing to additional mechanisms regulating CDPK function. Previous work has shown that *in situ* autophosphorylation “primes” Arabidopsis CPK28 for Ca²⁺ activation *in vitro* (53). Here, we demonstrated that phosphorylation at one site, CPK28-Ser318, is responsible for

autophosphorylation-based priming when Ca^{2+} concentrations are limiting (Fig 4A-B). Additionally, *in vivo* phosphorylation at Ser318 was required for CPK28 function in immune homeostasis (Fig 1C-E) but not stem elongation (Fig 1B), suggesting a role in stimulus-specific activation of a multifunctional protein kinase through Ca^{2+} -sensitivity priming.

Autophosphorylation has been correlated with the activation (15, 53, 73–75) or inhibition (72, 75, 76) of several CDPKs, although the mechanisms of regulation remain largely unknown. Phosphorylation could influence interactions with protein substrates (75, 77) or induce changes in secondary protein structure causing transitions between functional enzyme states (78, 79). A complete crystal structure for a plant CDPK has not yet been resolved; however, a mechanism for Ca^{2+} activation has been proposed based on the structures of apicomplexan CDPKs (31–33). Experiments using *Toxoplasma gondii* TgCDPK1/2 and *Cytosporidium parvum* CpCDPK1 demonstrate that Ca^{2+} activation is reversible with contact sites between the CaM-like domain and kinase domain stabilizing both active and inactive forms (31). Many of the residues that stabilize these conformations are conserved between plants and protists (32) suggesting similar contact sites may exist in plants.

CPK28-Ser318 resides in the C-terminal portion of the kinase domain in close proximity to the AIJ (Fig 1A). Although we could not generate a high confidence structural model of CPK28 using the crystal structures of Ca^{2+} -bound CDPKs, modeling of CPK28 using inactive TgCDPK1 (31) indicated that Ser318 is likely surface-localized,

directed away from the active site of the kinase domain (Fig S6). In this position, phosphorylated Ser318 would not interact with established contact sites, such as the autoinhibitory triad (31), or other interactions between the pseudosubstrate region and the active site of the kinase domain. We rather propose that phosphorylation of Ser318 could induce a structural change in the AIJ that prohibits stabilization of the inactive conformation. This could cause the protein to adopt an “intermediate” conformation that can more readily move to the active state upon Ca^{2+} binding (Fig 6). In support of this idea, our analysis of intrinsic Trp fluorescence of CPK28 and CPK28^{S318A} suggests that Ca^{2+} -dependent conformational changes can occur at a lower concentration of Ca^{2+} in the hyper- compared to de-phosphorylated protein and that the conformational change at low Ca^{2+} requires Ser318 phosphorylation (Fig 4C). Phosphorylation of Ser318 could also stabilize the active conformation, serving a similar function to autophosphorylation of a residue in the autoinhibitory region (Thr286) of CaMKII from rat brain, which renders CaMKII substrate phosphorylation independent of both Ca^{2+} and CaM (80, 81).

Overall, our analysis of CPK28 autophosphorylation, peptide kinase activity, and conformational changes collectively suggest that phosphorylation of Ser318 near the AIJ promotes an open, active conformation of CPK28 at low Ca^{2+} concentrations (Fig 6). Currently, it is not clear whether this conformational state results in enhanced affinity of the CaM-like domain for Ca^{2+} , or whether pSer318 exerts allosteric effects promoting release of the AIJ from the kinase domain. Notably, we recently demonstrated that CaM binds to an area of the CPK28 AIJ to inhibit both *in vitro* auto- and trans-phosphorylation

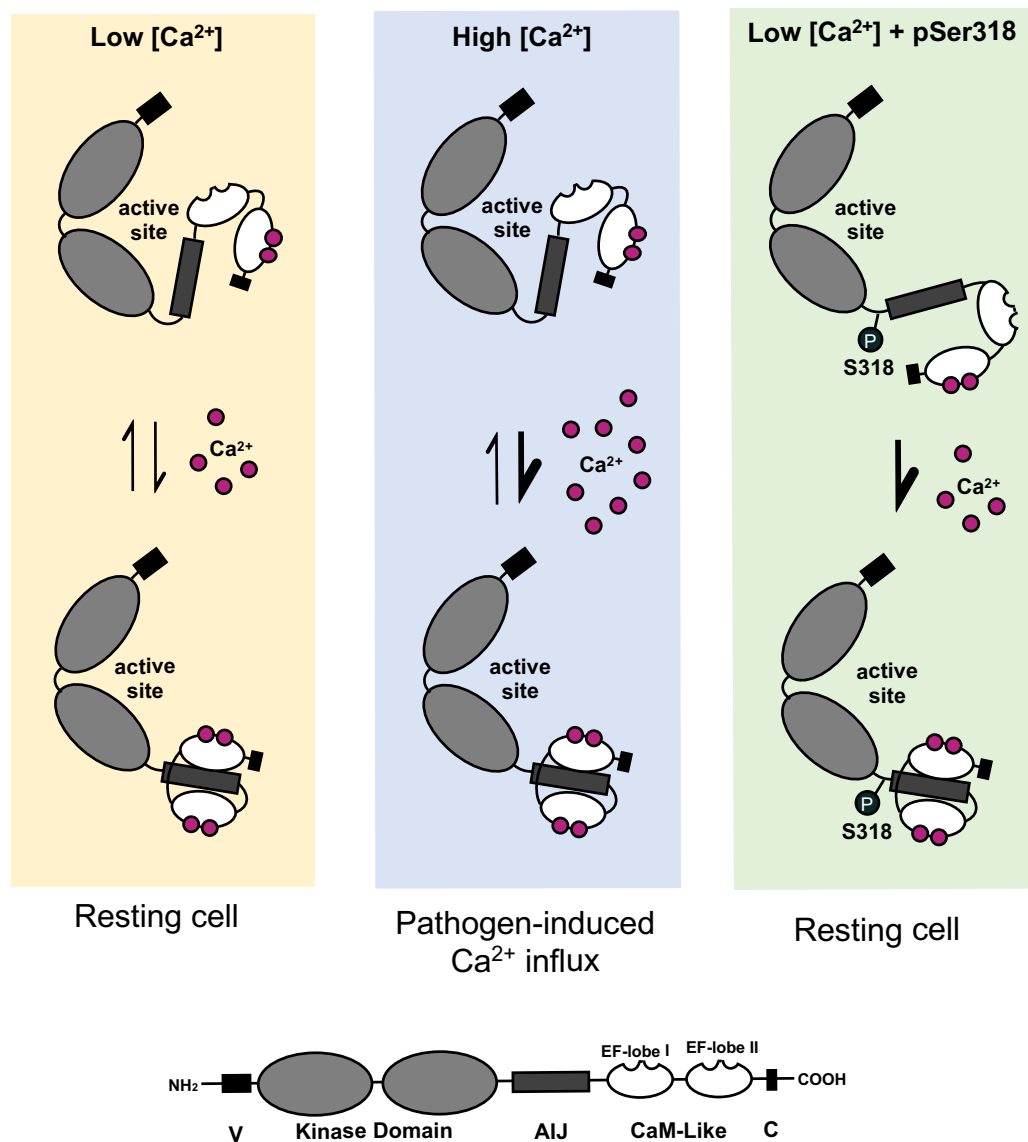


Figure 6. Model for CPK28 activation. Proposed mechanism of Ca²⁺-sensitivity priming of CPK28 by phosphorylation of Ser318. In a resting cell, CPK28 transitions between active and inactive conformations, binding and releasing Ca²⁺ from the amino-terminal EF-hand lobe of the calmodulin (CaM)-like domain. Ca²⁺ elevation during signaling events shifts this equilibrium towards the activated state via Ca²⁺-induced conformational changes. When Ser318 is phosphorylated, the transition of CPK28 from an inactive to an active state occurs at lower Ca²⁺ concentrations possible via stabilizing a conformation in which the AIJ is excluded from the active site.

activity (53), and that CPK28 autophosphorylation relieves this inhibition (53). Ser318 phosphorylation could conceivably block CaM binding or, alternatively, CaM could prevent Ser318 phosphorylation. Resolving an intact crystal structure for CPK28, and other plant CDPKs, will provide valuable insight into the activation of these kinases and allow for investigation into the possible structural roles of phosphorylation.

From a physiological perspective, phosphorylation of Ser318 would allow CPK28 to be active in a cell under resting conditions. Indeed, CPK28 promotes the degradation of BIK1 prior to the activation of immune signaling (49, 50). Limiting BIK1 accumulation is critical to prevent mounting an immune response in the absence of pathogen invasion. Ser318 was identified as an *in vivo* phosphorylation site in unstimulated cells (51), indicating no requirement for immune activation. A 25-fold increase in phosphorylated peptides corresponding to pSer318 were identified in *cpk28-1* protoplasts expressing CPK28-YFP compared to the kinase inactive variant (CPK28^{D188A}-YFP), suggesting that Ser318 is an autophosphorylation site *in vivo* (51). Our *in vitro* data indicates that CPK28 undergoes both intra- and inter-molecular autophosphorylation at Ser318 (Fig 2) and can also be transphosphorylated by BIK1 (Fig 3A and 3B), although a higher level of phosphorylation was detected on autophosphorylated CPK28 in our assays (Fig 3B). Whether Ser318 phosphorylation occurs by autophosphorylation and/or BIK1-mediated transphosphorylation *in vivo* is unknown, but our *in vitro* analyses clearly establish the potential for both mechanisms

as drivers of Ser318 phosphorylation *in vivo*. How these distinct events would contribute to CPK28-mediated BIK1 proteostasis remains an open and challenging question.

Nevertheless, it is tempting to speculate that BIK1 transphosphorylation could contribute to CPK28 regulation. Our epistasis analysis indicates that CPK28-mediated immune signaling is dependent on BIK1 and its homolog, PBL1 (Fig 3D). However, loss of *bik1 pbl1* in *cpk28-1* mutants restored *cpk28-1* growth inhibition to levels observed in Col-0 seedlings (Fig 3D), suggesting the involvement of additional RLCKs in response to endogenous immune peptide elicitation. In rice, OsRLCK176 phosphorylates OsCPK4 at three sites: Thr73, Ser210 and Ser381 (64), corresponding to CPK28-Thr76, -Ser213, and -Val384. Phosphorylation at these sites activates OsCPK4 as part of a regulatory feedback loop to control immune output through continual degradation of OsRLCK176 (64). Our *in vitro* kinase assays suggest that BIK1 phosphorylates CPK28 at Ser318 and additional, currently unknown, residues (Fig 3A). Given the high conservation of this immune signalling network (82), Thr76 and Ser213 are likely candidates for future analysis. In Arabidopsis, BIK1 turnover is mediated by CPK28-dependent phosphorylation and activation of the E3 ubiquitin ligases PUB25 and PUB26, which target BIK1 for 26S proteasomal degradation (49). Previous work indicates that CPK28 is also capable of phosphorylating BIK1 *in vitro* (50), although the biochemical and biological consequences of this transphosphorylation are not known. It is therefore plausible that BIK1 accumulation could be modulated by an interplay of

BIK1 ubiquitination and trans-phosphorylation events between CPK28 and BIK1, which is a current area of investigation.

Our cumulative data indicate that phosphorylation of Ser318 would render CPK28 highly responsive to slight increases in Ca^{2+} following immune activation, preventing initiation of a robust immune response. Ser318 phosphorylation could additionally slow CPK28 deactivation following a primary pathogen attack, making plants more susceptible to secondary infection. In accordance with its role in BIK1 turnover, overexpression of CPK28 dampens the MAMP-triggered Ca^{2+} (48) and oxidative (50) bursts, which are dependent on BIK1 and PBL1 (48, 50). This implies that CPK28 overactivation could additionally prevent the establishment of systemic acquired resistance which is reliant on ROS/ Ca^{2+} signal propagation (34, 83, 84). In order to buffer these attenuation mechanisms the plant would need to adopt a safeguard against sustained activation of CPK28. Recent work has demonstrated that following cell stimulation with AtPep1 (85) or the bacterial flagellin immunogenic epitope flg22 (86), alternative *CPK28* transcripts are produced that generate a truncated isoform that lacks the C-terminal EF-hand lobe. This CPK28 variant could act to outcompete Ca^{2+} “competent” proteins for downstream substrates, alleviating immune attenuation (87). Thus, CPK28 signaling appears to be intricately regulated at both the post-transcriptional and post-translational levels.

Despite the clear requirement for Ser318 phosphorylation in immune signaling (Fig 1C-E), *cpk28-1* plants expressing CPK28^{S318A} displayed normal stem elongation

(Fig 1B). The catalytic activity of CPK28 is indispensable for all known biological functions (50, 51); however, the lower kinase activity of CPK28^{S318A} at physiologically relevant Ca²⁺ concentrations (Fig 4A-B) did not impair stem elongation (Fig 1B), suggesting pathway-specific requirements for full CPK28 catalytic activity. We speculate that more processive genetic programs, such as those that occur in developmental and reproductive processes, would not require CDPKs to be as responsive to Ca²⁺ as stress-induced signals. In support of this hypothesis, prolonged exposure to low levels of Ca²⁺ relieved the requirement of Ser318 phosphorylation for full kinase activity in autophosphorylation assays (Fig 4A). In a physiological context, the phosphorylation status of CPK28 is likely dictated by a combination of kinase and phosphatase activities to precisely control CPK28 function. Although pathway-specific CPK28 binding partners have not yet been identified in the reproductive phase transition, it is possible that such associations could increase kinase activity or lower Ca²⁺ requirements.

The development of pathogen resistant crops can be complicated by growth trade-offs associated with the overactivation of immune signalling (88, 89). For example, prolonged activation of immune receptors by MAMP stimulation causes seedling growth inhibition (90, 91) and the formation of lesions (92, 93). Ablation of Ser318 phosphorylation allowed us to generate a *CPK28* allele that displays enhanced resistance to *Pto* DC3000 (Fig 1E) with no consequences to plant growth (Fig 1B). Group IV CDPKs are highly conserved across all land plants (26) and fulfill conserved roles as regulators of immune signaling (82) and reproductive development (51, 94–96)

in multiple plant species. Accordingly, our *in vitro* analysis of OsCPK4 indicated that, on a biochemical level, phosphorylation of Ser315 (analogous to CPK28-Ser318) has a conserved function in rice (Fig 4D). Additionally, a Ser residue at this site was identified as a unique feature of group IV CDPKs across all surveyed land plants (Fig 4C). Cumulatively, our data suggests that ablation of “Ser318” phosphorylation in species with agricultural value could serve as an effective tool for the development of disease resistance without associated costs to fitness or yield.

EXPERIMENTAL PROCEDURES

Plant growth conditions

Arabidopsis thaliana plants were grown either in soil or sterile media depending on the assay. For soil assays, seeds were stratified for 2-3 days at 4°C, sown on soil, and transplanted as one plant per pot in Sunshine Mix 1 soil (Sungro) for 5 weeks in temperature-controlled growth chambers in the Queen’s University Phytotron at 22°C with 10 h light (150-160 $\mu\text{E m}^{-2} \text{s}^{-1}$) and no humidity control. Oxidative burst and pathogen infection assays were conducted on soil-grown plants 3-4 weeks post germination (wpg), prior to reproductive stage transition. For assessment of stem elongation, plants were subsequently transferred to a growth chamber maintained at 22°C, with a 16 h photoperiod (150-160 $\mu\text{E m}^{-2} \text{s}^{-1}$), and 30% relative humidity for 1-2

weeks or until all plants had produced reproductive bolts. For sterile assays, seeds were surface-sterilized using 50% bleach, stratified for 2-3 days at 4°C, and germinated on 0.8% agar plates with 0.5x Murashige and Skoog (MS) media for 3-4 days and then transplanted into liquid 0.5x MS supplemented with 1% sucrose. Sterile seedlings were grown at ambient temperature with 10 h light 150-160 $\mu\text{E m}^2 \text{s}^{-1}$ and assays were conducted at 2 wpg. Soil-grown *A. thaliana* plants were fertilized biweekly with 1.5 g L⁻¹ 20-20-20 NPK. Predatory *Amblyseius swirskii* mites (Koppert Biological Systems) were released into growth chambers biweekly as a precautionary measure against greenhouse pests, according to manufacturer's instructions.

Plant materials

Stable *A. thaliana* transgenics were generated via *Agrobacterium tumefaciens* (GV3101)-mediated floral dip transformation (97). T₁ plants were selected on MS agar plates containing 50 $\mu\text{g/mL}$ hygromycin. Only lines displaying a 3:1 segregation ratio on selective media in the T₂ generation were bred to homozygosity and used in complementation experiments. Stable *cpk28-1/35S:CPK28-YFP*, *cpk28-1/35S:CPK28^{S318A}-YFP*, and *cpk28-1/35S:CPK28^{D188A}-YFP* *Arabidopsis* lines were previously described (51). Higher-order mutants were generated by crossing *bik1* or *bik1 pbl1* (65) mutants with *cpk28-1* (51) and bred to homozygosity using PCR-based genotyping. Table S1 includes a list of all germplasm used and generated in this study.

Molecular cloning

The *pCPK28:CPK28-FLAG* construct was cloned by fusing the coding sequence of *CPK28* downstream of its native promoter (1742 bp upstream of the start codon) and in frame with a C-terminal FLAG peptide using digestion-ligation cloning into a pGREENII-based binary vector carrying the aminoglycoside phosphotransferase gene from *E. coli* for hygromycin B resistance in plants (98). Both the *pT7:His6-CPK28* construct in pET28a+ (EMD Biosciences), and the *pT7:MBP-His6-CPK28* construct in pOPINM (Novagen), have been described previously (50, 53). Site-directed mutagenesis was used to generate CPK28 mutant constructs using overlapping complementary primers as described previously (50), using either pGREENII-based binary plasmids or pET28a+ clones as the template. The coding region of *BIK1* was PCR-amplified from previously described pENTR-BIK1 or pENTR-BIK1^{K105A/K106A} vectors (65) and cloned into bacterial expression vector pGex6.1 (GE Healthcare) by Gibson Assembly (NEB) to generate *pT7:GST-BIK1* and catalytically-inactive *pT7:GST-BIK1*^{K105A/K106A} constructs. *pET100:His6-OsCPK4* and *pET100:His6-OsCPK4*^{S315A} constructs were synthesized by GeneArt™ (Fisher Scientific). The coding region of PUB25 was PCR-amplified from previously described pET28a:PUB25 vectors (49) and cloned into bacterial expression vector pMAL-c2x (GE Healthcare) by digestion and ligation cloning using *Xba*I and *Pst*I-HF (NEB) to produce pMAL-c2x:MBP-PUB25. PUB26 was PCR amplified from pCAMBIA1300-35S:PUB26-FLAG (49) and cloned into pMAL-c2x using *Xba*I and *Pst*I-HF to produce pMAL-c2x:MBP-PUB26. All clones were confirmed by Sanger Sequencing using plasmid- and/or gene-specific primers (The Center for Applied

Genomics, Hospital for Sick Children, Toronto Canada, or Eurofins Genomics, Ebersberg, Germany). All primers used for cloning are listed in Table S1.

Confocal Microscopy

Leaf discs were sampled from 4-6 week-old Arabidopsis soil grown plants using a 4 mm biopsy punch (Integra Miltex) and were wet-mounted in water with the abaxial surface facing upwards prior to confocal imaging. Imaging was performed using a LSM 710 (Zeiss) confocal microscope with excitation at 488 nM for YFP and a range of 510-540 nM for measuring emission. To detect chlorophyll autofluorescence, an excitation wavelength of 543 nM and a range of 680-760 nM for detecting emission was used.

Immune assays

AtPep1(99) and elf18 (100) used for immune assays were synthesized by EZBiolab (USA). AtPep1-induced SGI and ROS burst assays were performed as previously described (101). Infection assays were conducted using virulent *Pseudomonas syringae* pv. *tomato* (Pto DC3000) on soil-grown *A. thaliana* plants using a needleless syringe as outlined previously (50).

Generation of the anti-pSer318 antibody

The CPK28 pSer318 antibody was generated and purified by LifeTein (New Jersey, USA). Briefly, rabbits were immunized with KLH-coupled synthetic peptide corresponding to the region of CPK28 surrounding Ser318 (NH₂-CKDPRARLTAAQALpSHAWV-COO-). KLH coupling was facilitated by the addition of Cys to the N-terminus of the peptide. Antibody was purified first by enrichment against the pSer318 phospho-peptide and then by negative enrichment against an unphosphorylated version of the peptide to remove non-phospho-specific IgGs. Purified antibodies were validated by immunoblotting against wildtype, kinase-dead (K91E), or S318A recombinant CPK28 proteins. Purified antibodies were determined to be phosphorylation and site-specific.

Recombinant protein expression and purification

All recombinant CPK28 clones were transformed into lambda phosphatase-expressing BL21 (DE3) *E.coli* cells for the production of dephosphorylated proteins or into T7 Express cells (New England Biolabs) for production of hyperphosphorylated protein (53). Cultures were grown in Luria-Bertani (LB) broth at 37 °C to an OD₆₀₀ of ~0.6-0.8. Expression was induced using 1 mM of β-D-1-thiogalactopyranoside (IPTG) for 16-18 h at room temperature with gentle shaking. Bacterial cells were harvested at 3,500 x *g* for 25 min at 4 °C and resuspended in 50 mL of extraction buffer containing 50 mM Tris-HCl (pH 7.5), 100 mM NaCl and 1 protease inhibitor cocktail tablet (SigmaAldrich). Cells

were lysed by passing the resuspended culture through a French press (Glen Mills® High Pressure Cell Disruption) 3 times. Lysates were clarified by centrifugation at 35,000 x *g* for 40 min at 4 °C. His₆-CPK28 proteins were immobilized on a nickel-nitrilotriacetic acid (NTA) gravity flow column (ThermoFisher) as described previously (53). Elution fractions were dialyzed against two exchanges of 2,500 volumes of 25 mM Tris-HCl (pH7.5), 50 mM NaCl and 1 mM DTT at overnight 4 °C. Recombinant production of GST-BIK1 and GST-BIK1-KD in BL21(DE3)-VR2-pACYC-LamP *E. coli* cells was conducted as described above in a phosphate buffered saline (PBS) solution (ThermoFisher) containing 1 mM DTT, 1 mM PMSF, and 6 mM MgCl₂. Proteins were immobilized on a glutathione agarose gravity flow column (Qiagen) washed 5 times with PBS solution and eluted in 50 mM Tris-HCl (pH 8.0), 5 mM DTT, and 10 mM reduced glutathione. All proteins were concentrated using Pierce™ 3000 MWCO concentration columns (ThermoFisher) to a final concentration of approximately 1.5 mg/mL, as determined by Bradford analysis (Bio-Rad) against bovine serum albumin standards. Recombinant production of MBP-PUB25 and MBP-PUB26 were conducted as described above with the following modifications. pMAL-c2x:MBP-PUB25/26 were transformed into BL21(DE3) *E. coli* cells. Cultures were grown in a baffled flask with LB broth at 37°C to an OD₆₀₀ of ~0.6-0.8 then expression was induced using 0.1 mM IPTG for 3 hours at room temperature with gentle shaking. Pelleted cells were resuspended in MBP column buffer containing 20 mM Tris HCl pH 7.4, 200 mM NaCl, 1 mM EDTA, 1 mM DTT, and 1 mM PMSF. MBP-PUB25/26 were purified using Amylose Resin (NEB) by batch purification according to manufacturer's instructions. Protein was eluted using

100 μ L elution buffer and used for assays on the same day as the purification. Purity was assessed by SDS-PAGE analysis followed by staining with Coomassie Brilliant Blue total protein stain. Protein aliquots were flash frozen in liquid N₂ and stored at -80 °C until use.

***In vitro* autophosphorylation assays**

Autophosphorylation assays were conducted by incubating 5 μ g of purified His₆-CPK28/His₆-OsCPK4 or mutant variants in a 50 μ L reaction containing 25 mM Tris-HCl (pH7.5), 10 mM DTT, 100 μ M ATP, and 100 μ M CaCl₂ or 10 mM EGTA, where specified. Proteins were allowed to autophosphorylate at room temperature for 1-60 min, as specified in figures. Reactions were stopped by the addition of 6x Laemmli sample buffer (LSB) and heating at 80 °C for 5 min. Reactions were analysed immediately or stored at -20 °C before SDS-PAGE and immunoblotting. Autophosphorylation was detected using the pIMAGO kit (Tymora Analytical) according to manufacturer's instructions.

***In vitro* trans-phosphorylation assays**

Trans-autophosphorylation assays were performed using 2 μ g of His₆-MBP-CPK28 or His₆-MBP-CPK28^{D188A} and 4 μ g of His₆-CPK28^{D188A} in the same reaction buffer as in the autophosphorylation assays at 30 °C for 30 min. Trans-phosphorylation assays were conducted using 2 μ g of purified GST-BIK1 or GST-BIK1^{K105A/K106A} and 4 μ g of

His₆-CPK28^{D188A} or His₆-CPK28^{D188A/S318A} in a 20 µL total reaction volume of 25 mM Tris-HCl (pH 7.5), 10 mM MgCl₂, 1 mM DTT and 100 µM ATP at 30 °C for 30 min. Reactions were stopped by adding 6x LSB buffer and heating at 80 °C for 5 min. Reactions were analysed immediately or stored at -20 °C before visualizing phosphorylated proteins using Phospho-Tag gel stain (APB Bio) according to the manufacturer's instructions.

Ca²⁺-activation assays

Analysis of CPK28 peptide kinase activity was carried out as exactly as previously described (53) using the ACSM+1 peptide (NH₂-NNLRLSMGKR-COO⁻) as substrate. Briefly, reactions contained 40 mM Tris-HCl, pH 7.5, 1 mM DTT, 10 mM MgCl₂, 100 µM ATP, 0.1 µCi/µl [γ-³²P]ATP (150 cpm/pmol), 500 ng purified of His₆-CPK28 or the S318A site directed mutant as indicated in the figures, and 10 µM peptide substrate. Reactions were initiated by addition of an ATP/[γ-³²P]ATP mixture. Reactions contained combinations of CaCl₂, or EGTA as indicated in the appropriate figures. For experiments at physiological Ca²⁺, final free Ca²⁺ concentrations were achieved by buffering CaCl₂ with EGTA, calculated using the online WEBMAXC Extended calculator (102). Final reaction volumes were 40 µl. After addition of the ATP/[γ-³²P]ATP mixture, reactions were allowed to proceed for 10 min at room temperature and were stopped by spotting 35 µl of each reaction onto P81 phosphocellulose cation exchange paper followed by washing three times for 5 min each in 0.45% (v/v) *o*-phosphoric acid. Incorporation of ³²P was assessed by liquid scintillation counting.

Intrinsic Trp fluorescence measurements

Intrinsic Trp fluorescence of recombinant purified dephosphorylated or hyperphosphorylated His₆-CPK28 or His₆-CPK28^{S318A} was performed in a PTI QuantaMaster steady-state spectrofluorimeter (Horiba Scientific) in a quartz cuvette with a 1 cm pathlength (Hellma USA Inc.). Data acquisition and background subtraction were performed using the FeliXGX software package (Horiba Scientific). Measurements were carried out on samples of CPK28 at a concentration of 200 nM in a buffer containing 20 mM HEPES-NaOH pH 7.2, 100 mM KCl, and 1 mM DTT. Trp fluorescence was measured at background Ca²⁺ levels ('non-treated') and after the titration of 100 μ M CaCl₂ into the same sample. Samples were measured at an excitation wavelength of 288 nm and fluorescence was collected between 300-450 nm in 1 nm steps with a dwell time of 1 second at each step. Each curve represents an average of two replicate scans of the same sample after appropriate background subtraction of buffer alone or buffer titrated with 100 μ M CaCl₂. Experiments were performed twice on independent preparations of all recombinant proteins.

Phylogenetic analysis

To determine the conservation of Ser318 in group IV CDPKs, the full-length AtCPK28 protein sequence was used as a query in the Phytozome 12 BLAST tool, which identified a total of 114 amino acid sequences from 53 species (File S1). Similarly, the full-length sequences of all group I, II, and III AtCPKs were queried in Phytozome 12

BLAST limited to twelve species spanning the plant lineage (*M. polymorpha*, *P. patens*, *S. fallax*, *S. moellendorffii*, *A. trichopoda*, *O. sativa*, *A. thaliana*, *V. vinifera*, *R. communis*, *B. rapa*, *T. cacao*, and *M. truncatula*) and a total of 327 amino acid sequences were retrieved (File S2). FASTA sequences were aligned using MUSCLE in MEGAX and the 11-amino acid window spanning Ser318 was extracted for visualization of conservation using WebLogo (103).

Protein modeling

CPK28 was modeled using PHYRE2.0 Protein Fold Recognition Server (104) on Intensive Mode and visualized using PyMol Molecular Graphics System Version 2.4.0. The crystal structure of inactive TgCDPK1 (PDB:3KU2) was used as a template.

Statistical analysis

Statistical significance was determined by a Student's T-test or one-way ANOVA followed by Tukey's post hoc test using GraphPad Prism version 8, as indicated.

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SUPPLEMENTARY DATA

		Ser228	Ser318	Ser495
AT4G36070.2	(AtCPK18)	QDIVG S AYYVA	AAQAL S HSWVK	EDGR I SINEFR
KF169738	(BnaCDPK18)	QDIVG S AYYVA	AAQAL S HSWVR	EDGR I S S IHEFR
Bradi3g02600	(BdCDPK17)	RDIVG S AYYVA	AAQAL S HPWVR	KDGR I SLSEFR
GRMZM2G157068	(ZmCDPK22)	HDIVG S AYYVA	AAQAL S HPWVR	KDGK I SLSEFR
GRMZM2G053868	(ZmCDPK40)	HDIVG S AYYVA	AAQAL S HPWVR	KDGK I SLSEFR
Os02g0126400	(OsCDPK4)	HDIVG S AYYVA	AAQAL S HPWVR	KDGR I SLSEFR
AT2G17890.1	(AtCPK16)	HDIVG S AYYVA	AAQAL S HPWVR	NDGK I SLQEFR
GRMZM2G365035	(ZmCDPK33)	RDIVG S AYYVA	AAQAL S HDWVR	KDGK I SLDEFR
Bradi1g52567	(BdCDPK07)	RDIVG S AYYVA	AAQAL S HEWVR	KDGK I SLDEFR
Os07g0409900	(OsCPK18)	RDIVG S AYYVA	AAQAL S HEWVR	RDGK I SLDEFR
AT5G66210.2	(AtCPK28)	HDIVG S AYYVA	AAQAL S HAWVR	RDGK I SLHEFR
JX122909	(BnaCDPK28)	HDIVG S AYYVA	ASQAL S HAWVR	RDGK I SLHEFR
Solyc02g083850.2.1	(SlCDPK28)	QDIVG S AYYVA	AAQAL S HPWVR	KDGK I SLSEFR
Solyc03g033540.2.1	(SlCDPK29)	QDIVG S AYYVA	AAQAL S HPWVR	KDGK I SLSEFR
VIT_04s0023g03420	(VvCPK3)	QDIVG S AYYVA	AAQAL S HPWVR	KDGR I SLAEFR
Glyma02g05440	(GmCPK3)	HDIVG S AYYVA	AAQGL S HPWVR	KDGK I SLPEFR
Glyma16g23870	(GmCPK31)	HDIVG S AYYVA	AAQAL S HPWVR	KDGK I SLPEFR
Glyma11g08180	(GmCPK24)	QDIVG S AYYVA	AAQAL S HPWVR	KDGK I SLPEFR
Glyma01g37100	(GmCPK1)	QDIVG S AYYVA	AAQAL S HPWVR	KDGK I SLPEFR
Smo164119	(SmCPK28)	HDIVG S AYYVA	AAQAL S HPWVR	GDGR I SLREFQ
Contig_10120	(MpCPK28)	QDVVG S AYYVA	ASQAL S HPWAR	GDGR I SLPEFQ
Smo92726	(SmCPK18)	HDVVG S AYYVA	AAQAL S HPWVR	GDGR I SLAEFQ
Pp1s83_172V6		RDVVG S AYYVA	AAQAL S HPWVK	KDGR I SLSEFQ
Pp1s370_37V6		GDVVG S AYYVA	AAQAL S HPWVK	GDGR I SLPEFQ
Pp1s83_8V6		QDVVG S AYYVA	AAQAL S HPWAK	GDGR I SLPEFQ
Pp1s199_57V6		HDVVG S AYYVA	AAQAL S HPWAK	GDGR I SLSEFQ
		*:*****	**:*.******:	* :*: :*

Figure S1. Ser228, Ser318 and Ser495 are conserved across group IV CDPKs. Amino acid sequences of representative group IV CDPKs from eudicots (*Arabidopsis thaliana*, *Glycine max*, *Solanum lyopersicum*, *Vitis vinifera* and *Brassica napus*), monocots (*Brachypodium distachyon*, *Zea mays*, and *Oryza sativa*), bryophytes (*Psychomiteralla patens*), liverworts (*Marchantia polymorpha*), and pteridophytes (*Selaginella moellendorffii*) were aligned using Clustal Omega Multiple Sequence Alignment Tool and the residues corresponding to positions 228, 318, and 495 of *Arabidopsis thaliana* CPK28 were compared. “*”=perfect alignment; “:”=strong similarity; “.”=weak similarity.

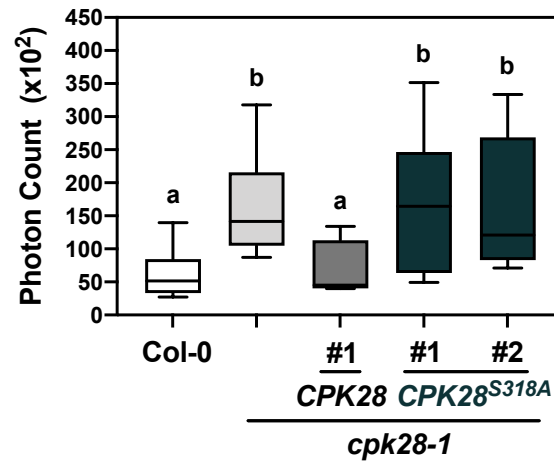


Figure S2. CPK28^{S318A} does not complement *cpk28-1* in response to elf18 treatment. Oxidative bursts of Col-0, *cpk28-1*, *cpk28-1/pCPK28:CPK28-FLAG*, and *cpk28-1/pCPK28:CPK28^{S318A}-FLAG* lines following continual growth in elf18 (100 nM) for 12 days (n=6). Values are presented as boxplots indicating first and third quartiles, split by a median line, and whiskers representing maximum and minimum values. Statistically different groups (p<0.005) are indicated with lowercase letters, as determined by ANOVA analysis followed by Tukey's posthoc test. Experiments were conducted three times with similar results.

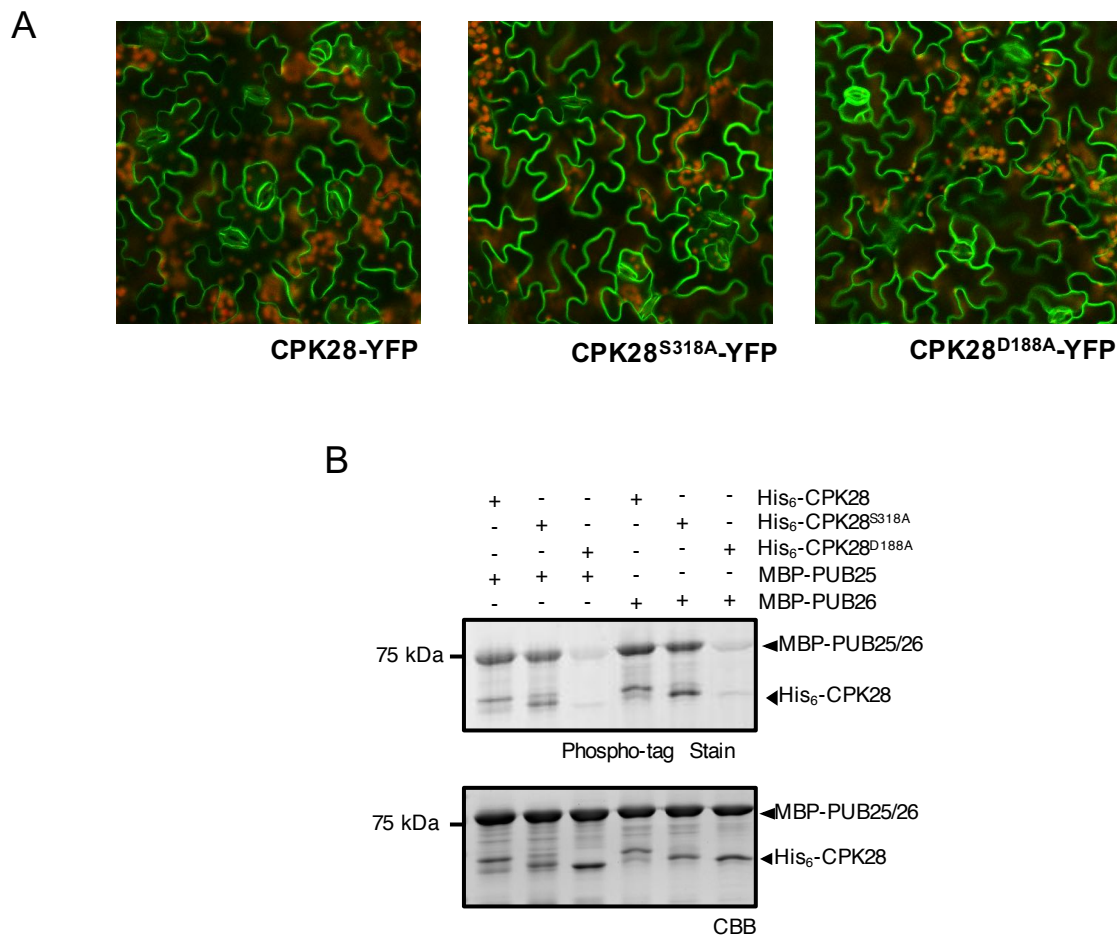


Figure S3. CPK28^{S318A} localizes to the plasma membrane and phosphorylates PUB25 and PUB26. (A) Subcellular localization of CPK28-YFP, CPK28^{S318A}-YFP, and CPK28^{D188A}-YFP stably expressed under the CaMV 35S promoter in *cpk28-1* mutants. Imaging was performed using a LSM 710 (Zeiss) confocal microscope with excitation at 488 nm for yellow fluorescent protein (YFP; coloured green) and a range of 510-540 nm for measuring emission. Chlorophyll autofluorescence (coloured red) was detected with an excitation wavelength of 543 nm and an emission wavelength range of 680-760 nm. (B) Phospho-tag gel stain of *in vitro* kinase assay using recombinantly produced His₆-CPK28, His₆-CPK28^{S318A}, or His₆-CPK28^{D188A} and MBP-PUB25 or MBP-PUB26. Gels were stained with Coomassie Brilliant Blue (CBB) to assess loading. Experiments were conducted at least three times with similar results.

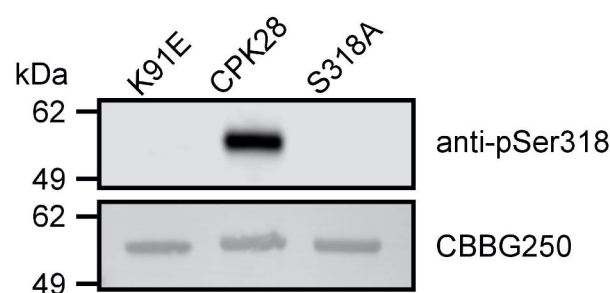


Figure S4. Specificity of the α -pSer318 antibody. Specificity of the CPK28 pSer318 antibody was determined by immunoblotting against wildtype (CPK28), kinase-dead (CPK28^{K91E}), or CPK28^{S318A}. 200 ng of *in situ* phosphorylated purified recombinant protein was separated by gel electrophoresis and blotted to a PVDF membrane before probing with 2 μ g/ml anti-CPK28 pSer318 IgGs. Only the wildtype protein was detected, demonstrating specificity of the antibody for the pSer318 site. Gels were stained with Coomassie Brilliant Blue (CBBG250) to assess loading. Experiments were conducted twice with similar results.

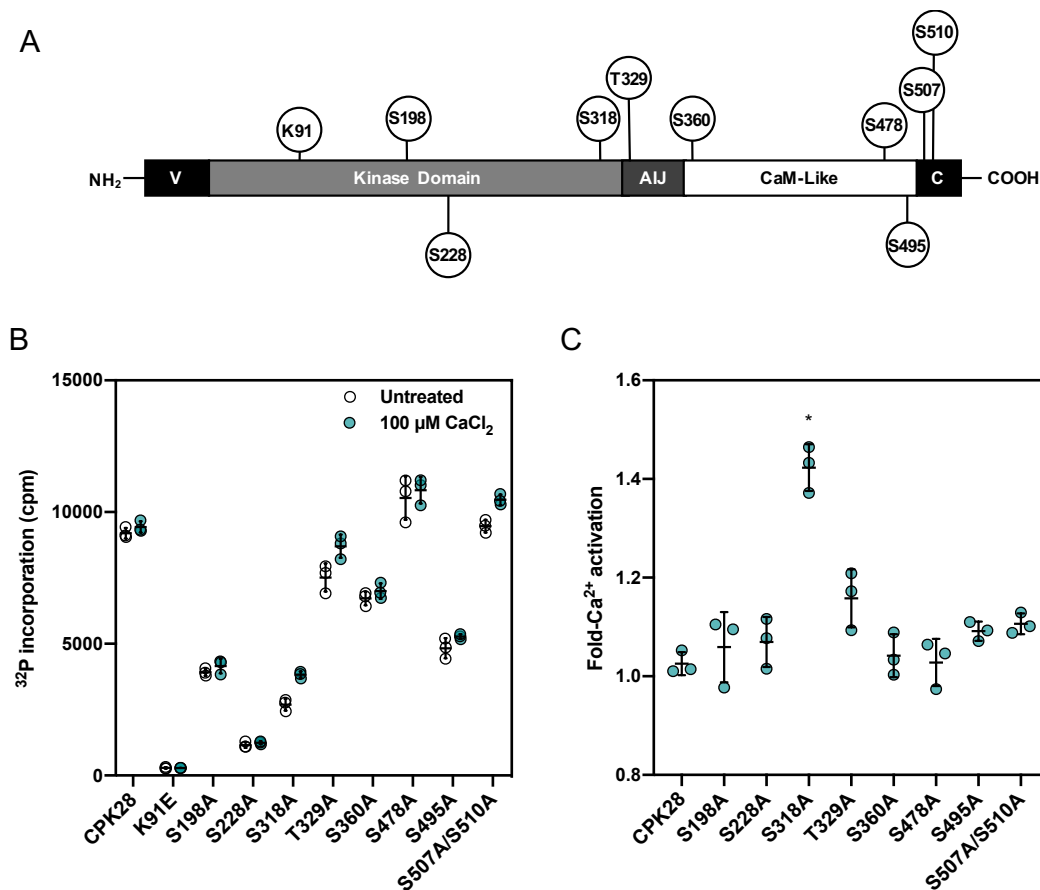


Figure S5. Ser318 phosphorylation uniquely primes CPK28 for Ca²⁺-activation. (A) Position of tested phosphorylation sites across CPK28 protein domains. (B) Biochemical screen of CPK28 phospho-null mutants for Ca²⁺ activation of peptide kinase activity using the ACSM+1 peptide as substrate. Activity was assessed using *in situ* phosphorylated purified recombinant proteins at either background (open circles) or 100 μM CaCl₂ (teal circles) and is shown as ³²P incorporation in cpm. Individual data points (three technical replicates) are shown with mean and standard deviation. (C) Fold-activation of CPK28 phospho-null mutants by the addition of excess Ca²⁺ derived from data shown in (B). No difference is observed for wildtype CPK28 between these two conditions and only the S318A site-directed mutants showed statistically significant activation by Ca²⁺ (Kruskal-Wallis ANOVA, $p = 0.024361$, $n = 3$ technical replicates). The screen with all phospho-site mutants was performed once and S318A was selected for confirmation of altered calcium sensitivity.

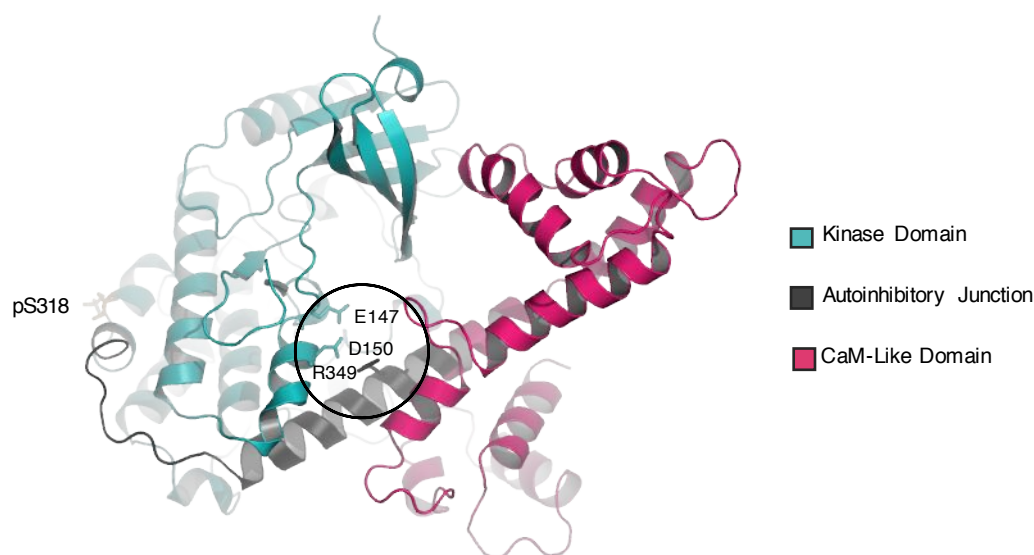


Figure S6. Structural modeling of CPK28. A model for CPK28 was generated using the PHYRE2.0 Protein Recognition Server (104) with inactive TgCDPK1 (iTgCDPK1; 3KU2) as a template (95% confidence score). Phosphorylated Ser318 is indicated in orange. The residues in the autoinhibitory triad that stabilizes TgCDPK1 (Lys338-Glu135-Asp138) (31), corresponding to Arg349-Glu147-Asp150 in CPK28, are labelled. CPK28 was visualized using the PyMOL Molecular Graphics System, Version 2.0 Schrödinger, LLC with PyTMs legacy add-on for post-translational modifications.

Table S1. List of germplasm, constructs, and primers used in this study.

Germplasm	
Genotype	Reference
<i>cpk28-1</i>	Matschi et al., 2012
<i>bik1</i>	Zhang et al., 2010
<i>bik1 pbl1</i>	Zhang et al., 2010
<i>cpk28-1 bik1 pbl1</i>	This study
<i>cpk28-1/pCPK28.CPK28-FLAG</i> line #1	This study
<i>cpk28-1/pCPK28.CPK28-S228A-FLAG</i> line #3	This study
<i>cpk28-1/pCPK28.CPK28-S228A-FLAG</i> line #6	This study
<i>cpk28-1/pCPK28.CPK28-S318A-FLAG</i> line #1	This study
<i>cpk28-1/pCPK28.CPK28-S318A-FLAG</i> line #2	This study
<i>cpk28-1/pCPK28.CPK28-S495A-FLAG</i> line #1	This study
<i>cpk28-1/pCPK28.CPK28-S495A-FLAG</i> line #2	This study
<i>cpk28-1/pCPK28.CPK28-S318D-FLAG</i> line #2	This study
<i>cpk28-1/pCPK28.CPK28-S318D-FLAG</i> line #3	This study
<i>cpk28-1/35S.CPK28-YFP</i>	Matschi et al., 2012
<i>cpk28-1/35S.CPK28-D188A-YFP</i>	Matschi et al., 2012
<i>cpk28-1/35S.CPK28-S318A-YFP</i>	Matschi et al., 2012
Constructs	
Construct name	Primers used (5'-3') or Reference
pRZ949-pCPK28.CPK28-FLAG	Promoter: FW: 5'-atcgGGTACCggggcagcaggaagaccaactc-3' RV: 5'-atcgCCATGGggctctgatgaatcgagaaag-3' CDS cloning: FW: 5'-actgCCATGGGTGTCTGTTCTCCGCCATTAG-3' RV: 5'-atcgGGATCCCTACTTATCATCATCATCCTTGTAATCTCGAAGATTCTGTGACC-3'
pET28a(+)-T7.His6-CPK28	Bender et al., 2017
pET28a(+)-T7.His6-CPK28-K91E	Bender et al., 2017
pRZ949-pCPK28.CPK28-S228A-FLAG	FW: 5'-CATTTGTTGGTggcCCTATTATGTG-3' RV: 5'-TCATGGAACCTTTTCCCTG-3'
pET28a(+)-T7.His6-CPK28-S228A	FW: 5'-CATTTGTTGGTggcCCTATTATGTG-3' RV: 5'-TCATGGAACCTTTTCCCTG-3'
pRZ949-pCPK28.CPK28-S318A-FLAG	FW: 5'-GCTGCACAAGCACTAGCACATGCGTGGGTAGAGAAGGCGGGAATGC-3' RV: 5'-GCATTCCCGCCTTCTCTAACCACGCATGTGCTAGTGTGTCAGC-3'
pET28a(+)-T7.His6-CPK28-S318A	FW: 5'-GCTGCACAAGCACTAGCACATGCGTGGGTAGAGAAGGCGGGAATGC-3' RV: 5'-GCATTCCCGCCTTCTCTAACCACGCATGTGCTAGTGTGTCAGC-3'
pRZ949-pCPK28.CPK28-S495A-FLAG	FW: 5'-GAGATGGGAAAAATAGCCCTGCATGAGTTCA-3' RV: 5'-TGAATCATGCAGGGGCTATTTCCCATCTC-3'
pET28a(+)-T7.His6-CPK28-S495A	FW: 5'-GAGATGGGAAAAATAGCCCTGCATGAGTTCA-3' RV: 5'-TGAATCATGCAGGGGCTATTTCCCATCTC-3'
pET28a(+)-T7.His6-CPK28-D188A	FW: 5'-GTCTTGTACATAGAGCTATGAAACCAGAGA-3' RV: 5'-TCTCTGGTTTCATAGCTCTATGTACAAGAC-3'
pRZ949-pCPK28.CPK28-S318D-FLAG	FW: 5'-ACAAGCACATAgacCATGCGTGGGTAGAGAAGG-3' RV: 5'-GCAGCAGTTAGCCGTGC-3'
pET28a(+)-T7.His6-CPK28-S198A	FW: 5'-GAAACCAAGAGAACTTTTGTTCAAAGCAGCTCAACTAGATTGCGCTCTAAAGG-3' RV: 5'-CCTTTAGAGGCGAATCTAGTTGAGCTGCTTTGAACAAAAAGTTCTCTGTTTC-3'
pET28a(+)-T7.His6-CPK28-T329A	FW: 5'-GGGTTAGAGAAGGCGGGAATGCTGCTGATATCCCTGTCGACATTTCAGTTC-3' RV: 5'-GAATCGAAATGTCGACAGGGATATCAGCAGCATTCCCGCCTTCTTAACCC-3'
pET28a(+)-T7.His6-CPK28-S360A	FW: 5'-CAATTGTCTTTAAGGGCGCTTGCTGCCACACTTGACGAGGCAGAGATCTC-3' RV: 5'-GAGATCTCTGCCCTCGTCAAGTGTGGCAGCAAGCGCCCTTAAAGCAAATTG-3'
pET28a(+)-T7.His6-CPK28-S478A	FW: 5'-GAATGCACACGGGGTTAAGAGGAGCAATAGATCCACTGCTGGATGAAGC-3' RV: 5'-GCTTCATCCAGCAGTGGATCTATTGCTCCTTTAACCCCGTGTGCAATTC-3'
pET28a(+)-T7.His6-CPK28-S507A/S510A	FW: 5'-GTTTCAGGAGACTTCAAGAACAGCGGGCCATAAGTGCACAGAGAGCACCAGGCC-3' RV: 5'-GGGCTTGGTGCTCTCTGTGCACTTATGGCCGCTGTTCTTAGAAGTCTCCTGA
pMAL-c2x:MBP-PUB25	FW: 5'-AATCTCTAGAAATGCCATAGGAATATAGAAC-3' RV: 5'-GATTCGCAAGTCAAAAAGGGAGCCACTTGG-3'
pMAL-c2x:MBP-PUB26	FW: 5'-AATCTCTAGAAATGCCGCGGGAATTAGAGCC-3' RV: 5'-GATTCGCAAGTCAAAAAGGGAGCCACTTGG-3'
pGex6.1-T7:GST-BIK1	FW: 5'-TCGAGCGGGCCGATCTGTGACATGGGTTCTTGTTCAGTTC-3' RV: 5'-GCGAGGCAGATCGTCAGTCACACAAGGTGCTGCCAAAAG-3'
pGex6.1-T7:GST-BIK1-K105A/K106A	FW: 5'-TCGAGCGGGCCGATCTGTGACATGGGTTCTTGTTCAGTTC-3' RV: 5'-GCGAGGCAGATCGTCAGTCACACAAGGTGCTGCCAAAAG-3'
pXCSG-35S:CPK28-YFP	Matschi et al., 2012
pXCSG-35S:CPK28-D188A-YFP	Matschi et al., 2012
pXCSG-35S:CPK28-S318A-YFP	Matschi et al., 2012

File S1. Amino acid sequences of group IV CDPKs across the plant lineage.

This text file includes all FASTA-formatted sequences retrieved following a query for group IV CDPKs using the Phytozome 12 BLAST tool (114 sequences from 53 species).

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>164119 Org_Smoellendorffii peptide: 164119 (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE
16-RELATED (PAC:15408038)
MGICFSADKSEKAEKEKNKKHGDHAAKDQVKNKEQRSKNQSAHVPLGKRTNFGYGRDFQAKYKLGKLLGHGQFGYTYAATKIGSGENAVVKRIEKKKML
LPISVEDVRREVRILQLLSGHENVVQFYASFEDDDYVYIVMELCEGGELLDRILSKKNGCYSEKDAAELVRQMLKVVARCHLHGTVHRDLKPENFLFKSQ
RDNTPLKATDFGLSDFIRPGRRFHDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEAGIFNEVLKKKPEFRIKPWPSISANAKDFV
KRLLVKDPRARPTAAQALSHFPWVREGGCAPDFPLDIIVLSNMREFVKFSRLKQFAFRALATTLEPEEIHNLRDQFNIIDVDGSGTITLLEIRQALLKDRP
WTLKESKVLIVQAMDANMDGFIDEFVFAATLHVRLQLELDSKWLRTKCAFDFDKDGDGFIISPDEIKETGLKGLDITLLEADADGDGRISLREF
QKLLRQASLSGRTNHHHIQPHLKHPKLEMHAPSPKISEESSQ*
>29830.t000004 Org_Rcommunis peptide: 29830.m001387 calcium-dependent protein kinase, putative
(PAC:16810129)
MGACSTIKVSGSSSNTATTTTTVGGHHYQRKEIAGNPQRISTATKTNKQTKNNNNNNNNNNNNESRQKQSQSQSQKQVKEKQTLRRPGGVI PCGKRT
DFGYAKDFDKRYSIGKLLGHGQFGYTYVATDKANGDRVAVKKIEKNKMVLP IAVEDVKREVKILQELAGHENNVHFYNAFEDDSFVYIVMELCEGGELL
RILLKKDSRYTEKDAAVIVRQMLKVAEACHLHGLVHRDMKPENFLFKSTKDDSPKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLKRSGPESDVWSI
GVITYILLCGRRPFWDKTEAGIFKEVLNRKPDFFRRKPWPSISSAKDFVKLLVKDPRVRLTAAQALSHFPWVREGGNASEIPIDISVLNNMRQFVKYSRF
KQFALRALASTLDEELSDLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFSEFVAAALHVHQLEEHNSEKQHRSQ
AAFEKFDIDKDGFIITSEELRMHTGLRGSIDPLLEEADIDKDGKISLSEFRLLRTASISSRNAPSPSGHRNSRKM
>92726 Org_Smoellendorffii peptide: 92726 (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE
16-RELATED (PAC:15420653)
MGVCFVSPKRRKQDPATGNAKSRVRPAGHNKRNAIPLGLRTNFGYGRDFKSKYRIGKLLGHGQFGYTYSAVELMTGDKVAVKRIEKKKMLLPISIEDVK
REVKILDALSGHENNVQFHAAFEDEDFVYIVMELCEGGELLDRILAKKEGRYTEKDAAVIVRQMLRVVARCHLNGVVRDLKPENFLFKSQQDDSLRAV
DFGLSDFIRPGRRFHDVVGSAAYYVAPEVLKRKSGPESDVWSVGIVITYILLCGRRPFWDKTEAGIFNEVLKRKPDLRERPWPSIGSSAKDFVRKLLVKDPR
ARLTAAQALSHFPWVREGGDALEIPLDISVLNNMRQFVKYSRLKQLAFRALATTLDPEDIAALRDQFDAIDADKSGSISLEEMKQALAKDRPWLKESMVM
EILQAMDCNCDGLVDFEEFVAATLHVHQLEDMGSDKWQKRKAFAFDQFVDGDDGYITSEELKQYTGKLSGLTLEEGDIDGDGRISLAEFQKLLRQASL
GSRN*
>Aco015726 Org_Acomosus peptide: Aco015726.1 calcium-dependent protein kinase 28 (PAC:33034109)
MGNCYSNSSKVRGSSSGRGGGGGAANAGGANHERRPPEEREKEKEKGERKGVVPCGKRTDFGYDKDFESRYAIGKLLGHGQFGYTYVATDKANGDK
VAVKRIDKNKMVLPVAVEDVRREVKILKALKGHENNVHFFNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVRQMLKVAEACHLHGLVHR
DMKPENFLKSTKEDSPKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRSGPESDVWSIGVITYILLCGRRPFWDKTEAGIFKEVLKKNKPDFFRRNP
WPSISDSAKDFVQRLLVKDPARLTAAQALSHFPWVREGGNASDIPDISVLNNMRQFVKYSRKFQFALRALASTLNEEELADLRDQFNAIDVDKNGTISL
EEMKHALAKDLPWRMREPRVLEILEAIDSNTDGLVDFDEFVAATLHVHQLELDSKWSLSQAADFQFVDVDRDGYITPDELRMHSGLKGSIDPLLEEAD
IDKDGKISLDEFRRLLKTASMSRNIPNHSAVRNTSKS*
>Aco027228 Org_Acomosus peptide: Aco027228.1 calcium-dependent protein kinase 28 (PAC:33049140)
MFRDIVGSAYYVAPEVLKRSGPESDVWSIGVITYILLCGRRPFWDKTEAGIFKEVLNRKPDFFRRKPWPTISASAKDFIKLLVKNPRARLTAAQALSH
WVREGGDASEIPVDISVLNNMRQFVMYSRMKQFALRALASTLDEEELSDLRDQFDAIDVDKNGSISLEEMRHALAKDLPWRLRGPVLEILQAIDSNTDG
LVDFKEFVTATLHVHQMAEHDSEKWHLRCAAFDKFDLDGDGYITPEELRLHTGLKGSIEPLLEEADIDKDGKISLYEFRKLLRTASMSNLPSPPTGVRNP
HQL*
>AHYPO_018869 Org_Ahypochondriacus peptide: AHYPO_018869-RA (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:32834481)
MGSCSLSTTKVNGSNSNSTTTTTNNALTVIKNQRKEPAKSVANTAPKNDGSHQKQTQKRNEIEGNGKNHKNNNNNNVGMFKHREKTSRRQGAIPCGKRT
DFGYDKDFEYKYITIGKLLGHGQFGYTYVATDKSNGDRVAVKKIDKSKMVLPIAVEDVKREVKILKALAGHENNVQFHNAFEDENYVYIVMELCEGGELL
RILAKKDSRYTEKDAAVVVRQMLKVAEQCHLNLVHRDMKPENFLFKSPKEDSALKATDFGLSDFIKPGKFTDIVGSAYYVAPEVLKRSGPESDVLRN
KPDFFRRKPWPTISNDAKDFVKLLVKDPRARYTAAQALSHFPWVREGGNALDIPIDISVLNNMRQFVKYSRMKQFALRALASTLNEEELADLRDQFDAIDV
DKSGTISLEEMRQALAKDLPWNNTDGLVDFTEFVAATLHVHQLEHDNEKQQLSQAFAFEKFDVDKDGFIITPEELKLHTGLKGSVDPLLEEADIDKDGKI
SLSEFRLLRSASISSRKIASPTCRKNRSRL*
>AL3G50930 Org_Alyrata peptide: AL3G50930.t1 (1 of 1) PF13202//PF14531 - EF hand (EF-hand_5) // Kinase-
like (Kinase-like) (PAC:35941968)
MGLCFSSGHNRRSRNPNNHPLTVAKTRPPQSPCSFMAVTIQKDHRTQPRRNNAAKKTPTRQTPPHGRGREKVISNNGRRHGEAIPYGRKIDFGYAKDFD
HRYTIGNLLGHGQFGYTYVATDKKTDVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENNVRFYNAFEDKNSVYIVMELCEGGELLDRILARKDSR
YSERDAAVVVRQMLKVAEACHLRLGLVHRDMKPENFLFKSTEEEDSPKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRSGPESDVWSIGVISYILL
GRRPFWDKTEAGIFKEVLKKNKPDFFRRKPWPTISNSAKDFVKLLVKDPRARLTAAQALSHFPWVREGGDASEIPIDISVLNNMRQFVKFSRLKQFALRALA
TTLDEEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKARVAEILQAIDSNTDGFVDFGEFVAAALHVNQLEEHDSKWKQSRRAFEKFDID
GDGFTAEELRMHTGLKGSIEPLLEEADIDNDGKISLQEFRRLLRTASIKSRNVSPPGYLISRKV*
>AL7G14970 Org_Alyrata peptide: AL7G14970.t1 (1 of 1) PF13499//PF13833//PF14531 - EF-hand domain pair
(EF-hand_7) // EF-hand domain pair (EF-hand_8) // Kinase-like (Kinase-like) (PAC:35937856)
MGLCFSSPKATRGTSRRNPNNLHSPQTQKASNNKNNKKTKSKNKIQWRHGGGIPYGRKIDFGYAKDFDNRYIIGRLLGHGQFGYTYVATDNNNGNVRVAVK
RIEKAKMTQPIEVEDVREVKILQALGGHENNVGFHNAFEDNNYIYIVMELCEGGELLDRILAKKDSRYTEKDAAVVVRQMLKVAEACHLRLGLVHRDMKP
ENFLFKSTEEGSSLKATDFGLSDFIKPGMKFQDIVGSAYYVAPEVLKRSGPESDVWSIGVITYILLCGRRPFWDKTDGIFNEVMRKKPDFREVPWPTI
SNGAKDFVKLLLVKEPRARLTAAQALSHFPWVKEGGEASEVPIDISVLNNMRQFVKFSRLKQIALRALATTIDEDELDDLRDQFDAIDIDKNGSISLEEMR
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QALAKDVPWKLKDARVAEILQAIDSNTDGLVDFTEFVVAALHVNQLEEHDSSEKQQRSRAAFDKFDIDGDGFITPEELRLQTGLKGSIEPLLEEADIDKD
GRISINEFRRLRSASLKSRSNVKSPPGYQLSQKM*

>AL8G45320 Org_Alyrata peptide: AL8G45320.t1 (1 of 3) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE
16-RELATED (PAC:35949817)
MGVCFSAIRVTGASSSRPSSQTNNPKSKAAPSPIDTKRRTGSI PCGKRTDFGYAKDFHDHYTIGKLLGHGQFGYTYVAIHKPNGDRVAVKRLDKTKMVL
IATEDVKREVQILIALSGHENNVQFYNAFEDDDYVYIMVCEGEGELLDRILSKKGNRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMKPNFLFKSAQL
DSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRRKPDFSRKPWLITSDSAKDFVKK
LLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEEMRQALAKDLPWK
LKDSRVAEILEAIDSNTDGLVDFTEFVVAALHVNQLEEHDSSEKQQLRSRAAFEFKFDIDKGYITPEELRMHTGLRGSIDPLLEADIDRDGKISLHEFR
LLRTASISSQRAPSPQGHNR*

>AqcoelG376400 Org_Acoerulea peptide: AqcoelG376400.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:33079349)
MGICFSTSNKVTGGTSNTTTTTTNATTTTTTINNNVNNNQRESIKPSSSTIHHVPSQQRPYESHNRNSQHQQSQLHQHRSRPSGVPFCGKRTDFG
YLKDFDDKYSIGKLLGHGQFGYTFVATDKINGDRVAVKRIEKNKMLPIAVEDVKREVKILRALTGHENNVQFHNAFEDSEYVYIMVCEGEGELLDRIL
SRKDSRYTEKDAAIIVRQMLKVAAECHLHGLVHRDMKPNFLFKSSKEDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVI
TYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPSIGNSAKDFVQKLLVKDPRARLTAAQALSHPWVREGGDASEIPVDISVLNNMRQFVKYSRLKQF
ALRALASTLNEELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKMKPEPRVLEIVEAIDSNTDGFVDFSEFVAATLHVHQLLEEHDTDKWQVRSQA
EFKFDVDRDGFITPEELKMHMTGLKGSIDPLLEEADVDKDGKISLSEFRRLRTASMSRRNVPTPAGFRNSRKL*

>Aqcoe5G209900 Org_Acoerulea peptide: Aqcoe5G209900.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:33089879)
MGLCLSTTSNKNRKRDNQOQSQSNNNNNKKKITQKKKPPQQQLQOQEKKSNNLRSSVVGKRTDFGYEKDFDEKYSIGKLLGHGQFGYTFVATDKSNGDRV
AVKRIKDKKMTLPIAVEDVKREVKIFQALTGHENNVQFYNAFEDDSYVYIMVCEGEGELLDRILAKKDKRYSEKDAAIIVRQMLKVAAECHLHGLVHRD
LKPENFLFKSTKDDSPKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWNKTEDGIFKEVLKNKPDFHRKPW
PSISNSAKDFVQKLLVKDPRVRLTAAQALSHPWVREGGDASDIPVDILVLSNMRFVKYSRKFQFALRALASTLNEEELSVLRDQFDAIDVDKSGCISFD
EMKQALEKDLPWKIKPEPRVLEILQAIDSNTDGHIDFSEFVAATLHVHQLLEEHDSQKWHLLSQAFAEFKFDVDDGDFITSEELRMHTGLKGSIVPLLEADI
DKDGKINLLEFRKLLRTASMTSPNVPSPSGVGNSKRS*

>Araha.1084s0035 Org_Ahalleri peptide: Araha.1084s0035.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:28844220)
MARESDAPSVTGIAKEIISFVVTFFHFWHEKFNSKKSNEPVYVKKGNASTKRRTGSI PCGKRTDFGYAKDFHDHYTIGKLLGHGQFGYTYVAIHKPNGDRV
AVKRLDKTRMVLPIAVEDVKREVQILIALSGHENNVQFYNAFEDDDYVYIMVCEGEGELLDRILSKKGNRYSEKDAAVVVRQMLKVAGECHLHGLVHRD
MKPNFLFKSAQLDSPKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRRKPDFSRKPW
LTISDSAKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLE
EMRQALAKDLPWKLKDSRVAEILEAIDSNTDGLVDFTEFVVAALHVNQLEEHDSSEKQQLRSRAAFEFKFDIDKGYITPEELRMHTGLRGSIDPLLEADI
DRDGKISLHEFRRLRTASISSQRAPSPQGHNR*

>Araha.13406s0005 Org_Ahalleri peptide: Araha.13406s0005.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:28853710)
GRGREKVISNNGRRHGEAIPYGRKIDFGYAKDFDHRYTIGNLLGHGQFGYTYVATDKKTDNRVAVKKIDAKMTIPIAVEDVKREVKILQALTGHENNV
FYNAFEDKNSVYIMVCEGEGELLDRILARKDSRYSERDAAVVVRQMLKVAAECHLRLGLVHRDMKPNFLFKSTEDSPLKATDFGLSDFIKPGKRFHDI
VGSAYYVAPEVLKRRSGPESDVWSIGVISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLALATTLDEEELADLRDQFDAID
VDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFGEFVVAALHVNQLEEHDSSEKQWQERSRAAFEFKFDIDGDGYITAEELRMHTGLKGS
IEPLLEEADIDNDGKISLQEFRRLRTASIKSRNVRSPPGYLISRKV*

>AT2G17890 Org_Athaliana peptide: AT2G17890.1 calcium-dependent protein kinase 16 (PAC:19642660)
MGLCFSSAAKSSGHNRRSSRNPHPLTVVKSRRPSPCSFMAVTIQKDHRTPRRNATAKKTPTRHPTPHGKVKREKVISNNGRRHGETIPYGRKRVDFGY
AKDFDHRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDAKMTIPIAVEDVKREVKILQALTGHENNVFYNAFEDKNSVYIMVCEGEGELLDRILA
RKDSRYSERDAAVVVRQMLKVAAECHLRLGLVHRDMKPNFLFKSTEDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVIS
YILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKFSRLKQFA
LRALATTLDEEELADLRDQFDAIDVDKNGVISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFGEFVVAALHVNQLEEHDSSEKQWQERSRAAF
KFIDIDGDGFITAEELRMHTGLKGSIEPLLEEADIDNDGKISLQEFRRLRTASIKSRNVRSPPGYLISRKV*

>AT4G36070 Org_Athaliana peptide: AT4G36070.2 calcium-dependent protein kinase 18 (PAC:19645425)
MGLCFSSPKATRRGTGSRNPNPDSPTQGGKASEKVSNNKNNKTKKIQLRHQGGIPYGRKIDFGYAKDFDNRYTIGKLLGHGQFGFTYVATDNNNGNRVAVK
RIDKAKMTQPIEVEDVKREVKILQALGGHENNVGFHNAFEDKTYIYIMVCEGEGELLDRILAKKDSRYTEKDAAVVVRQMLKVAAECHLRLGLVHRDMK
ENFLFKSTEEGSSKATDFGLSDFIKPGVKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTDGIFNEVMRKKPDFREVWPWTI
SNGAKDFVKKLLVKEPRARLTAAQALSHSWVKEGGEASEVPIDISVLNNMRQFVKFSRLKQIALRALAKTINEDELDDLDRDQFDAIDIDKNGSISLEEMR
QALAKDVPWKLKDARVAEILQANDSNTDGLVDFTEFVVAALHVNQLEEHDSSEKQWQERSRAAFEFKFDIDGDGFITPEELRLQTGLKGSIEPLLEEADVD
GRISINEFRRLRSASLKSRSNVKSPPGTEHIICHNLLDGICIEDTEERTSAVRFEYVSQVL*

>AT5G66210 Org_Athaliana peptide: AT5G66210.2 calcium-dependent protein kinase 28 (PAC:19666939)
MGVCFSAIRVTGASSSRSSQTKSAAPTIDTKASTKRRTGSI PCGKRTDFGYSKDFHDHYTIGKLLGHGQFGYTYVAIHRPNGDRVAVKRLDKSKMVL
PIAVEDVKREVQILIALSGHENNVQFHNAFEDDDYVYIMVCEGEGELLDRILSKKGNRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMKPNFLFKSAQ
LDSPKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRRKPDFSRKPWATISDSAKDFV
KLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEEMRQALAKDLPW
KLKDSRVAEILEAIDSNTDGLVDFTEFVVAALHVNQLEEHDSSEKQQLRSRAAFEFKFDLDKDGITPEELRMHTGLRGSIDPLLEADIDRDGKISLHEFR
RLRTASISSQRAPSPAGHRNL*

>Bo1012461 Org_Boleraceacipitata peptide: Bo1012461 (1 of 2) PF13202//PF13499//PF14531 - EF hand (EF-
hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:37347443)
MGLCFSSAKVSGRRNHSPSPNPPLTVAKHRPPQTPCSFLAVTIQKDHRTPRRSPATTKKTPPQTQTQTQTPPHGKGREKGGNNNNNNNTNKGKRHG

EAIPYGRKRVDFGYAKDFDNRYTIGKLLGYGQFGYTYVATDKKTGDRVAVKKIDKAKMRIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIAME
LCEGGELLDRLILAKKESRYSERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRS
GPESDVWSIGVISYILLCGRFPWFDPKTEDGIFKEVLKKNKDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDAEIPIDISVLNNM
RQFVKFSRLKQFALRALATTLDEEESADLRDQFDAIDVDKNGAISLDEMQRALAKDHPWKLKDARVAEILQAIDSNTDGFVDFEEFVAAALHVNQLEEH
SEKWQQRSAFAFEKFDIDGDGFITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLRTASIKSRNVNPPGYLVSRKV*

>Bol018678 Org_Boleraceacapitata peptide: Bol018678 (1 of 2) PF13202//PF13499//PF14531 - EF hand (EF-
hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:37361402)
MGLCFSSPKTTGHGTNHPNPNTPTDIPKPPQAKGREKVCNKNKKTKNNKIQRHVGGNPFGKRIDFGYARDFDNRYIIGKLLGHGQFGFYTAATDNNN
GDRVAVKRLDKAKMTQPIEIEDVKREVKILQALGGHENVVGFHNVFEDKSYVYIVMELCEGGELLDRLILSKKDSRYTEKDAAVVVRQMLKVAAECHLRGL
VHRDMKPENFLFKSTGEDSSLKATDFGLSDFIKPGMKFKDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRFPWFDPKTEDGIFNEVMRKEPDK
TNPWPTISDGAKDFVKKLLVKEPRARLTAAQALSHSWVREGGEASEIPLDISVLENMRQFVKFSRLKQIALKALATTIDEDELDDLRDQFDAIDIDKNGS
ISLEEMRQALAKDLPWKLKDARVAEILQAIDSNTDGLVDFTEFVVATLHVNLQLEEHDSKWEQSRSAFAFEKFDVDRDGFITPEELRLQTGLKGSIEPLLE
EADVDEDEGRISIEHEFRLLRSASLKPRPTVKSPPGYQLSRKM*

>Bol019292 Org_Boleraceacapitata peptide: Bol019292 (1 of 1) PF13499//PF14531 - EF-hand domain pair
(EF-hand_7) // Kinase-like (Kinase-like) (PAC:37350374)
MGLCFSDIRVTGTSSSSSRSSSQTNNNNNNNKPNKSNKTRPPPPENNNNDKPSSTTTTKRRTGSVPCGKRTEFGYAKDFHDQYSIGKLLGHGQFGYTYVAI
HKSNGDRVAVKRLDKSKMVLPAVEDVKREVQILKALSGHENVVQFYNAFDDDDVYIVMELCEGGELLDRLILSKKDSRYSEKDAAVVVRQMLKVAGECH
LHGLVHRDMKPENFLFKSAKLDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRFPWFDPKTEDGIFKEVLNRK
PDRFRKPWSTISDSAKDFIKGLLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVYRSRLKQFALRALASTLDEAEISDLRDQFDAIDVD
KNGVISLEEMRQALAKDLPWKLKESRVAEILEAIDSNTDGLVDFTEFVAAALHVNQLEEHDSKWLRSRAFAFEKFDIDKDGITYITPEELRMHTGLRGSID
PLLEADIDRDKGKISLHEFRRLRTASISSPRVPSTAGHRIPR*

>Bol027148 Org_Boleraceacapitata peptide: Bol027148 (1 of 1) PF13499//PF13833//PF14531 - EF-hand domain
pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) // Kinase-like (Kinase-like) (PAC:37361248)
MGVCFSAIRVTGASSSRQTNNNNNKAHKKGCKKPPENKPSSTTTTNAKRRATGSVPCGKRTEFGYAKDFHEQYTIQKLLGHGQFGYTYVAIDKANGDRVAV
KRLDKSKMVLPIAVEDVKREVEILKALSGHENVVQFYNAFDDDDVYIVMELCEGGELLDRLILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMK
ILSKKDSHYTERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSVLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIG
VITYILLCGRFPWFDPKTEDGIFKEVLKKNKDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDATEIPIDISVLNNMRQFVKFSRLK
QFALRALATTLDEEELADLRDQFGAMADKNGAISLDEMQRALAKDHPWKLKDARVAEILQAIDSNTDGFVDFEEFVAAALHVNQLEEHDSKWKQQRSA
RAFAFEKFDIDGDGFITAEELRMHTGLKGSIEPLLEEADIDHDGKISLHEFRLLRTASIKSRNVNPPGYLISRKA*

>Bostr.0568s0032 Org_Bstricta peptide: Bostr.0568s0032.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:30669325)
MGLCLSSIRVTGASSSRSSQTNNNHNGCKKAVPNPKDIDTKRRTDSSIPCGKRTEFGYAKDFHDQYSIGKLLGHGQFGYTYVAIDKANGDRVAVKRLD
KSKMVLPIAVEDVKREVQILKALSGHENVVQFYNAFDDDDVYIAMELCEGGELLDRLILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMKPENF
LFKSAKLDSPLKATDFGLSDFIKPGKRFDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRFPWFDPKTEDGIFKEVLNRKPDFFRRKPWSTISDS
AKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVYRSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEEMRQAL
AKDLPWKLKDSRVAEILQAIDSNTDGLVDFTEFVAAALHVNQLEEHDSKWLRSRAFAFEKFDIDKDGITYITPEELRMHTGLRGSIDPLLEADIDRDKGI
SLHEFRLLRTASISSQVRVSSPSGHRNPR*

>Bostr.18351s0257 Org_Bstricta peptide: Bostr.18351s0257.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:30676600)
MGLCFSSAAKASGHNSRRNPIPHPLTVAKPRPPQTPCSFMAVTIQKDHRTPRNRNAAKKTPTWQTPPHGRERDKVSSNNNNNNNNGRRHGEAIPYGRK
IDFGYAKDFHRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGGELL
DRILARKDSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWS
IGVISYILLCGRFPWFDPKTEDGIFKEVLKKNKDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDAEIPIDISVLNNMRQFVKFSR
LKQFALRALATTLDEEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFTEFVAAALHVNQLEEHDSKWKQQR
RAFAFEKFDIDGDGYITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLRTASIKSRNVRSPPGYLISRKV*

>Bradi1g52567 Org_Bdistachyon peptide: Bradi1g52567.1.p (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32792415)
MGLCSSSSAASPADPAGNGNKEKRGSGRGIVACGKRTEFGYDKDFEARYTIGKLLGHGQFGYTFAAVDRYSDERAVKRIKDNKMVLPAVEDVKR
EVKILKALQGHENNVHFNFAFEDDNNYVYIVMELCEGGELLDRLILAKKDSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSSKEGSPKATD
FGLSDFIRAGKQFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRFPWFDPKTEDGIFKEVLKKNKDFRRKPWNTITPSAKDFVQKLLVKDPRA
RLTAAQALSHWVREGGQASEIPLDISVLNNMRQFVKYSRKFQFALRALASTLNSEELSDLRDQFNAIDIDKSGTISLEELKQALAKDVPWRLKGPRVLE
IVEAIDSNTDGLVDFEEFVAATLHVHQLVEHDSKWKSLQAADFDFVDGDGYITSDELRMNTGLKGSIDPLLEEADIDKDGKISLDEFRLLRTASMS
SRNATPKSVSKSYRFA*

>Bradi3g02600 Org_Bdistachyon peptide: Bradi3g02600.2.p CAMK_CAMK_like.26 - CAMK includes
calcium/calmodulin dependent protein kinases, expressed, subfamily CAMK_like(CAMK_1) (PAC:32812227)
MGGCFSTNTPATPAEERRRRRRRQRAASPEKSGGGAEGVARVVEFGYERDFEGRYEVRGLLGHGQFGYTFAAVDRGSGDRVAVKRIKAKMNRVAVE
DVKREVKILKALQGHENIVHFNFAFEDDSYVYIVMELCEGGELLDRLILAKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTKEDSPL

KATDFGLSDFINPGKKFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKPWPSPISSTSAKDFVKRLLVK
NPRARLTAAQALSHPWVREGGDASEIPVDISVLNMRQFVKYSRKFQFALRALASTVNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLPWRLKGP
RVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGLRCAAFSKFDLDGDGYITPDELRMHTGLKGSIEPLLEEADIDKGRISLSEFRKLLRT
ASMSNLPSPPTGVPNPQAL*

>Brara.F02520 Org_BrapaFPsc peptide: Brara.F02520.1.p (1 of 2) PF13202//PF13499//PF14531 - EF hand (EF-
hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:30630447)
MGLCFSSAKVSGRRNHSRSPENPNPLTVAKHRPPQTPCSFLAVTIQKDHRTQPRRSPATTKKTPPQTQTQTRQTPPHGKGREKAGNNNNNNNKGKRHGEA
IPYGRVDFGYAKDFDNRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTIPIAVEDVVKREVKILQALTGHENNVRFYNAFEDKNSVYIAMELC
EGGELLDRILAKKESRYSERDAAVVVRQMLKVAEACHLRLGLVHRDMKPENFLFKSTDEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGP
ESDVWSIGVISYILLCGRRPFWDKTEDGIFKEVLKKNKPDFRRKPWPPTVSNASAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNMRQ
FVKFSRLKQFALRALATTLDEEESADLRDQFDAIDVDKNGAISLDEMQRALAKDHPWKLKDARVAEILQAIDSNTDGFVDFFEEFVAAALHVNQLEEHDS
KWQQRSAFAFEKFDIDGDFITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLRTASIKSRNVNRNPPGYLVSRKV*

>Brara.G00225 Org_BrapaFPsc peptide: Brara.G00225.1.p (1 of 1) PF13202//PF13833//PF14531 - EF hand (EF-
hand_5) // EF-hand domain pair (EF-hand_8) // Kinase-like (Kinase-like) (PAC:30634206)
MGLCFSSAKVSGRQHSRSPENPPHHPLTVAKPKPEQTPCSFLAVTIQKDHKAQQRRNAATTTNKKTPPTQTPTHGKAREKAKRHGEKIPYGRVDFGY
AKDFDNRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTLPIAVEDVVRREVKILQALTGHENNVRFYNAFEDKNSVYIAMELCGEGELLDRILA
KKDSHYTERDAAVVVRQMLKVAEACHLRLGLVHRDMKPENFLFKSTEDSALKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVIS
YILLCGRRPFWDKTEDGIFKEVLKKNKPDFRRKPWPPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNMRQFVKFSRLKQFA
LRALATTLDEEELADLRDQFGAMADKNGAISLDEMQRALAKDHPWKLKDARVAEILQAIDSNTDGFVDFFEEFVAAALHVNQLEEHDSKQQRSAFAFE
KFDIDGDFITAEELRMHTGLKGSIEPLLEEADIDHDGKISLHEFRRLRTASIKSRNVNRNPPGYLISRKT*

>Brara.G01274 Org_BrapaFPsc peptide: Brara.G01274.1.p (1 of 2) PF13499//PF14531 - EF-hand domain pair
(EF-hand_7) // Kinase-like (Kinase-like) (PAC:30633535)
MGVCFSAIRVTGASSSRQTNNNKAHKGCKKPPENKPSNTTKRRATGSGVPCGKRTDFGYAKDFHEQYTIKLLGHGQFGYTYVAIDKSNNGDRVAVKRLDKS
KMLVPIAVEDVVKREVEILKALSGHENNVQFYNAFDDDDYVYIMELCEGEGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMKPENFLF
KSTQLDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRRKPWSTISDSAK
DFVKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNMRQFVYRSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEEMRQALAK
DLPWKLKDSRVAEILQAIDSNTDGLVDFTEFVAAALHVNQLEEHDSKQWQLRSRAFAFEKFDIDKDGYYITPEELRMHTGLRGSIDPLLEADIDRDGKISL
HEFRRLRTASISSQRVISAPGHRNPR*

>Brara.I00917 Org_BrapaFPsc peptide: Brara.I00917.1.p (1 of 2) PF13499//PF14531 - EF-hand domain pair
(EF-hand_7) // Kinase-like (Kinase-like) (PAC:30645318)
MGVCFSAIRVTGTSSSRSSSQTNNNNKNPKSNKTPPPENNNNPKSTTTTKRRTGSGVPCGKRTEFGYAKDFHEQYSIGKLLGHGQFGYTYVAIHKSNG
DRVAVKRLDKSKMVLPAVEDVVKREVQILKALSGHENNVQFYNAFDDDDYVYIMELCEGEGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLV
HRDMKPENFLFKSAKLDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRR
KPWSTISDSAKDFIKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNMRQFVYRSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVI
SLEEMRQALAKDLPWKLKESRVAEILEAIDSNTDGLVDFTEFVAAALHVNQLEEHDSKQWQLRSRAFAFEKFDIDKDGYYITPEELRMHTGLRGSIDPLLE
ADIDRDGKISLHEFRRLRTASISSPRVASTAGHRIPR*

>Brara.K01328 Org_BrapaFPsc peptide: Brara.K01328.1.p (1 of 2) PF13202//PF13499//PF14531 - EF hand (EF-
hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:30623319)
MGLCFSSPKATRHGTNHPNPNPPDPIDPKPQSQGKGREKVCNQNKKTTKNNKIQRHVGGTLFGKRIDFGYARDFDNRYTIGKLLGHGQFGFTYAATDNN
NEDRVAVKRIDKAKMTQPIEDVVKREVKILQALGGHENNVGFHNVFEDKNYVYIMELCEGEGELLDRILSKKDSRYTEKDAAVVVRQMLKVAEACHLRL
LVHRDMKPENFLFKSAKLDSPLKATDFGLSDFIKPGMKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKQTNGIFNEVMRKKPDF
ETTPWPTISDGAKDFVKKLLVKEPRARLTAAQALSHSWVREGGEASEIPIDISVLNMRQFVKFSRLKQIALKALATTIDEDELDDLDRDQFDAIDIDKNG
SISLEEMRQALAKDLPWKLKDARVAEILQAIDSNTDGLVDFTEFVVATLHVQNLEEHDSKWEQSRSAFAFEKFDVDRDGFITPEELRLQTGLKGSIEPLL
EEADIDEDGRISIEHEFRRLRLRSASLKPRTVKSPPGYQLSRKM*

>Brast04G317700 Org_Bstacei peptide: Brast04G317700.1.p (1 of 1) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32863370)
MGGCFSTASATPAAERRRRRQRAASPEKSGGAEGVAPRVVEFGYERDFEGRYEVGRLLGHGQFGYTFATDRGSGDRVAVKRIDKAKMNRPAVED
VKREVKILKALKGHENIVHFYNAFEDDSYVYIMELCEGEGELLDRILAKKNSRYSEKDAAVVVRQMLKVAEACHLRLGLVHRDMKPENFLFKSTKEDSPLK
ATDFGLSDFIKPGKKFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKPWPSPISSTSAKDFVKRLLVK
PRARLTAAQALSHPWVREGGDASEIPVDISVLNMRQFVKYSRKFQFALRALASTVNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLPWRLKGP
VLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGLRCAAFSKFDLDGDGYITPDELRMVQHTGLKGSIEPLLEEADIDKDGKISLSEFRKLLR
TASMSNLPSPPTGVPNPQAL*

>Brast06G146700 Org_Bstacei peptide: Brast06G146700.1.p (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32852110)
MGLCSSSSAARPADPAGSNGNKEKGRKSGSGRGLVACGKRTDFGYDKDFEARYTIGKLLGHGQFGYTFAAVDRYSDERVAVKRIDKNMVLPAVEDVVKR
EVKILKALQGHENNVHFYNAFEDDNYVYIMELCEGEGELLDRILAKKDSRYSEKDAAVVVRQMLKVAEACHLRLGLVHRDMKPENFLFKSSKEGSPLKATD
FGLSDFIRAGKFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKPWPNTITPSAKDFVQKLLVKDPRA
RLTAAQALSHWVREGGQASEIPLDISVLNMRQFVKYSRKFQFALRALASTLNSEELSDLHDQFNAIDIDKSGTISLEELKQALAKDVPWRLKGPVLE
IVEAIDSNTDGLVDFEEFVAATLHVHQLVEHDSEKWKSLQAADFDFVDGDGYITSDELRMNSGLKGSIDPLLEEADIDKDGKISLSEFRRLRTASMS
SRNATPKSVSKS*

>Cagra.10427s0030 Org_Cgrandiflora peptide: Cagra.10427s0030.1.p (1 of 3) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:28917453)
MGVCFSAIRVTGASSRRSSQTTHNHRKGCQKKKKAASPCPNPAIDAKRSRTGSI PCGKRTDFGYPKDFHDQYSIGKLLGHGQFGYTYVAIDKSN
GDRVAVKRLDKSKMVLPIAVEDVVKREVQILKALSGHENNVQFYNAFDDDDYVYIAMELCGEGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLV
HRDMKPENFLFKSKLDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRRK

PWSTISDSAKDFVKKLLVKDPRLARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVIS
LEEMRQALAKDLPWKLKDSRVSEILQAIDSNTDGLVEFTEFVAAALHVVHQLLEHDSEKWQQRSAFAFEKFDIDKDGYYITPEELRMHTGLRGSIDPLLDEA
DIDRDGKISLHEFRRLRLRTASISSQVRSSPSGRHRNPR*

>Cagra.2236s0004 Org_Cgrandiflora peptide: Cagra.2236s0004.1.p (1 of 1) PF13202//PF13833//PF14531 - EF
hand (EF-hand_5) // EF-hand domain pair (EF-hand_8) // Kinase-like (Kinase-like) (PAC:28906597)
MGLCCSSPKATRHGTSRPNPNHSGPTQGGKANEKVSNNKNGKTKNKNKIQRQGGRTPYGKRIDFGYAKDFDNRYTIGKLLGHGQFGFTYVATDNNNGNSV
AVKRIDKAKMSLPIEVEDVKREVKILQALGGHENVVGFHNAFDDKNVYIVMELCEGGELLDRIILGKKDSRYTEKDAAVVVRQMLKVAAECHLRGLVHRD
MKPENFLFKSTEEDSSSLKATDFGLSDFIKPGTKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTDQDGFNEVMRKKPDPFKTVPW
PTISNSAKDFVKKLLVKEPCARLTAAQALSHPWVREGGEASEIPIDISVLNNMRQFVKFSRLKQIALRALATTIDEDELDDLRDQFDAIDIDKNGSISLE
EMRQALAKDVPWKLKDAARVAEILQAIDSNTDGLVDFTFVAVTLHVNQLEEHDSSEKWQQRSAFAFEKFDIDKDGYYITPEELRMHTGLRGSIDPLLEADV
DEDGRLSIHEFRRLRLRSASIKSRNTKSPPGYQLSRKM*

>Cagra.3126s0021 Org_Cgrandiflora peptide: Cagra.3126s0021.1.p (1 of 1) PF13202//PF13499//PF14531 - EF
hand (EF-hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:28902422)
MGLCFSSAAKATGHNRSRNPVPHPLTVAKHRPPQSPCSFMAVTIQKDHRTQPRRKTPTTRQTPPHGRGREKVISNNNNNNNKRHGEAVIIPYGRVD
FGYAKDFDHRITIGKLLGHGQFGYTYVATDKKTGDRVAVKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGGELLDRI
ILARKDSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTDEDSALKATDFGLSDFIKPGKFFHDIVGSAYYVAPEVLKRRSGPESDVWSIG
VISYILLCGRRPFWDKTEDGIFKEVLKKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRLARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKFSRLK
QFALRALATTIDEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDAARVAEILQAIDSNTDGFVDFSEFVAAALHVNQLEEHDSSEKWQQRSA
AFEKFDIDGYYITAEELRMHTGLKGSIEPLLEADIDNDGKISLHEFRRLRLRTASIKSRNVRSPPGYLISRKV*

>Carubv10006766m.g Org_Crubella peptide: Carubv10006766m (1 of 1) PF13202//PF13833//PF14531 - EF hand
(EF-hand_5) // EF-hand domain pair (EF-hand_8) // Kinase-like (Kinase-like) (PAC:20895390)
MGLCCSSPKATRHGTSRPNPNHSLTQGGKANEKVSNNKNGKTKNKNKIQRRRGGRTPYGKRIDFGYAKDFDNRYTIGKLLGHGQFGFTYVATDNNNGNSV
AVKRIDKAKMSLPIEVEDVKREVKILQALGGHENVVGFHNAFDDKNVYIVMELCEGGELLDRIILGKKDSRYTEKDAAVVVRQMLKVAAECHLRGLVHRD
MKPENFLFKSTEEDSSSLKATDFGLSDFIKPGTKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTDQDGFNEVMRKKPDPFKTVPW
PTISNSAKDFVKKLLVKEPCARLTAAQALSHPWVREGGEASEIPIDISVLNNMRQFVKFSRLKQIALRALATTIDEDELDDLRDQFDAIDIDKNGSISLE
EMRQALAKDVPWKLKDAARVAEILQAIDSNTDGLVDFTFVAVTLHVNQLEEHDSSEKWQQRSAFAFEKFDIDKDGYYITAEELRMHTGLRGSIDPLLEADV
DEDGRLSIHEFRRLRLRSASIKSRNIKSPPGYQLFRKM*

>Carubv10013325m.g Org_Crubella peptide: Carubv10013325m (1 of 1) PF13202//PF13499//PF14531 - EF hand
(EF-hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:20897988)
MGLCFSSAAKATGHNRSRNPVPHPPPLTVAKHRPPQSPCSFMAVTIQKDHRTQPRRKTPTTRQTPPHGRGREKVISNNNNNNNKRHGEAVIIPYGRV
DFGYAKDFDHRITIGKLLGHGQFGYTYVATDKKTGDRVAVKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGGELLD
RILARKDSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTDEDSALKATDFGLSDFIKPGKFFHDIVGSAYYVAPEVLKRRSGPESDVWSI
GVISYILLCGRRPFWDKTEDGIFKEVLKKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRLARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKFSRL
KQFALRALATTIDEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDAARVAEILQAIDSNTDGFVDFSEFVAAALHVNQLEEHDSSEKWQQRSA
AAFEKFDIDGYYITAEELRMHTGLKGSIEPLLEADIDNDGKISLHEFRRLRLRTASIKSRNVRSPPGYLISRKV*

>Carubv10028399m.g Org_Crubella peptide: Carubv10028399m (1 of 3) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:20911700)
MGVCFSAIRVTGASSRRSSQTNTNHNRTKGCQKKKKAASPCPNKAIDAKRSRTGSI PCGKRTDFGYPKDFHDQYSIGKLLGHGQFGYTYVAIDKSN
RVAVKRLDKSKMVLPIAVEDVKREVQILQALSGHENVVQFHNAFEDDDVYIAMELCEGGELLDRIILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVH
RDMKPENFLFKSDKLDSPKATDFGLSDFIKPGKFFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKKNKPDFRRK
PWSTISDSAKDFVKKLLVKDPRLARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVIS
LEEMRQALAKDLPWKLKDSRVSEILQAIDSNTDGLVEFTEFVAAALHVVHQLLEHDSEKWQQRSAFAFEKFDIDKDGYYITPEELRMHTGLRGSIDPLLDEA
DIDRDGKISLHEFRRLRLRTASISSQVRSSPSGRHRNPR*

>Ciclev10025251m.g Org_Cclementina peptide: Ciclev10025251m (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:20800576)
MGICLSTTKVSGSNSGNNNNANHHNRNANKEEAKRRHRNRHARNDTTHKHQHQHQAERAKNYQQLKTKQHQTNSRRQTGVIPCGKRTDFGYDKDFDRRYTI
GKLLGHGQFGYTYVATDKANGDRVAVKKIEKNMILPIAVEDVKREVKILQALAGHENVVVFYNAFEDDNYVYIAMELCEGGELLDRIILAKMISITLTS
WFLAIRKDSRYTEKDAAVVVRQMLRVAAECHLHGLVHRDMKPENFLFKSAKEDSSSLKATDFGLSDFIKPGKFFQDIVGSAYYVAPEVLKRRSGPESDVWS
IGVITYILLCGRRPFWDKTEDGIFKEVLKKNKPDFRRKPWPSISNSAKDFVKKLLVKDPRLARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKYSR
LKQFALRALASTLDEELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDCNTDGLVDSEFVAAATLHVHQLLEHDSEKWHLRS
QAAFEKFDIDRDGFITPEELRMHTGLKGSIDPLLEADIDKDGIRLSLSEFRRLRLRTASISSRNVPPSPSGHRNPRKL*

>DCAR_016603 Org_Dcarota peptide: DCAR_016603 hypothetical protein (PAC:36076972)
MGSCFSTKKITGSSSNTTNTNTHVKKPASSATSTSATTKLYRNNNNKNNKNDNDHRNQQLIRHRDKASSRKQNGVIPCGRKRTDFGYDKDFDLRYSIGK
LLGHGQFGYTYVAVDRSNGDRVAVKIDKKNMILPIAVEDVKREVRILKALSGHENVVQFYNFEDDSYVYIAMELCEGGELLDRIILAKSSRYTEKDA
RVVRQMLKVAAECHLHGLVHRDMKPENFLFKSPKDDSAKATDFGLSDFIRPGKFFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWD
KTEDGIFKEVLKKNKPDFRRKPWPTISNGAKDFVKKLLVKEPRARYTAAQALSHPWVREGGNALEIPLDISVLYNMRQFVKYSRLKQFALRALASTLDEE
LADLRDQFHAIDVDKNGAISLEEMRQALAKDIPWKVKESRVLEILQAMDSNTDGLVDFHEFVAATLHVHQLLEHNSEKQQISHAAFEKFDVVDKDGYYITA
EELKMHTGLRGSIDPLLEADIDKDGKISLSEFRKLLRTASMGTRNVNSPAAHGRSRRQ*

>DCAR_021501 Org_Dcarota peptide: DCAR_021501 hypothetical protein (PAC:36084600)
MGKLLGHGQGYTYVATDNNNGDRVAVKIDKKNMILPIAVEGVKREVRIMKALSGHENVVQFHNSFEDDSYVYIAMELCEGGELLDRIILAKSSRYTEK
DAAAVARQMLKVAAECHLHGLVHRDMKPENFLFKSPEEDSTLKVTDGFLSDFIRPGKFFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRP
FWDETEDGIFKEVLKKNKPDFCRKPWPTISDDAKDFVKNLLVKEPRARYTAAQALSHPWVREGGNALEIPLDISVLYNMRQFVKYSRLKQALALASTLD
EELADLRDQFLAIDVDKNGTISLEEMRQALAKDIPWKVKESRVLEILQAMDSNTDGLIDFHEFVAATLHVHQLLEHNSEKQQISHAAFEKFDVVDKDGYY
ITAEELRMEQVELSV*

>Eucgr.I02347 Org_Egrandis peptide: Eucgr.I02347.1.p (1 of 1) PF07714//PF13202//PF13499 - Protein

tyrosine kinase (Pkinase_Tyr) // EF hand (EF-hand_5) // EF-hand domain pair (EF-hand_7) (PAC:32064182)
 MGICASSAARRAGGSAGASTRRNGNRRRRERDQDGAGEANRKRKDDRRQAEFGGGGGGGNGKQGGGAVPCGKRADFGYARDFAERYSLGKLLGHGQFGYTY
 VAVDKVNGDRVAVKRIKSKMVLPIAVEDVKREVILKALTGHEENVVQFYNAFEDDSYVYIAMEYCEGGELLDRILAKKDSRYTEKDAAVVVRQMLRVAA
 ECHLHGLVHRDMKMPENFLFKSSKEDSPLKATDFGLSDFINPGKRFDIVGSAYYVAPEVLKRKSGPESDVWSIGVITFILLCGRPFWDKTEDGIFKEVL
 KKKPDFRRRPWPTISNSAKDFVKLLVKDPRARLTAAQALSHPWVREGGNASDIPIDISVLNNMRQFVKYGRKQFALRALASTLDGEEELADLKQDFAAI
 DVDKNGSISLEEMREALAQDLPWKMKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQMEEHDSKQWQLRSQAFAFEKFDIDRDGYITPEELRLQTLGKG
 SLGPLLEEADIDKDGKISLSEFRLLRTASMGSQLPSSSGYRNLRKI*
 >Eucgr.J02432 Org_Egrandis peptide: Eucgr.J02432.1.p (1 of 1) PF13499//PF14531 - EF-hand domain pair
 (EF-hand_7) // Kinase-like (Kinase-like) (PAC:32034103)
 MGLCISTTRVSGSSSNAAAAANQKRHEIGRPQAGAAGGTAGANEKNKQKVRGEGGKKKSGVPCGKRTDFGYAKDFDRRYTIGKLLGHGQFGYTYVAT
 DKANGDRVAVKRIEKNKMLPIAVEDVKREVILKALTGHEENVVQFYNAFEDDSYVYIAMEYCEGGELLDRILSKKDSRYTEKDAAVVVRQMLKVAQCH
 LHGLVHRDMKMPENFLFKSKKDDSSLKATDFGLSDFIKPGKFPDVGSAAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRPFWDKTEDGIFKEVLKSK
 PDFRRRPWPSISNSAKDFVKLLVKDPRARLTAAQALSHPWVREGGSASEIPIDISVLNNMRQFVKYNRFKQFALRALASTLDEEELADLKQDFAIDVD
 KNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFHEFVAATVHVNQLEEHNSKWLRRSQSAFEKFDLDGDGYITPEELRMHTGLRGSID
 PLLEEADIDKDGRISEFRLLRTASMSKTVSSPSNFRNSRKM*
 >evm.TU.supercontig_6.254 Org_Cpapaya peptide: evm.model.supercontig_6.254 (1 of 2) PTHR24349:SF87 -
 CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:16423436)
 MGTCLSTTKVSGANSNTATTTTNVHHNRKATKQSTTAAATATTTTTTTNQKEQGSQNHHHHANKTQNQRNSQQLKAKEKTSRRPGGVI PCGKRTD
 FGYAKDFDKRYAIGKLLGHGQFGYTYVATDKVNGDRVAVKRIEKSVMVLPIAVEDVKREVILKALTGHEENVVQFYNAFEDENYVYIVMELCEGGELLDR
 ILAKFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRPFWDKTEDGIFKEVLNRKPDFRRKPWPTISNAAKDFVKLLVKDPRARLTAAQAL
 SHPWVREGGEASEIPIDISVLNNMRQFVKYSRLKQFALRALASTLDDEELADLRDQFAAIDVDKNGSISLEEMRQALAKDLPWKLKDSRVLEILQAIDCN
 TDGLVDFTEFVAALHVHQLEEHDSKQWQRSRAAFEKFDIDRDGYITPEELRLHTGLKGSIDPLLEEADIDKDGKISLSEFRLLRTASIGSRNIPSP
 GQRIPRKI*
 >Glyma.01G166100 Org_Gmax peptide: Glyma.01G166100.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT
 PROTEIN KINASE 16-RELATED (PAC:30544862)
 MGLCFSSTKVSGSSNNNNNNNASNRNRKCSAAPAAAAPPEPVTQKKQPSQAQRRRVPEESRKNPRAKDAGARRQGTVP CGKRTDFGYEKDFENRF
 SLGKLLGHGQFGYTYVIGIDKNGDRVAVKRLKSKMVLPIAVEDVKREVILKELTGHEENVVQFFNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYTE
 KDAAVVVRQMLKVAEECHLHGLVHRDMKMPENFLFKSTKEDSPLKATDFGLSDFIKPGKRFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGR
 PFWDKTEDGIFKEVLNRKPDFRRKPWPTISNAAKDFMKLLVKDPRARYTAAQALSHPWVREGGEALEIPIDISVLNNMRQFVKYSRLKQFALRALASTL
 NEGELSDLKQDFAIDVDKNGSISLEEMRQALAKDQPKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSKQWQRSQAFAFEKFDLDKDG
 YITPDELRMHTGLRGSIDPLLEEADIDKDGKISLPEFRLLRTASMSRTVMSPSHRHRKI*
 >Glyma.02G048300 Org_Gmax peptide: Glyma.02G048300.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT
 PROTEIN KINASE 16-RELATED (PAC:30506592)
 MGACFSATKVSGSNGNVNKKRRGTTKPKKSETAKANQRHKAASSRHVPCGKRTDFGYKKDFNQRYSLGKLLGHGQFGYTYVIGIDKANGDRVAVKRL
 EKSKMVLPIAVEDVKREVILKALTGHEENVVQFYNAFEDDSYVYIVMELCEGGELLDRILAKKDGRYTEKDSAVVVRQMLKVAEECHLHGLVHRDMKMPEN
 FLFKSIKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRKSGPQSDVWSIGVITYILLCGRPFWDKTEDGIFKEVLRRKPDFRRKPWPTISN
 AAKDFLKRLLVKDPRARLTAAQGLSHPWVREGGEALEIPIDISVLNNMRQFVKYSRMKQFALRTLASTLNEEELADIKDQDFAIDVDKNGSISLEEMRQA
 LAKDLPWKLKESRVLEILQAIDSNTDGLVDFREFVAATLHVHQLEEDSDKWQQLSQAAFEKFDIDKDGITTEELRMHTCLRGSVDPLLEEADIDKDGKI
 SLPEFRLLRTASMSKSNVSSPSVHRRRF*
 >Glyma.11G077300 Org_Gmax peptide: Glyma.11G077300.1.p (1 of 1) PF13202//PF13499//PF14531 - EF hand
 (EF-hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:30528853)
 MGICFSATKVSGSSSNNAAASNRNRKGLAAPAPAPPAQPELEPVTGKQKQPSQAQRRQVPEDSQKNPRSKDKAGARRQGHVPCGKRTDFGYEKDFENR
 FSLGKLLGHGQFGYTYVIGIDKNGDRVAVKRLKSKMVLPIAVEDVKREVILKELTGHEENVVQFHNAFDES YVYIVMELCEGGELLDRILAKKDSRYT
 EKDAAVVVRQMLKVAEECHLHGLVHRDMKMPENFLFKSTKEDSPLKATDFGLSDFIKPGKRFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGR
 RPFWDKTEDGIFKEVLNRKPDFRRKPWPTISNAAKDFVKLLVKDPRARYTAAQALSHPWVREGGEALEIPIDISVLNNMRQFVKYSRLKQFALRALAST
 LNEGELSDLKQDFAIDVDKNGSISLEEMRQALAKDQPKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSKQWQRSQAFAFEKFDLDKD
 GFITPDELRMHTGLRGSIDPLLEEADIDKDGKISLPEFRLLRTASMSRPI MSPSHRHRKI*
 >Glyma.16G128600 Org_Gmax peptide: Glyma.16G128600.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT
 PROTEIN KINASE 16-RELATED (PAC:30560415)
 MGTCSATKVSGSHGNAVTVNKNRGAAPKPKSETATANPLRHKASSRHVPCGKRTDFGYEKDFDQRYSLGKLLGHGQFGYTYVIGIDKANGDRVAVKRLK
 SKMVLPIAVEDVKREVILKALTGHEENVVQFYNAFEDGSYVYIVMELCEGGELLDRILAKKDSRYTERDAAVVVRQMLKVAEECHLHGLVHRDMKMPENFL
 FKSTKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRKSGPQSDVWSIGVITYILLCGRPFWDKTEDGIFKEVLRRKPDFRRKPWPTISNAA
 KDFVKLLVKDPRARLTAAQALSHPWVREGGEALEIPIDISVLNNMRQFVKYSRKFQFALRALASTLNEEELADIKDQDFAIDVDKNGSISLEEMRQALA
 KDLPWKLKESRVLEILQAIDNNTDGLVDFREFVAATLHVHQLEEDSDKWQQLSQAAFEKFDLDKDGITPEELRMHTCLRGSVDPLLEEADIDKDGKISL
 PEFRLLRTASMGSQLNVSSPSVHRRQR*
 >Gorai.003G009500 Org_Graimondii peptide: Gorai.003G009500.1 (1 of 3) PTHR24349:SF87 - CALCIUM-
 DEPENDENT PROTEIN KINASE 16-RELATED (PAC:26798333)
 MGACLSATKVSGSSGNTTAHHRKTATNAEKQSQKPNQVRCQPLKNKQKPEKQSGIIPWGKRTDFGYDKDFDQRYTIGKLLGHGQFGYTYVAIDKVN
 GDRVAVKKIDKNKMILPIAVEDVKREVILKALKGHEENVVQFYNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAEECHLHGL
 VHRDMKMPENFLFKSTRPDSPLKATDFGLSDFIKPGKRFDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRPFWDKTEDGIFKEVLKKNKPDFR
 RKPWPTISDDAKDFLKMVLKDPARLTAAQALSHQWVREGGNASDIPVDISILSNLRQFVKYSRLKQFALRALASTLNEEEIADLRDQDFAIDVDKSGS
 ISLEEMRQALAKDLPWKLKDSRVLEILQAIDSNTDGLVDFTEFVAALHVNQMEEHDCDKWQMLQAFAFEKFDVDRDGYITPEELRMHTGLRGSIDPLLE
 EADIDKDGKISLSEFRLLRTASMSRNVSSPSGNNRNTQKL*
 >Gorai.007G194500 Org_Graimondii peptide: Gorai.007G194500.1 (1 of 3) PTHR24349:SF87 - CALCIUM-
 DEPENDENT PROTEIN KINASE 16-RELATED (PAC:26781420)

MGACLSSTTKVIGSSSNAAAHHRKHQPSATTVTVNEKKESRKPNNQQGQRQVRSSQPLKVKGKPSSTRQTGIIPCGKRTDFGYHKDFDQRYTIGKLLGHG
QFGYTYVAIDKANGDRVAVKKIDKNKMVLPMAVEDVKREVKILEALKGHENNVQFYNAFEDDSYVYIVMELCEGGELLDRI LAKKDSRYSEKDAAVVVRQ
MLKVAACHLHGLVHRDMKPNFLFKSTKEDSLPKATDFGLSDFIRPGKRFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGKRPFWDKTEDG
IFKEVLKKKPDFRRKFPWPTISNGAKDFVKLLVVKDPRARLTAAQALSHRWVREGGNASDIPVDISVLNNLRQFVKYSRLKQFALRALASTLNEEEIADLR
DQFDAIDVDKNGSISLEEMRQALAKDLPWKMKPEPRVLEILQAIDSNTDGLVDFKEFVAAALHVNQMEEHSDSKWQMLSQAFAFEKFDVDRDGFITPEELRM
HTGLRGSIDPLLEEADIDKDGKISLSEFRLLRTASISSRNVPCSSDQRNSRKL*

>Gorai.011G098300 Org_Graimondii peptide: Gorai.011G098300.1 (1 of 1) PF13499//PF13833//PF14531 - EF-
hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) // Kinase-like (Kinase-like)
(PAC:26812417)

MGICLSSTTKVFGTSSNPSPDHHEEKQPVSPTTTTNAKKESHKPTVKHQQQQFKAKPSSSRKQGGNVPCGKRTDFGYRKDFEKRYTTGKLLGHGQFGYTYV
AIGNENGNRAVAVKKIEKMKMVLPIAVEDVKREVKILEALKGHENNVQFYNAFEDDSYVYIVMELCEGGELLDRI LAKKDSRYSEKDAAVVVRQMLKVAEE
CHLRGLVHRDMKPNFLFKSTKEDSLPKATDFGLSDFIRPGKRFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGKRPFWDKTEDGIFREVLK
NKPDFRRKFPWPTISDSAKDFVKLLVVKDPRARLTAAQALSHRWVREGGDASEIPIDISVLNMRQFVKYSRLKQFALRALASTLNEEEIADLRDQFHAID
VDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDINTDGLVDFTEFIAAALHVNQMEEHSDSEKQMRSEAAFQKFDVDRDGFITPDELRMHTGLKGS
IDPLLEEADIDRDGKISLSEFRLLRTASISVRPNPSHRTTWKL*

>GRMZM2G053868 Org_Zmays peptide: GRMZM2G053868_P01 (1 of 2) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:31049975)

MGACFSSASAAPAGAAVDERRPSKEGDKRRRAAGASPDAAAPRVVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRSGSDRVAVKRIDKAKMTRPVA
VEDVKREVKILKALKGHQNIHVHFNFAFEDDSYVYIVMELCEGGELLDRI LAKKNSRYSEKDAAVVVRQMLKVAEECHLRLVHRDMKPNFLFKSNKEDS
PLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNRNKPDRFRKPWSSISPGAKDFVKRLL
VKNPRARLTAAQALSHRWVREGGEASDIPVDISVLNMRQFVKYSRKFQFALRALASTLNEEELSCLKDQFDAIDIDKSGSISIEEMRHALAKDLPWRLLK
GPRVLEIIQAIDSNTDGLVDFKEFVAATLHIIHQMAELDSERWGIQAAAFSKFDLDGDGYITPEELRMVQHTGLKGSIEPLLEEADIDKDGKISLSEFRK
LLRTASMSNVPSRGPNNPQAL*

>GRMZM2G157068 Org_Zmays peptide: GRMZM2G157068_P01 (1 of 2) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30986103)

MGACFSSASAAPAGAAVDERRPSKEGDKRRRAAGASPDAAAPRVVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRSGSDRVAVKRIDKAKMTRPVA
VEDVKREVKILKALKGHQNIHVHFNFAFEDDSYVYIVMELCEGGELLDRI LAKKNSRYSEKDAAVVVRQMLKVAEECHLRLVHRDMKPNFLFKSNKEDS
PLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNRNKPDRFRKPWSSISPGAKDFVKRLL
VKNPRARLTAAQALSHRWVREGGEASDIPVDISVLNMRQFVKYSRKFQFALRALASTLNEEELSCLKDQFDAIDIDKSGSISIEEMRHALAKDLPWRLLK
GPRVLEIIQAIDSNTDGLVDFKEFVAATLHIIHQMAELDSERWGIQAAAFSKFDLDGDGYITPEELRMVQHTGLKGSIEPLLEEADIDKDGKISLSEFRK
LLRTASMSNVPSRGPNNPQAL*

>GRMZM2G365035 Org_Zmays peptide: GRMZM2G365035_P01 (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30965679)

MGLCSSSTAARAASDPGAAAAGDAAAAGKGRGIVACGKRTDFGYDKDFEVYSLGKLLGHGQFGYTFAAADRATERVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENNVHFNFAFEDDNYVYIVMELCEGGELLDRI LAKKDSRYSEKDAAVVVRQMLKVAEECHLHGLVHRDMKPNFLFKSKKEDSPLKATDF
GLSDFIKPGQRFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKKKPDFRRKPWSNITSSAKDFVQKLLVVKDPRAR
LTAAQALSHDWVREGGKASEIPLDISVLNMRQFVKYSRKFQFALRALASTLNSEEMSLDRDQFNAIDVDKNGTISLEELKQALAKDVPWRLLKGPVLEI
IEAIDSNTDGLVDFEEFVAATLHVHQLVEHDTWKWSLSQAADFDFDVRDGYITPDELRMHTGMKGSIDPLLEEADIDKDGKISLSEFRLLKKTASMSA
RNVQTPRGVRKS*

>GSMUA_Achr1G08900_001 Org_Macminata peptide: GSMUA_Achr1P08900_001 (1 of 1) PF13202//PF13499//PF14531
- EF hand (EF-hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:32312516)

MGACFSADAKIRGGTSSAGTRSSSRQQLQPEQKNKAPTTPQPKQKDRGSKRRSSGLVPCGRRRTDFGYAKDFDSRYSVGKLLGHGQFGYTTFVATENATGERV
AVKRIDKNKMVLPVAVEDVKREVKILQALKGHENNVNHNFAFEDDSYVYIVMELCEGGELLDRI LAKKDSHYTEKDAAVVVRQMLKVAEECHLHGLVHRD
MKPNFLFKSKKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLNRNKPDRFRKPW
PTISNAKEFVKLLVVKDPRVRLTAAQALSHRWVREGGNASEIPLDISVLNMRQFVKYSRKFQFALRALASTLDEDELADLKQFQAIIDIDKSGSISLD
EMRQALAKDIPWRLLKGPRLDILQAIDSNTDGLVDFTEFVAATLHVHQMEEHDSKWRSRCKAAFEKFDVDRDGYITPEELRMHTGLKGSIEPLLEEADI
DKDGKISLSEFRKLLRTASMSNVPSPSGVRNPQKF*

>GSMUA_Achr2G00480_001 Org_Macminata peptide: GSMUA_Achr2P00480_001 (1 of 1) KOG0198//KOG0580//KOG0659
- MEKK and related serine/threonine protein kinases // Serine/threonine protein kinase // Cdk
activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor
TFIIH/TFIIK, kinase subunit CDK7 (PAC:32304571)

MILPVAVEDVKREVKILQALKGHENNVNHNAYEDDSYVYIVMELCEGGELLDRI LAKKDSRYTEKDAAVVVRQMLKVAEECHLHGLVHRDMKPNFLFK
STEENSPLKATDFGLSDFIEPGKFHAIIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFREVLNRNKPDRFRKPWPSISNSAKD
FVKLLVVKDPRVRLTAAQALSHRWVREGGNALEIPLDISVLNMRQFVKYSRVRLTADSKLGIDLFRRTSLELYRGSSLSQVAAQRLQKRFIYCL*

>GSMUA_Achr5G18720_001 Org_Macminata peptide: GSMUA_Achr5P18720_001 (1 of 1) PF13499//PF14531 - EF-
hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:32326160)

MGACLSSTQVSSRNKATAVAAAAAEGKHGQPGAKNEQQKQKPRARNCGKLKAVARLSCGRRTNFGYERDFERRYSIGKLLGHGQFGYTTFVATDKANG
DRVAVKRIDKNKMILPVAVEDVKREVKILKALKGHENNVHFNFAFEDDSYVYIVMELCEGGELLDRI LAKKESRYTEKDAAVVVRQMLKVAEECHLHGLV
HRDMKPNFLFKSTKEDCPLKATDFGLSDFIRPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIYKEVLRTPEDFRR
KPWPNISAKDFVKLLVVKDPRARLTAAQALSHRWVREGGDALEIPLDISVLNMRQFVKYSRKFQFALRALASTLNEEELADLKQFHAIDVDKSGAI
SLEEMRHALAKDLPWKLEKPCVSEIVQAMDSNTDGFIDFEEFVAATLHVHQLVEHDNGKWSRLTAAAFDFDKVDKNGYITPDELRMHTGLKGSIDPLLEE
VDIDKDGKISLSEFRLLKKTASMKPRSVPRQSTTRDRNTCFFTKQVFVLFLLFQALIIISQSLSHN*

>GSMUA_Achr8G19290_001 Org_Macminata peptide: GSMUA_Achr8P19290_001 (1 of 4) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:32309843)

MGACISSADPNSDTAAAAAEEQQGRPEANRQQQQQRVLDGGKEKAAAGGLVPCGRRTNFGYDRDFASKYTIGKLLGHGQFGYTTFVATDKAHGDRVAVK

RIDKNKMILPIAVEDVKREVMILKALKGHENVVHFYNAYEDDSFVYIAMELCEGGELLDRLAKKNSRYTEKDAAVVVRQMLKVAAECHLHGLVHRDMKP
ENFLFKSTKEDSPLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRTSGPESDVWSIGVITYILLCGKRPFWNRTENGIFKEVLKTEPDFQRKPWPSI
SNSAKDFVKKLLVKDPRVRLTAAQALSHSWVREGGDALEIPLDISVLSNMQRQFVKYSRKFQFALRALATTLNEEELADLKDQFDAIDVDKSGAISLEEMR
HALAKDLPWKSKEHSVLEILQAMDSNTDGLIDFEEFVAAALHMHQLVELDSEKWSLSQAADFDFVDRDGYITPEELRMHTGLKGSIDPLLEEVDIDKD
GKISLDEFRRLLKTASMGSRNVNPNRSTGH*

>GSVIVG01018778001 Org_Vvinifera peptide: GSVIVT01018778001 (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:17828604)

MGACLSATKVRSSNSNTTANAAATKNTRPRGSSKTSNKNQKKPQEGDRNRSNQHRNPQPQKVDRANGRRGTGIIPCGKRTDFGYAKDFDARYTIGKL
LGHGQFGYTYVATDKANGDRVAVKRIEKNKMILPIAVEDVKREVKILEALTGHENVVQFHNAFEDDSYVYIVMELCEGGELLDRLAKKDSRYSEKDAAK
VVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYILLCGKRPFWDK
TEDGIFKEVLKKNKPDFRRKPWPTISNGAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLSNMREFVKYSHLKFALRALASTLDDEEL
ADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSKDKWQRQSQAADFDFVDRDGYITPE
ELKLHTGLRGSIDPLLEEADIDKGRISLAEFRLLRTASISSRQVPSSSGFRNPRKI*

>Kaladp0028s0017 Org_Kfedschenko peptide: Kaladp0028s0017.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:35759078)

MGVCFSATKISGSSSSNGNRKSRRAAQQQPASTAPGRHKDKPRGDAEGRGRRDVGRMVPCGKRTDFGYLKNFDERYKIGKLLGHGQFGYTYVATDKSNGDR
VAVKRIDKSKMVLPIAVEDVKREVKILQALTGHENVVQFYNAFEDDNYVYIAMELCEGGELLDRLAKKDSRYTEKDAAIIVRQMLKVAAQCHLHGLVHR
DMKPENFLFKSTKEDSPLKATDFGLSDFIRPGKFFHDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNRKPDFRRKP
WANISNSAKDFVKKLLVKDPRARLTAAQALSHSWVREGGSASEIPVDISVLNNMRQFVKYSRMKQIALRALASTLDEEEIADLRDQFDAIDVDGNGSISL
EEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHNSDKWQQRQSQAADFDFVDRDGYITPEELKLHTGLKGSIDPLLEAD
IDKDGKISLPEFRLLRTASISSRAITSPRRVPSRNK*

>Kalax.0174s0042 Org_Klaxiflora peptide: Kalax.0174s0042.1.p (1 of 6) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:32567177)

MGVCFSATKISGSSSSNGNRKSRRAAQQQPASTAPGRHKDKPRGDAEGRGRRDVGRMVPCGKRTDFGYLKNFDERYKIGKLLGHGQFGYTYVATDKSNGDR
VAVKRIDKSKMVLPIAVEDVKREVKILQALTGHENVVQFYNAFEDDNYVYIAMELCEGGELLDRLAKKDSRYTEKDAAIIVRQMLKVAAQCHLHGLVHR
DMKPENFLFKSTKEDSPLKATDFGLSDFIRPGKFFHDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNRKPDFRRKP
WANISNSAKDFVKKLLVKDPRARLTAAQALSHSWVREGGSASEIPVDISVLNNMRQFVKYSRMKQIALRALASTLDEEEIADLRDQFDAIDVDGNGSISL
EEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHNSDKWQQRQSQAADFDFVDRDGYITPEELKLHTGLKGSIDPLLEAD
IDKDGKISLPEFRLLRTASISSRAITSPRRVPSRNK*

>LOC_Os02g03410 Org_Osativa peptide: LOC_Os02g03410.1 CAMK_CAMK_like.12 - CAMK includes
calcium/calmodulin depeudent protein kinases, expressed (PAC:33137776)

MGACFSSHTATAAADGGSGKRQQRKGDHKGKLPDGGGGEKEKEAARVEFGYERDFEGRYQVGRLLGHGQFGYTFAATDRASGDRVAVKRIDKAKMVRPVA
VEDVKREVKILKELKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRLAKKNSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDS
PLKATDFGLSDFIKPGKKFFHDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNRKPDFRRKPWPGISSGAKDFVKKLL
VKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMQRQFVKYSRKFQFALRALASTLKEEELADLKDQFDAIDVDKSGSISIEEMRHALAKDLPWRLK
GPRVLEIIQAIDSNTDGLVDFEEFVAATLHIIHQMAELDSEWRGLRCQAAFSKFDLDGDDGYITPDELRMVQHTGLKGSIEPLLEEADIDKGRISLSEFRK
LLRTASMSNLPSPRGPPNPQPL*

>LOC_Os07g22710 Org_Osativa peptide: LOC_Os07g22710.1 CAMK_CAMK_like.32 - CAMK includes
calcium/calmodulin depeudent protein kinases, expressed (PAC:33114003)

MGLCSSSSARRDAGTPGGNGAGNKDNAGRKIVACGKRTDFGYDKDFEARYALGKLLGHGQFGYTFAAVDRSSERVAVKRIDKNKMVLPIAVEDVKRE
VKILKALDGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRLAKKDSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSSKATDF
GLSDFIRPGKHFRDVGSAAYYVAPEVLRRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNRKPDFRRKPWPNITPCAKDFVQKLLVKDPRAR
LTAAQALSHWVREGGQASDIPLDISVLNNMRQFVKYSRKFQFALRALASTLNAEELSDLRDQFNDAIDVDKNGTISLEELKQALAKDVPWRLKGPRVLEI
VEAIDSNTDGLVDFEEFVAATLHVHQLEHDETEKWSLSQAADFDFVDRDGYITSDELRMQTGLKGSIDPLLEEADIDRDGKISLDEFRRLLKTASMS
RNVQTPRSVHRS*

>Lus10028459.g Org_Lusitatissimum peptide: Lus10028459 (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:23166166)

MGSRRVSGTVFPGKRTDFGYDKDFNKRYTIGKLLGHGQFGYTYVATDKNGDRVAVKRIDKGMILPIAVEDVKREVKILRQLAGHENVVHFVNAFEDDS
YVFIIVMELCEGGELLDRLAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSALKATDFGLSDYIKPGKKFFHDIVGSAYYVAP
EVLQRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNRKPDFRRKPWPTISHSAKDFIRKLLVKDPRARLTAAQALSHPWVREGGDASEIPID
ISVLKNMRQFVKYSRLKQFALRALASTINEEELADLKDQFDAIDIDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFEFAAALHV
HQLQEHNSKEWEERSQAADFDFIDGDDGYITPDELRMHTGLRGSIDPLLEEADIDKDGKISLSEFRLLRTASMGSRTPSPSGHRNSRRL*

>Manes.01G145800 Org_Mesculenta peptide: Manes.01G145800.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:323358707)

MGVCFSTIKVSGSSSSNNNTASAGHHYHRKERTDTTQSTTNKQSSDQKNNKDDNNSTNNGTPESRQLQTKPKQQQQQQQQQHKVKEKQTSRRQSGV
IPCGKRTDFGYAKDFDRRYMTGKLLGHGQFGYTYVATDKASGDRVAVKRIEKNKMVLPIAVEDVKREVKILRELAGHENVVQFYDAFEDDSYVYIVMELC
EGGELLDRLAKKDSRYTEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKVDSPKATDFGLSDFIKPGKKFFHDIVGSAYYVAPEVLRRKSGP
ESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNRKPDFRRKPWPSISNSAKDFVKKLLVKDPRVRLTAAQALSHPWVREGGDASEIPIDISVLSNMQR
FVKYSRLKQFALRALAGTLDDGELADLRDQFDAIDVDNRNGSISLEEMRQALAKDLPWKLKDSRVLEILQAIDSNTDGLVDFSEFVAALHVVHQLEEHNS
KWHMRSQSAFEKFDLKDGFITPEELRMHTGLKGSIDPLLEEADIDKDGKISLSEFRLLRTASISSQNLPSPSAHRNSWKI*

>Manes.02G104800 Org_Mesculenta peptide: Manes.02G104800.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:32333786)

MGACFSTIKISGSSNSNSTGAAAGHHYHRKEITNNPQSTTANRQSSNQKNDNNNNETRKSRLQQTQQQQQHHKIKEKQTSRRQSGMIPCGKRTDFGYAKD
FDRRVVIGKLLGHGQFGYTYVATDKANGDRVAVKRIDKNKMVLPIAVEDVKREVKILQELAGHENVVQFYDAFEDDSYVYIVMELCEGGELLDRLAKKD
SRYTEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLKSSKENSPLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYIL

LCGRFPFWDKTEDGIFKEVLRNKPDFRRKPWPSISNSAKDFVKKLLVKDPRVRLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKYSRLKQFALRALSTLDDDAELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKMKDSRVLEILQAIDSNTDGLVDFSEFVAAALHVVHQLEEHNSEKWHLSRQTAFKFDLKDGYITPEELRMHTGLKGSIDPLLEEADIDKDGKISLSEFRLLRTASISSRTAPSPSARRNSRMI*

>Mapoly0098s0040 Org_Mpolymorpha peptide: Mapoly0098s0040.1.p (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:33021029)

MGGCLSAHPHGRARAKAQVAGQDASAENSANASAPPQQPKKVTPRKSPKNNTPKKKTTERKRSRITVNHKDNSTQASIPLGKRTNFGYEREFKTKYKLGKLLGHGQFGYTYAAVEISTGLKVAVKTIKKQMLLPISVDDVKREVEILGTLSGHENNVVQFHAAFEEDDLVYIVMELCEGGELLDRIILSKKDSRYSEKDAKIVRQMLKVAARACHLNGVVRHDMKPENFLFKSQKEDSPLKATDFGLSDYIKIGKRFQDVVGSAYYVAPEVLRRKSGPESDVWSIGVITYIILCGRFPFWAKEEQGIFNEVLKKKPDFKEKPWPSISASAKDFVKKLLVKDPRARLTAAQALSHPWAREGGDASDIPLDISVLNNMRQFVKYSRLKQFALRALASTLDGEEIADLRDQFDAIDMDKNGTITLLEEIKQALAKDTPWSVKETRVVEILKAMDSNRDGMVDFDEFVAATLHVHQLEESDTDKWQRRSRAAFEKFDIDKDGFIITAEELKVVQLQATGTGKGNMETLLEEADTDGGRISLPEFQRLLRQASLGSRNTNGSGSLQHFHGRK*

>Medtr5g022030 Org_Mtruncatula peptide: Medtr5g022030.1 (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:31091524)

MGLCFSSSTKVVSGSNSNTTNNDRNRKNQSTTTDTTVTVTATTAAQKQTAQRKKGSGNETAQKKNHHQHHLRLEKGTGSKHVPCKGKRTDFGYEKDFDKRFSLGKLLGHGQFGYTYVGVKDSNGDRVAVKRIEAKMVLPIAVEDVKREVKILKELTGHENNVVQFYNAFDDDSYVYIVMELCEGGELLDRIILNKKDSRYTEKDAAVVVRQMLKVAACHLHGLVHRDMKPENFLFKSKNKEDSALKATDFGLSDFIKPGKRFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYIILCGRFPFWDKTEDGIFKEVLRNKPDFRRKPWPTISNAAKDFVKKLLVKDPRARLTAAQALSHPWVREGGEASEIPIDISVLNNMRQFVKYSRLKQFALRALASTLNEGLSDLDKQDFAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHSDSKWQQRSAAFEKFDIDKDGFIITPEELRMHTGMGRGSIIDPLLEEADIDKDGKISLPEFRLLRTASIGSRNVTSPTLRHRI*

>Migut.H01152 Org_Mguttatus peptide: Migut.H01152.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:28953593)

MGICFSTKKGSA PSTTTTGNVHQNNRRSSATSKPSSFKTTFTASSKKQEGSQNNNLKTRDNHKNQQQKRSHKIKIKNSSKSTSGAIPCGKRTNFGYDKDFVKKYINIGKLLGHGQFGYTYVAIDKSNNGDRVAVKRIEKNMVLPIAVEDVKREVKILKALAGHENNVHFYNAFEDDSFVYIVMELCEGGELLDRIILSKKDSRYTEKDAAVVVRQMLKVAACHLHGLVHRDMKPENFLFKSPKEDSHLAKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLRRKSGAESDVWSIGVITYIILCGRFPFWDKTEDGIFKEVLRNKPDFRRKPWPGISNAAKDFVKNLLVKDPRARLTAAQALSHPWVREGGEALEIPIDISVLNNMRQFVKYSRKFQFALRALASTIDEELADLRDQFDAIDVDKNGSISLDEMRQALEKDLFPWKMKDSRVVEILQAIDSNTDGLVDFSEFVAATLHVHQLEEHNSEKWWQQRSLAFAQKFDVDRDGFITPHELKMHGTGLKGSIDPLLEEADIDKDGKISLHEFRLLRTASMSRGGVST*

>Migut.L00702 Org_Mguttatus peptide: Migut.L00702.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:28935439)

MGFKWEGGGVINAHWPYGNWNNNSRQQQHRHTQQNSKTSKSRPSSGGAIPCGKRTDFGYDKDFNSRYTIGKLLGHGQFGYTYVAVDKFNDRVAVKRIEKNMVLPIAVEDVKREVRIKALAGHENNVVQFYNAFEDDSYVYIAMELCEGGELLDRIILSKKDSRYTEKDAAVVVRQMLKVAACHLHGLVHRDMKPENFLFKSPKDDSSSLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYIILCGRFPFWDKTEDGIFKEVLRNKPDFRRKPWPGISNAAKDFVKKILVKDPRARLTAAQALSHPWVREGGEASDIPLDISVLNNMRQFVKYSRKFQFALRALASTLDDEELADIRDQFDAIDVDKNGSISLEEMRQALEKDIPWKIKDSRVHEILQAIDSNTDGLVDFPEFVAATLHVHQLEHSSSEKWHQRSAAFEKFDIDKDGFIITPDELKMTCLKGSIEPLLEEADIDKDGKISLSEFRLLRTASLSSRGGVGT*

>gene14609-v1.0-hybrid Org_Fvesca peptide: mrna14609.1-v1.0-hybrid (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:27244231)

MGGCLTTAKVTGSNNTNNNPATTVTAVVNRKQTTRPQPAQTNNHHPNEAQKKHKKHKSQSSRQKTGVI PCGKRTDFGYDKNFDRRYTIGKLLGHGQFGYTYVATDRSNGDRVAVKRIKDNKMILPIAVEDVKREVEILQALAGHENNVVQFFNACEDDTYVYIVMELCEGGELLDRIILEKKDSRYTEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSKALDSPLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVISYIILCGRFPFWDKTEDGIFKEVLRNKPDFRRKPWPGISNAAGKDFVKKILVKDPRARLTAAQALSHPWVREGGEASDIPLDISVLNNMRQFVKYSRKFQFALRALASTLDDEELADIRDQFDAIDVDKNGSISLEEMRQALEKDIPWKIKDSRVHEILQAIDSNTDGLVDFPEFVAATLHVHQLEHSSSEKWHQRSAAFEKFDIDKDGFIITPDELKMTCLKGSIEPLLEEADIDKDGKISLSEFRLLRTASLSSRGGVGT*

>orangel.1g008127m.g Org_Csinensis peptide: orangel.1g008127m (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:18099036)

MGICLSTTKVSGSNSGNNNNANHHNRNANKEEAKRRHNNHARNDTTHKHQHQHQAERAKNYQQLKTKQHKTNSRRQTGVIPCGKRTDFGYDKDFDRRYTIGKLLGHGQFGYTYVATDKANGDRVAVKKIEKNKMILPIAVEDVKREVKILQALAGHENNVVQFYNAFEDDNYVYIAMELCEGGELLDRIILAKMISTTLTSAWFLAIRKDSRYTEKDAAVVVRQMLRVAAECHLHGLVHRDMKPENFLFKSAKEDSSSLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYIILCGRFPFWDKTEDGIFKEVLRNKPDFRRKPWPSISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKYSRLKQFALRALASTLDDEELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDCNTDGLVDFSEFVAATLHVHQLEEHDSKWKQQLSRAAFEKFDIDRDGYITPDELRMHTGLKGSIDPLLEADIDKDGKISLSEFRLLRTASMSRQKADPSGQRNSRQV*

>orangel.1g008127m.g Org_Csinensis peptide: orangel.1g008127m (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:18099036)

MGICLSTTKVSGSNSGNNNNANHHNRNANKEEAKRRHNNHARNDTTHKHQHQHQAERAKNYQQLKTKQHKTNSRRQTGVIPCGKRTDFGYDKDFDRRYTIGKLLGHGQFGYTYVATDKANGDRVAVKKIEKNKMILPIAVEDVKREVKILQALAGHENNVVQFYNAFEDDNYVYIAMELCEGGELLDRIILAKMISTTLTSAWFLAIRKDSRYTEKDAAVVVRQMLRVAAECHLHGLVHRDMKPENFLFKSAKEDSSSLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYIILCGRFPFWDKTEDGIFKEVLRNKPDFRRKPWPSISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKYSRLKQFALRALASTLDDEELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDCNTDGLVDFSEFVAATLHVHQLEEHDSKWKQQLSRAAFEKFDIDRDGYITPDELRMHTGLKGSIDPLLEADIDKDGKISLSEFRLLRTASISSRNVPPSPSGHRNPRKL*

>Oropetium_20150105_14239 Org_Othomaeum peptide: Oropetium_20150105_14239A (1 of 1)

PTHR24349//PTHR24349:SF137 - SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:36005025)

MGVCFSAAAAAARPSKEEKRKRRGAASPDGQKTVRVEFGYDRDFEARYEVGRLLGHGQFGYTFATADRDSGDRVAVKRIKAKMDRPVAVEDVKREVKILKALQGHENIVSFYNAFEDDSYVYIVMELCEGGELLDRIILAKKNSRYSEKDAAVVVRQMLKVAACHLRLGLVHRDMKPEVLNRNKPDFRRKPWPSISPGAKDFIKRLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLNNMRQFVKYSRKFQFALRALASTLNEELADLRDQFDAIDVDKNGSISIEEMRHIDSDGLVDFREFVAATLHIHQMAELDSERWGLRCAAFRKLDDGDGYITPEELRMHTGLKGSIEPLLEEADIDKDGKISLSEFRLLRTASMSNIPSPRGV PNPQALSNSGAAIGQEHGL*

>Oropetium_20150105_26612 Org_Othomaeum peptide: Oropetium_20150105_26612A (1 of 1)

PTHR24349//PTHR24349:SF123 - SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:36012113)

MGLCTSSTASADHTDDGAAGRKSAGGGRGIVACGKRTDFGYDKDFEARYLLGKLLGHVVKREVKILKALRGHENNVHFYNAFEDDNYVYIVMELCEGGELLDRIILAKKDSRYSEKDAAVVVRQMLKVAACHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGFEKQARFSSETLAKHYAKCKRFCTKVT SQGSPCKTNCCTGVMGEGKASEIPIDISVLNNMRQFVKYSRKFQFALRALASTLNAEELSDLRDQFDAIDVDKNGTISLEELRQIDSNTDGLVDFEEFVAATLHVHQLEHDETEKWRSLSQAAFDFKFDVDGDGYITSDLELRMHTGLKGSIDPLLEEADVDKDGKISLYEFRLLRTASMSARIVQTTPRGARINSELIGVKH*

>Pahal.A00155 Org_Phallii peptide: Pahal.A00155.1 (1 of 1) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32529447)
MGACFSSASAAPAGAERRPSKEDRKRRRGASPEGAAKAAAAAAPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMT
RPVAVEDVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSN
KEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRPFWDKTEDGIFKEVLNRNPKDFRRKPWSSISPGAKDFV
KRLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRKFQFALRALASTLNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLP
WRLKGRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCAAFSKFDLDGDGYITPEELRMHTGLKGSIEPLLEEADIDKDGRIISLSEF
RKLLRTASMSNVPSRGPFPNPQAL*

>Pahal.B01532 Org_Phallii peptide: Pahal.B01532.1 (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32489711)
MGLCSSCTAAADTTTRPGAGAGAAAGKREKEKGRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTFAAVDRASGDRVAVKRIDKNKMVLPVAVEDV
KREVKILKALQGHENNVHFYNAFEDDNFVYIVMELCEGGELLDRILAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKA
TDFGLSDFIRPGKQFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRPFWDKTEDGIFKEVLNRNPKDFRRKPWPNITPAAKDFVQKLLVKDP
RARLTAAQALSHDWVREGGKASEIPLDISVLHNMQRQFVKYSRKFQFALRALASTLNSEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGRV
LEIIEAIDSNTDGLVDFEEFVAATLHVHQLVEHDTQKWKSLSQAAFDFKFDVGDGYITSDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTAS
MSARTVQTPRGVRMS*

>Pavir.Aa03445 Org_Pvirgatum peptide: Pavir.Aa03445.1.p (1 of 3) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30250634)
MGACFSSASAAPAGAERRPSKEGEKRRRGASPEGAAKAAAAAPVRAEFYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMTRPVAV
EDVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVIVRQMLKVAAECHLRGLVHRDMKPENFLKSNKEDSP
LKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRPFWDKTEDGIFKEAIIYLARLSFSDFCRQNTTNTVNPPLV
NLKSGDNLWPAQNAWTLLVLRNPKDFRRKPWSSISPGAKDFVLRLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRKFQFALRA
LASTLNEEELADLKDQFDAIDIDKNGSISIEEMRNALAKDLPWRLKGRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCAAFSKFD
LDGDGYITPEELRMQHTGLKGSIEPLLEEADIDKDGRIISLSEFRKLLRTASMSNVPSRGPFPNPQAL*

>Pavir.Ab00120 Org_Pvirgatum peptide: Pavir.Ab00120.1.p (1 of 3) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30234536)
MGACFSSASAAPAGAERRPSKEDDKGRRGASPEGAAKAAAAAPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMTRPV
AVEDVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVTAACHLRGLVHRDMKPENFLFKSNKED
SPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGLESVDWSIGVITYILLCGRPFWDKTEDGIFKEVLNRNPKDFRRKPWSSISPGAKDFVLR
LVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRKFQFALRALASTLNEEELADLKDQFDAIDIDKNGSISIEEMRNALAKDLPWRL
KGRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCAAFSKFDLDGDGYITPEELRMQHTGLKGSIEPLLEEADINKDGRIISLSEFR
KLLRTASMSNVPSRGPFPNPQAL*

>Pavir.Ba02369 Org_Pvirgatum peptide: Pavir.Ba02369.1.p (1 of 3) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30291111)
MGLCSSSTAAADTPRRPGAAAGKREKRDGKRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTFAAVDRASGDRVAVKRIDKNKMVLPVAVEDVKRE
KILKALQGHENNVHFYNAFEDDNFVYIVMELCEGGELLDRILAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFG
LSDFIRPGKQFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRPFWDKTEDGIFKEVLNRNPKDFRRKPWPNITPAAKDFVQKLLVKDPARL
TAAQALSHDWVREGGKASEIPLDISVLHNMQRQFVKYSRKFQFALRALASTLNSEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGRVLEII
EAIDSNTDGLVDFEEFVAATLHVHQLVEHDTKWKSLSQAAFDFKFDVGDGYITSDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMSAR
TVQTPRGVRMS*

>PGSC0003DMG400003564 Org_Stuberosum peptide: PGSC0003DMP400006361 Calcium-dependent protein kinase
CPK4 (PAC:37426490)
MGNICFSSSKVSGSNSNTPTSTNTATVNGHRNRRSSAKPVSATTNTSRKQEGSHYNRQKGDNGGVKQQTQKNVKNHNTRRQSGVPCGKRTDFGYDKDFDK
KFTIGKLLGHGQFGYTYVATDKSNGNRVAVKRIEKKKMVPIAVEDVKREVKILKALAGHENNVDFYNAFEDDNVYIVMELCEGGELLDRILAKKDSRY
TEKDAAIIVGQMLKVAAQCHLHGLVHRDMKPENFLFKSPKEDSPLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITFILLCG
RRPFWDKTEDGIFKEVLNRNPKDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLSNMRQFVKYSRLKQFALRALAS
TLDEEELADVRDQFSAIDVDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFPEFVAATLHVHQLLEEHNLLKWQQRSTAFEKFDVDR
DGFITPEELRMHTGLKGSIDPLLEEADIDKDGKISLSEFRLLRTASISSRMVTSPTVRGSRKI*

>PGSC0003DMG400022562 Org_Stuberosum peptide: PGSC0003DMP400039123 Calcium-dependent protein kinase
(PAC:37463999)
MGSCFSSSKVSGSNSNTPTSTNTATNTNTVNVHPNRRETSKAPSTTVNSNRNQEGSNYNRGKGNINQKNQKQPRNSQQNVKPSRRQGGVPCGKRTD
FGYDKDFEKRYTIGKLLGHGQFGYTYVATDKSSGDRVAVKRIEKNKMVPIAVEDVKREVKILKALGGHENNVQFYNSFEDDNVYIVMELCEGGELLDR
ILSKKDSRYTEKDAAIIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRRSGPESDVWSIG
VITYILLCGRPFWDKTEDGIFKEVLNRNPKDFRRKPWPNISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLSNMRQFVRYSHLK
QFALRALASTLDEEELADLRDQFSAIDVDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFPEFVAATLHVHQLLEEHNLLKWQQRSA
AFEKFDVDRDGFITPEELKMHTGLRGSIDPLLEEADIDKDGKISISEFRLLRTASMSSPTVRDSRGM*

>Phvul.002G108700 Org_Pvularis peptide: Phvul.002G108700.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:37176995)
MGICFSATKVSNSNAGASNRNRKWSAPMTAQVTLQPLTAQKQSSSHKQSSSHKQSSSHGQRRRVPEDSRKNPRAKEKTSGRQGGNLPCKGRTDFGY
EKDFDKKFSGLKLLGHGQFGYTYVGIDKANGDRVAVKRLEKNKMVLPPIAVEDVKREVKILKELTGHENNVQFYNAFEDDSYVYIVMELCEGGELLDRILA
KKDSRYTEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTREDSPLKATDFGLSDFIKPGKRFDPDIVGSAYYVAPEVLKRRSGPESDVWSIGVIT
YILLCGRPFWDKTEDGIFKEVLNRNPKDFRRKPWPTISNSAKDFVKKLLVKDPRARYTAAQALSHPWVKEGGEALEIPIDISVLNNMRQFVRYSRKQFA
LRALASTLNEEELSDLKDQFDAIDVDKNGSISLEEMRLALAQDLPWKLLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLLEEHSFKWQQRSA
KFDLDKDGYYITPEELRMHTGLRGSIDPLLEEADIDKDGKISLSEFRLLRTASIGSRNVLSPNQLRKRM*

>Phvul.003G261700 Org_Pvularis peptide: Phvul.003G261700.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-

DEPENDENT PROTEIN KINASE 16-RELATED (PAC:37145240)
 MGICYSATKVSFNGSPVTVKKNRRAAPEKRTPTANTERHKASSRHVPCGKRTDFGYEKHFDTTRYTLGKLLGHGQFGYTYVVIDKANGDRVAVKREK
 SKMVQPIAEVDKREVKILKALTGHENVVQFYDAFEDDSYVYIVMELCEGELLDRILAKKESRYTEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFL
 LKSTKEDSPLKATDFGLSDFIKPGKFKHDIVGSAYYVAPEVLKRKSGPQSDVWSIGVITYILLSGRRPFWDKTEGIFKEVLRRKPDFHRKPWTTISNAA
 IDFKVKKLLVKDPRARLTAAQALSHPWVREGGEASEIPIDISVLSNMRQFVKYSRLKQFALRALASTLNEEELADLKDQFDAIDVDKNGSISLEEMRQALA
 KDLPLWKLKEPRVLEILQAIDSNTDGLVDFSEFVAATLHVHQLEDDSDKWQLRSQAAFEKFDIDKGYISPEELKMHTGLRGSIDPLLEEADIDKDGKISL
 SEFRLLRTASMSSQKVSSPTVYKRI*
 >Potri.005G113600 Org_Ptrichocarpa peptide: Potri.005G113600.1 (1 of 2) PTHR24349:SF87 - CALCIUM-
 DEPENDENT PROTEIN KINASE 16-RELATED (PAC:27031190)
 MGACFSTIKVSGSNSNNVHSRKEPTKPTKTTKATTATRKKEVHVHHQNNKNVNNEAEKKLVKEKQSSKAIPCGKRTDFGYDKDFDMRYTIGKLLG
 HGQFGYTYVAIDKANGDRVAVKRIEKNKMVLPPIAEDVKREVILRELTHGENVVQFYNALEDDSYVYIVMELCEGELLDRILSKKDSRYTEKDAAVV
 RQMLKVAAEACHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGKFKQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTE
 DGIFKEVLKNKPDFRRKPWPWTISTSADKDFVNKLLVKDPRARLTAAQALSHPWVREGGVASEIPIDISVLSNMRQFVKYSRLKQFALRALASTIDEEELAD
 LKDQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEIVQAIDSNTDGLVDFTEFVAAALHVHQLEHNSEKWQLRSQAAFEKFDIDRDGYITPEEL
 RMHTGLRGSIDPLLEEADIDKDGKISLSEFRLLRTASMSSRNVPSPSGHRKSHKI*
 >Potri.007G057600 Org_Ptrichocarpa peptide: Potri.007G057600.1 calcium-dependent protein kinase family
 protein; CDPK family protein; calcium-dependent protein kinase family protein; CDPK family protein; [ortholog of At4g36070,At2g17890,At5g66210,] (PAC:27015393)
 MGACFSTINISGSNSNNNTKANHNKREPTKPTQTRTKAATRKKEVHVHHHQNNKNVNNEAEKKLVKEKQSSKAIPCGKRTDFGYDKDFDIRYTIGKLL
 GHGQFGYTYVATDKNGDRVAVKRIDKNKMVLPPIAEDVKREVILRELTHGENVVQFHNAFEDDSYVYIVMELCEGELLDRILAKKDSRYTEKDAAVV
 VRQMLKVAAEACHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGKFKQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTE
 EDGIFKEVLNRKPDFRRKPWPWTISTSADKDFVQKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLSNMRQFVKYSRLKQFALRALASTIDEEELA
 DLKDQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEIVQAIDSNTDGLVDFTEFVAAALHVHQLEHNSEKWQLRSQAAFEKFDIDRDGYITPEE
 LRMHSGLRGSVDPLLEEADIDKDGRIISLSEFRLLRTASMSSQNVDPSPSGHRNSKKL*
 >Pp3c15_5120 Org_Ppatens peptide: Pp3c15_5120V3.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN
 KINASE 16-RELATED (PAC:32926634)
 MGGCCSKSSVVEQRPQAPHRTEANGKEKEAAYQNKGRDLPVKVGGDPPEKKERDSPEHKGRLDVENTQGSPPPEKKARETPDKQVGATKRPIPERKQSRIS
 AANLKDQNSHSPQLGKRTNFGYERDFKEKYSGLKLLGHGQFGYTYVATEKATGNKVAACKIEKKQMKLPISVEDVKREVILRLTSGHENVVQFYAFEDDDLV
 DDLVYIVMELCEGELLDRILAKKDSRYSEKDAKIVRQMLNVAARCHLNGVVRDMKPENFLFKSSKDDSPKATDFGLSDYIKPGKFRDVGVSAYYV
 APEVLNRKSGPESDVWSIGVITYILLCGRRPFWDKTEAGIFNEVLKKKPDFREKWPSTISASAQDFVKKLLRKDPHMLRTAAQALSHPWVKEGGDASDMP
 LDISVLSNMRFEVVKYSRLKQALRALASTLESDEIRDLRDQFDAMDVDNRNGITILEEIKHALQKDRPWAVKESRVLEILQAMDSNADGMIDDFEFVAATL
 HVHQLEQANSKQWQSRKAASFQDFVDGDFITAEELKIATGLKGSVGTILLEADSDKDGRIISLSEFQKLLHQASFGSRTNTDHNRRQT*
 >Pp3c9_4620 Org_Ppatens peptide: Pp3c9_4620V3.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN
 KINASE 16-RELATED (PAC:32913651)
 MGNCKCKSSVAAEVTRKYKAPEQWITKNPEQAQTHQKQKQNGATHTKPRSRKPPPGVVHSNRNSKKVEKLAESKQPEPWKSPPESTADRKKKPRVRAAIN
 GKDNKEMAPLGKRTNFGYGRDFKSKYTLGKLLGHGQFGYTYVAIEKSTGSRVAVKTIEKKQMTLPISVEDVKREVILRLTSGHENVVQFYAFEDDDLV
 YIVMELCEGELLDRILAKKDSRYSEKDAKIVRQMLNVAARCHLNGVVRDMKPENFLFKSTSEDSPLKATDFGLSDYIRPGNRFDVVGVSAYYVAPEV
 LKKKSGPESDVWSIGVITYILLCGRRPFWDKTEKGFIDEVLKKNPDYGEKFPWTISSAKDFVKKLLVKDPAARLTAAQALSHPWAKEGGDALDIPDLIS
 VLSNMRFEVVKYSRLKQALRALASTLDSSDIADLQDQFNAIDIDRNGKITLEEMREALQKDRPWSIQESRIVEILQAMDSNSDGLVDFDEFVAATLHVHQ
 LEETDSEKQWQSRQAASFQDFDGDGYITADELKIATGLNGSMDSILVEADIDGDKISLSEFQKLLRQASLGSRNTNEHHTLVTHNHRKC*
 >Prue.7G168400 Org_Ppersica peptide: Prue.7G168400.1.p (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
 PROTEIN KINASE 16-RELATED (PAC:32104836)
 MGGCFSTVKVSGSNSNNNTTAPTANHNKQSTASSQSTTPPVKQEQRRTRNPNEMPRKQLANKPKGKPNRRQTGVI PCGKRTDFGYDKNFKRYTIGKLL
 GHGQFGYTYVATDKANGDRVAVKRIDKNKMILPIAEDVKREVILRELTHGENVVQFYNAFEDDSYVYIVMELCEGELLDRILEKKDSRYTEKDAAVV
 VRQMLKVAAEACHLHGLVHRDMKPENFLFKSKALDSPLKATDFGLSDFIKPGKFKQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTE
 EDGIFKEVLNRKPDFRRKPWPWTISTSADKDFVKKILVKDPRARLTAAQALSHPWVREGGNASEIPIDISVLSNMRQFVKYSRLKQFALRALASTLNAEELS
 DLKDQFDAIDVDKNGSISLEEMRQALAKDVPWKLKDSRVLEILEAIDSNTDGLVDFTEFVAATLHVHQLEEHDSEKWQQRSAAFEKFDIDKDGFTPEE
 LKMHTGLRGSIDPLLEEADIDKDGKISLSEFRLLRTASISSKTVTSPPGQRNARKV*
 >SapurV1A.0130s0480 Org_Spurpurea peptide: SapurV1A.0130s0480.1.p calcium-dependent kinase
 (PAC:31426758)
 MGVCFSTIKVSGSNSNNNVNHNKREATKQQTKTATAPTRKKQEVVDHQNNKNVNNEEKKLVKEKQGSKAIPCGKRTDFGYDKDFGMRYTIGKLLG
 HGQFGYTYVATDKANGDRVAVKRIEKNKMILPIAEDVKREVILRELTHGENVVQFYNALEDDSYVYIVMELCEGELLDRILSKKDSRYTEKDAAVV
 RQMLKVAAQCHLHGLVHRDMKPENFLFKSTKEDTLPKATDFGLSDFIKPGKFKQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTE
 DGIFKEVLKNKPDFRRKPWPWTISTSARDFVNKLLVKDPRARLTAAQALSHPWVREGGSASEIPIDISVLSNMRQFVKYSRLKQFALRALASTINEEELAD
 LKDQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFNEFVAAALHVHQLEEHNSEKWQVRSQAAFEKFDIDRDGYITPEEL
 RMHTGLRGSIDPLLEEADIDKDGKISLSEFRLLRTASMSSRNVPSPSGQRKSQKI*
 >SapurV1A.0515s0090 Org_Spurpurea peptide: SapurV1A.0515s0090.1.p calcium-dependent kinase
 (PAC:31451114)
 MGACFSTIKVSGSNSNNNTNHNKREKSTKPTSTATTKQEVVLSHHQINKNVNNEAEKKLVREKQSSKAIPCGKRTDFGYDKDFDIRYTIGKLLGHGQFG
 YTYVATDKANGDRVAVKRIEKNKMVLPPIAEDVKREVILRELTHGENVVQFHNAFEDDSYVYIVMELCEGELLDRILAKKDSRYTEKDAAVVVRQMLK
 VAAEACHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGKFKFRDMVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTE
 EVLRNKPDPFRKPWPWTISTSADKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLSNMRQFVKYSRLKQFALRALASTIDEEELADLKDQF
 DAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEIVQAIDSNTDGLVDFTEFVAAALHVHQLEEHNSEKWQLRSQAAFEKFDIDRDGYITPEELRMHSG
 LRGSIDPLLEEADIDKDGRIISLSEFRLLRTASMSSQNVPSPSGQNSKKL*
 >Seita.1G102100 Org_Sitalica peptide: Seita.1G102100.1.p (1 of 1) PTHR24349//PTHR24349:SF137 -

SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32695536)
MGACFSSASAAPAGAERRPSKEDKKRRRGASPEGATKAAAAAAPPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMTR
PVAVEDVKREVKILKALKGHEINVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFLFKSNK
EDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRWPSSISPGAKDFVK
RLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLNSMRQFVKYSRKFQFALRALASTLNEEELADLKDQFDAIDIDKSGSISIEEMRHAKDLPLW
RLKGRPVLEIIQAIDSNTDGLVDKFKEFVAATLHIHQMAELDNERWGIRCAAFSKFDLDGDGYITPEELRMMQHTGLKGSIEPLLEEADIDKDGRISLSE
FRKLLRTASMSNVPSRPGPPNPQAL*

>Seita.2G111700 Org_Sitalica peptide: Seita.2G111700.1.p (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32718390)
MGLCFSSSTAADSPPRPAAGGAAGKRERSRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTAAVDRASGDRVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFLFKSTKEDSPLKATDF
GLSDFIRPGKQFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNKNPDRFRKPWPNTIPAAKDFVQKLLVKDPRAR
LTAAQALSHDWVREGGKASEIPLDISVLHNMQRQFVKYSRKFQFALRALASTLNEEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGRPVLEI
IEAIDSNTDGLVDFFEFVAATLHVHQLVEHDTKEWKLLSQAAFDFKFDVDGDGYITSDELRMHTGMKGSIDPLLEEADIDKDGGKISLDEFRRLLKTASMSA
RIVQTPRGIRMS*

>Sevir.1G101400 Org_Sviridis peptide: Sevir.1G101400.1.p (1 of 1) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32664287)
MGACFSSASAAPAGAERRPSKEDKKRRRGASPEGATKAAAAAAPPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMT
RPVAVEDVKREVKILKALKGHEINVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFLFKSN
KEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRWPSSISPGAKDFV
KRLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLNSMRQFVKYSRKFQFALRALASTLNEEELADLKDQFDAIDIDKSGSISIEEMRHAKDLPL
WRLKGRPVLEIIQAIDSNTDGLVDKFKEFVAATLHIHQMAELDSERWGIRCAAFSKFDLDGDGYITPEELRMMQHTGLKGSIEPLLEEADIDKDGGKISLDEFRRLLKTASMSA
EFRKLLRTASMSNVPSRPGPPNPQAL*

>Sevir.2G117500 Org_Sviridis peptide: Sevir.2G117500.1.p (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32636163)
MGLCFSSSTAADSPPRPAAGGAAGKRERSRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTAAVDRASGDRVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFLFKSTKEDSPLKATDF
GLSDFIRPGKQFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNKNPDRFRKPWPNTIPAAKDFVQKLLVKDPRAR
LTAAQALSHDWVREGGKASEIPLDISVLHNMQRQFVKYSRKFQFALRALASTLNEEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGRPVLEI
IEAIDSNTDGLVDFFEFVAATLHVHQLVEHDTKEWKLLSQAAFDFKFDVDGDGYITSDELRMHTGMKGSIDPLLEEADIDKDGGKISLDEFRRLLKTASMSA
RIVQTPRGIRMS*

>Sobic.002G114800 Org_Sbicolor peptide: Sobic.002G114800.1.p (PAC:37951044)
MGLCSSSTAARAASDPGAAAAGDAAAAAAGKRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTFAAVDRASSERVAVKRIDKNKMVLPVAVEDVK
REVKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFLFKSTKEDSPLKAT
DFGLSDFIKPGKQFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLNKNPDRFRKPWPNTISSAKDFVQKLLVKDPR
VRLTAAQALSHDWVREGGKASEIPLDISVLHNMQRQFVKYSRKFQFALRALASTLNEEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGRPVLEI
EIIAIDSNTDGLVDFFEFVAATLHMHLVEHDTKEWKLLSQAAFDFKFDVDRDGYITSDELRMHTGMKGSIDPLLEEADIDKDGGKISLDEFRRLLKTASMS
SARNVQTPRGVRS*

>Sobic.004G025000 Org_Sbicolor peptide: Sobic.004G025000.1.p (PAC:37929853)
MGACFSSSASAAPAGAADDRPSKDDGKRRRRAAGASPEAAAAAAPPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRASGDRVAVKRIDKAKMTR
PVAVEDVKREVKILKALKGHEINVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFLFKSNK
EDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRWPSSISLGAKDFVK
RLLVKNPRARLTAAQALSHPWVREGGEASDIPVDISVLNSMRQFVKYSRKFQFALRALASTLNEEELADLKDQFDAIDIDKSGSISIEEMRHAKDLPLW
RLKGRPVLEIIQAIDSNTDGLVDKFKEFVAATLHIHQMAELDSERWGIRCAAFSKFDLDGDGYITPEELRMVQHTGLKGSIEPLLEEADIDKDGGKISLSE
FRKLLRTASMSNVPSRPGVPNPQAL*

>Solyc02g083850.2 Org_Slycopersicum peptide: Solyc02g083850.2.1 (1 of 1) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:36156830)
MGNICFSSSKVSGSNSNTPSTTTNTAANGHRNRSSANPVSATNTSRKQEGSHYNRQKGDNGGVKQQTRNSQKNVKHNTRKQSGIIPCGKRTDFGY
DKDFDNKFTIGKLLGHGQFGYTIVATDKSNGNRVAVKRIEKKKMVPIAVEDVKREVKILKALAGHENNVDFYNAFEDDNYVYIVMELCEGGELLDRILA
KKDSRYTEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFLFKSKEDSSLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVIT
FILLCGRRPFWDKTEDGIFKEVLRNKPDRFRKPWPNTISNSAKDFVKLLVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLNSMRQFVKYSRLKQFA
LRALASTLDEEELADLRDQFSAIDVDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFFEFVAATLHVHQLVEHNLLKWQQRSTAFE
KFDVDRDGFITPEELRMHTGLKGSIDPLLEEADIDKDGGKISLSEFRRLLRRTASISSRMVNSPTVRGSRKI*

>Solyc03g033540.2 Org_Slycopersicum peptide: Solyc03g033540.2.1 (1 of 1) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:36136238)
MGSCFSSSKVSGSNSNTPSTNTTNTAVNAHQNRRETSKAPSTTVNPRNQEGCRDKGNINQKNQKQPRNSQQNVKPSRRQGGVIPCGRKRTDFGY
HKDFEKRYTIGKLLGHGQFGYTIVATDKSNGDRVAVKRIEKNKMVLPVAVEDVKREVKILKALGGHENNVQFYNSFEDDNYVYIVMELCEGGELLDRILS
KKDSRYTEKDAAVVVRQMLKVAAEACHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVIT
YILLCGRRPFWDKTEDGIFKEVLRNKPDRFRKPWSNISNSAKDFVKILVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLNSMRQFVKYSRLKQFA
LRALASTLDEEELADLRDQFSAIDVDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFFEFVAATLHVHQLVEHNSTKWQQRSAAFE
KFDVDKDGFITPEELKMHTGLRGSIDPLLEEADIDKDGGKISISEFRRLLRRTASMSSTPTVRDSRGM*

>Sphfalx0060s0096 Org_Sfallax peptide: Sphfalx0060s0096.1.p (1 of 1) PF13202//PF13405//PF13499//PF14531
- EF hand (EF-hand_5) // EF-hand domain (EF-hand_6) // EF-hand domain pair (EF-hand_7) // Kinase-like
(Kinase-like) (PAC:32604604)
MGSCCTKTSAAQEEQNEHKFAHQNYDQNGAQKHQEQQLQHVANHKKHTPQHHHHHRHAREQERSVVEDLQQPAQAACKPPAAVAAPQSDRRKTRRRIV

GSNIRDNTSVPLGKKTNFGYQRDFKAKYTLGKLLGHGQFGYTYVAIQKATGMRVAVKTIEKKQMTLPISVEDVKREVKILDTLSGHENVVQFIASFEDNN
LVYIVMELCEGGEILLDRILAKKESRYSEKDAARIVRQMLNVAACHLNGVVHRDMKPNFLFKSTKEDSPLKATDFGLSDFIKPGKRFHVDVGSAYYVAP
EVLKRKSGPESDAWSIGVITYILLGRRPFWEKTEAGIFNEVLKKKPDFREKWPPTISASAKDFVKKLLVKDAFARLTAAQALSHPWVREGGDASDIPLD
ISVLNMRFEVVKYSHLQKIALRALASTLDSDEISDLRDQFDAMDMRNGTITILEEMRIALQKQDPWVLKESRVLEILQAMDNRDGLVDFEFVAATLHV
HQLKETDAKKWQMLQAADFDFDGDGYITAIELKIAMGLKGSMEAILCEADLDGGRISLPEFQNLVRQASLGSRRNDDNDVRMQHRRHHREAPLPC
ENQMMM*
>Sphfalx0184s0017 Org_Sfallax peptide: Sphfalx0184s0017.1.p (1 of 1) PF13499//PF14531 - EF-hand domain
pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:32623020)
MGSCCTKSLAEQEERNGKQEQKFHSHQNHQHGVTQHQEQHHVHNHYHAREQGAHYHHYAKEQEHVVELQQQQPGGQEGGKKEPPPPAVHRHSEGGKTK
VSSSSIKDNNVPLGKKTNFGYARDFAKYTLGKLLGHGQFGYTYVAVEKATGMRVAVKTIEKKQMALPISVEDVRREVKILETSLGHENVVQFIASFED
DDLVIYVIMELCEGGEILLDRILAKKDSRYSEKDAARIVRQMLNVAACHLNGVVHRDMKPNFLFKSPKEDSPLKATDFGLSDYIRPGKRFHVDVGSAYYV
APEVLKRKSGPESDVWSIGVITYILLGKRPFWDKTEAGIFNEVLKKKPDFRDKPWPTVSASAKDFVKKLLVKDAFARLTAAQALSHPWAREGGDASDIP
LDISVLNMRFEVVKYSRKQIALRALASTLDADEISDLRDQFDAMDMRNGTITILEEMRIALQKDRPWIVKESRVLEILQAMDSNRDGLVDFNEFVAATL
HVHQLBETDSEKWQMLQAADFDFDGDGYITANELKIATGLKGSMEAILDEADMDGGRISLPEFKNLLRQASLGSRRNNDHVDHTQHQRVRVQEAHE
ARIIS*
>Sphfalx0226s0012 Org_Sfallax peptide: Sphfalx0226s0012.1.p (1 of 1) PF06293//PF13499//PF13833 -
Lipopolysaccharide kinase (Kdo/WaaP) family (Kdo) // EF-hand domain pair (EF-hand_7) // EF-hand domain
pair (EF-hand_8) (PAC:32617120)
MGCCVSKNPVHQTIQREAGAGGQKEIVHGPGGHRQQLPPDHGIVNHQLHHDVGEQIHNRRGDGEMKKKAVAAASAAAVKPIRKSSRITAASCDIQNNAP
LHPTAPLQGRINFGYGRDFDEKYSGLGKLLGHGQFGYTYVGTAKTSNEVAVKCIKKMKLPVEVEDVKREVRILKTLSGHKNVVQFYAAFEDDFQVYI
VMELCEGGEILLDRILAKKNHRYTEKDAKVVREMLNVVARCHLNGVVHRDIKPNFLFKSQDEDAPLKAVDFGLSDFIRPGKRFHVDVGSAYYVAPEVLK
RRSGPESDVWSIGVITYAILLCGVRPFWDKTEAGIFNEVQKKKPNFTQKPWPRISSAKDFVKKLLEKDPHLRLTAAQALSHWVREGGVASDMPDLIAVL
SNMREFVKYSRLKQIALRALASTLTKSEIILNLQDQFDAIDVDQNGTITILEEMKNALSADKPWSVREPRISEILQAMDANMDGMIIDFDEFVATMHHMQLE
ENNSKKWQSRSSAAFAKLMDGDGYVTADELKVAMGLKSSVSILLDEADTDRDGRISLPEFQKLLHQASLGSRTNHNHPHHRH*
>Spipol16G0021400 Org_Spolyrhiza peptide: Spipol16G0021400 Calcium dependent protein kinase 16
(PAC:31516197)
MGACFSTATKAASAAGDPQGPQQAHPKPREAQRSTSSQSQQNRKQGQNYQREKQGEKRAAGAI PCGKRTNFGYARDFESKYTTGKLLGHGQFGYTFVATQK
ATGDRVAVKRIDKSKMLHSAVEDVKREVKILQALTGHENVVQFHNAFEDDSYVYIVMELCEGGEILLDRILAKKDSRYSEKDAAVVVRQMLKVAEECHLH
GLVHRDMKPNFLFKSTKEDSPLKATDFGLSDFIKPGKRFHDI VGSAYYVAPEVLKRKSGPESDVWSIGVITYILLGRRPFWDKTEDGIFKEVLKRPD
FRRKWPNISSAKDFVTKLLVKDPRARLTAAQALSHPWVREDGDASEIPLDISILNNIREFVKYSRLKQIALRALASTLNPEEMANLRDQFDAIDVDKN
GAISLEEMRHAKDLPLWKLEPRVMEILQAMDSNTDGLVDFDEFVAATLHVHQLLEHDSEKWQSRSSAAFEKFDVDGDGFI TPEELRVHTGLKSSIEPL
LEEADIDKDGKISLPEFRLLRSVSSRNVPAPSAARNSRKM*
>Spipol17G0030600 Org_Spolyrhiza peptide: Spipol17G0030600 Calcium-dependent protein kinase
(PAC:31514565)
MGACLSNATKVTGCSSTATSGSATDPPRQHKDRPPREGKSPSTQDDHHEHQRRERDQGRRTTGII PCGKRTSFGYGRDFLSRYTIGKLLGRGQFGHTFV
ATDKANGDKVAVKRIDKKNMILPIAVEDVKREVKILQALTGHENVVQFHNAFEDDSYVYIVMELCEGGEILLDRILAKKDSRYTEKDAKVVVRQMLKVAEK
CHLHGLVHRDMKPNFLFKSTKEDSPLKATDFGLSDFIKPGQRFDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLGRRPFWDRTEDGIFKEVLK
NKPDRFRKPWPSISPSAKDFVKKLLVKDPRARLTAAQALSHPWVREDGDASEIPLDISVLGSMREFVKYSRMKQIALRALASTLDPEELADLRDQFNAID
VDKNGSISLEEMRHAKSKDI IWRLEPRVLEILQAIDSNTDGLVDFDEFVAATLHVHQLLEKQDSRKWLSRSQAAFEKFDVDGDGFI TPEELRMHTGMKGS
IDPLLEEADIDKDGKISLSEFRLLRNASMGSHNVL*
>Spipol1G0063900 Org_Spolyrhiza peptide: Spipol1G0063900 Calcium dependent protein kinase 18
(PAC:31521583)
MGACFSDPTKVGSSSSSTGSVKNLAGKHQHQARTQKKSSNGKDQQRKQEQNQPRNQNHREKGEVKRTNGVVPYGKRTNFGYPRDFESKYEIGKLL
GHGHFGYTFVAIDKANGNHVAVKINKQKMHHTAVEDVKREVKILRALTGHENVVQFYNAFEDDSYVYIVMELCEGGEILLDRILAKKDSYAEKDAAI V
VRQMLRVAAECHLRLGLVHRDMKPNFLFKSALENSPLKATDFGLSNFIVPGKRFYDIVGSAYYVAPEVLKQSRGPESDVWSIGVITYILLGRRPFWDKT
EEGIFKEVLKPKPDRFRKPWPSISNSAKDFVGLKLVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLNMRRFVKYSCFKQFALRALASTIDQEEEL
DLHDQFDAIDVDKNGSISLEEMRHAKDVPWRTKEPRVLEILRAIDSNTDGRVDFEFVAATLHVHQLVEHDSEKWLLRSQSAFEKFDLDGDGFI TPEE
LRTHIGLRGSDPLLEEADIDKDGKISLSEFRLLRTASMNS*
>ThecclEG00206 Org_Tcacao peptide: ThecclEG00206t1 Calcium dependent protein kinase 16 (71%U)
(PAC:27435494)
MGACLSSTTKVSGSSSNAGVNRKEQQSTTTTNEKKESQKPSGQQGQQQQQVRNSQPLVKGKPSARRQSGIIPCGKRTDFGYHKDFDKRYTIGKLLGH
GQFGYTYVATDKANGDRVAVKKIEKNMVLPIAVEDVKREVKILEALKGHENNVQFYNAFEDDSYVYIVMDFALAI SLVLALQLYTFISILLSLDSIICL
LSDARLCEGGEILLDRILANQCYFLSVDVSNVSTTSSTLCLPSSVRKDSRYSEKDAAVVVRQMLKVAEACHLRLGLVHRDMKPNFLFKSTRADSPLKATDF
GLSDFIRPGKRFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLGKRPFWDKTEDGIFKEVLKKNPDRFRKPWPTISNSAKDFVKKLLVKDPQAR
LTAAQALSHPWVREGGNASEIPVDISVLNLRQFVKYSRLKQFALRALAGTLNEEIIADLRDQFDAIDVDKNGSISLEEMRQALAKDLPLWKLESRVLEI
LQAIDSNTDGLVDFTEFVAAALHVNQMEEHSDKWQQRSSQAAFEKFDVDGDGFI TPEELRMHTGLRGSIDPLLEEADIDKDGKISLSEFRLLRTASMGS
KNVPSPSGQRNTCKL*
>Thhalv10003969m.g Org_Esalsugineum peptide: Thhalv10003969m (1 of 1) PF13499//PF14531 - EF-hand domain
pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:20198771)
MGVCFSAIRVTGASSSSRRSSQTNRKGCKKDKAYKAPIKEENDKPSTKRRTGAIPCGKRTDFGYAKDFHDQYSIGKLLGHGQFGYTYVAIHKSNGDRVA
VKRLDKSKMVLPIAVEDVKREVQILKALSGHENNVQFYNAFEDEDYVYIVMELCEGGEILLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVHRDM
KPNFLFKSAKLSPLKATDFGLSDFIKPGKRFHDI VGSAYYVAPEVLKRKSGPESDVWSIGVITYILLGRRPFWDRTEDGIFKEVLKRNKPDFRRKPWS
TISDAKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNLRQFVYRSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEE
MRQALAKDLPLWKLDNRVAILQAI DSNTDGLVDFTEFVAAALHVNQLEEHDSKWLRSRAAFEKFDIDKDGITPEELRMHTGLRGSIDPLLEADID
RDGKISLHEFRLLRTASISSQVRVSPACHRNPR*

>Thhalv10022615m.g Org_Esalsugineum peptide: Thhalv10022615m (1 of 1) PF13202//PF13499//PF14531 - EF hand (EF-hand_5) // EF-hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:20202464)
MGLCFSSAKVSGRHNRSRPNPNPPLPLTVAKHRPPQTPCSFMTVSIQKDHRTQPRRPAKKTTPQTQTRQTPTHGRAREKVSNNHNGRRHGEAIPY
GKRIDFGYAKDFDHRYSIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGG
ELLDRILAKKDSRYSERDAAVVVRQMLKVAEECHLRGLVHRDMKPENFLFKSTEEASPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESD
VWSIGVISYILLCGRRPFWDKTEDGIFKEVLKKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDATEIPIDISVLNNMRQFVK
FSRLKQFALRALATTLDDEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFEEFVAAALHVNQLEEHDSSEKWQ
QRSRAAFEKFDIDGDGYITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRLLRTASIKSRNVNPPGYLISRKV*
>Thhalv10027243m.g Org_Esalsugineum peptide: Thhalv10027243m (1 of 1) PF00069//PF13202//PF13833 - Protein kinase domain (Pkinase) // EF hand (EF-hand_5) // EF-hand domain pair (EF-hand_8) (PAC:20193139)
MGLCFSSPKATRHGTSRRKPNPTPEMPKPQPGQKARKKVSNNKKKTNNNKIQWRHGGETPYGKGVDFGYAKDFDNHYTIGKLLGHGQFGYTYVATDNVN
EDRVAVKRIDKAKMTVPIEVEDVKREVKILQALGGHENVVAFHNVFEDKNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQYANFLFKSTGEDS
SLKATDFGLSDFIKPGMKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTDGIFNEVMRKKPDFKTIPTWPTISNSAKDFVKKLL
VKEPLARLTAAQALSHPWVREGGEASEIPIDISVLNNMRQFVKFSRLKQALRALATTIDEDELDDLRDQFDAIDIDKNGSISLEEMRQALAKDVPWKLK
DARVAEILQAIDSNTDGLVDFTEFVATLHVNVQLEEHDCWKQQRSAFAFDKFDIDRDGYITPEELRLQTGLKGSIEPLLEEAEVDKDGRIISHEFRLL
RSASLSIKVKSPPGYQLS*
>Tp57577_TGAC_v2_gene18198 Org_Tpratense peptide: Tp57577_TGAC_v2_mRNA18832 (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:35968253)
MGICFSSTKVVSNSNTNNENRKNSTSTTKTENAPVTTTSATASTTRKQVPSSNQRRKGSEEAQKKTHQSRHKDKVSSRVPCGKRTDFGYEKDFDK
RFSGLKLLGHGQFGYTYVGVDSNGDRVAVKRLEKAKMVLPIAVEDVKREVKILKELTGHENVVQFYNAFEDDSYVYIVMELCEGGELLDRILGKKDSRY
TEKDAAVVVRQMLKVAEQCHLHGLVHRDMKPENFLFKSNKDDSAKATDFGLSDFIKPGKRFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCG
RRPFWDKTEGIFKEVLKKNKPDFRRKPWPTISNAKDFVKKLLVKDPRARLTAAQALSHPWVREGGEASEIPVDISVLNNMRQFVKYSRLKQFALRALAS
TLNEGEFSDLDKQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLLEEHDSSEKWQQRSAFAFDKFDLDK
DGFITPEELRMHTGMRGSDIDPLLEEADIDKDGKISLPEFRLLRTASIGSRNVSSPTHRNRMM*
>Zm00008a008476 Org_ZmaysPH207 peptide: Zm00008a008476_P01 (1 of 1) PTHR24349//PTHR24349:SF123 - SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:37205832)
MGLCSSTAARAASDPGAAAAGDAAAAGKGRGIVACGKRTDFGYDKDFEVRYSLGKLLGHGQFGYTFAAVDRASERVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAEECHLHGLVHRDMKPENFLFKSKKEDSPLKATDF
GLSDFIKPELLPTFLSAFCQVLFGRMGWFLAEQWEHSVLKKKPDFRRKPWSNITSSAKDFVQKLLVKDPRARLTAAQALSHDWVREGGKASEIPLDIS
VLHNMQRQFVKYSRKFQFALRALASTLNSEEMSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPVLEIIEAIDSNTDGLVDFEEFVAATLHVHQ
LVEHDETEKWSLSQAADFDFVDLDGTYITPDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMSARNVQTPRGVRSK*
>Zm00008a020829 Org_ZmaysPH207 peptide: Zm00008a020829_P01 (1 of 1) PTHR24349//PTHR24349:SF137 - SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:37208826)
MEVARSLVCRGTGKMPRPVAVEDVKREVKILKALKGHQNIHVYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAEECHLRGL
VHRDMKPENFLFKSNKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKKNKPDFR
KRPWSSISPGAKDFVKKLLVKNPRARLTAAQALSHPWVREGGEASDIPVDISVLNNMRQFVKYSRKFQFALRALASTLNEEELSCLKDQFDAIDIDKSGS
ISIEEMRHAKADLPWRLKGPVLEI IQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCAAFSKFDLDGDGYITPEELRMHTGLKGSIEPLLE
EADIDKDGKISLSEFRKLLRTASMSNVPSRPGPPNPQAL*
>Zosma34g00020 Org_Zmarina peptide: Zosma34g00020.1 Calcium dependent protein kinase 16 (PAC:33182282)
MGNCIVFRQTKSVVTAQTSHRPNTPARQHRHEQRKHQDGDKMVASGKMDFGYDKNFGERYVLGKLLGHGQFGYTFVGTDKINGDRVAVKRIDKNKMM
GVKDVKREVNILRELTGHENVVQFHNAYEDDTYVYIVMELCEGGELLERILSKKNSRYSEIDAEEIVRQMLKVAEQCHLHGLVHRDMKPENFLLESKEED
SRLKATDFGLSDYIKPEKKFSDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWGRTEGIFNSVLKKNKPDFKSKPWPHTISDSAKDFVKKL
LVKSPSVRLTASQALSHPWVRENGDASEIPLDISVLSNLKFMFTYNGLKQFALGALASTLNKEELADIRDQFDVIDVDKNGTISLDEMSQALAKYRPWKL
KERHVRILQAIDTNTDGLVDFSEFVTATLRVHQMEVHDSKWKLSQTAFDQFDKDKGFIPTPEELKMHAGLLGSINSLLEEADTDKDGKLSLAEFRKL
LKPANIHQPSPPSSKRNHRQ*
>Zosma72g00360 Org_Zmarina peptide: Zosma72g00360.1 Calcium-dependent protein kinase (PAC:33169652)
MGACATKVGSGASSRRSNTASKTKPNGGDLLEKKTEGTSGEKVEVPPTQKKQKGRAVTVPCGKQTNFGYDRDFTRYSIGKLLGHGQFGYTFVATDKEN
DDRVAVKRISKNMKTLPIAVEDVKREVQILRELTGHENVVQFHNAYEDDSYVYIVMELCEGGELLDRILSKKESRYTENDAAVVVRQMLKVAEECHLHGL
VHRDMKPENFLFISKNNESMLKATDFGLSDYIKPGKNFRDIVGSAYYVAPEVLKRRSGPQSDVWSIGVITYILLCGRRPFWNKTEDGIFKEVLKKNKPDFN
RKPWHSISESAKDFVNKLLVKNPDARLTASQALSHPWVREGGDALEIPLDISVLSNLRDFVKYSRLKQFALRVLMARTLDDNEELGNIRDQFNAIDTDGN
GIISPEEMKQALEKNRPWKLKEPKVKEIVQAIDSNTDGYVDFPEFVAATLHIHQMEERDSKWKALSQTAFDQFDKDKGFIPTPEELKMHAGLRGSDILI
LEEADIDKDGKISLSEFRKLRTASIQTR*
>Zosma8g01530 Org_Zmarina peptide: Zosma8g01530.1 Calcium-dependent protein kinase 28 (PAC:33183934)
MGNCFRSHIRIINRSTSSKNATATATADDSKSPKPNAAVLKTNQTPRNNDKRLHEKKSTNSVPYGLKTDGFGYKDFDKNYAIGKLLGHGQFGYTFIATNK
STHESVAVKRIEKKMVLPIAVEDVRREVKILKQLTGHENVVQFHNAYEDDAYVYIVMELCEGGELLDRILSKKDSRYTEKDAAVVVRQMLKVAEECHLH
GLVHRDMKPENFLFGSKREDSVLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRSGPESDAWSIGVITYILLCGRRPFWDKTEGIFKEVLKKNKPD
FKRNPWPTISDSAKDFVNKLLVKNPRARLTAAQALSHPWVREGGNASEIPLDISVLSNLRDFVKYSRMKQALRALASTVDDDELADLRDQFDAIDVDKS
GTISFEELKLALAKDLPWRVKEARVVEILEAIDSNTDGLVDFREFVTATLHVHQMEHDSSETWNSRCKAFAQKLDVDGNGFLTPEELRLHTGIKGSIDMLL
DEADTDKDGKISLIEFLTTLKTASTPRQRCAVSDHRNSSHK*

File S2. Amino acid sequences of representative group I, II, and III CDPKs across the plant lineage.

This text file includes 327 FASTA-formatted sequences retrieved from the Phytozome 12 BLAST tool following a query for group I, II, and III CDPKs in 12 species spanning the plant lineage (*M. polymorpha*, *P. patens*, *S. fallax*, *S. moellendorffii*, *A. trichopoda*, *O. sativa*, *A. thaliana*, *V. vinifera*, *R. communis*, *B. rapa*, *T. cacao*, and *M. truncatula*).

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>105020 Org_Smoellendorffii peptide: 105020 (1 of 1) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE
10-RELATED (PAC:15411844)
MGNCCATPGIKRKRKPNPFAQDGFKGTPPKVIMKEHAPGMSVQQGVDINEKYVLGKELGRGEFGITYLCTGKESQEDLACKSISKSLKRTAVDIDDVR
REVQIMHHLPRHPNVVALKDVFEDGNAVHLMELCEGGELFDRIIARGHYSERAAAGITRTIVEVVQVCHKHGMHRDLKPENFLFANKKENSPLKAIDF
GLSVFRPGERFSEIVGSPYYMAPEVLKRNYPGEIDVWSAGVILYILLSGVPPFWAESEQGVAQAILRGQIEFKRDPWPKISENAKSLVQNMMPDPKQR
YTAQVQLDHPWLQNAKKASNVPLGPDVVRNRLKQFSAMNKLKRKALQMITELLSGDEVESYKDMFKVMDQKNEGSITYDELKVGLAKIGSQLAESEAKLLM
EAADVNNKGTLDYQEFVAMMIHIQRMNDDEYLRKAFNRDLKDESGFIEKEELREALYDDRGASETEMIDDILQEVLDLDKGKISYEEFASMMRTGTDWRK
ASRHSYRGRYNSLSIRLLRDGSLQSGNYEKR*
>105846 Org_Smoellendorffii peptide: 105846 (1 of 1) PTHR24349:SF126 - CALCIUM-DEPENDENT PROTEIN KINASE
32 (PAC:15417957)
MGNCCATPPREAGDQDSHKPRGKKRFGKGNPYAKDSENGQRKLTVLEAEQRTGSSIKERYNLGRELGRGEFGVTYLCMEQESQELLACKSISKSLKRTAV
DIEDVRREVAIMRHLPPHPNIVALKGAYEDERAVHIVMELCAGGELFDRIIARGHYTERAAAGVIRTIVEVVQACHRQGMHRDLKPENFLFANKKENS
LKAIDFGLSVFRPGERFNEIVGSPYYMAPEVLKRNYPGEIDVWSAGVILYILLCGVPPFWAESEQGVAQAILRGVLDFFRREPWPAPVSESAKSLVRMLE
PDPRLRLSASQVLEHPWLHRAGKHAPNVPLDAVTRRLKQFAALNKLKKALEIIAEELSQEENAGMREIFEAMDSSGRGGITLDELKIGLAKSPTIVTNE
YAEVELKSVMDAAEDNDGVLNNGYGEFVTVIVYLQQRFDSDHLRKAFAFDRLDKDANGFLDKEDLAAALAEPPGGDGGGEVADILAEVDADKDLGVSYYEF
ARVMRTGTDWRKASRRYSKGRFNSLSNKLKDGSLTATA*
>118877 Org_Smoellendorffii peptide: 118877 (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE
3 (PAC:15411727)
MRNTKSAIAGSSTPLRGSAAFKAGNVLGRPFSDLRQEFALARELGAGQFGVTRLCSSRRSTGERLACKSIAKRKLLDRSDAEDVRREVQIMHHLGHAHIV
ALREVFEDKGSVHLIMELCEGGELFDRIIVQRGHYSERAAATLCRTMVLVLQTCVSLGVMHRDLKPENFLFASADEDSPLKATDFGLSVFFKPGETFCDLV
GSAFYVAPEVLRNRYGPEADIWSAGVILYILLSGVPPFWAESEQGIFDEVLRGHLDLSSDPWPSISDGAkdLLRKLKQDPKERMTPLEVLNHPWLKEDG
EAPDVLPLDNAVLSRMKQFSAMNKLKLLKLVIAESLSEEEIMGLKEMFKSIDTNSGTITYDELKAGLANLGSALAEHEVQQLMRAADVNGNSIDYTEF
ITATMHLNTEKEDHLYSAFQFFDKDNGSYITVEELEQALGDLNMQDLTEIIEKVDTDNDGKIDYDEFVAMMRGANPPRTAAVAAKAAEKSSS*
>152133 Org_Smoellendorffii peptide: 152133 (1 of 1) PF07714//PF13499//PF13833 - Protein tyrosine
kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8)
(PAC:15417480)
MYVLGRELGRGQFGVTHLCTDRASGKTYACKTIAKRKLISKADVEDVKREVQIMHHLRGNEINIVELRGSYEDKHSVHLMELCEGGELFDRIIARGHYSE
RAAAALCRTIVRVVYICHSLGVMHRDLKPENFLADKSESAPLKATDFGLSVFFKHGDKFTDLVGSAYYVAPEVLRNRYGPEADVWSAGVILYILLSGVP
FWAESEQGIFDAVLRGQVDFVSDPWPSISSAKDLVKKMLTQDVKKRVTAAEVLSHPWVREDGDAPDAPLDNAVLSRMKQFTAMNKLKLLKLVIAASL
SEEEITGLKEMFSSMDTDGSGTITFDELKAGLERLGSNLRDAEIRQIMNAADVNGNTIDYLEFITATMQNMKQKEDHLYSAFQFFDNDNSGYALSFLK
LFMDDWLLRDSYITMEELEALVKYGMGDHETMKEILKEVDTDNDGKINYDEFVAMMTKGAAPSEQQNNRRKGQELPVGAPRHRK*
>165073 Org_Smoellendorffii peptide: 165073 (1 of 2) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE
20 (PAC:15410490)
MGDSRPTAAAVVSPRHGGLTSSVLGRRTENVKDLVYLGRKLGGQFGTITYCTEKSSGKHYACKSIPKRKLISLEDVEDVRREIHHMHLGHPNVVEI
KGAYEDSSCVHLMVMDLCAGGELFDRIIQRGHYSESAAQLTRTIVGVVVACHSLGVMHRDLKPENFLLANADEDSPLRATDFGLSVFFQPGEVFKDVVGS
PYVVAPEVLRKQYGPEDVWSAGVILYILLSGVPPFWAESEQGIFQVLQGDIDFESDPWPKISESAKDILRKLMLTRNPRKRLKAQEVLTHPWIMEGGVA
PDAPIDSAVLSRLKHFSAMNKKIKIALRVIAERCTEDEIAGLKEMFKMMDADNSGAITFDELKAGLQVRGNSNLKESEIHALMDAADLDKNGTIDYTEFIT
ATLHLNKIEREENLFAAFSYFDRDSSGYITIDELQSACKEHYMGDDLLEMLREIDQDNDGRIDYNEFVTMMRNGNGGVGRGQMRNSLSLRDVMVG*
>231127 Org_Smoellendorffii peptide: 231127 (1 of 1) PTHR24349//PTHR24349:SF135 - SERINE/THREONINE-
PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:15414521)
MPQQHIACHRPQRSQAEQQQNTKALPASPPRAASPAAPSPSPSPAKPSTAATAKNIVIPSSQPKTDGSNVGLPLKDVRSAYALGKELGRGQFGITYA
CTDKITGEKLACKTISKRSILNRNTDMEDVQREMQIMQRLAGQHANIVELKAVYEDKQSVHLMELCAGGELFDRIIVSRGHYTEKAAAVFRTIVIRVQHC
HATGVIHRDLKPENFLASPAEDAPLKATDFGLSVFYKTGQIFTEVGSAYYVAPEVLKRYGPEADIWSAGVILYILLGLPPFWAETEKGIFDSVLRG
ELDFSDDPWPKISSAKELIRRLNQNPSERLAIPILDHFPWRPDGEASDQPLQSVLARMKGTAMNKMKKIALKIIAESLSEKEIKGLKELFKKMDV
DKSGTITFEELKSLAKQGYDMAESEVRAIMESADVNGNTIDYLEFISATMHMNMKDRENNLLAAFKQFDTDNSGFISVEELEQALYRYGMVDEGMIKD
IIEKVDVNKARREDRLQRCYDAAASGIEC*
>27777.t000008 Org_Rcommunis peptide: 27777.m000274 calcium-dependent protein kinase, putative
(PAC:16799163)
MGFCLSKSKRSQQHHYNGATGLQHSREPVAYQSKSPAQPSYQFPSQTPGAQIPRKPVPVAPSPKPVHKPDTILEKPYEDVKLHYTIGKELGRGQFGVTY
LCTEISTGKLYACKSISKRLVTRNDKEDMKREIQIMQHLSGQPNIVEFKGAYEDKQSVHLMELCAGGELFDRIIAKGHYSEKAAASICRSIVNVVHAC
HFMGMHRDLKPENFLSSKDQNALLKATDFGLSVFIEEGKTYRPIVGSAYYVAPEVLRRLRYGKEMDIWSAGVMLYILLSGVPPFWAESEKGFDAILQG
DIDFESPPWPPTISSAKDLVRRMLTQDPKKRITSTQVLEHPWLKEGGDASDKPIDSAVLSRMKQFRAMNKLKMKALKVIAENLSDEIQGLKSMFANIDT
```

DNSGTITYDELKAGLARLGSKLTETEVKQLMDAADVDNGTIDYLEFITATMHRHRLEREEHLYKAFQYFDKDNSGFITRDELETAMKDYEMGDDATIKE
IISEVDADNDGRINYEFCMTMMKTGNQHQGKLF
>28308.t000002 Org_Rcommunis peptide: 28308.m000065 calcium-dependent protein kinase, putative
(PAC:16800511)
MGNCCRSAPAAVAREDVKSNSYSSHDHSHKKNDAATKKQPIITVLTVGAKENIEEKYLVDRLEGRGEFGVTYLCIDRDNRELLACKSISKRKLRTAVDIEDVRR
EVAIMKHLPLKNSSIVSLKEACEDDNAVHLMELCEGGELFDRIVARGHYTERAAAAVTRTIVEVQVLCCHKHGVHRLDLKPENFLFANKKENSPLKAFDFG
LSIFFKPGERFSEIVGSPYYMAPEVLKRNYPGEIDWSAGVILYILLCGVPPFWAESEQGVAAQLRGIIDFKRDPWPNISESAKSLVKQMLEPDPKRLRL
TAKQVLEHPWLQNAKKAPNVPLGDDVKSRLKQFSMMNRFRKALRVIAEFLSTEEIEDIKDMFRKMDTDNDGIVSIEELKSGLQNFNSQLAESEVQMLIE
AVDANGKGTLDYGEFVAVSLHLQRMANDEHLHKAFSYFDKDSNGYIEPDDLRLDALMEDGADDCTDMANDIFQEVDTDKDGKISYDEFVAMMKTGTDRKA
SRHYSRGRFNLSMKMLMDGSLNLG
>29333.t000041 Org_Rcommunis peptide: 29333.m001078 calcium-dependent protein kinase, putative
(PAC:16802692)
MGNNCVGSRASQSIWWLTHPTDCFLSHHHAKKEAIKGLPYNKQEQESTTSQPQNTTPPEQMKIAKEEIKQAALPASSAPPKQEQANQKPALPSQPKEEIKQA
PLPPKPKDETQVQSEVNGIIRNQRGEIKSTRQVSVKEKKPAVPPRPKPHNVKRLYSAGLLAESVLRKTGHLKEYYNLGRKLGHGQFGTTFCLVEKGTG
KEYACKSIAKRKLSTIDDEDVRRRIQIMHHLSGNPNVISIKGAYEDAVAVHVMELCAGGELFDRIIKRGHYTERKAAQLTRTIVGVVEACHSLGVMHR
DLKPENFLFVNQEDSPLKAIDFGLSVFFKPGEIFTDVVGSPYYVAPEVLKRYGPEADVWSAGVMVYILLSGVPPFWAETEQEIEFEEVLHGQDLFTSDP
WPHISESAKDLVRRMLVRDPKRITAHEVLCHPWVRDDGVAPDKPLDPAVLSRMKQFSAMNKLKMLALRVIAENLSEEEIAGLTEMFKMIDTNSGQITF
EELKVGRLRRFGANLNESEIYDLMQAADIDNSGTIDYGEFIAATLHLNKVEREDHLFAAFSYFDKDGSGYITLDELQQACIEFGMEDVHLEEMIREVDQDN
DGRIDYKEFVAMMQKGNSEMGKNGLQGTSTFSIGFREALQVC
>29333.t000051 Org_Rcommunis peptide: 29333.m001088 calcium-dependent protein kinase, putative
(PAC:16802702)
MGNTCVGPNLSPNGFLQSVTAAVWTRPPEDRLPPPSKEDQNSNKS DISKSEESSKKGSNHAPIQDTPPEMVKITDAPPKAMEHEKSIRPEMNRVSIKV
AEDPKPKSNHFKRVSSAGLQMSVSLGRKTGNLKEIYSLGRKLGGQGFGTTFCLIEKATGRDFACKSIAKRKLTTQEDVEDVRRRIQIMHHLGHPNVIK
IDAYEDAVAVHVMELCAGGELFDRIIQRGHYTERKAAELARLIVGVVQACHSLGVMHRDLKPENFLFDVHEEEAALKTIDFGLSVFFRPGETFSDVVG
SPYYVAPEVLKHHYGECDVWSAGVYIYILLSGVPPFWDETEQGIQFQVLKGLDFISEPWPNISESADLVRKMLVRDPKRLTAHEVLCHPWVQVDGL
APDRPLDSAVLSRLKQFSAMNKLKRIAIRVIAETLSEEEIAGLKEMFKMIDTDGSGQISLDELKTGLERVGAILKDESIDSLMQAADIDNSGTIDYGEFI
AAMLHLNKIDKEDHLFAAFSYFDKDGSGYITQDELQQACDQFGLGDIHIEDIIREVDQDNDGRIDYSEFVAMMQDSGWSERRSK
>29728.t000018 Org_Rcommunis peptide: 29728.m000812 calcium-dependent protein kinase, putative
(PAC:16806882)
MKKSAGGSSTTKPAHTVLPYQTSRLRDHYLIGKKLGGQFGTTYLCTNKATNAQYACKSIPKRKLCKEDYEDVWREIQIMHHLSEHPNVVQIKGTYED
SMFVHLMELCAGGELFDRIVAKGQYSEKEAAKLIKTIVGVVEACHSLGVMHRDLKPENFLFDTPGDDAKLKATDFGLSVFYKPGQYFSDVVGSPYYVAP
EVLKRYGPEVDVWSAGVILYILLSGVPPFWAETESGIFRHLQKIDFESEWPWKISDSADKLIKMLERDPRQRISAHEVLCHPWIVDDTVAPDKPLD
SAVLSRLKKFSAMHKLKMLALRVIAERLSEEEIGGLKELFKMLDTSSTGTTFEELKEGLLRVGSSELMECEIKALMEAADIDNSGTIDYGEFLAATLHLN
KMEREENLLAAFSYFDKDGSGYITVDELQQACKDFGLDDVHLEDEMIKEIDEDNDGRIDYAEFTSMMRKGDIEDIGRSRTMRSHLNFNLADALGVKDLN
>29761.t000015 Org_Rcommunis peptide: 29761.m000421 calcium-dependent protein kinase, putative
(PAC:16808108)
MGNCATPPSDPHENKKYKKKPNPFSIDYGLNNGVSHRLTVLKDPTGREIEQRYELGGELGRGEFGVTYLCIDKESGEKFACKSISKKKLRTAVDIEDVR
REVQIMKHLPKHPNIVSLKDTYEDDNAVHLMELCEGGELFDRIVSRGHYTERAAAAVTKTIVEVVMCHKHGVMHRDLKPENFLFANKKESAAKKAIDF
GLSVFFKPGERFNEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQGVAAQAIIRSVVDFKRDWPVKVSDNAKDLVKMLDPPDKRR
LTAQVQLDHPWLQNAKKAPNVSLGETVKARLKQFSVMNKLKRALRVIAEHLSEVEEVAGIKEGFRMLDTSNKGKINLDELRIGLQKLGHQITDTDVQMLM
EAGDVDRDGHLDYGEFVTISVHLRKMGNDEHLRKAFFEYFDKNQSGHIEIEELRNALADELDENSEEIIISAIHVDVTDKDGRIISYDEFATMMKAGTDWRK
ASRQYSRERFNLSLKLMDGSLQMNENR
>29842.t000094 Org_Rcommunis peptide: 29842.m003597 calcium-dependent protein kinase, putative
(PAC:16810728)
MGCCGSKEKPSKPKNDNGYRPANTGNSRPQQQQQQPQYPQQWDLQQQNLIIPQIQAKPKAPSPQPSTPPPVKPAPAPIKPVQKPETILGKPLDDIR
QFYTLGKELGRGQFGITYLCTENSTGHTYACKSILKRKLISKSDREDIKKEVQIMQHLSGQPNIVEFRGAYEDRQSVHLMELCAGGELFDRIIAKGHYS
ERDAARICKDIVNVHACHFMGVHRLDLKPENFLASKDEGATLKATDFGLSVFIEEGKYRDKVGSAYVAPEVLSRSYGEIDVWSAGVILYILLSGV
PPFWAETENGIFDAILQGDIDFESKPWPSISDSADKLIRMLTQDPKKRITSQVLDHPWIKDGAASDKPIDSAVLSRMKQFRAMNKLKLLKLVIAES
LSEEEIKGLKVMFRNMDTDKSGTITYEELKTGLARLGSRLSETEVQVLMKAGLKRVLNKESEIYDLMQAADVNSGTIDYGEFIAATLHLNKIEREDHLFAAFSYFD
LESAMKEYMGDEATIKEIIEVSDTDNDGRINYEFCAMMRSGIQQAEKLF
>29852.t000019 Org_Rcommunis peptide: 29852.m002000 calcium-dependent protein kinase, putative
(PAC:16811562)
MGNTCVGPTISKNGFFQSVSAAMWRSRSPESGSVSQANGESVHDTTSKEPESPLPVQSNPPQQVVIKPEKEPEKPGNPEQPSKPKKAPQIKRVASAGLKVD
SVLQTKTGNFKEFYSGLKKLGGQFGTTFCLVEKATGKEYACKSIAKRKLTTDEDEDVRRRIQIMHHLGHPNVISIKGAYEDAIAVHVMELCAGGEL
FDRIIQRGHYSERQAAELTRTIVGVVEACHSLGVMHRDLKPENFLFVNQKEDSLKTIIDFGLSIFFKPGEKFNDVVGSPYYVAPEVLKRYGPEADVWSA
GVIVYILLSGVPPFWAETEQGIQFHEVLHGDLDFSSDPWPSISEGAKDLVRMMLDRPRLTAHEVLCHPWVQEDGVAPDKPMSAVLSRMKQFSAMNKL
KKMALRVIAESLSEEEIAGLKEMFKMIDTNSGTISFDELKAGLKRVLNKESEIYDLMQAADVNSGTIDYGEFIAATLHLNKIEREDHLFAAFSYFD
KDGSYITPDELQQACEFGLDFRLEEMIREVDQDNDGLIDYNEFVAMMQKGNVGGGPRKALENSFSIGFREALKL
>29896.t000003 Org_Rcommunis peptide: 29896.m000119 calcium-dependent protein kinase, putative
(PAC:16812395)
MGGCISAPLKAGRIISRLHYDNRSKPLADNSAASQPCTNFQVGNVLKSPAGNNIRQKYEFKGELGRGEFGVTYRCLHKETGETYACKTISKAKLKTEID
VEDVRREVEIMRHLPKHPNIVSYKEAYEDKEVIYLMELCEGGELFDRIVAKGHYTERAAAMVTKTILEIVKVCHKHGVHRLDLKPENFLFADVHENSQ
KAIDFGLSIFFPQGRFSEIVGSPYYMAPEVLRNYPGEVDVWSAGVILYILLCGVPPFWAETEEGIAHAIVGGKIDFTRDPWPRVSEAKDLVQNMLDQ
NPYSRLTVQVLEHPWIHNASDPVNVNLGENVRARIKQFSLMKNFKKRVLRVADNLTDQVDGKIQMFHMDTDNTGDLTFFELKSGLHKIGHVPDPD
VRTLMDAADIDNGTLSIEEFVAMSIHLIKIGNDEHLSQAFKFFDKNQTYIEFEELRDAMVHDLGNPCNEVVKIDIMSDVDLDDKGRISFDEFKAMMS

GMDWKMASRQYSRAMLNALSMKLLKDGSMQLKT
>30100.t000014 Org_Rcommunis peptide: 30100.m000791 calcium-dependent protein kinase, putative (PAC:16817768)
MGNTRGSGFKGKLYQGYSQPEDQSTASHTNRNPSSNNSNTEHSPTSVAQEFADKNPKKDNFPLISPNNRDLIMRRGADNQSYVVLGHKTANIRDLYTL
GRKLGQGGFGTTYLCVENSTGTEYACKSISKRLKSKEDVEDVRREIQIMHHLGAGHKNIVTIKAYEDQLYVHIVMELCSGGELFDRIIQRGHYSERKAA
ELTKIIVGVVEACHSLGVMHRDLKPENFLVNKDDDFSLKAIDFGLSVFFKPGQIFTDVVGSPPYVAPEVLLKHGYPEADVWTAGVILYILLSGVPPFFWA
ETQQGIFDAVLKGYIDFESDPWPLISDSAKDLIHKMLCGRPSDRLTAEVLCWPICENGAVPADRALDPAVLSRLKQFSAMNKLKLMALRVIAESLSEEE
IAGLREMFQMTDNDNGAITFDELKAGLRRYGSTMKDTEIRDLMDAADVDNSGTIDYGEFIAATVHLNKLREEHVLAFAFYFDKDGSGYITVDELQQAC
AEHNMTDVLLEDIIREVDDQNDGRIDYSEFVAMMQKGNAGIGRRTRMNSLNMSMRDAPGAQ
>30142.t000025 Org_Rcommunis peptide: 30142.m000651 calcium-dependent protein kinase, putative (PAC:16819478)
MGNCCSRGDSGDAENKGEAVANNNGSVANNANQENSTTPPKSTAPSPSPAASPKPAKAAPIGPVLRPMEEVKSVTYTIGELGRGQFGVTHLCTH
KATGEQFACKTIAKRKLNVKEDVEDVKREVQIMHHLTGQPNIVELKAYEDKHSVHLVLMELCAGGELFDRIIAKGHYTERAAASLLRTIVQIVHTCHSMG
VIHRDLKPENFLLLNKDENSPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLKRRYGPEADIWSVGVMYIILLSGVPPFWAESEHGIFNAILRGHVDF
TSDPWFQISPAKDLVRKMLNSDPKQRLTAIQVLSHPWIKEDGEAPDTPLDNAVLRLKQFKAMNNFKKVALRVIAAGCLSEEEIMGLKEMFKGIDTDNSG
TITLEELKQGLAKQGKTLSEYEVKQLEMAADADGNGTIDYDEFITATMHLNMRDREHLYTAFQHFDDKNSGYITTEEEQLALREYGMHDGRDIKEIIE
VDSHDHGRINRYDEFVAMMRKGNPEANPKRRDRTVFV
>30147.t000328 Org_Rcommunis peptide: 30147.m014057 calcium-dependent protein kinase, putative (PAC:16820071)
MGNCNTCVRPDTSPDTKTHRTNRKRRKKSKDGKPNPYSDNTIPSPAPIRVLKDVIPLSHRTRIGDKYILGRELGRGEFGITYLCTDRETCDGLACKSISK
RKLRTAVDIEDVRREVAIMSNDLPDHPNIVKLKATYEDNENVHLMELCEGELFDRIIVARGHYSERAAANVARTIAEVVRMCHENGVMHRDLKPENFLFA
NKKENSVLKAIDFGLSVFFKPGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVALAILRGQIDFKREWPQISDSAKS
LVRQMLEADPKRLTAQQVLDHSLWQNAKAPNVLPGDIVRTRLKQFSLMNRFKKALRVIAEHLVVEEVKIDMFALMDTDNDGKVTYNELRAGLRKV
GSQLAPEIKMLMEAADVDGNGVLDYGEFVAVTIHLQKMEDEHIRRAFMMFFDKDGSGYIELEELREALADEYGETDNDVLDHILREVDTDKDGCISYEE
FVVMKAGTDWRKASRQYSRERFKSLSLNLMKDGSLQLHDGLTGQCYAV
>30169.t000219 Org_Rcommunis peptide: 30169.m006442 calcium-dependent protein kinase, putative (PAC:16821242)
MGNCCITPSSSSSSEKKKAKGNNKNQNPFPGNDYVNVSGSGYIDHKLVLVLEPTGRDISAHYDLGRELGRGEFGITYLCTDVNTDEKLACKSISKKKLR
TAVDIEDVRREVEIMKHLPHHPNIVSLRATYEDDNAVHIVMELCEGELFDRIIVARGHYTERAAAVMRTIVEVQMCCHKHGMHRDLKPENFLFGNKKE
TAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAIIRSVIDFKRDPWPKVSDNAKDLVKK
MLNPDPKRLRLTAQQVLGHPWLQNAKAPNVSLGETVKARLKQFSVMNKLKKRALRVVAEHLVVEEVAGIKEAFDMMDDTTRRGKINLEELRIGLQKIGQQI
PDADLQILMEAADVDGGSGLNYGEFVAVSVHLKMGNDHEIHKAFAFFDQNSGYIEELREALNDEVDTCSEVDINAIMHDVDTDKDGRISYEEFATM
MKAGTDWRKASRQYSRERFNSLSLKLMDGSLQVAS
>30170.t000694 Org_Rcommunis peptide: 30170.m014282 calcium-dependent protein kinase, putative (PAC:16822115)
MGLCFTKFHRSRSHDITISSASDSPHPHYQSQPKRPPQQRHNNPPPPYNPRPRTSQAPPPTSSASNIGPILGKPYVDIASIYDLDELGRGQFGITYLCTE
KTTGLKYACKSISRKLNVNDKDEDVRREILILQHLTGQPNIVEFKGAYEDRQNLHLMELCSGGELFDRIIAKGYTEREAATITRQIVNVVHACHFMG
VIHRDLKPENFLLSKAEDSPLKATDFGLSVFIEEGVVYKDIVGSAYYVAPEVLNRSYGKEVDVWSAGIILYILLSGVPPFWGENEKGFIAIIGKQLDL
QSSPWPKISASAKDLIRKMLARDPKKRITAAEALEHPWLKVGGEEASEKPIDSAVLRRLKQFRAMNKLKKLALKVIAENLSEEEIKGLKQMFNNMDTDKSG
TITYEELKDLGLKRLGSRLTEAEIMQLMDAADVDKSGTIDYEFITATMHRHKLKDEEHMFQAFQYFDKNSGYITRDELQAMSQYGMGDDATIDEILED
VDSNKDGRINRYEEFVAMMRKGNPELVNRRRK
>30190.t000579 Org_Rcommunis peptide: 30190.m011343 calcium-dependent protein kinase, putative (PAC:16823697)
MGNCSNLPSTSTFTADRPPPPPPSHGITHVPHPTASPPRPPPPHSLQPTSNRPSAAPAAVGRVLGRPMEDVRSIYAFGRELGRGQFGVITYLVTHKETK
QQFACKSIATRKLINRDDIEDVRREVQIMHHLTGHRNIVELKAYEDRHSVNLVLMELCAGGELFDRIIAKGHYSERAAANLCRQIVTVVHCHSMGVIHR
DLKPENFLFLSTDENSPKATDFGLSVFFKPGDTFKDLVGSAYYVAPEVLRRNYGPAIDIWSAGVILYILLSGVPPFWGETEQAIQFDTVLRGHIDFSSDP
WPSISSAKDLVKMLTADAKDRISAAEVLNHPMRVVDGASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIMGLKEMFKSMDTDNNGTITY
EELKAGLPKLGKTLSESEVKQLEMAADVDGNGTIDYIEFITATMHRMNRMEREDHLYKAFYFDKDKSGYITMEELEHALKEYNMGDARTIKEIIAEVDTD
HDGRINRYEEFVAMMRKGNPELVNRRRK
>96034 Org_Smoellendorffii peptide: 96034 (1 of 1) PF00069//PF13499 - Protein kinase domain (Pkinase)
// EF-hand domain pair (EF-hand_7) (PAC:15404581)
MGNCLGGGDEKKQ SARQALVANVLGQPHKDIKQYITIGRELGRGQFGVITYLCTDKKSAQQFAVKTISKRLMNKDDVDDVKREVQIMKHLTGKDNIVELY
STFEDKSTVYLVLMELCQGELFDRIIVSKGHYTEKAASAVCRTIVKVHTCHSHGVIHRDLKPENFLANKREDAPVKATDFGLSVFFRSQGVFREIVGSA
YYVAPEVLKKSYPGEADVWSAGVILYVLLAGVPPFWAETEQQGIFEAVLRGLHDLNGSPWPTISASAKDLVRKMLKQNPRLRLSAADVLPQHPWIKEDGDAP
DKLIDGEVLSRMKNFSAMNKLKKVALKIISESLSEEEIIKLKDMFKQMDTNSGTITFEELKAGLANQGSNMIDAEIRQLMEAADVDGNGTIDYLEFIQA
SMHLNKMMDRGDHLHAAFQNIIDTDGSGYITMEELEALVKHGLGVEDAKDIIKEVDTDNDGRINRYDEFAMMLKRNTPPAGAGHRRSINDLPVGIKK*
>99178 Org_Smoellendorffii peptide: 99178 (1 of 2) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20
(PAC:15414412)
MKAAGGIAASTPRSAITASVLGRSTESVRELYTLGRKLGQGGQFGVITYLCEVKSSGQYACKTIPKRKLISQEDVDDVRREIQIMHHLGAGQPNVQIKGAY
EDAGSVHLMELCAGGELFDRIIQRGHYSERKAELIRVIVGVVQACHSLGVMHRDLKPENFLLSKHEDSLMKATDFGLSVFFKPGEVTDVVGSPYYV
APEVLRRKKYGEADVWSAGVILYILLSGVPPFWAETEKGIFEQVLKGEIDFESHWPVVISQDAKDLIRKMLCPVPANRLKAHEVLGHPWARADGVADPKP
LDSAVLSRMKQFSAMNKKIKIALRVIAESLSEEEIAGLKEMFKMMDTNSGSIITFDELKAGLERVGSNLVESEIRDLMAAADVDNSGTIDYKEFITATLH
LNKIEREEHLLAFAFYFDKNSGYITKDELQVCAENHMGDEVIEEMMREADQNDGRIDYSEFVTMMRKAGGIGRKTMRNSLSITFRDLLTV*
>Brara.A00300 Org_BrapaPsc peptide: Brara.A00300.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:30636881)

MGNSCRSSSKDKIHQGNNTKPEDSNSKSSDRSTEIIIPQELPKEAHNKDPALVIPLKEPIMRRNMDNQAYYVLGHKTPNIRDLYTLRKLGGQGGFTT
YLCTELATGVGYACKSISKRLKSKEDVEDVRREIQIMHHLAGHGNIVTIKAGYEDSLVHIVMELCAGGELFDRIIQRGHYSERKAAELTKIIVGVVEA
CHSLGVMHRDLKPNFLNKKDDDFSLKAIDFGLSIFFKPGQIFTDVVGSPYVAPEVLLKRYGPEADVMTAGVILYILLSGVPPFWAETQQGIFDAVLK
GYIDFSDPWPVVISDSAKDLIRMLCSKPAERFETAHEVLRHPWICENGVAEPDRALDPAVLRLKQFSAMNKLKKMALKVIAESLSEEEIAGLRREMFQAMD
TDNSGAITFDELKAGLRKYGSTLKDTEIHLMEAADVDNSGTIDYSEFIAATIHNLKLEREEHLVAAFQYFDKDGSGYITIDELQQACVEHSMTDVFLED
IIKEVDQNDGKIDYGEFVEMMQKGNAGVGRRTMRNSLNMISMRDA*

>Brara.A01217 Org_BrapaFPsc peptide: Brara.A01217.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:30638668)
MGCFFSKHRRQTQSDVNVGNVHRSFPTNQSQTHVPRDVTAHSSIPTNQSQTHVSRDVTPEQISTTTQNHNNHPQEQQESKPVNQIIEEYQVFKPLKPIA
LLETETILGKPFQIKRLYTLGHEIGRGQFGITYTCKENSTGNTYACKSILKRLKTRKQDRDDVKKEIQIMQHLSGQQNIVEIRGAYEDRQSIHLVMELC
GGELFDRIIAQGHYSERAAAGVIRSVLNVVQICHFMGMHRDLKPNFLNKKDDDFSLKAIDFGLSIFFKPGQIFTDVVGSPYVAPEVLLKRYGPEADVMTAGVILYILLSGVPPFWAETQQGIFDAVLK
DIWSAGIILYILLCGVPPFWAETKEGIFEEIIGKEIDFESQWPWSISESAKDLVRKLTTMDPRKRISAAQALEHPWIRGGEAPDNPIDSAVLSRMKQFRA
MNKLLKALKVIAESLSEEEIKGLKTMFANMDTDQSGTITYEELKTGLARLGSKLSEAEVKQLMEAADVDNGTIDYIEFISATMHRYLDRDEHLFKAF
QYFDKDNSGFTMDELESAMKEYGMDETSIKEVIAEVDTDNDGRINYEFCAMMRSGTTQPPQKGTSSIPLTD*

>Brara.A01377 Org_BrapaFPsc peptide: Brara.A01377.1.p (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:30640163)
MGHRHSKSKTSSSSSSSDNVVHHVKPSGERRGSSGSGSPVSSSGSGTGGSRSSQNGRILGKPMEDVKGTIDYDLGRELGRGQFGVTHLVTHKTKKVFAC
KSIPTRRLLVQSDDIEDVRREVQIMHHLGSHRNIVDLKAYEDRQSVNLIMELCEGELFDRIIAKGHYSERAAADLCRQMMVHVSCHSMGMHRDLKPE
NFLFLSKDESSPLKATDFGLSVFFKPGDKDLVGSAYYVAPEVLKRYGPEADIWSAGVILYILLSGVPPFWGENETGIFDAILEGKLDFADPWPDPVS
NGAKDLVKKMLTYDPKDRLTASEVLNHPWIKEDGEASDKPLDNVLSRMKQFRAMNKLKKMALKVIAENLSEEEIIGLKEMFKALDNDKNGIVTLEELRT
GLPLKLSKISEAEIKQLMEAADMDGDSIDYLEFISATMHMNRIEREDHLYTAFQYFDKDNSGYITMEELEQAMKKYNMGDDKSKEIIAEVDTDRDGKI
NYEEFVAMMKKGHPVLVTNRNRVNM*

>Brara.B00448 Org_BrapaFPsc peptide: Brara.B00448.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30609053)
MGNCCSQGRDSADNADGYTQDKGITASTAEPSVPQSKHAPPSPPPATKQGPFGVLPGRPMEDVKSSYSLGKELGRGQFGVTHLCTQKATGQQFACKTIK
RKLNVNKEDIEDVRREVQIMHHLTGQPNIVELKGAIEDKHSVHLVMEELCAGGELFDRIIAKGHYSERAAASLLRTIVQIIHTCHSMGVIHRDLKPNFLNKK
SKDENAPLKATDFGLSVFFKPGDKDIVGSAYYIAPEVLKRYGPEADIWSIGVMLYIILLCGVPPFWAESENGIFNAILKGHVDFSSDPWPSLSPQAKD
LVKKMLNSDPKQRLTAAQVLNHPWIKEDGEAPDVLNNAVMSRLKQFKAMNNFKKVALRVIAAGCLSEEEIMGLKEMFKGMDTDDSGTITLLEELRQGLAKQ
GTRLSEYEVQQLMEAADADNGTIDYGEFIAATMHINRLDREEHLYSAFQHFQDKDNSGYITMEELEQALREFGMNDGRDIKEIISEVDGNDGRINYEDEF
VTMMRKGNDPIPKKRRELSFK*

>Brara.B00817 Org_BrapaFPsc peptide: Brara.B00817.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30607754)
MGNCCGRDTGNNNGEPTYENGVSAAESVKASRHPASPPATKQGPFGVLPGRPMEDVKSSYSLGKELGRGQFGVTHLCTQKATGLQFACKTIKRRKAN
KEDIEDVRREVQIMHHLTGQPNIVELKGAIEDKHSVHLVMEELCAGGELFDRIIAKGHYSERAAASLLRTIVQIIHTCHSMGVIHRDLKPNFLNKKDEN
SPLKATDFGLSVFFKPGDKDIVGSAYYIAPEVLKRYGPEADIWSIGVMLYIILLCGVPPFWAESENGIFNAILSGQIDFSTDPWPAISHQAKDLVRKM
LNSDPKQRLTAAQVLNHPWIKEDGEAPDVLNNAVMSRLKQFKAMNNFKKVALRVIAAGCLSEEEIMGLKEMFKGMDTDDSGTITLLEELRQGLAKQGTRLS
EYEVQQLMEAADADNGTIDYGEFIAATMHINRLDREEHLYSAFQHFQDKDNSGYITMEELEQALREFGMNDGRDIKEIISEVDGNDGRINYEDEFVAMMR
KGNPDNPNNKKRREMSFK*

>Brara.B00823 Org_BrapaFPsc peptide: Brara.B00823.1.p (1 of 3) PTHR24349:SF116 - CALCIUM-DEPENDENT
PROTEIN KINASE 7 (PAC:30610970)
MGNCCASPGSDTKSKASRPKTKSNPFYSEAYTTTNSSGTGFKLSVLKDPTGHDISLMDYDLGREVGRGEFGITYLCTDIKTGEKYACKSISKKKLRTAVDI
EDVRREVEIMKHMPKHPNIVTLKDAFEDDDAVHIVMELCEGELFDRIIVARGHYTERAAAAVMKTILEVQVICHKNGVMHRDLKPNFLFANKKENSPLK
AIDFGLSVFFKPGEGFNEIVGSPYYMAPEVLRHYGPEVDIWSAGVILYILLCGVPPFWAETQGVAAIIRSVIDFKRDPWPRVSDTAKDLVRRLMPLD
PKKRLSAAEVLHPWIQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSEEVAGIKEAFEMMDSKKTGKINLEELKHGLHLKQQQIPDPTD
LQILMEAADVDGDTLNYGFEVAVSVHLKMANDEHLKAFSFFDKNQSNYIEIEELREALNDEVDTSSEEVIAAIMQDVDTDKDGRISYEEFAAMMKAG
TDWRKASRQYSRERFNSLSLKLMDRGSLQLEGET*

>Brara.B02654 Org_BrapaFPsc peptide: Brara.B02654.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:30608873)
MGCLSSKHRQEETAAPKSTPITPAQTHVPEHRKPQTPPTHQISAPPATVRDPDITLGPFPEDIRKFYSLGKELGRGQFGITYRCREISTGNTYACKSI
LKRKLISKQDKEDVKREIQIMQYLSGQANIVEIKGAYEDRQSVHLVMEELCAGGELFDRIIAQGHYSERAAAGIIRSVNVVQICHFMGVHRDLKPNFL
LSSKEENAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRSSYGEIDIWSAGVILYILLSGVPPFWAENEGIFDEVVKGEIDFESQWPWSISESA
KDLVRKMLTKDPRRRITAAQVLEHPWIKGGEAPDKPIDSAVLSRMKQFRAMNKLKKLALKVIAESLSEEEIKGLKTMFANMDTDKSGTITYEELKTGLTR
LGSKLSETEVKQLMEAADVDNGTIDYFEFISATMHRYLKDRDEHVYKAFQHFQDKNSGHITRDELESAMKEYGMGDEASIKEVISEVDTNDGRINFE
FCAMMRSGTTQPPQKGLLPFH*

>Brara.B03710 Org_BrapaFPsc peptide: Brara.B03710.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30607565)
MASESRTRWVLPYRTKNLKDYLGRVLGQGGQFGTFLCSHNETGQKLACKSIPKRTLLCQEDCDQVLRREIQIMHHLSEYPNVVRIQSTYEDETSVHLVM
ELCEGELFDRIAEKGHYSERDAKVIKTIVSVVEACHSLGVMHRDLKPNFLFSSSDEASLKSTDFGVSVFCEPDTTFSELVGSAYYVAPEVLLKHYG
RECDVWSAGVILYVLLCGFAPFDAGTDNGIFREILQGKLDFTDPWPSISESAKDLTMKMLESDPKKRLTAHQVLCHPWIVDDTVAPDKPLDFAVVSRK
RFSAMNKLKKMALRVVAERLSEEEIIGLKELFKMIDRDNSTITFKELKDCIRRVGSELVESEIQELLQAADVDGSGTIDYGEFLAATIHNLKLEREENL
VAAFSSFFDKSSGCITLLEELQQAQWQFGIKDSNLDMIKIDIDQNDGQINYEFCAMMRKGNNGVGSIRRTMRNTLNFENFLPE*

>Brara.B03711 Org_BrapaFPsc peptide: Brara.B03711.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30607630)
MVLPHSLVKQDSHTMASERTRWVLPYKTKNLQDDYLLGVRVLGQGGQYGTTFCLTHNETGQKLACKSIPKRLLRQEHFDRVLRREIQIMHHLSENPNVRI
QSTYEDATSVHLVMEELCEGELFERIAKKGHHSEREAALKTKTIVAVIEACHSLGVMHRDLKPNFLFSSCDEEDASIKSIDFGLSVFCKPGSTFSKLVS

AYYVAPEVLRHHYDRECDVWSAGVILYMLLCGFPFPFAGTERGIFRKILQGKLDKETDPWPSISESAKDLIKKMLSESDPKRRRLTAHQVLCHPWIVDDTVA
PDKPLGFAVVSRLKRFSAAMNKLKMLALRVVAERLSEEEIGGLKELFKMIDTDNSGTITFEELKDSVRCVGSSELVESEIQELLQAADVDESGTIDYGEFLA
ATIHLNKLEREENLVAASFDDKASGCITVDELQQAWKQFGIKDSNLDMIKDIDQSDGRIDYGEFVAMMRKGNNGSGDISRGTMRNIQLWNFLDRTE
CFCKSSSYVFNKN*

>Brara.B03712 Org_BrapaFPsc peptide: Brara.B03712.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30608180)
MASESRTRWVLPYKTKNLRDDYVLGRFLGQGYGTSTSLCTHKTETGQKLACKTIPKRKLLCQEDYDDVLRREIQIMHHLSEYPNVVRIQETVEDDTSVHLVM
ELCEGEGELFDRIITQKGYHSERDAKVIKTIIVSVVEACHSLGVVHRDLKPENFLFSSDDESSLLKSTDFGLSVFFKPGATFTDLVGSAYYVAPEVLRNHYG
RECDVWSAGVILYILLCGFPFPFAGTERGIFRKIRQKGVFETSPWPSISESAKDLIGKMLSENPQKRLTAHQVLCHPWIVDDTVAADPKPLDFAVVSRLK
RFSAMNKLKKTALRVVAERLSEEEIGGLKELFKMIDTDNSGTITFEELKDSVRRVGSSELVESEIKELLEAADVDESGTIDYGEFLAATIHLNKLEREENL
VNAFSSFFDKDSSGCITMDELQQAWKQFGIKDSHLDEMIDKIDHDNDGQINYGFEFVAMMRKGNNDVNGISRRRTMRNTLNFNENPLPDESNELS*

>Brara.C00182 Org_BrapaFPsc peptide: Brara.C00182.1.p (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:30618202)
MGNTCVGPSRNGFLHSVSAAMWRPRDAADDSVSQTNVDTASEAVSGELRSPSSDQVLNKPPEQLTMPKPGGTNIEIKAKDNVEIQPESKLEEKETKPKET
KEETPADAKPKPKPKHMKRVTSAGLRTEVLRQKTENFKEFYSLGRKLGGQGFGTITFLCEKSTGKEFACKSIAKRKLLTDEDVEDVRREIQIMHHLSGH
QNVISIKGAYEDVMAVHLVMECCAGGELFDRIIQRGHYTERKAAELTKTIVGVVEACHSLGVMHRDLKPENFLFVSKDEDSLLKTIDFGLSIFFFKPDVDF
TDVVGSPYYVAPEVLRKQYGEADVWSAGVIVYILLSGVPPFWAESEQGFQVLHGDLDFSSDPWPSISESAKDLVRKMLVRDPKKRLTAHQVLCHPWV
QVDGVADPKPLDSAVLSRMKQFSAMNKKFKMALRVIAESLSEEEIAGLKEMFNMDADKSGQITFEELKAGLKRVGANLKESEILDLMQAADVDSGTIDY
YKEFIAATLHLNKIEREDHLFAAFTYFDKDGSGYITPDELQQACEFEGVEDVRIEEMMRDQVQDNDGRIDYNEFVAMMQKGSMTGGGGPVKMGGLEKSFS
NIALKL*

>Brara.C00506 Org_BrapaFPsc peptide: Brara.C00506.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30618726)
MGNCSSGRDSEDGHTQDKGLTDSNTAGPTAEPVQSKHAPSPPPATKQPIGVLPGRPMEDVKASYSLGKELGRGQFGVTHLCTQKATGQQFACKTIA
KRKLVNKEDIEDVRREVQIMHMTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGYHSERAAASLLRTIVQIIHTCHSMGVIHRDLKPENFL
LSKDESSPLKATDFGLSVFYKPGVFKDIVGSAYYIAPEVLRKRYGPEADIWSIGVMYIILLCGVPPFWAESENGIFNAILKSHVDFSSDPWPSISPQAK
DLVKMLNSDPKQRLTAAQVNLNHPWIKEDGEAPDVLDNAEAMNFKKVALRVIAAGLSEEEIMGLKEMFKGMDTDSGGTITLEELRQGLAK
QGTRLSEYEVQQLMEAADADNGTIDYGEFIAATMHINRLDREEHLYSAFHFDKDNSGYITMEELEQALREFGMSDGRDIKEIIEVDGDNDGRINDE
FVAMMRKGNPDQIPKKRRELSFK*

>Brara.C01607 Org_BrapaFPsc peptide: Brara.C01607.1.p (1 of 3) PTHR24349:SF160 - CALCIUM-DEPENDENT
PROTEIN KINASE 24 (PAC:30616615)
MGSCVSSPLKGSPPFGKRPVRRNRNNSHKTSSSNPKFVSSTNLSRLLFQPPSRVLPPEIGDGILLKYELGKELGRGEFGVTHECIEITTRKRFACKRISK
EKLRTIEDVEDVRREVEIMSCLPKHPNIVTFKEAFEDEDAVALVMEICEGELFDRIIVARGHYTERAAASVTKTILEVVVKCHEHGVHRDLKPENFLFS
NGTETAQLKAIDFGLSINFKHGQRFNEIVGSPYYMAPEVLRDRDYGEIDVWSAGVILYILLCGVPPFWAESENGIAHAIVRGHIDFERDPWPKVSKEAKQ
LVKSMMLDANPYSRLTVQEVLEHPWIQNAERAPNVNLGDNVRTNIQGFVLMNRFFKKVLRIVADNLPNEEIAAIVQMFMETMDTKNGHLTFEELRDGLKLN
GQVCPDGDVKMLMDAADTDGNGMLSCEEFVTLSTIHLKRIGCDEHLQEAIFYFDKNGNGFIELDELKEALFDDKLGQGSQWIKDIFFDVLDNKDGRISFD
EFKAMMKSCTDWMASRQYSRALLNLSMKMFEDFGDSAPKQSMEFPFIARKRAKILDSPKNKSMELGLSKTYKPSGLRY*

>Brara.C01607 Org_BrapaFPsc peptide: Brara.C01607.2.p (1 of 3) PTHR24349:SF160 - CALCIUM-DEPENDENT
PROTEIN KINASE 24 (PAC:30616616)
MGSCVSSPLKGSPPFGKRPVRRNRNNSHKTSSSNPKFVSSTNLSRLLFQPPSRVLPPEIGDGILLKYELGKELGRGEFGVTHECIEITTRKRFACKRISK
EKLRTIEDVEDVRREVEIMSCLPKHPNIVTFKEAFEDEDAVALVMEICEGELFDRIIVARGHYTERAAASVTKTILEVVVKCHEHGVHRDLKPENFLFS
NGTETAQLKAIDFGLSINFKHGQRFNEIVGSPYYMAPEVLRDRDYGEIDVWSAGVILYILLCGVPPFWAESENGIAHAIVRGHIDFERDPWPKVSKEAKQ
LVKSMMLDANPYSRLTVQEVLEHPWIQNAERAPNVNLGDNVRTNIQGFVLMNRFFKKVLRIVADNLPNEEIAAIVQMFMETMDTKNGHLTFEELRDGLKLN
GQVCPDGDVKMLMDAADTDGNGMLSCEEFVTLSTIHLKRIGCDEHLQEAIFYFDKNGNGFIELDELKEALFDDKLGQGSQWIKDIFFDVLDNKDGRISFD
EFKAMMKSCTDWMASRQYSRALLNLSMKMFEDFGDSAPKQSMEFPFIARKRAKILDSPKNKSMELGLSKTYKPSGLRY*

>Brara.C01984 Org_BrapaFPsc peptide: Brara.C01984.1.p (1 of 1) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:30618339)
MGNTCTGPKLNPNGFLQSVSAAVWRNQPDESLESNKDDSSKKKSVHGGDNAPSADPTPTPPPVKMANEEAPKCINNNDENPKPKKEAHMKRMASAGL
QIDSVLGRKTENLKEIYSVGRKLGGQGFGTITFLCVDKKTNKLACKTIAKRKLTTPEDIEDVRREIQIMHHLSGHPNVIQIVGAYEDAVGVHVMEICAG
GELFDRIIQRGHYTERKAAELARTIVGVIEACHSLGVMHRDLKPENFLFVSGDEEAALKTIDFGLSVFFKPGETFSDDVGSPPYYVAPEVLRKHYSHCEDV
WSAGVILYILLSGVPPFWDETEQGFQVLKGLDLFVSEPWPSVSESAKDLVRRLIRDPKKRMTAHEVLCHPWARVDGVALDKPLDSAVLSRLKQFSAM
NKLKKAIAKVIAESLSEEEIAGLKEMFKMIDTDNSGHITLLEELKGLDRVGANLKDSEILGLMQAADIDNSGTIDYGEFIAAMVHLNKKIQKEDHLFTAFS
YFDKDGSGYITREELQGGCKQFGLADVHLDDIIEVDKDNDGRIDYSEFVEMMQDTGFGKMGRLVS*

>Brara.C02607 Org_BrapaFPsc peptide: Brara.C02607.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30617300)
MEKPSRRPSSSVLPYETPRLRDHYLLGKKGQGFGTITLCTEKSSSANYACKSIPKRKLVCREDEDYEDVWREIQIMHHLSEHPNVVRIKGTIEDSVFVH
IVMEVCEGELFDRIIVSKGHFSEREAALIKTILGVVEACHSLGVMHRDLKPENFLFDSPNDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYYVAPEVLRK
CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQKGLDFKSDPWTISEGADLIYKMLDRSPKKRISAEALCHFWIVDEQAAPDKPLDPAVLS
RLKQFSQMNKIKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKERE
ENLVVAFSYFDKDGSGYITIDELQQACTEFGLCDTFLDDMIKEIDLNDGRIDFSEFTAMMKKGDGVGRSRTMMKNLNFNIADAFGVEETSSAETDDKPN
*

>Brara.C03333 Org_BrapaFPsc peptide: Brara.C03333.1.p (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:30617367)
MGNVCGPTISGNSFVQAVSAAIWRPRIGAEQQASSHGKEASKEAASSHGKGEASKEAASSHGKAEVSKEASSSEPLDQVQNKPPQVMTSNPRTIPE
AETKSKPEEVKQEVVVQVETTKPETKSETKPDNPKPKHMRVSSAGLRTEVLRQKTENFKEFYSLGRKLGGQGFGTITFLCEKSTGKEFACKSIAKRKLLT
KRKLLTDEDVEDVRREIQIMHHLGHPNVISIKGAYEDVVAVHLVMELCSGGELFDRIIQRGHYTERKAAELARTIVGVLETCVSLGVMHRDLKPENFLF

VSKEEDSLLKTIDFGLSMFFKPDIEFTDVVGSPYYVAPEVLRRKRYGSESDVWSAGVIVYILLSGVPPFWAETEQQGIFEQVLHGDLDFSSDPWPSISEGAK
DLVQKMLVRDPKRRILTAHQVLCHPWVQIDGVAPDKPLDSAVLSRMKQFSAMNKKFKMALRVIAESLSEEEIAGLKEMFKMIDADNSGQITFEELKVGLKR
VGNLKESEILDLMQAEDVNSGTTIDYKEFIAATLHLNKIEREDHLFAAFSYFDKDDSGFITHDELQQACEEFGVEDARIEEMIRVDQDKDGRIDYNEF
VAMMQKGSIMGGGPMKMGLEKSSISLSLK*

>Brara.C03790 Org_BrapaFPsc peptide: Brara.C03790.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:30617675)
MGNCFAKNHGLMKPQQNGQTSRSEVDQTHQDPPSYTPQPRSQTPEKPSSETNQPPWRMAAPAPSPKAAKSSSTSIENAYEDVKLFYTLGKELGRGQFG
VTYLCSTENSTGKKYACKSISKKKLVTKADKDDMRREIQIMQHLSGQPNIVEFKGAYEDEKAVNLVMELCAGGELFDRIIAKGHYSERAAASVCRQIVNVV
KICHFMGVLRDLKPENFLSSSKDDKALIKATDFGLSVFIEEGKVYRDIIVGSAYYVAPEVLRRLRYGKEVDIWSAGIILYILLSGVPPFWAETEKGIFDAI
LEGHIDFESQFPWPSISNSAKDLVRKMLTADPKRRISAADVLGHFWLREGGEASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAENINTEEQGLKAMFAN
IDTNSGTTITYEELKEGLAKLGSKLTEAEVKQLMDAADVDGNGSIDYIEFITATMHRHRESDENLYKAFQHFDDKDGSGYITIDELEVALKEYGMGDDAT
IKEVLSDDVSDNDGRINYEFCAMMRSGNPQQQQQQPPRLF*

>Brara.C04385 Org_BrapaFPsc peptide: Brara.C04385.1.p (1 of 3) PTHR24349//PTHR24349:SF145 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30616576)
MGNCCRSAPASVAREDVKSNSYSGNDHRRKDAAGGKKPAPIRVLGDVPKENIEDRYLLDRELGRGEFGVTYLCIVRSTRDLLACKSISKRLRTDVEDVK
REVAIMQHLPSESSIVTLKEACEDDNAVHLMVMELCGGELFDRIIVARGHYTERAAAGVTKTIMEVVQLCHKHGVIRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGEKFSTIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAEESEQGVQAAILRGIIDFKREPWPNISETAKSLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFRKRALRVIAEFLSTQEVEDIKEMFNKMDTDKDGIVTIEELKAGLRDFGTQLAESEVQMLI
EAVDTKGKGTLDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPQELCEALKEDGGDDCVDVANDIFQEVDTDKDGRISEYEEFAAMMKTGTDWRK
VSRHYSRGRFNSLSIKLMKDGSLNLGNE*

>Brara.D00630 Org_BrapaFPsc peptide: Brara.D00630.1.p (1 of 3) PTHR24349//PTHR24349:SF145 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30621870)
MGNCCRSAPAAVAREDVKSNSYSGRDHHRKDDASGGKKLAPIRVLSEVPKENIEERYLLDRELGRGEFGVTYLCIERSTRDLLACKSISKRLRTAVDIEDVK
REVAIMKHLPKSSSIVTLKEACEDDNAVHLMVMELCGGELFDRIIVARGHYTERAAAGVTKTIVEVVQLCHKHGVIRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGEKFSEIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAEESEQGVQAAILRGIIDFKREPWPNISETAKNLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFRKRALRVIAEFLSTQEVEDIKEMFNKMDTDKDGIVTIEELKAGLRDFGTQLAESEVQMLI
EAVDTKGKGTLDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPQELCEALKEDGGDDCVDVANDIFQEVDTDKDGRISEYEEFAAMMKTGTDWRK
ASRHSYRGRFNSLSIKLMKDGSLNLGNE*

>Brara.D00630 Org_BrapaFPsc peptide: Brara.D00630.2.p (1 of 3) PTHR24349//PTHR24349:SF145 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30621871)
MGNCCRSAPAAVAREDVKSNSYSGRDHHRKDDASGGKKLAPIRVLSEVPKENIEERYLLDRELGRGEFGVTYLCIERSTRDLLACKSISKRLRTAVDIEDVK
REVAIMKHLPKSSSIVTLKEACEDDNAVHLMVMELCGGELFDRIIVARGHYTERAAAGVTKTIVEVVQLCHKHGVIRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGEKFSEIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAEESEQGVQAAILRGIIDFKREPWPNISETAKNLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFRKRALRVIAEFLSTQEVEDIKEMFNKMDTDKDGIVTIEELKAGLRDFGTQLAESEVQMLI
EAVDTKGKGTLDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPQELCEALKEDGGDDCVDVANDIFQEVDTDKDGRISEYEEFAAMMKTGTDWRK
ASRHSYRGRFNSLSIKLMKDGSLNLGNE*

>Brara.D01902 Org_BrapaFPsc peptide: Brara.D01902.1.p (1 of 1) PF00036//PF00069//PF13499 - EF hand (EF-
hand_1) // Protein kinase domain (Pkinase) // EF-hand domain pair (EF-hand_7) (PAC:30622182)
MGSCVSSPLKGSPPFRKRPVRRRKSSTSTNPRVDSSTNLRRILFQPPSRVLPPIGDGIFVKYELGKELGRGEFGVTHECIEITTRERFACKRISKE
KLRTAIDVEDVRREVEIMRSLPKHPNIVSFKEAFEDKEAVYLVMEICEGGELFDRIIVSRGHYTERAAASVAKTILEVVVKCHEHGVIRDLKPENFLFSN
ETETAIDKAIIDFGLSPGQFNEIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAETEAGIAHAIVRGNIIDFERDPWPKVSAEAKEL
VKDMLDANPYSRLTQVEVLEHPWIQNAERAPNVNLGDNVTKIQQFLLMNRFRKKVLRIVADNLPNKEIEEIVQMFRMTBTDKNGRLTFEELRDGLKFKG
TVCPDGDVLMMDAADTDGNGMLSCEEFTVLAHLKRMGCDHLQQAQFYFDKNGNSIELDELKEALFDDDKLGQGNQWIKDIFFDVLDNKDGRISFD
EFKAMMKSGETDWMASRQYSRALLNALSIFKFKEDGGNGNPKFHSMEFPVARKKANILDPKNKSMELVHSRTYKPSGLRN*

>Brara.D02174 Org_BrapaFPsc peptide: Brara.D02174.1.p (1 of 2) PTHR24349:SF128 - CALCIUM-DEPENDENT
PROTEIN KINASE 25 (PAC:30621670)
MGNVCIHMVNNCVDTKSNTWVRPTDLIMDHPVKQLPDKPPQQLMLMHKDDDKPKLETSGEDPKLLEESDSHQEQQEGSTSEERKKRAARIACGNSKRKPH
NVKRLMSAGLQAESVLTKTGHLEKEYNLGSKLGHGQFGTTFVCTEKGTEGEEYACKSIPKRKLENEEDVEDVRREIEIMKHLGQPNVISIKGAYEDAVA
VHMVMELCRGGELFDRIVERGHYSERKAAHLAKVILGVVQTCBSLGVMMHRLKPENFLFVDDQEDSPLKAIDFGLSMFVKPGENFSDVVGSPYYIAPEIL
NKDYGPEADIWSAGVMYIYVLLSGSAPFWGETEEEIFNEVLEGEGLDSSDPWPQVSESADKLRKMLERDPKKRLTAQQVLGHFWIRDEGNAPDTPLDATV
LNRLKKFSETDKLKKIALQVTVRELSEEKIRSLRETFKIIDSEKSGKVITYKELKSILERFDTNLNSDISGLMQMPMNEHLEDTVDYEEFIAAIVRLKEL
QDEEANDRLDSSTKV*

>Brara.D02546 Org_BrapaFPsc peptide: Brara.D02546.1.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT
PROTEIN KINASE 14 (PAC:30623178)
MGNCCGTGGTLIGNDKNKKGFKIANPFSIDYGRHDGDKLVVLKEPTGRDIKRLYNLRELGRGEFGVTYLCSTNETGESFACKSILKKKLRTAVDIDDV
RREAEMRMPEHPNIVTLKETIEDDKAVHLMVMELCGGELFDRIIVARGHYTERAAASVIKIMEVVQMCHKHGMHRLKPENFLFANKKETAPLKAID
FGLSIFFKPGEKFNEIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAETHGVAKAILKSVIDFRRDPLPKVSSNAKDLIKRMLHPDPKL
RLTAQQVLDHPWIQDGKNASNVSLGESVRLKQFTVMNKLKKRALRVIAEHLSEVEASGIIERFQVMDTSNRGKITIQELRLGLRKLGIIVPQDDIQIL
MDAGVDKDGIDINEFVAISVHIRKMGNDHLKKAFFDLKSGYIEIDELDALADEFTTSEEVEAIIYDVTNKDGRISYEEFATMMKTGTDWR
KASRQYSRDRFKNLSRKLMDGSLQSHGDTK*

>Brara.E00252 Org_BrapaFPsc peptide: Brara.E00252.1.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT
PROTEIN KINASE 14 (PAC:30626664)
MGNCCGTAGSLIVNEKLKKGLKANPFSIDYGRHDGDKLVVLKEPTGREIKRLYKLGRELGRGEFGVTYLCSTNETGDFACKSILKKKLRTAVDIDDV
RREAEMRMPEHPNIVTLKETIEDDKAVHLMVMELCGGELFDRIIVARGHYTERAAASVVKIMEVVQMCHKHGMHRLKPENFLFANKKETASLKAID
FGLSVFFKPGERFNEIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAETHGVAKAILKSVIDFRRDPLPKVSSNAKDLIKRMLHPDPKR

RLTAQQVLEHPWLQDGKNAPNVSLGETVVRARLKQFTVMNKLKKRALRVIAEHLSEVEASGKERFQVMDTSNRGKITIEELRIGLRKLGIIVVPQDDIQIL
MDAGVDVKDGYLDVNEFVAISVHIRKMGSEHLKTAFSFFDQNKSGYIEIEELREALANEFDTTSEEVEAIIILDVDTNKDGRISYEEFATMMKTGTDRW
KASKQFSRDRKFNLSIKLKEEGLSNNNCDAE*

>Brara.E01210 Org_BrapaFPsc peptide: Brara.E01210.1.p (1 of 1) PF00036//PF07714//PF13499 - EF hand (EF-
hand_1) // Protein tyrosine kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_7) (PAC:30625067)
MGSCVSSPLKGSFPFKRPARRRNNSSSTKTSSNPKTDTSTSTLSRRLIFQPPSRVLPEPIGDGIFLKYELGKELGRGEFGVTHECIEISTRERFACKRI
SKEKLRTIEDVEDVRREVEIMRSLPKHANIVSFKEAFEDKDAVYLVEICEGGEFDFRIVSRGHYTERAAASVAKTILEVVKVCEHGVHRLDKPENFL
FSNETETAQLKAIDFGLSIFFKPAQRFEIVGSPYYMAPEVLRNRYGPEIDVWSAGVILYILLCGVPPFWAETEEGIAHAIVRGNIDFERDPWPVKSREA
KELVKNMLDANPYSRLTVQVEVLEHPWIQNAERAPNVNLGDGVRTKIQQFLLMNRFFKKVLRVVDNLNPEEIESIIQMFQTMDDTKNGHLTFEELRDGLK
KIGQVCPDGDVKMLMDAADTDGNTLSCEEFTVLAHLKRMGCDEHLQQAFKYFDKNGNGSIELDELKEALFDDDKLGHGGDQWIKDIFFDVDLNDKGRI
SFDEFRRAMKSGTDWKMASRQYSRALLNLSIKMFKEDVDGNGPKSYSMEFPLARKKAKLLDAPKNKSMELVHVKTYRPSGLRN*

>Brara.E01219 Org_BrapaFPsc peptide: Brara.E01219.1.p (1 of 1) PF07714//PF13833 - Protein tyrosine
kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_8) (PAC:30625239)
MGCFWSKNQPPSDGELQNILGKPLGDIKNYYSFGKELGKGNLGTTCMEEILTGRSYACKSIPKGLKSKQEDKEAVKKEIEIMFRLSCQHNIIVSIKSVYE
DRECHVVMELCGGELSSRIEASHYSSEKDSAGILKSIYNALQTCCHSMVVIHRDVKPNFLFSSEVENTVLKATIGFGSSVYIKQETELKRKVESKYLLA
PEVLQKGSYGEKIDISWAGVILYLLLCGKHFPFETESKIRRGSLDLESKPWPCVSESADKDLVKKMLTKDPKSRISASDVLEHSHWIKMQAPYKPIDNVLVLC
MKRFGAMNKLKALNADVDGNGRIDLCEYISATTETNVLVTDENLHKAQFFQFDKDGSGYITKDNLMKHVVGNANAKDIISEVDTDNDGRIDYEEFCAM
MRDGKLPQPGKRRVRIN*

>Brara.E01819 Org_BrapaFPsc peptide: Brara.E01819.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30623678)
MEKANPRRPSNTVLPYQTPRLRDHYLLGKKGQGGFGTTLCTEKSTSANYACKSIPKRLVLCREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVH
LVMEVCEGGELFDRIVAKGHFSEREAVKLIKTILAVVEACHSLGVMHRDLKPNFLFDSPKEDAKLKATDFGLSVFYKPGQYLYDVVGSPPYYVAPEVLKK
CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQKGLDFKSDPWPITISEAAKDLIYKMLERSPKKRISAHEALCHFWIVDEEAAPDKPLDPAVLS
RLKQFSQMNKIKKMLRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRVGSELMSEIEKSLMDAADIDNSGTIDYGEFLAATLHMNMKERE
ENLVAAFSYFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVRRTMMKNLNFNIADAFGVDEQSAQKSD*

>Brara.E02997 Org_BrapaFPsc peptide: Brara.E02997.1.p (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:30626505)
MGNVCVGNLSSGNGFLQTVSAALWKPRIGAEQASSSHGNAQQVPKEAAAEVSKEAVPDQVQNKPPQVMTNPNPSSIPEAETKPKPEPEEAKQEVVVQVET
STKTETKPEPKPEPTKPKETNPETKPDPNPKHMRVRSSAGLRTEVLQRKTENFKEFYSLGRKLQGGFGTTLFCLCKGTGNEYACKSISKRLT
DEDVEDVRREIQIMHHLAGHPNVISIKGAYEDVAVHLVMELCGGELFDRIIQRGHYTERKAAELARTIVGVLETCCHSLGVMHRDLKPNFLFVSREED
SLKKTIDFGLSMFFKPDVEFTDVVGSPPYYVAPEVLRKRYGPESDVWSAGVIVYILLSGVPPFWAETEQGIFQVLHGDLDFSSDPWPSISDGAKDLVQKM
LVRDPKRLTAHQVLCHPWVQIDGVAPDKPLDSAVLSRMKQFSAMNKKFKMALRVIAESLSEEEIAGLKEMFKMIDADNSGQITFEELKAGLKRVGANLK
ESEILDLMQAADVDSNGTIDYKEFIAATLHLNKEIEKEDHLFAAFSYFDKDGSGFITPDELQHACEEFGVEDARIEEMMRDQDKDGRIDYNEFVAMMQK
GSIMGGPMKMGLEKISISLKH*

>Brara.F01336 Org_BrapaFPsc peptide: Brara.F01336.1.p (1 of 3) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:30630361)
MGNVCNVCKPNSSEDSTQPKPTPNDRKPNPYAAGAIVRSPGTTLKDAVIPTSHRTKISKDYILGRELGRGEFGITHLCTDRETREALACKSISKRLRT
AVDVEDVRREIVAIMTLPDPHNVVLRATYEDGENVHLVMELCGGELFDRIVARGHYTERAAAGVARTIAEVMMCHSNGVVRDLKPNFLFANKKEN
SALKAIDFGLSVFFKPGDKFTEIVGSPYYMAPEVLRKRDYGPESDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVIDFKRDPWPQVSESASLVRQM
LDPPAKRLTAQQVLAHPWQIHAHKAPNVPLGDIVRSRLKQFSMMNRFFKKVLRVIAEHLSEVEVIEKDMFSLMDEDNDGRITYPELKAGLQKVGSQLG
EPEIKMLMEVADVVDGNGFLDYGEFVAVIIHLQKIENDELFLKAFMFDDKDGSTYIELDELREALTDELGEFDPVSVLNDIMREVDADKDGRIYNEFVMTM
KAGTDWRKASRQYSRERFKSLSLNLMKDGSLHLHDALTGQSVPV*

>Brara.F02560 Org_BrapaFPsc peptide: Brara.F02560.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:30631163)
MGNSCRGSFKDKVYEGNNSEPEENSRTTTTNDHSPTEAQDFPKEDSNNNPVPVKEPFIRRNMDNQAYYVLGHKTPNIRDLYTLRKLQGGFGTTLCTEV
ATGVYDACKSISKRLISKEDVEDVRREIQIMHHLAGHKNIVTIKAYEDPLYVHIVMEVCAGGELFDRIIQRGHYSERKAAELTKIVGVVEACHSLGV
MHRDLKPNFLLVNKDDDFSLKAIDFGLSVFFKPGQIFKDVVGSPPYYVAPEVLLKHGYPEADVWTAGVILYILLSGVPPFWAETQGGIFDAVLKGDVDFE
SDPWPVSDSAKDLISKMLCSRPSERLTAHEVLRHPWICENGAVAPDRALDPAVLSRLKQFSAMNKLKMKALKVIAESLSEEEIAGLRAMFEAMDTNNSGA
ITFDELKAGLRRYGTLDKTEIRDLMEAADVDNSGTIDYSEFIAATIHNLKLDREHVLVSFAFYFDKDGSGYITIDELQQSCVEHGMTDVFLDVIKEVD
QDNDGRIDYGEFVAMMQKGNAGVGRRTMKNLSNISMARDV*

>Brara.F02597 Org_BrapaFPsc peptide: Brara.F02597.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30631379)
MHHLSEYPNVVRIQDITYEDSNSVHLVMELCGGELFDRIVKKGHYSEREAALKMKTIVGVVETCHSLGVLHRDLKPNFLFASCDDEDASLKSTDFGLSVF
CKPGATFSELVGSAYYVAPEVLHKHYSRECDVWSAGVILYILLCGFPPFWAEESEIGIFRKILQGKLNFTETNPWPSISESAKDLIKKMLEGNPKRLTAHQ
VLCHPWIVDDTVAPDKPLDCAVVSRLKKFSAMNKLKMLRVIAERLSEEEIGGLKEMFKMIDTDSGTITFEELKDSMKRVGSELMSEIEIQLLHAADV
DESGTIDYGEFLAATLHLNKLREENLVAASFDDKDGSGYITIDELQQAWKEFGINDSHLDEMIDQDNDGQIDYGEFVAMMRKGNNGGIGRRTMR
NTLSFENPLPDESING*

>Brara.F03923 Org_BrapaFPsc peptide: Brara.F03923.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:30629157)
MKHSGGNQACFVLGQKTPSIRDLYSLGHKLQGGQGGTTCMCREISTGREYACKSITKRKLISKEDVEDVRREIQIMHHLAGYKNIVTIKAYEDPLYVHI
VMELCGGELFDRIIQRGHYSERKAAELIKIIVGVVEACHSLGVMHRDLKPNFLLVNKDDDFSLKAIDFGLSVFFKPGQIFEDVVGSPYYVAPEVLLKH
YGPEADVWTAGVILYILVSGVPPFWAETQGGIFDAVLKGHIDFSDPWLISDSADKDLIRGMLCSRPSERLTAHQVLRHPWICENGAVAPDRALDPAVLSR
LKQFSAMNKLKQMALRVIAESLSEEEIAGLKEMFKAMDTNNSGAIITFDELKAGLRRYGTLDKTEIRDLMEAADIDKSGTIDYGEFIAATIHNLKLDREE
HLLSAFSYFDKDGSGYITIDELQQACAEQMSDVFLDVIKEVDQDNDGRIDYGEFVAMMQKGIAGRTMRQSNMMLSRKNA*

>Brara.G01743 Org_BrapaFPsc peptide: Brara.G01743.1.p (1 of 2) PTHR24349:SF126 - CALCIUM-DEPENDENT

PROTEIN KINASE 32 (PAC:30633874)
 MGNCCTAGSFPQNDSSNPKPKKKKKQNPFSIDYGLHHNGGGGGGLKLTVLSDPTGREIEQKYTLGRELGRGEFGVTYLCTDKETGGVLACKSILKKKL
 TAVDIEDVRREAEIMRHPPEHNPVTLKETYEDEYAVHLVMECEGGELFDRIVARGHYTERAAAVTKTIEVVQVCHKHGMVHRDLKPENFLFANKKE
 TAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYPGEVDIWSAGVILYILLCGVPPFWAETEQQGVAQAIIRSQDLFRDPWPVKVSEHAKDLIRK
 MLDPDQKRRLTAQQVLDHPWLQONANTAPNVSLGETVTRARLKQFTVMNKLKKRALRVIAEHLSDDEASGIREGFQIMDTSQRGKINIDELKIGLQKLGHNI
 PQDDIQILMDAGDITDKDGYLDCDEFIAISVHLRKMGNDEHLKKAFAFFDQDNNGYIEIEELREALSDEVGTSEEVDVAIIRDVDITDKDGRISYEEFVTMM
 KTGTDWKASRQYSRERFSTSISLKLMDASLHANGDTR*
 >Brara.G03159 Org_BrapaFPsc peptide: Brara.G03159.1.p (1 of 3) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:30635005)
 MGNCIACVNFDEADSKQTKNQTKKRHRVKNPNAHDPDGLRSHGPIRVLPDVPMSHRTQISDKYILGRELGRGEFGITYLCTDRETREALACKSISKRL
 RTAVDVEDVRREVTIMSTIPDHPNVVVKLKATYEDNENVHLMELCEGGELFDRIVARGHYTERAAATVARTIAEVVMCHMNGVMHRDLKPENFLFANKK
 ENSALKAIIDFGLSVLFKPGERFTEIVGSPYYMAPEVLKRDYGPGEVDVWSAGVILYILLCGVPPFWAETEQQGVALAILRGVLDKFRDPWSQISSESASLVK
 QMLNPDPKRLTAQQVLDHPWIQNAKKAPNVPLGDIVSRSLKQFSMMNRLKKKALRVIAEHLISQIEVEVIRDMFTLMDDDNDGKITYPELRAGLKKVGSQ
 LGEPEIKMLMEVADVNGNGCLDYGEFVAVIIHLQKMEDEHFRQAFMFDDKDGSGYIESDELRRALTDELGEPDNSVVIDIMREVDITDKDGRINIDEFVV
 MMKAGTDWKRASRQYSRERFKSLSLNLMKDGSLHLHDALTGQSVAV*
 >Brara.G03397 Org_BrapaFPsc peptide: Brara.G03397.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
 PROTEIN KINASE 29 (PAC:30635009)
 MFRKLNKATRNKRNQTRTKHFFNRMGFCFSKSQTQEIPISSSSDSTPPHRYQPLPKPTNPQTQTSTFTPTPKPKPAPPPSSSGSQIGPILNRPMDLSA
 LYDLHKELGRGQFGITRYCTDKSNGREYACKSISKRLIRQKDIEDVRREVMILQHLTGGQPNIVEFRGAYEDKDNLHVVMELCSGGELFDRIIKKGSYSE
 KEAANIFRQIVNVVHVCHFMGVVHRDLKPENFLVSADDDSPIKATDFGLSVFIEEGKVYKDVVGSAYYVAPEVLHRYNKEIDVWSAGVMLYILLCGVP
 PFWGETEKTIFEAVLEGNLDLESSPWPTISSESADLIRKMLARDPKKRITAAEALAHPLWTDSEVSDKPIDSAVLIRMQKFRAMNKLKKALKVIAENLS
 EEEIKGLKQMFKNIDTDGSGTITFDELRTGLHRLGSKLSEIEIKLMEAADVKDGSITIDYIEFITATMHRHRLEKEEHLLEAFKYFDKDRSGYITRDELK
 HSMTQYGMGDATIDEVINDVDTDNDGRINYEFEFVAMMTKGTTHSDAKLIR*
 >Brara.I00608 Org_BrapaFPsc peptide: Brara.I00608.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
 PROTEIN KINASE 11-RELATED (PAC:30643355)
 MANKSRTRWVLPYTTKNVEDDYFLGQILGQGFQGTFLCTHKKTAQKLACKSIPKRLKLCQEDYDDVLRREIQIMHHLSEFPNVVRIEGAYEDTSSVHVM
 ELCEGGELFDRIVKRGHYSEREAALIKTIVGVVEACHSLGVMHRDLKPENFLFASCDEASLKSTDFGLSVFCKPGATFSELVGSAYYVAPEVLHKKYS
 RECDVWSAGVILYILLCGFPFWDESEFGIFRKILQGKIDFETSPWPSISSESADLIVKMLEKDPKKRLTAHQVLCHPWIVDDKVPADKPLDCAVLSRLK
 NFSAMNKLKMAFRVIAERLSEEEIGGLKELFRMIDTDSGTITFEELKDTVKRVGADLMESEIQELLRSADVDENGSIDYGEFLAATIHNLKLEREENL
 VAAFSFFDKDGSYITVDELQHALKEFGINDSHLDEMIKDIDQDNDGQIDYGEFVAMMRKNGSGGISRRTMRNTLNFANWVASS*
 >Brara.I01019 Org_BrapaFPsc peptide: Brara.I01019.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
 PROTEIN KINASE 6 (PAC:30646539)
 MGNSCRGSFKDKTYEGNNNLPEENSITITHVSSVHSPTTEQDFPKEDNNNNNNKSPLVLVPVKEPFMRNMDNQAYYVLGHKTPNIRDLYTLRSLKLGQGO
 FGTTYLCTEVATGVYACKSISKRLISKEDVEDVRREIQIMHHLAGHKNIIVTIGAYEDPLYVHVIMEVCAGGELFDRIIQRGHYTERKAAELTKIVVG
 VVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFKDVVGSPPYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFD
 AVLKGDIDFESDPWPVISDSADLIRKMLCSNPSERLTAHEVMRHPWICENGAVPADRALDPAVLSRLKQFSAMNKLKMKALKVIAESLSEEEIAGLRAMF
 EAMDTDNSGAIITFDELKAGLRRYGSTLKDTEIQDLMEAADVDNSGTIDYSEFIAATIHNLKLDREEHLVSAFQYFDKDGSGYITIDELQQSCVEHGMDTV
 FLEDVIKEVDQDNDGRIDYGEFVAMMQGNAGIGRRTMRNSLNI SMRDA*
 >Brara.I02207 Org_BrapaFPsc peptide: Brara.I02207.1.p (1 of 3) PTHR24349:SF23 - MAP KINASE-ACTIVATED
 PROTEIN KINASE 5 (PAC:30643178)
 MGCCGSKSLPASDLVTEREPAGTILGKPLVEFKKLYKLGEELGKGFATTYMCQEISTGRSFACKSIPKRLNLSQEAVKTEIEIMENLSGVSNIQFHAS
 YEDKNFVHIVMELCRGGELFDRIHALVKSHRYYTEKDAAGIFKSI VNAVQICHSMNVIHRDVKPENFLFSSDDEESSKLKAIDFGCSVYIEGVELKEKV
 GSLYYIAPEVLREESYKEIDIWSAGVILYILLSGSPFFGNDDEIKKGIIDFDSQPWPCISVGAADLIRMLNKNQKERISAENVLEHPWILSEAPDKPI
 DGVIAEGLSEEEIRSLKTMFESMDTDKSGSITYEELKTGLNRLGSKLPEAEVKQLMEAADVDNGTIDYIEFITATMQRHRLEDEHLHKAFLHFDKDNS
 GYITKDELEIAMKEHGMGDACAKEIISEIDKNYDGKIDYEEFCAMMRSVNLQGLIHH*
 >Brara.I03514 Org_BrapaFPsc peptide: Brara.I03514.1.p (1 of 3) PTHR24349//PTHR24349:SF145 -
 SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30643998)
 MGNCRRSPAAVAREDVKSNSYSGHDHPRKDSSTNGKKSAPIRVLTDPVKENIEDRYLLDRELGRGEFGVTYLCIERATRDLLACKSISKRLRTAVDIEDVK
 REVAIMRHLPKSSSIVTLKEACEDDSAVHLVMECEGGELFDRIVARGHYTERAAAGVTKTIVEVVQLCHKHGVHRDLKPENFLFANKKENSPLKAIDF
 GLSIFFKPGKFSEIVGSPYYMAPEVLKRSYGPEDIWSAGVILYILLCGVPPFWAEESEQQGVAQAILRGIIDFKREPWPNISETAKSLVRQMLEPDPKRR
 LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFKRALRVIAEFLSSQEVEDIKEMFNKMDTDKDGIVTIEELKAGLRDFGTQLAESEVQMLI
 EAVDTKGKALDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPEELCEALKEDGGDDCDVDVANDIFQEVDTDKDGRISYEEFAAMMKTGTDWK
 ASRHYSRGRFNSLSIKLMKDGSLNLGNE*
 >Brara.I03972 Org_BrapaFPsc peptide: Brara.I03972.1.p (1 of 2) PTHR24349:SF126 - CALCIUM-DEPENDENT
 PROTEIN KINASE 32 (PAC:30646230)
 MGNCSSAGSLANNDNNKPTKGRKKQNPFSIDYGLHHNNNGGVKVKPLKLVLTDPGTGREISQKYKLRELGRGEFGVTYLCTDKETEEVFACKSILKK
 KLRTAVDIEDVRREVEIMRHPPEHNPVTLKETYEDEIAVHLVMECEGGELFDRIVARGHYTERAAAGVTKTIVEVVQVCHKHGMVHRDLKPENFLFAN
 KKETAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYPGEVDIWSAGVILYILLCGVPPFWAETEQQGVALAIIRSQDLNFRDPWPVKVSENADL
 IRKMLDPDQKRRLTAQQVLDHPWLQNAKTAPNVSLGETVTRARLKQFTVMNKLKKRALRVIAEHLSDDEASGIREGFQIMDNTQRGKINIDELKIGLQKL
 HAVPQDDLQILMDAGDIDKGYLDCDEFIAISVHLRKMGNGEHLKKAFAFFDQDNNGYIEIEELREALSDEVGTSEEVVEAIIRDVDITDKDGRISYEEFA
 TMMKTGTDWKRASRQYSRERFNSISQKLMQDASLHVNSEAI*
 >Brara.I04763 Org_BrapaFPsc peptide: Brara.I04763.1.p (1 of 3) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:30641261)
 MGNCNVCVRPPNPESKPTPKPKTNQNRKLNPFSTDIFRSPVTRAAKDAVPTSHQTKITDKYILGRELGRGEFGITYLCTDRESREALACKSISKR
 KLRTAVDVEDVRREVSIMSTLPDHPNVVKLRATYEDGENVHLVMECEGGELFDRIVARGHYTERAAAGVARTIAEVMMCHVNGVVRDLKPENFLFAN

KKENSALKAIDFGLSVFFKPGKEFKFKEIVGSPYYMAPEVLKRDYGPVEDVWSAGVVIYILLCGVPPFWAETEQQGVALAILRGVIDFKRDPWPQISESAKSL
VRQMLNPDPTKRLTAQQVLAHPWVQNAKKAPNVPLGDIVSRSLKQFSMMNRFKKKVLRVIAEHLISIQEVEVIKDMFSLMDEDDNDGRITYLELKAQKQV
SGLGEPEIKMLMEVADVDGNGFLDYGEFVAVIHLQKIENDELFLKLAFFDKDGSTYIELDELREALTDELGEPEVSVLNDIMREVSDPKDGRINIDEF
VTMMKAGTDWRKASRQYSRERFKSLINLMKDGSLSLHDLATGQSVPV*

>Brara.J01554 Org_BrapaFPsc peptide: Brara.J01554.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30611977)

MSDSQTMASESRTSVWLPYKTKNLKDDYVLDRLVGQGGFTTFLCTHSETGQKLACKSIPKRKLLCQEDCDDVLREIQIMHHLSEYPNVRIQSTYEDAN
DVHLMELCEGGELFDRIEKKGHYSEREAALKIKTIVAVVEACHSLGVMHRDLKPENFLFSSDDEASLKSTDFGLSVFCKPGATFTQLVGSAYYVAPEV
LHRHYGRECDVWSAGVILYIMLCGFAPFDAGTQYGFIRKILQGGKLDFTSPWPSISESAKDLIKKLMESNPKKRLTAHQVLCHPWIVDDTVAPDKPLDFA
VVSRLKRFSAAMNKLKMLARIVAERLSEEEIGGLKELFKMIDTNSGTITFEELKDSIRRVGSELVESEIQELLQAADVDESGETIDYGEFLAATIHNLK
EREENLVDAFSFFDKDASGCITIDELQQAWNQGFGIKDSHLDEMIKDIDQNDGQIDYGEFVAMMRKGNVNGISRRTRMNTLSFENPPPPQESNE*

>Brara.J01642 Org_BrapaFPsc peptide: Brara.J01642.1.p (1 of 3) PTHR24349:SF116 - CALCIUM-DEPENDENT
PROTEIN KINASE 7 (PAC:30611728)

MGNCCATPGSDSKSKDAKPKTRNNPFYSEAYTTNRSAGFKLSVLKDPDTHDITLMYDLGREVGRGEFGITYLCTDINTGEKYACKSISKKKLRTAVDI
EDVRREVEIMKHMPKHPNIVSLKDAFEDDDAVHIVMELCEGGELFDRIIVARGHYTERAAAVMKTILEVVQVCHKNGVMHRDLKPENFLFANKKETSP
AIDFGLSVFFRPGEGFNEIVGSPYYMAPEVLRRNYGPEVDIWSAGVILYILLCGVPPFWAETEQQGVAQAIIRSVIDFKRDPWPVSDTAKDLVRKMLEPD
PKKRLSAAEVLHESWIQNAKKAPNVSLGETVKARLKQFSVMNKLKRALRVIAEHLSEVEVAGIKEAFEMMDSNKTGKINLEQLKHGLHKLGGQQMADAD
LQILMEAADVDGDTLNYGEFVAVSVHLKMANDEHLKAFSFFDQNGSYIEIEELRQALNDEEDTSSEEVIAAIMQDQVDTDKDGRISYEEFVAMMKAG
TDWRKASRQYSRERFNSLSLKLMDRGSLLQLEGET*

>Brara.J01648 Org_BrapaFPsc peptide: Brara.J01648.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30611859)

MGNCCAHGREPTQEKGLGDGAEASVKASRHSPPATKQGGPIGPVLGRPMEDVKSSSYSLGKELGRGQFGVITYLCTQKATGLQFACKTIAKRLVNKE
DIEDVRREVQIMHHLTGQPNIVELKGAYEDKHNVHLMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIHTCHSMGVIHRDLKPENFLLLNKEENSP
LKATDFGLSVFYKPGEEFKDIVGSAYYIAPEVLKRYKGPEADIWSIGVMYIILLCGVPPFWAEESENGIFNAILSGQIDFASDPWPAISHQAKDLVRKMLN
SDPKQLRTAAQVLNHPWIKEDGEAPDVLNDAVMSRLKQFKAMNNFKKVALRVIAAGCLSEEEIMGLKEMFKGMDTDSGTITLLELRQGLAKQGTSLSEY
EVQQLMEAADADNGTIDYGEFIAATMHINRLDREHLSAFQHFDDKNSGYITMEELEQALREFGMSDGRDIKEIIEVDGDNDGRINYEFEVAMMRK
NPDNPNKKRRELSFDTT*

>Brara.J02143 Org_BrapaFPsc peptide: Brara.J02143.1.p (1 of 3) PTHR24349:SF116 - CALCIUM-DEPENDENT
PROTEIN KINASE 7 (PAC:30612058)

MGNCCGSPSSATIESGHGKPKNNPFFHSNEANGSGAGFKLSVLKDPDTHDISSQYDLGREVGRGEFGVITYLCTDIQTGDYACKSISKKKLRTAVDIGD
VRREVEIMRHPKHPNIVSLKDSFEDDDAVHIVMELCEGGELFDRIIVARGHYTERAAAAVMKTIVEVVQICHKQGMHRDLKPENFLFANKKESALKAI
DFGLSVFFKPGEQFNEIVGSPYYMAPEVLRRNYGPEIDVWSAGVILYILLCGVPPFWAETEQQGVAQAIIRSVIDFKRDPWPVSVESAKDLVRKMLEPDPK
KRLSAAEVLHETWILNAKKAPNVSLGETVKARLKQFSVMNKLKRALRVIAEHLSEVEEAGIKEAFEMMDVNRGKINLEELKYGLQKAGQQIADADLQI
LMEATDVGDTLNYGEFVAVSVHLKMANDEHLKAFNFFDQNGSGYIETEELREALNDELDETSSEEVIAAIMQDQVDTDKDGRISYEEFAAMMKAGTD
WRKASRQYSRERFNSLSLKLMDRGSLLQLAGEA*

>Brara.J02172 Org_BrapaFPsc peptide: Brara.J02172.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30612624)

MGNCCSNGRDSGDNDGTRGITASNAGPTAEASVPQSKHAPSPPPATKQGGPIGPVLGRPMEDVKSSSYSLGKELGRGQFGVTHLCTQKATGQQFACKTIAK
RKLNVKEDIEDVRREVQIMHHLTGQPNIVELKGAYEDKHSVHLMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIVHTCHSMGVIHRDLKPENFLLL
SKDEKAPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLKRYKGPEADIWSIGVMYIILLCGVPPFWAEESENGIFNAILKSHVDFSSDPWPSISPQAKD
LVKMLNSDPKQLRTAAQVLNHPWIKEDGEAPDVLNDAVMSRLKQFKAMNNFKKVALRVIAAGCLSEEEIMGLKEMFKGMDTDSGTITLLELRQGLAKQ
GTRLSEYEVQQLMEAADADNGTIDYGEFIAATMHINRLDREHLSAFQHFDDKNSGYITMEELEQALREFGMNDGRDIKEIIEVDGDNDGRINIDEF
VAMMRKGNPDPIPKRRDLSFK*

>Brara.J02705 Org_BrapaFPsc peptide: Brara.J02705.1.p (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:30611720)

MGNCTCVGPSRNGFLQSVSAAMWRPRDGDSDSVSQSNGDSTSEAAVSGELRSPSPDPHQVLNKPPEHLTMPKPVETAKSDVLETQPEPKPETKADASPAK
PKKPKHMKRVTSAGLRTEVLQRKTENFKEFYSLGRKLGGQGGFTTFLCVEKATGKEFACKSIAKRKLLSDEDVEDVRREIQIMHHLSGHPNIVISIKGAY
EDVVAVHLVMECCAGGELFDRIIQRGHYTERKAAELTRTIVGVVEACHSLGVMHRDLKPENFLFVSKHEDSLKKTIDFGLSMFFKPDVFTDVVGSPPYYV
APEVLKRYKGPEADVWSAGVIVYILLSGVPPFWAEESEQGIFEQVLHGDLDFFSSDPWPSISESAKDLVRKMLVRDPKKRLTAHQVLCHPWVQVGDVAPDKP
LDSAVLSRMKQFSAMNKKFKMALRVIAESLSEEEIAGLKEMFNMDADQSGQITFEELKAGLKRVGANLKESEIIDLMAQADVNSGTIDYKEFIAATLH
LNKIEREDHLFAAFYFDKDGSGYITPDELQQACEEFGVEDVRIEEMMRDQDNDGRIDYNEFVAMMQKGSITGGPVKMGLEKSFSLAKL*

>Brara.K00298 Org_BrapaFPsc peptide: Brara.K00298.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:30646929)

MGNSCRGSFKDKLFQTNNSNKLKEDNSKTSTNVTNSRSSSTNTEEFSPKKDNNSKNSPLVIPSKEPIMRRNMDNQAYYILGHKTPNIRDLYTLRKLGGQ
QFGTTYLCTELTTSVDYACKSISKRKLISKEDVEDVRREIQIMHHLAGHGNIVTIKAYEDFLYVHIVMELCAGGELFDRIIQRGHYSERKAAELTKIIV
GVVEACHSLGVMHRDLKPENFLVNKDDDFSLKAIDFGLSDFFKPGQIFTDVVGSPPYYVAPEVLKRYKGPEADVWTAGVILYILLSGVPPFWAETEQQGIF
DDVLKGYIDFSDPWPVINSARLTAHEVLPMYIHIKAYIYLFAGHFWICKNGVAPDRPLDPAVLSRLKQFSAMNKLKMAKLVIA
ESLSEEEIAGLREMFQAMDTNSGAIITFDELKAGLRKYGSTLKDTEIHDLMEEAADVNSGTIDYSEFIAATIHNLKLEREEHLVAAFQYFDKDRSGYITI
DELQQTCEVHSMTDVFLIEDIKEVDQNNDDQIDYGEFVEMMQKGNAGVGRRTMRNSLNINMRDA*

>Brara.K00706 Org_BrapaFPsc peptide: Brara.K00706.1.p (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:30614569)

MGHRHSKSKSSGPPSSSSSSSSSTNVVHVQPSGERRGSSSGPTPVGSSSTGGSRSAAASQNGRILGRPMENVRGTYDFGKELGRGQFGVITYLVTHKE
TKLFLACKSIPTRRLVHRDDIEDVRREVQIMHHLSGHRNIVDLKAGYEDRHSVNLMELCEGGELFDRIIAKGHYTERAAADLCRQMVMVHSCSMGMV
HRDLKPENFLFSLKEDNSPLKATDFGLSVFCKPGDKFDLVGSAYYVAPEVLKRYKGPEADIWSAGVILFISLVGPPFWGENETGIFDAILKGLDLSA
DPWPTVSAGAKDLVKMLKYDPKDRLTASEVLNHPWIKEDGEASDKPLDNVLSRMKQFRAMNKLKMAKNVIAENLSEEEIIGLKEMFKALDTDKNGIV

TLEELRTGLPKLGKISEAEIKQLMEADMDGDGSDIDYLEFISATMHMMNRIEREDHLYTAFQYFDKNSGYITMEELEQAMKKYNMGDDKSIKEIIAEVD
TDRDGKINYEFEVAMMKGNPELVNRRRVNM*

>Brara.K01255 Org_BrapaFpsc peptide: Brara.K01255.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:30614939)

MACLCINFKKKPKKPIPVSNQENTEFESGESTKKQPLRQQTAPRANIQIVVQPHKLPLVPVISHPQEQQKLMHQPEPISGKPFEDVKETYSLGRELQ
ISSGKNFACKSILKRKLIRTQDREDVRREIQIMQYLSGQPNIVEIKGAYEDRQSVHLMELCEGGELFDKISKRGHYSEKAAAEIIRCVVKVVEICHFMG
VIHRDLKPENFLLSGKDEASAMKATDFGVSVFIEEGKVYKDIVGSAYYVAPEVLKRNYGKEIDWSAGVILYILLCGTPPFWAETDKGIFEEILRGEID
FEFKPWPSISSEAKDLVMNMLKSDPKSRYTASQVLEHPWIREGGEASDKPIDSAILSRMKQLQAMNKLKLLALKFIAQSSSKFDR*

>evm_27.TU.AmTr_v1.0_scaffold00001.145 Org_Atrichopoda peptide:
evm_27.model.AmTr_v1.0_scaffold00001.145 (1 of 2) PTHR24349:SF89 - CALCIUM-DEPENDENT PROTEIN KINASE 29
(PAC:31551023)

MGDCFSKPKFPESPPRRLTPVSNSSPVPSPLPKKEQPTRPANRPSTHQQTRKPPATSPNPSANRQPLPLTSALKSHVSAENTILGKPMVDVSSLYALDREL
GRGQFGVITYLCTERTTGLQYACKSVSKRKLMSKSDVEDIKREVLILQHLTGQPNIVEFKGAYEDKQSVHVMELCSGGELFDRIIAKGSYSERAAAASVCR
AIVNVVYVCHFMGMHRDLKPENFLLTSKDENAALKATDFGLSVFIEEGKVHREIVGSAYYVAPEVLRNYGKEIDVWSAGVILYILLSGVPPFWAETEK
GIFDAILQGDIDFASDPWPSISNSAKDLIRKMLTQDPKNRITASQVLEHPWMKADAASDKPISSAVLTRMKQFRAMNKLKLLALKVIAENLSEEEIKGLK
QMFKNMDTDGSGTITYEELRAGLNRLGSLSEAEVKQLMDAADVDRSGSIDYIEFITATMHRHRLEREENLYKAFQYFDTDNSGFIITRDELEIAMKDYGM
GDDATIKEVIEQVDTDNDGRINYQEFVAMMRK*

>evm_27.TU.AmTr_v1.0_scaffold00002.445 Org_Atrichopoda peptide:
evm_27.model.AmTr_v1.0_scaffold00002.445 (1 of 1) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE
10-RELATED (PAC:31562350)

MGNCCVKVGNSSSSSTSSRRKRHNKEKRPNPFADLGLDPCGTPRLRLVLEEAAVGCNITDKYILGRELGRGEFGVITYLCTDKETREALACKSISKRK
LRTAVDVEDVRREVAIMSSLEPHPNVRLKAAYEDSEAVHLMELCEGGELFDRIIVARGHYSERAAANVTRTIVEMCHKNVGMHRDLKPENFLYANKKEN
APLKAIDFGLSVFFRPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQQVAQAILRVVIDFKRDPWPKVSDSAKSLVRQM
LES DPRRLSAQQVLEHPWLNTAKAPNIPGLDIVSRRLKQFSVMNRFFKKALGVIAEHLSEVEEIIIDRMFKLMDTDNNGKVTFEELKAGLKKVGSQLA
ESEMKLMEAADVDGNGALDYGEFVAVTIHLQRMENDEHFRRAFMFDDKDGSGFIEIDELREALMDESGQTDTEVLNNIMREVDTDKDNRISEEEFVSM
KTGTDRKASRHSYRERFKNLSVNLMDGSLKMTDDFGV*

>evm_27.TU.AmTr_v1.0_scaffold00004.174 Org_Atrichopoda peptide:
evm_27.model.AmTr_v1.0_scaffold00004.174 (1 of 1) PTHR24349:SF161 - CALCIUM-DEPENDENT PROTEIN KINASE 1-
RELATED (PAC:31550478)

MGNCTCVGPSLTKNQGFQTVSAAASGPYRLWRARTPEEMLPPDNTENTDDHHQPNSTETETPIPNKPPETVRIQENESNPTEPTKPKKPNASVMKRISAG
LQIDSVLQRKTEILKEHYSGLRKLQGGQFGTTFLCIEKATGKEYACKSIKRKLTEEDVEDVRREIQIMHHLAGHPNVISIKGAYEDAVAVHVMELCA
GGELFDRIIQRGHYSERKAADLARIIVSVVEACHSLGVMHRDLKPENFLVDTNEESPLKTIIDFGLSIFFKPGETFTDVVGSPYYVAPEVLKHYGPEAD
VWSAGVILYILLSGVPPFWAETEQQGIFEQVLHGELDFSEFPWPGISESAKDLIKRMLMRNPKKRITAHEVLCHPWVQDDGVAPDKPLDSAVLTRLKQFSA
MNKLKMLARVIAESLSEEEIAGLKEMFKMTIDTSGSGSITFEELKAGLKRVGANLDEIHALMEAADI DNNGSIDYGEFIAATLHLNKAEREDHLFAAF
SYFDKDGSGYITQDELQQACEEFGIEDVRLEEMIREVDQDNDGSDIDYNEFVAMMQGNPVFGKKGLQNNFSIGFRGALKLG*

>evm_27.TU.AmTr_v1.0_scaffold00007.62 Org_Atrichopoda peptide: evm_27.model.AmTr_v1.0_scaffold00007.62
(1 of 1) PTHR24349//PTHR24349:SF145 - SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED
(PAC:31557595)

MGNCCRSPAAAAREDVKSNSVHDQSKKEGNSNKKLTVLSGSIKGGVDEKYVVDRELGRGEFGVITYLCIDRSTQELLACKSISKRKLRTTVDIEDVRREV
AIMNHLPIHSNIVSLKETCEDENAVHLMELCEGGELFDRIIVARGHYTERAAAGVTKTIMEVQVCHKHGVIHRDLKPENFLFANKKENSPLKAIDFGLS
IMFKPGETFEISEVSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAESEQQVAQAILRGLIDFKRDPWPSISENAKSLVRQMLEPDPKLRRLTA
KQVLEHPWLQNAKKAAPNVLPGDIVKTRLKQFSMLNRFKRRLRVIAEHLSEIEVEDIKEMFKMMDTDNDGTVTYEEELKAGIQKLGSQLSADVQLMEAV
DADGNGLTDYGEFIAVSLHLQRMANDEHLRKAFSYFDKDGNGFIEPEELREALVEDGITDSVDVANDIFLEVDTDKDGRISEEEFLAMMKTGTDWRKASR
HYSRGRFNSLSIRLMKDGSLNAGSKK*

>evm_27.TU.AmTr_v1.0_scaffold00010.325 Org_Atrichopoda peptide:
evm_27.model.AmTr_v1.0_scaffold00010.325 (1 of 2) PTHR24349:SF131 - CALCIUM-DEPENDENT PROTEIN KINASE
17-RELATED (PAC:31573023)

MGMCLSHQETPPEYPTKPGNHTPHHPSPGNHTPRHGNHTPNHPSPGNHTPHRRSPNHTPPLSPARFFNLPRVGTVLGRPLADVWASYSKKGELGRGQFG
ITHLCTDLSTGRQLACKTIAKRKLTHKDDIEDMRREVQIMHHLAGHESIVELVDSFEDRHSVNLVMGLCSGGELFDRIIKRGHYSEREAAGLVRAMARV
HTCHSMGVVHRDLKPENFLFLSEEDSPLVVTDFGLSVFYKPGDVFKDVGSAYYVAPEVLKRNYGPEIDIWSIGVILYILLCGTPPFWAESDEGIFDEI
MRGLIDFRSEFPWPSISAGAKDLVRKMLNPDPKQRLTAFQVLNHRWTKEDGEASDTPLDNAVLNRLKQFRAMNFKKIALRVIAKGLSEEEIMGLKEMFKG
MDRDKSGTITFEELRRLAAGQSKLTETEVKQLMEAADVDGNGTIDYDEFVTATMRLNKHEDHLYTAFQYFDRDNGSYITKEELEQALREHGLYDGRD
IRDIIAEVDADNDGRINYDEFAAMNKENAEPKAKKRQDIFAYDPK*

>evm_27.TU.AmTr_v1.0_scaffold00017.52 Org_Atrichopoda peptide: evm_27.model.AmTr_v1.0_scaffold00017.52
(1 of 1) PTHR24349:SF166 - CALCIUM-DEPENDENT PROTEIN KINASE 11-RELATED (PAC:31570163)

MKKGLAASIMASPVLRQQNGNLRDLYLIGRKLQGGQFGTTLCTEKTATGKEYACKSIKRKLMEIEDVRREIEIMHLSGHPNVVTIKGAYEDSVFV
HLVMELCAGELFDRIIQKGHYSEKQAHLIKVIVGVVEACHSLGVMHRDLKPENFLFLEDEDAPLKATDFGLSVFVYQGETFTDVVGSPYYVAPEVLR
KHYGPESDVWSAGVILYILLSGVPPFWAETEQQGIFRQILQGPLDFESEFPWPGISESAKDLIRKMLNRNPKKRVTAEHVLCHPWIVDDSVAPDRPLDSAVL
SRLKQFTAMNKLKMKALKVIAESMSEEEIGGLKELFKMIDTDGSGTITFEELKEGLKRVGSELMESEIKALMDAADLDHSGTIDYGEFLAATMHLNKM
EENLASAFSYFDKDGSGYITIDELQQACREFGLSDFHLDMDIQQEIDQDNDGRIDYSEFAAMMRNGGVRKTMRSNLNIMRDLKISDQ*

>evm_27.TU.AmTr_v1.0_scaffold00044.74 Org_Atrichopoda peptide: evm_27.model.AmTr_v1.0_scaffold00044.74
(1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT PROTEIN KINASE 6 (PAC:31575378)

MGNSCRGSFRNTVIQGYKEPTDRSGRTNGSVSDGRSNSDPSHLSQVIAEEFAKDNSKRGNPGSNNIFDLSTKDNIMRRGGENQTYTVLGHKTENIRDL
YTLGRKLGGQFGTTLCTEATGKEYACKSIKRKLISDEVEDVRREIQIMHLSGHPNVVTIKGAYEDSLFVHVMELCSGGELFDRIIQRGHYSER
KAAELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDSSSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLCKHYGPEADVWTAGVILYILLSGVPP

FWAETQQGIFDAVLKGVDFETDPWPVISDSAKDLIKKMLCWRPSERLTAHEVLCHPWICENGVPDRPLDPAVLSRLKQFSAMNKLKKMALRVIAESLS
 EEEIAGLREMTAMDITDMSGAITFDELKAGLKRYGSNLKESEIRDLMDAADVDNSGTIDYGEFVAATVHLNKLEREHLVAAFSYFDKDGSGYITVDELQ
 HACSEHNISDVPIEDIREVDQDNDGRIDYNEFVAMMLKGNGLGRRTMRNSLNVSMDAPGAH*
 >evm_27.TU.AmTr_v1.0_scaffold00103.111 Org_Atrichopoda peptide:
 evm_27.model.AmTr_v1.0_scaffold00103.111 (1 of 1) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN KINASE 14
 (PAC:31567028)
 MGNCSSNPGEFNQKTQKKQKKNPFSVDYPGSYNSSNSGSKPPVLKDPTGRDIASRYDLGRELGRGEFGITYLCTDRDTGEVLACKSISKKKLRTAVDIE
 DVRREVAIMGHLPKHPNIVSLKDTYEDDNAVHLMELCEGGEFDFRIVARGHYTERAAAVVTRTIVEVVLCHKHGVMHRDLKPENFLFANKKETSPKLA
 IDFGLSVFFKPGEHFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAIIRSVIDFKRDPWPKVSDNAKNLVKRMLEPDP
 KLRLTAQEVLDHPWLQNAKKAPNVSLGETVRARLKQFSVMNKLKKRALRVIAEFLSVEEAAGIKDTFQMMDINNNGKITFEELKVGLQKIGQQAQDADVQ
 MLMEAADADGDTLNYAEFVAVSIHLRKGNDHDLRKAFLYFDQNGQSGYIEIEELRDSLADDLADNCEEVINAIHDVDTDKDGRISYDEFATMMKAGTD
 WRKASRQYSRERFTSLSLKLLQDGSLLQLTN*
 >evm_27.TU.AmTr_v1.0_scaffold00158.18 Org_Atrichopoda peptide: evm_27.model.AmTr_v1.0_scaffold00158.18
 (1 of 1) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE 3 (PAC:31561650)
 MGNCNGVPTDEEQHEAAAALPHNSKTGIHVSPAPPPKPVSHLQTHSLASPSPPQHIAIGRILGRPMEDGRSTYIFGKELGRGQFGVTYTMCHTHRET
 KEVLACKSIATRKLITKDDIEDVRREVQIMHHLTGHRNIVELKGAIEDRNSVNLVLMELCAGGEFDRIIAKGHYTERAAATLCREIVTVVHTCHSMGVMH
 RDLKPENFLFLNKDEASPLKATDFGLSVFFKPGEVFRDLVGSAYYVAPEVLRHYGVEADIWSAGVILYILLSGVPPFWAENEHGFIDAILRGHIDFSSD
 PWPSSISGAKELVKMLKADPTDRLSAIQILNHPWIREDGVASDQPIDVTVLTRMKQFRAMNKLKKVALKVIAENLSEEEIMGLKEMFRSMDTDSNGTIT
 FEELKAGLPKLGTRISSEVVRQLMEAADVDGNGTIDYIEFITATMHLNRMEKEDHLYTAFEYFDKDKSGYITMEELEQALKKYNMGDEKTINEIIAEVDT
 DRDGRINYDEFVTMMRKGNDMAANRRRSVTVGAPKYK*
 >evm_27.TU.AmTr_v1.0_scaffold00269.4 Org_Atrichopoda peptide: evm_27.model.AmTr_v1.0_scaffold00269.4 (1
 of 2) PTHR24349:SF131 - CALCIUM-DEPENDENT PROTEIN KINASE 17-RELATED (PAC:31567349)
 MGMCFSQAGRKGPDPDANAEPPSPGPKDPPIATSKPTPTPPPSKPPPIGVPLGRPMEDVRATYIMGKELGRGQFGITHLCTHKATGQPFACKTIAKRKL
 VNKEDIEDVRREVQIMYHLTGQPNIVELKGAIEDKQSVHLMELCAGGEFDRIIAKGHYTERAAAALMRTIVQIVHTCHSMGVHRDLKPENFLLLSKD
 EDAPLKATDFGLSVFFKQGEVFRDIVGSAYYIAPEVLKRYGPEVDIWSIGVMYILLSGVPPFWAENEHGFNAILRGQIDFTSDPWPSSISVGAKDLVK
 KMLNSDPKHLRLTAFQVLSHPWIKDGEAPDPLDNAVLSRLKQFRAMNKKKVALKVIAENLSEEEIMGLKEMFKNMMDTDSNGTITLLEELKQGLSKQGTKL
 SEYEVKQLMEAADADGDTIDYDEFITATMNMNRMDREEHLYTAFQYFDKDNQSGYITPEELEQALLEYGMHDGRDIKDILSEVDADNDGRINYDEFVAMM
 RKGNEANPKKRRDKFV*
 >GSVIVG01000238001 Org_Vvinifera peptide: GSVIVT01000238001 (1 of 1) PTHR24349:SF166 - CALCIUM-
 DEPENDENT PROTEIN KINASE 11-RELATED (PAC:17816817)
 MHRDLKPENFLDFTTAEDAALKATDFGLSVFYKPGETFSDVVGSPYYVAPEVLCKHYGPEADVWSAGVILYILLSGVPPFWAETETGIFRQILQGLDFE
 SEPWPCISETAKELELRKMLDRNPKKRLTAHEVLSPWVVDRLMAPDKPLDSAVLSRLKQFSAMNKLKKMALRVIAEGLSEEEIGGLRELKFMIDTDSNGT
 ITFDELKGLKRVGSSELMSEIRDLMDNAADIDNSGTIDYGEFLAATVHLNKLEREENLVSAFSSFFDKDKSGYITIDELQQAQCEFFGLSEAHLDMDIKEID
 QDNDGQIDYGEFAAMMRKGNNGGIGRRTMRNNLNLGDVLGIPDMRLTN*
 >GSVIVG01001931001 Org_Vvinifera peptide: GSVIVT01001931001 (1 of 1) PTHR24349:SF161 - CALCIUM-
 DEPENDENT PROTEIN KINASE 1-RELATED (PAC:17817910)
 MHRDLKPENFLLVNEEDSLKTIIDFGLSVFFKPGEKFTDVVGSPYYVAPEVLKRYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLHGDLDIFS
 SDPWPSSISESAKDLVRRMLVRDPRRLTAHEVLCHPWVQVDGVAPDKPLDSAVLSRLKQFSAMNKLKKMALRVIAENLSEEEIAGLKEMFKMIDTDSNGQ
 ITFEELKAGLRVGANLKESEIYDLMDAADVDNNGTIDYGEFIAATLHLNKLVEREDHLFAAFSYFDKDKSGYITPDELQQAQCEFFGLSEAHLDMDIKEID
 QDNDGRIDYNEFVAMMQKGNPGIGKGLQTSFSMGEALRKH*
 >GSVIVG01008077001 Org_Vvinifera peptide: GSVIVT01008077001 (1 of 2) PTHR24349:SF167 - CALCIUM-
 DEPENDENT PROTEIN KINASE 10-RELATED (PAC:17820750)
 MELCEGGEFDFRIVARGHYTERAAAGVARTIAEVVRMCHENGVIHRDLKPENFLFANKRESSPLKAIDFGLSVFFRPGERFSEIVGSPYYMAPEVLKRN
 YGPEVDIWSAGVILYILLCGVPPFWAETEQQGVALAILRGVIDFKREPWPQISDNKSLVRQMLEQDPRKRRLTAQQVLEHSLWQNAKKAPNVPLGDIVRTRL
 KQFSCMRNFKKKAMRVIAEHLSEVEVEVIRDMFTLMDTDNDGKVTYEELKAGLRVGSQGLPEIKLLMEVADVDGNGVLDYGEFVAVTTHLQRMENDEH
 FQRAFMFDDKDGNGFIDLIELQEALADESGETDADVVNEIMREVDTDKDGRINYDEFVAMMKTGTDRWKASRQYSRERFKSLSLNLMKDGSLHLEDRITG
 QSIAY*
 >GSVIVG01008749001 Org_Vvinifera peptide: GSVIVT01008749001 (1 of 4) PTHR24349:SF89 - CALCIUM-DEPENDENT
 PROTEIN KINASE 29 (PAC:17821297)
 MGFCFSRPRDIPISSSSSSGDFTNHHYQPIPISSSKESLDIPPLSMSVPKPPTSSQIGTVLGRPLCEITSYIDIGKELGRGQFGITYLCTEKSTGLKY
 ACKSISKRLKLSGKDIEDVKREILILEHLTGQPNIVEFKGAYEDKQNLHLMELCSGGELFDRITAKGSYSEREAADICRQIVTVVHVCHFMGMVHRDLK
 PENFLMVSRENSPLKATDFGLSVFIEDNEVYKDVVGSAYYVAPEVLRYSYGEIDVWSAGVILYILLSGVPPFWGENEKSIFDAVLQGYVDFDSAPWPS
 ISSAKDLIKKMLMKDPKRRITASDALNHPWLREDGEASDKPIDSAVLVRMKQFRAMNKLKKLALKVIAENLSEEDIKGLKQMFNNMMDTDRSGTITFEEL
 KTGLSRLGSKLSELEIKQLMDAVDQNGTLDYTEFITATMQRRHLEKEENLFKAFQFFDKDGSGFITREELKQAMTQYGMGDEATIDEVIDDVDTDKDG
 RINYEFEVAMMKGPQDTELKQR*
 >GSVIVG01010743001 Org_Vvinifera peptide: GSVIVT01010743001 (1 of 3) PTHR24349:SF126 - CALCIUM-
 DEPENDENT PROTEIN KINASE 32 (PAC:17822813)
 MHSYSMNGAHTLIMTSLRNNPMGGCISMPAKAGQKKKAKAKKIIPESGDDVFRKSVTIRPISVLKEPSGKDIYKTYRLGKELGRGEFGVTHQCFDLETG
 EIFACKTISKSLTTEIDIQDVRREVEIMKHLPKHPNIVRLKEAYEDKDNVHLMELCEGGEFDFRIVARGHYTERAAADVTRISIVEILQICHQHGMHR
 DLKPENFLFADASEASPLKAIDFGLSIFFKPGQRFNEIVGSPYYMAPEVLRHYGPEVDVWSAGVILYILLCGVPPFWAETEEGIAQAIKVSVDFERDP
 WPHVSEDAKDLVRSMLDPNPNYRLTVEEVLAPWIKNATSI PNVS LGENVTRIKQFSLMNKFKKRVLRVADNLPNEQRDGIRQIFHMMMDTDKNGNLSF
 EELKDGLHKIGHPVADPDVKMLIEAADMDGTGLNCDFTVTSVHLRKISSDENLSEAFRAFDKNDSGYIEFEELREALREDNLGPNNEQVIQDIIFDVD
 LDKDGRISYDEFKAMMKTGMWKMSRRQYSRAMLNALSMRIFKDKSMPLQNKSMQLENRSMLLKNRSMRLQNQVVF*
 >GSVIVG0101167001 Org_Vvinifera peptide: GSVIVT0101167001 (1 of 3) PTHR24349//PTHR24349:SF145 -
 SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:17823124)

MVDRELGRGEFGYCELEGGGLCHKHGVHRDLKPENFLFANKKENSPLKAIDFGLSIFFFKPGERFSEIVGSPYYMAPEVLKRNYPGEIDIWSAGVILYILL
CGVPPFWAESEQGVQAAILRGLIDFKRDPWPNISESAKSILVRQMLEPDPKRLRLTAKQVLEHSLWLNQAKKAPNVPLGDDVVKARLKQFSMMNRFKRKALRVI
ADHLSTEEVEDIKESFFKMDTDNDGIVSIEELKSGLRKFGSQLAEAEVQMLIETVDTNGKGTLDYGEFVAVSLHLQRMANDEHLRKAFSYFDRDNGNGYIE
RDELRLDALMEDGADCTDVANDIFQEVDTDKDGKISYDEFAAMMKTGTDRKASRHSYRGRFNSLSIKLMKDGSNLNGNE*

>GSVIVG01012730001 Org_Vvinifera peptide: GSVIVT01012730001 (1 of 4) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:17824232)

MGCFSKSERVTERDIKGRSERGAPTQTYHQPPPPQPLKPSHPNTRAIQKPDITLGRPFDDIKHYITLGKELGRGQFGVITYLCTQNSTGNTYACKSILKR
KLVTNKDKEDIKREIQIMQHLTGQPNIVEFKGAYEDRHSVHLVLMELCAGGELFDRIISQGHYSERAAAAICRAIVNVVHICFMGMVHRDLKPENFLLS
KDEAAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRNRYGKEIDIWSAGVILYILLSGVPPFWAETEKGIFDAILQGEIDFESQPWPAISNGAKDL
VRKMLTQDRNKRITSQVLEHPWIREDGEASDKPIDSAVLSRMKQFRAMNKLKLLKLVIAENLSEEEIKGLKAMFTNMDTKSGTITYEELKSGLARLG
SRLESETEVQQLMEAADVDGNGTIDYIEFITATMHRHRLERDEHLYKAFNYFDKDNSGFI TRDELENAMKEYGMGDEDSIKEIINEVDTDKGRINRYKEFC
TMMRSGTQPPVKLF*

>GSVIVG01019446001 Org_Vvinifera peptide: GSVIVT01019446001 (1 of 1) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:17829068)

MHHLTGHRNIVELKGAIEDRHSVNLVLMELCAGGELFDRIIAKGHYSERAAAAALCRQIVTVVHNCHTMGMVHRDLKPENFLFLSTAEDSPLKATDFGLSVF
FKPGDVFVKDLVGSAYYVAPEVLRNRYGAEADIWSAGVILFILLSGVPPFWGENEQSIFDITLGRGHIDFSSDPWPSISNSAKDLVKMLRADPKERLTAID
VLNHPWMKEDGASDKPIDIAVLTRVKQFRAMNKLKLLKLVIAENLSEEEIKGLKEMFKSMDDTNSGTITYEELKNGLPKLGTKLSESEVRQLMEAADVD
NGTIDYIEFISATMHHMNRMEREDHLYRAFEYFDKDKSGYITMEELEHALKRYNMGDEKTIKEIIAEVDTDHDGRINYEFAAMMRKGNPDITNRRRK*

>GSVIVG01022524001 Org_Vvinifera peptide: GSVIVT01022524001 (1 of 1) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:17831346)

MGNTCVGPNLAANGFLQSVSAVWRTRPPEDMLPPNADGSSSGDNAGSDGAKGSDPPMPKAEKSDGNSGKQKKQTHMKRLSSAGLQIDSVLQRNTENLK
EIYSLGRKLQGGQFGTITYLCEKANGKEFACKSIARKRLTTREDVEDVRREIQIMHHLAGHPNVISIVGAFEDAVAVHVMELCVGGELFDRIIQRGHYT
ERKAADLARVIVGVVEACHSLGVMHRDLKPENFLFINQDEDSPLKIDFGLSMFFRPGEIFTEVVGSPYYVAPEVLRKHYGPECVDSAGVITYILLSGV
PPFWDETEQGFIFEQVLKGDLDVSEFPWPSISDSAKDLVRKMLVRDPKKRLTAHEVLCHPWVQVNGVAPDKPLDSAVLTRLKQFSAMNKLKKIAIRVIAES
LSEEEIAGLKEMFKMIDVNSGNTILEELKTGLERVGADLKDSEIIRLQQAADIDNSGTIDYGEFVAAMLHLNLIKEDHLYAFAFSYFDKDGSGYITQDE
LQQACEQFGLAEIHLIEDVIREVDQDNDGRIDYSEFVAMMQDRDFFGKKGYKIT*

>GSVIVG01022606001 Org_Vvinifera peptide: GSVIVT01022606001 (1 of 1) PTHR24349:SF128 - CALCIUM-
DEPENDENT PROTEIN KINASE 25 (PAC:17831388)

MGNNCVGSVMPEHGLFESISNSIWWTRASDKQKSPPPVQNKPPPEEVELINPPEVMKITKEETKPTPTPKRPLLMKRLPSAGLEVLDLVLDKTDHLKEHY
NLGRKLGHGQFGTTFPCVEKETGKEYACKSIARKRLTTREDVEDVRREIQIMHHLAGHSNIIISIKGAYEDAVAVHVMELCTGGELFDRIAKRGHYTERK
AAQLARTIIGVVEACHSLGVMHRDLKPENFLFVNEQEESLKTIDFGLSVFFKPGEIFTDVVGSPYYVAPEVLRKCYGPEADVWSGVITYILLSGVPPF
WAESEQEIEFQEVHLGLDNLFSSDPWPHISESAKDLIRRLVRDPKKRLTAHEVLCHPWQVQDGVAPDKTLDSAVISRLKQFSAMNKLKKMALRVIAENLSE
EEIAGLKEMFKIIDTNSGQITFEELKAGLRKFGANLNEAEIYDLMQAADVDNSGTIDYGEFIAATFHLNKIEREDHLFAAFSYFDKDGSGYITPDELQK
ACEEFGMEDVHLEEMIQEVQDNDGRIDYNEFVAMMQGNNNDFFGKKGLQNGISGFRQPLPVY*

>GSVIVG01023866001 Org_Vvinifera peptide: GSVIVT01023866001 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:17832178)

MGNTCRGSFRGKYFQGYGQPEEQSTSKRNSDRSNSDYSPSSLSNQQLTANIRDLYSGLRKLQGGQFEDVRREIQIMHHLAGHKNILFDRIIQRGHYSERK
AAELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLRKCYGPEADVWTAGVITYILLSGVPPF
WAETQQGIFDAVLKGFIDFESEPWPLISDSAKDLIRKMLCSRPAADRLTAHEVLCHPWICENGVAAPDRSLDPAVLRLKQFSAMNKLKKMALRVIAESLSE
EEIAGLREMFKAMDTDSSGATFDELKAGLRRYGSTLKESEIRDLMDAADVDNSGTIDYGEFIAATVHLNKLEREHLVAAFQYFDKDGSGYITVDELQQ
ACAEHMTDVFLEDIIEVDQDNDGRIDYSEFVAMMQGNAGIGRRTMRNSLMSMRDAPGAF*

>GSVIVG01025249001 Org_Vvinifera peptide: GSVIVT01025249001 (1 of 3) PTHR24349:SF126 - CALCIUM-
DEPENDENT PROTEIN KINASE 32 (PAC:17833278)

MGNCCASPGEKENPYLIDYNVLHGSVSRNRGPVLKDPTGRDISLKYELGREGMGRGEFGVTYMCETKSTNEKYACKSIAKKKLRTAVDIEDVRREVQIMK
RLPMHFNIVSLKDTFEDENAVHIVMELCEGGELFDRIIVSRGHYTERAAAGVMRTIVEVQICHKHGVMHRDLKPENFLFANKKEAAPLKIDFGLSVDFK
HGERFSEIVGSPYYMAPEVLKHNYPGEIDIWSAGVILYILLCGIIPFWAETEQGVQAIRAVVDFKRDWPVKVSDKAKELVKKMLDPDPKKRLTAQEV
DHPWLQDAKSVPNVSLGESVKARLKQFSMMNKLKKALQVMAEHLSMEEVAGIKEAFKTMIDNNRGQINLDELRSGLQKLQGPIDPSDLQILMEAADLDG
DGTLYNAEFVAVSIHIKKITNEEHLHKAFAFFDQNGQSGYIEIEELQNALADELSTNSEEVINAIMHDVDTDKDGRISYEEFAAMMKAGTDWRKASRQYSR
ERFNTLSLKLTRDGKDGQ*

>GSVIVG01033306001 Org_Vvinifera peptide: GSVIVT01033306001 (1 of 3) PTHR24349:SF126 - CALCIUM-
DEPENDENT PROTEIN KINASE 32 (PAC:17839046)

MELCEGGELFDRIIVARGHYTERAAAAVTKTIVEVQMKHKGVMHRDLKPENFLFANKKETAPLKAIDFGLSVFFKPGERFTEIVGSPYYMAPEVLKRN
YGPEDVWSAGVILYILLCGVPPFWAETEQGVQAIRSVLDFKRDWPVKVSENAKDLVKMLDPDPKKRLSAQEVLDHPWLQNAKKAPNVSLGETVRARL
KQFSMMNKLKKRALRVIAEHLVSVEEVAGIKEGFQMLDGTGNKGKINMDELVRVGLQKLGHQIPEQDLQILMEAGDVGDDGLHDYGEFVAISVHLRKMGNDDH
LLKAFEFFDQNNNGSYIEIEELRDALAGELESNSEEVINAIHVDVTDKDGRIISYDEFAAMMKAGTDWRKASRQYSRERFNNLSLKLIRDGSLVLRP*

>GSVIVG01034489001 Org_Vvinifera peptide: GSVIVT01034489001 (1 of 1) PTHR24349:SF117 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:17839939)

MHRDLKPENFLFESTDEDAKLKATDFGLSVFYKPGEVFFEVVGSPYYVAPEVLRKHYGHEVDVWSAGVILYILLSGVPPFWAENDTGIFKEILKGLDFK
SDPWPSISESAKDLIKKMLEMDPKKRISAEVLRCHPWIVDDRVAPDKPLDSAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTNSGT
ITFEELKEGLRKVGSELMESEIKTMDAADIDNSGTIDYGEFLAATLHLNKMEREENLIAAFSFFDKDGSGYITIDELQQACREFGLGDAHLEDEMIREID
QDNDGRIDYGEFTAMMRKGDGGIGSRTMRNNLNFNLADAFGINDTT*

>GSVIVG01037295001 Org_Vvinifera peptide: GSVIVT01037295001 (1 of 1) PTHR24349:SF131 - CALCIUM-
DEPENDENT PROTEIN KINASE 17-RELATED (PAC:17841971)

MGNCCSQGNTNDGPANDKGTIPEPTNPETAAPESSAAQNKPAARKELGRGQFGVTHLCTSKATGEQFACKTIAKRKLVNKEDIEDVRREVQIMHHLTG
QPNIVELKGAIEDKQSVHLVLMELCAGGELFDRIISKGHYTERGAASLLRTIVQIVHTCHSMGVVHRDLKPENFLLLNKDENAPLKATDFGLSVFFKQGEV

NNDGQIDYAEFVAMMQGSNVGLGWQTMESLNLVALRDAPQVH*

>LOC_Os03g03660 Org_Osativa peptide: LOC_Os03g03660.3 CAMK_CAMK_like.17 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (PAC:33128276)

MGNQCQNGTLGSDYHNRFPREHAVGYVQGD SYLDLKKFDDTWPEVNNFKPTAASILRRGLDPTSINV LGRKTADLREHYIIIGRKLGGQGFQGTYYLCTEIN TGCEYACKTIPKRKLITKEDVEDVRREIQIMHHL SGHKNVVAIKDVYEDGQAVHIVMELCAGGELFDRIQEKGHYSEKAAELIRIIVSIVAMCHSLGVM HRDLKPENFLLLDKDDLSIKAI DFGLSVFFKPGQVFTELVGSPPYVAPEVLH KRYGPESDVWSAGVILYVLLSGVPPFWAETQQGIFDAVLKGHIDFQS DPWPKISDSAKDLIRKMLSHCPSERLKAHEVLRHPWICENG VATDQALDPSVISRLKQFSAMNKLK LALRVIAERLSEEEIAGLREMFKA VDTKNRGVITFGELREGLRRFGAEFKDTEIGDIMEAAHNDNNVTIHYEEFIAATLPLNKIEREEHLLAAFTYFDKDGSGYITVDKLRACGEHNMEDSLLEEIISEVDQ NNDGQIDYAEFVAMMQGSNVGLGWQTMESLNLVALRDAPQVH*

>LOC_Os03g03660 Org_Osativa peptide: LOC_Os03g03660.4 CAMK_CAMK_like.17 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (PAC:33128277)

MGNQCQNGTLGSDYHNRFPREHAVGYVQGD SYLDLKKFDDTWPEVNNFKPTAASILRRGLDPTSINV LGRKTADLREHYIIIGRKLGGQGFQGTYYLCTEIN TGCEYACKTIPKRKLITKEDVEDVRREIQIMHHL SGHKNVVAIKDVYEDGQAVHIVMELCAGGELFDRIQEKGHYSEKAAELIRIIVSIVAMCHSLGVM HRDLKPENFLLLDKDDLSIKAI DFGLSVFFKPGQVFTELVGSPPYVAPEVLH KRYGPESDVWSAGVILYVLLSGVPPFWAETQQGIFDAVLKGHIDFQS DPWPKISDSAKDLIRKMLSHCPSERLKAHEVLRHPWICENG VATDQALDPSVISRLKQFSAMNKLK LALRVIAERLSEEEIAGLREMFKA VDTKNRGVITFGELREGLRRFGAEFKDTEIGDIMEAAHNDNNVTIHYEEFIAATLPLNKIEREEHLLAAFTYFDKDGSGYITVDKLRACGEHNMEDSLLEEIISEVDQ NNDGQIDYAEFVAMMQGSNVGLGWQTMESLNLVALRDAPQVH*

>LOC_Os03g48270 Org_Osativa peptide: LOC_Os03g48270.1 CAMK_CAMK_like.21 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (PAC:33127982)

MGNCTCCVAPATTDEVGAPPRDHHAAKSPAPSATTTTATRQRHGQEPKPKPKPRARAKPNPYDWAPPVLPARGGAAAASAVRVLEGVVPHPRLRVTDK YQLGRELGRGEFGVTHLATDRATERLACKSIPKRRLRTAVDADVVRREVAIMASLPDHPALVRLRAAYEDADAVHLVME LDCGGELFDRIVARGRYTERAAAAARTVAEVRACHAGVMHRDLKPENFLYAGKAEDAQLKAI DFGLSVFFRPGERFREIVGSPYMAPEVLRDYGEV DIWSAGVILYIILCGVPPFWAETEQQVARAILRGAAFDREPWPRISRAAKSLVRQMLDVPDRRRPTAQQVLDHPWLHHAARAFNPVPLGDVVRARL KQFSLMNRLKKKAMRVIAEHL SVEEVVVKDMFALMDTDNNGRVTLQELKDGLTKVGSKLAEPPEMELLMEAADVDGNGYLDYGEFVAVTIHLQRLSNDNHLRTAFLFFDKDGSGYIDRAELA DALADDSGHADDAVLHDHILREVDTDKGRISYEEFVAMMKS GTDWRKASRQYSRERFKTSLNSLIKDG SITMAR*

>LOC_Os03g57450 Org_Osativa peptide: LOC_Os03g57450.1 CAMK_CAMK_like.2 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (PAC:33131946)

MGNCTCVGPSISKNGFFQSVSTVLWKARQDGD DALPGANGAPDGGGQGRLPAPPPPTSDAPLAVQNKPP EHVKIVSTTDTASAEQDASKSSAGSDSGEAAR PRPRVPVVKRVSSAGLLVGSVLKRKTESLKD KYSIGRKLGGQGFQGTYYLCTEINATGKEFACKSILKRKLVTD DVEDVRREIQIMYHLAGHPNVISIRGA YEDAVAVHLMELCAGGELFDRIVQKGHYTERKAAELARIVGVVEVCHSMGMHRDLKPENFLFADQTEEAALKTIDFGLSIFFRPGQVFTDVVGSPYY VAPEVLKKKYQEADVWSAGVYIIYLLCGVPPFWAENEQGFEEVLHGR LDFQSEFPWPSISEGAKDLVRRLVDRPKKRLTAHEVLRHPVWQVGLAPDK PLDSAVLSRMKQFSAMNKLKKMALRVIAENLSEDEIAGLKEMFKMIDT DNSGQITFEELKVGLKKVGANLQEEIYALMQAADVNSGTIDYGEFIAATL HMNKIEREDHLFAAFQYFDKDGSGYITADELQLACEEFG LGDVQLEEMIREVDENDGRIDYNEFVAMMQKPTMGLPAKKSGGLQNSFSIGFREALRMS*

>LOC_Os03g57510 Org_Osativa peptide: LOC_Os03g57510.1 CAMK_CAMK_like.23 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (PAC:33131565)

MGNNCVGPSAAGQNGFFANVALWRPRPAD AAPPALPPSSAPSDQAPEVPTIPSEHSSHSSRSTDPSTPTSAAEQPANKAAPKV KRVQSAGLLADSVL KRDVNTARLKDLYTIGKKLGGQGFQGTYYLCTEINATGKEFACKSIAKRKLLTQEDVEDVRREIQIMHHLAGHANVVSIVGAYEDAVAVQLVME LDCGGELFDRIVQKGHYSEKAAQLARIVGVIEACHSLGVMHRDLKPENFLFIHQKEDSPLKAI DFGLSIFFKPGETFTDVVGSPYYVAPEVLMKHYGREVDVWSAG VYIIYLLSGVPPFWDESEQGFIFEQVLKGDLDFSSEFPWNISSES AKDLVRKMLIRDPKKRLTAHEALCHPWVCVDGVAPDKPLDSAVLSRLKQFSAMNKLK KMALRVIAESLSEEEIAGLKEMFKMLD TDNSGHITLEELKTGLQVRGANLMDSEIDALMEAADIDNSGTIDYGEFIAATLHINKVEKEDKLF AAFSYFDK DGSGYITQDELQKACEEFGIGDTRIEDIIGDIDQNDGRIDYNEFVEMMQKGNAMGMKGQHS TGNFGLGEALKLR*

>LOC_Os03g59390 Org_Osativa peptide: LOC_Os03g59390.1 CAMK_CAMK_like.24 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (PAC:33133053)

MGNCCGTPATAEEGGKRRRRRGKQKKANPFTVAYNRPASSAGAAAGRPGLMVLDRDPTGRDLGARYELGGELGRGEFGITYLCTEATGDRYACKSISKRKL RTPVDEDVRREVEIMRHMP SHPNIVSLRAAYEEDNVHLVME LCEGGELFDRIVARGHYTERAAA AVTRTIVEVVQMCHRHGMHRDLKPENFLYANKK DSSPLKAI DFGLSVFFRPGERFTEIVGSPYMAPEVLKRHYGPEVDVWSAGVILYIILCGVPPFWAETEQQVAQAIIRSVVDFKREPWRVSEPAKDLVK RMLDPNPMTRLTAEQVLEHPWLHDSKKMPDIPLGD AVRARLQQFAAMNKLKKALKVIAEHL SAAEADIKDMFDKMDVSKNGQLTFEDFKAGIRKLG NQMPDSDLKILMDAADIDKNGILDYQEFVAVSIHVRKIGNDEHIQKAFSYFDQNKSGYIEIEELREALVDEIDGNDEDIINSIIRVD TDKDGKISYDEFAV MMKAGTDWRKASRQYSRQFSNL SLKLQKDGSISSDTQ*

>LOC_Os04g47300 Org_Osativa peptide: LOC_Os04g47300.1 CAMK_CAMK_like.26 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (PAC:33109983)

MGNCTFKTYEIPITSGTMRRPASTAERSKARGGDEPGTWRRPSFPRHGAPHRPPTGSSSAAGALSRRASGGGGEMGPVLQRAMVSVRSLYQLDRKL GSGQFGTYYLCTERATGNRYACKSVSKRKLVRRTDVDDVRREITILQHLSGQPNIAEFRGAYEDNDHVHLVMEFCSGGELFDRIITAKGSYSE RQAAAACRDILTVVHVCHFMGVIHRDLKPENFLLASADDDAPLKAIDFGLSVFFIEEGKVYKDIVGSAYYVAPEVLQRNYGKEADIWSAGVILYIILCGT PPFWAETKEGIFDAILVNQVDFSTSPWPSISESAKDLIRQLMRDPQKRITASQALEHRWLKEGGASDRPIDSAVLSRMKQFKAMNKLKQLAL KVIAENLSPEEIKGLKQMFNMMDTDRSGTITVEELKVGLTKLSRISEAEVQKLMEAVDVKSGSIDYSEFLTAMINKHKLKEEDLLRA FQHFDKDNGSYITRDELEQAMAEYGMGDE ANIKQVLDEVDKDKDGRIDYEEFVEMMRKGIQT*

>LOC_Os04g49510 Org_Osativa peptide: LOC_Os04g49510.1 CAMK_CAMK_like.27 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (PAC:33112648)

MGNACGGSLSRKYLSFKQTASQRHDTDDNNNA AADSPKKPSRPPAAAKTDDHPVSASAPAAAMRRGQAPADLGSVLGHPTPNLRDLYAMGRKLGGQGF GTTYLCTELSTGVYACKSISKRKLITKEDIEDVRREIQIMHHL SGHKNVVAIKGAYEDQLYVHIVMELCAGGELFDRIIQRGHYSEKAAELTRIIVGVV EACHSLGVMHRDLKPENFLLANKDDDSLKAIDFGLSVFFKPGQFTTDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYIILSGVPPFWAETQQGIFDAV LKGFIDFSDPWPVISESAKDLITKMLNRPKRLTAHEVLRCHPWIRDHGVADRPDLPAVLSRIKQFSAMNKLKKMALRVIAESLSEEEIAGLKEMFQT MDADNSGAIITYDELKEGLRKYGSTLKDTEIDRLMDAADIDNSGTIDYIEFTIATLHLNKL EREEHLVAAFSYFDKDGSGYITVDELQ QACKEHNM PDAFLDDVINEADQDNDGRIDYGEFVAMMTKGNMGVGRRTMRNSLNISMRDAPGAL*

>LOC_Os04g49510 Org_Osativa peptide: LOC_Os04g49510.2 CAMK_CAMK_like.27 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33112649)
MGNACGSSLRSKYLSFKQTASQKRHDTDDNNNAAAADSPKPKPSRPAAAKTDDHPVSASAPAAAMRRGQAPADLGSVGLGHPTPNLRDLIYAMGRKLGGQGF
TTLCTELSTGVDYACKSISKRLITKEDIEDVRREIQIMHHLGSHKNVVAIKGAYEDQLYVHIVMELCAGGELFDRIIQRGHYSERKAAELTRIIVGVV
EACHSLGVMHRDLKPENFLLANKDDDLKAIIDFGLSVFFKPGQTFTDVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAV
LKGFIIDFSDPWPVISESAKDLITKMLNRPKRLTAHEVLCHPWIRDHGVAPDRPLDPAVLSRIKQFSAMNKLKKMALRVIAESLSEEEIAGLKEMFQT
MDADNSGAITYDELKEGLRKYGSTLKDTEIRDLMDAVS*

>LOC_Os05g39090 Org_Osativa peptide: LOC_Os05g39090.1 CAMK_CAMK_like.29 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33159975)
MGNCCRSPPAAAARDVKTSHFPASTGGGKKKPHQARNGGGGGGGGGWEKKRLSVLGEEGSEVNGGIEEKYALDRELGRGEFGVYTLCDRCRSRELLA
CKSISKRLRTPVDVEDVRREIVAIMRHLPRASIVSLREACEDDGAHLVLMELCEGGELFDRIIVARGHYTERAAAATRTIVEVQLCHRHGVIHRDLKP
ENFLFANKKENSPLKAIIDFGLSIFFKPGEKFSEIVGSPYYMAPEVLKRYNGPEIDIWSAGVILYILLCGVPPFWAETEQQGVAQAILRGNIDFKREPWPV
SDNAKDLVRQMLQPDPKRLRLTAQVLEHTWLQNAKKAAPNVPLGDIVKSRLKQFSRMNRFRKRALRVIAHLSAEEVEDIKDMFKVMDTDNDGIVSYEELK
SGIAKFGSHLAESVQMLIEAVDTNNGRAGLDYGEFLAVSLHLQRMANGEHLRRAFLFFDKDNGYIEPEELQEALVEDGATDIMEVVKDILQEVDTDKDG
KISYEEFVAMMKTGTDRWKASRHYSRGRFNSLSIRLIKDGSVKLGNE*

>LOC_Os05g41270 Org_Osativa peptide: LOC_Os05g41270.1 CAMK_CAMK_like.4 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33156904)
MGNCCPPGSSSEPDPPASSGSSRPAGSAGAAASPATISPSAAPAPAKPPAPIGPVLGRPMEDVKSIIYTVGKELGRGQFGVTSCLTHKATGQRFACKTIS
KRKLTSTKEDVEDVRREVQIMYHLAQPGVVELKGAYEDKHAVHLVLMELCAGGELFDRIIAKGHYTEHAASSLLRTIVEIHTCHSMGVIHRDLKPENFLL
LSKDEHAPLKATDFGLSVFFKEGEVFRDIVGSAYYIAPEVLKRSYGPEADIWSIGVMLYILLCGVPPFWAEEHGFINSILRGHVDFSSEFPWSRISHGAK
DLVRMLHSDPKQRISAYDVLNHPWIKEDGEAPDTPLDNAVGLRLKQFRAMNQFKKAALRVIAAGCLSEEEIRGLKEMFKSMDSNSGTITVDELKRLGLAK
KGTKLTEAEVQQLMEAADADNGTIDYEEFITATMNMNRMDREEHLYTAFQYFDKNSGYITIEELEQALREKGLMDGREIKDIISEVDADNDGRINYTE
FVAMMRKGDPEANPKRRRDVVL*

>LOC_Os05g50810 Org_Osativa peptide: LOC_Os05g50810.1 CAMK_CAMK_like.5 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33157415)
MVSSSSSPQSKPKPKPKPLSPPMGARASRHRQSPDQSQSQSPSPHHKHHHHHQTTRAPKPKPKQPPPPQPPQPSQPPPPPRHQPPQAPQAAAEDGVGR
VLGRPMEDVRATYTFGRELGRGQFGVYTLATHKPTGRRYACKSIAARKLARPDLDLDDVRREVMHMHHTLGHNRNIVELRGAYEDRHSVNLVLMELCEGGELF
DRIIARGHYSERAAAAALCREIVSVVHSHCSMGVMHRDLKPENFLFLNKREDSPLKATDFGLSVFFKPGEQFRDLVGSAYYVAPEVLKRLYGAEADIWSAG
VILYILLSGVPPFWAENEDGIFDAVLQGHIDFSSEFPWPSISSGAKDLVKRMLRQDPKERLTAEEILNHPWIREDGEAPDKPLDITVISMKQFRAMNKLK
KVALKVAENLSEEEIVGLKEMFKSLDNDNSGTITLLEELRAGLPKLGTKISESELQRLMEAADVDGNGSIDYVEFISATMNMNRLEKEDHIYKAFEFYFDK
DHSGFITVDELEELTKYDMGDEATIKEIIAEVDTDHDGRINYTEFVAMMKNNSPEIVPNRRRMF*

>LOC_Os05g50810 Org_Osativa peptide: LOC_Os05g50810.2 CAMK_CAMK_like.5 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33157416)
MVSSSSSPQSKPKPKPKPLSPPMGARASRHRQSPDQSQSQSPSPHHKHHHHHQTTRAPKPKPKQPPPPQPPQPSQPPPPPRHQPPQAPQAAAEDGVGR
VLGRPMEDVRATYTFGRELGRGQFGVYTLATHKPTGRRYACKSIAARKLARPDLDLDDVRREVMHMHHTLGHNRNIVELRGAYEDRHSVNLVLMELCEGGELF
DRIIARGHYSERAAAAALCREIVSVVHSHCSMGVMHRDLKPENFLFLNKREDSPLKATDFGLSVFFKPGEQFRDLVGSAYYVAPEVLKRLYGAEADIWSAG
VILYILLSGVPPFWAENEDGIFDAVLQGHIDFSSEFPWPSISSGAKDLVKRMLRQDPKERLTAEEILNHPWIREDGEAPDKPLDITVISMKQFRAMNKLK
KVALKVAENLSEEEIVGLKEMFKSLDNDNSGTITLLEELRAGLPKLGTKISESELQRLMEAADVDGNGSIDYVEFISATMNMNRLEKEDHIYKAFEFYFDK
DHSGFITVDELEELTKYDMGDEATIKEIIAEVDTDHN*

>LOC_Os07g06740 Org_Osativa peptide: LOC_Os07g06740.1 CAMK_CAMK_like.31 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33117996)
MGNTCVGPSSAADRHGFFHSVSLAVLWRPGGRAEPSQPPGYPPRESSHSVTSSTAPERVTIADSDLSSTPNKGGNKPKVRRVQSAGLLADSVLKRDS
RLKDLTYLTKGLKGQGFQGTYYQCVEKATGKVLACKSIAKRLVSEEDVEDVRREIQIMHHLGHPVSVSVIGAYEDAVAVHLVLMELCAGGELFDRIIVQRG
HYSEKAAQALRVIIIGVVEACHSLGVMHRDLKPENFLFVNHKEDSPLKIDFGLSIFFKPGENYSDVVGSPYYVAPEVLMKHGREVDVWSAGVIIYILL
SGVPPFWDESEQGFIEKVLKGDLDSSDPWPAISDSAKDLVRKMLNRDPKRLTAHEALCHPWVCDGVAPDKPLDSAVLTRLKQFSAMNKLKKMALRVI
AENLSEDEIAGLREMFKMLDNDNSGTITLLEELKTLGRRVGANLKDSEITTLMEAADIDNSGSIDYGEFIAATMHLNKVEREDNLFAAFSYFDKDSGGYIT
QDELQKACEEFGIGDAHLEDIIKIDIDQDNDGRIDYNEFTVMQKGNPNLGGKGGQGLSFLGREALKLG*

>LOC_Os07g06740 Org_Osativa peptide: LOC_Os07g06740.2 CAMK_CAMK_like.31 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33117995)
MGNTCVGPSSAADRHGFFHSVSLAVLWRPGGRAEPSQPPGYPPRESSHSVTSSTAPERVTIADSDLSSTPNKGGNKPKVRRVQSAGLLADSVLKRDS
RLKDLTYLTKGLKGQGFQGTYYQCVEKATGKVLACKSIAKRLVSEEDVEDVRREIQIMHHLGHPVSVSVIGAYEDAVAVHLVLMELCAGGELFDRIIVQRG
HYSEKAAQALRVIIIGVVEACHSLGVMHRDLKPENFLFVNHKEDSPLKIDFGLSIFFKPGENYSDVVGSPYYVAPEVLMKHGREVDVWSAGVIIYILL
SGVPPFWDESEQGFIEKVLKGDLDSSDPWPAISDSAKDLVRKMLNRDPKRLTAHEALCHPWVCDGVAPDKPLDSAVLTRLKQFSAMNKLKKMALRVI
AENLSEDEIAGLREMFKMLDNDNSGTITLLEELKTLGRRVGANLKDSEITTLMEAADIDNSGSIDYGEFIAATMHLNKVEREDNLFAAFSYFDKDSGGYIT
QDELQKACEEFGIGDAHLEDIIKIDIDQDNDGRIDYNEFTVMQKGNPNLGGKGGQGLSFLGREALKLG*

>LOC_Os07g33110 Org_Osativa peptide: LOC_Os07g33110.1 CAMK_CAMK_like.33 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33116748)
MGSCSRATSPDSGRGGANGYGYSHQTKPAQTTPSYNHPQPPPPAEVRYTPSAMNPPVPPVPPVAPPKPTPDITLGPYDDVRSVYSLGKELGRGQFGVY
LCTEIASGQYACKSISKRLVSKADKEDIRREIQIMQHLSGQGNIVEFRGAYEDKSNVHVMELCAGGELFDRIIAKGHYSERAAATICRAVVNVVNIC
HFMGMHRDLKPENFLLATKEENAMLKATDFGLSVFIEEGMYRDIIVGSAYYVAPEVLRNRYGKEIDVWSAGVILYILLSGVPPFWAETEKGIFDAILQG
EIDFESQPWPSISESAKDLVRKMLTQDPKKRITSQVLQHPWLDRGEASDKPIDSAVLSRMKQFRAMNKLKKMALKVIASNLNEEEIKGLKQMFNTMDTD
NSGTITYEELKAGLAKGLSKLSEAEVKQLMEAADVDGNGSIDYVEFITATMHRHLKERDEHLFAKAFQYFDKNSGFIITRDELESALIEHEMGDTSTIKDI
ISEVDTDNDGRINYTEEFCAAMMRGGMGQPMRLK*

>LOC_Os07g33110 Org_Osativa peptide: LOC_Os07g33110.2 CAMK_CAMK_like.33 - CAMK includes calcium/calmodulin depeudent protein kinases, expressed (PAC:33116745)

MGSCSRATSPDSGRGGANGYGYSHQTKPAQTTPSYNHPQPPPPAEVRYTPSAMNPPVPPVAPPKPTPDTILGKPYDDVRSVYSLGKELGRGQFGVTY
LCTEIASGKQYACKSISKRLVSKADKEDIRREIQIMQHLGSGQNNIVEFRGAYEDKSNVHVVMELCAGGELFDRIIAKGHYSERAAATICRAVVNVVNIC
HFMGMVHRDLKPENFLLATKEENAMLKATDFGLSVFIEEGKMYRDIVGSAYYVAPEVLRNRYGKEIDVWSAGVILYILLGSGVPPFWAETEKGIFDAILQG
EIDFESQPWPSISESAKDLVRKMLTQDPKKRITSAQVQLQHPWLRDGEASDKPIDSAVLSRMKQFRAMNKLKMKALKVIASNLNEEEIKGLKQMFTNMDDT
NSGTITYEELKAGLAKGLSKLSEAEVQQLMEAADVDNGSIDYVEFITATMHRHKLDERDEHLFAFQYFDKDNSGFI TRDELESALIEHEMGDTSTIKDI
ISEVDTDNDGRINYEFEFCAMMRGGGMQPMRLK*

>LOC_Os07g33110 Org_Osativa peptide: LOC_Os07g33110.3 CAMK_CAMK_like.33 - CAMK includes
calcium/calmodulin depeident protein kinases, expressed (PAC:33116747)
MGSCSRATSPDSGRGGANGYGYSHQTKPAQTTPSYNHPQPPPPAEVRYTPSAMNPPVPPVAPPKPTPDTILGKPYDDVRSVYSLGKELGRGQFGVTY
LCTEIASGKQYACKSISKRLVSKADKEDIRREIQIMQHLGSGQNNIVEFRGAYEDKSNVHVVMELCAGGELFDRIIAKGHYSERAAATICRAVVNVVNIC
HFMGMVHRDLKPENFLLATKEENAMLKATDFGLSVFIEEGKMYRDIVGSAYYVAPEVLRNRYGKEIDVWSAGVILYILLGSGVPPFWAETEKGIFDAILQG
EIDFESQPWPSISESAKDLVRKMLTQDPKKRITSAQVQLQHPWLRDGEASDKPIDSAVLSRMKQFRAMNKLKMKALKVIASNLNEEEIKGLKQMFTNMDDT
NSGTITYEELKAGLAKGLSKLSEAEVQQLMEAADVDNGSIDYVEFITATMHRHKLDERDEHLFAFQYFDKDNSGFI TRDELESALIEHEMGDTSTIKDI
ISEVDTDNDGRINYEFEFCAMMRGGGMQPMRLK*

>LOC_Os07g33110 Org_Osativa peptide: LOC_Os07g33110.4 CAMK_CAMK_like.33 - CAMK includes
calcium/calmodulin depeident protein kinases, expressed (PAC:33116746)
MGSCSRATSPDSGRGGANGYGYSHQTKPAQTTPSYNHPQPPPPAEVRYTPSAMNPPVPPVAPPKPTPDTILGKPYDDVRSVYSLGKELGRGQFGVTY
LCTEIASGKQYACKSISKRLVSKADKEDIRREIQIMQHLGSGQNNIVEFRGAYEDKSNVHVVMELCAGGELFDRIIAKGHYSERAAATICRAVVNVVNIC
HFMGMVHRDLKPENFLLATKEENAMLKATDFGLSVFIEEGKMYRDIVGSAYYVAPEVLRNRYGKEIDVWSAGVILYILLGSGVPPFWAETEKGIFDAILQG
EIDFESQPWPSISESAKDLVRKMLTQDPKKRITSAQVQLQHPWLRDGEASDKPIDSAVLSRMKQFRAMNKLKMKALKVIASNLNEEEIKGLKQMFTNMDDT
NSGTITYEELKAGLAKGLSKLSEAEVQQLMEAADVDNGSIDYVEFITATMHRHKLDERDEHLFAFQYFDKDNSGFI TRDELESALIEHEMGDTSTIKDI
ISEVDTDNDGRINYEFEFCAMMRGGGMQPMRLK*

>LOC_Os07g38120 Org_Osativa peptide: LOC_Os07g38120.1 CAMK_CAMK_like.34 - CAMK includes
calcium/calmodulin depeident protein kinases, expressed (PAC:33116046)
MGNCCTPEGSGRGRKKQQQEQKQKQKEPKQQQQQKKGKKPNPFSIEYNRSSAPSGHRLVLVIREPTGRDIAARYELGGELGRGEFGVTYLTCTERETGDA
YACKSISKKKLRATAVDIEDVRREVDIMRHLPKHPNIVTLTRDTYEDDNVHLVLMELCEGGELFDRIIVARGHYTERAAALVTRTIVEVVMCHKHGMVHRDL
KPNFLFANKKEATAALKADDFGLSVFFTPGERFTEIYGSFYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEKQVAQAIIRSVIDFKRDPWE
RVSDNAKDLVKGLMPLDPRRRLQADQVLDHPWLQNIKKAPNVNLETGVKARLQQFSVMNKFKKHALRYIAEHLVSVEVAGIKDMFEKMDLNKDNMINFDE
LKLGLHKLGHQMAADADVQILMDAADVDNGNSLDYGEFVALSVHLRKIGNDEHLHKAFAFYFDRNQSGYIEIDELRESLADDLGANHEEVINAIIRDVDTDK
DGKISYDEFAAMMKAAGTDWRKASRQYSRERFTSLSLKLQKDGSLQLTTTQ*

>LOC_Os08g42750 Org_Osativa peptide: LOC_Os08g42750.1 CAMK_CAMK_like.37 - CAMK includes
calcium/calmodulin depeident protein kinases, expressed (PAC:33102766)
MGGCYSAYASSRKLGRISKISLVIPDPVPDAEASPRKDGVDGDGDDVRGGGGGCGDDGDDVVAIATTADEFARRYVLGKELGRGEFGVTRRCSDAATG
EALACKTIRKHRLAPPVRVTAAKAAAAHGEDVVKREVAIMRRMSSASSSRGGGAASSAAVVRLREACEDAADGSHVLMELCEGGELFDRIIVARGHYSERA
ANAFRTIVQAVVLRCHSDINREHRLDKPENFLFANKSEDSPLKVIDFGLSVFFKPDRTFTEVNGSAYYMAPEVLRRSYGEQVDVWSAGVILYILLCGVPPF
WGNDEKIAQVILQAGIDFNREPLPRVSNNAKDLVRRMLDNPNSTRLTAQVLEHPWLKNADAPNVSLGDAVRAPNVSLGEIIVRSRLMQFSAMNKFKKALGVARNLPG
EEVDKYVQMFHMDKDKNGHLSLDELLEGLHINGQFPVPEPEIRMLLEAADTDGNGTLDCDEFVTVSVHLKMKSNDEYLAFAFYFDKDGSGFIELDELRE
EVGPNEQAILEILRDVDTDKGRISYQEFELMMKSGADWRNASHFSTRANFSTLSRRICKDITLP*

>LOC_Os09g33910 Org_Osativa peptide: LOC_Os09g33910.1 CAMK_CAMK_like.39 - CAMK includes
calcium/calmodulin depeident protein kinases, expressed (PAC:33142352)
MGGCSAFAVSTRMIRFSRGRVPAAILPVTSNDEPCCSCSPENNNKNDGGGGGCGDGEHQKGSWRRWQYRRCGGGGGGGGGRKNAILGDAADVKTAAAG
FAERYLGAERLGAFTVTRCSDQALTEALCACTIRKRLLRCKGDAEDVREVEILRRISALGAGTQDVVRLDACESSDGVHLMELCEGGELFDRI
FARGHYTERAAAKGFEITVGRVQDLCHENGVMHRDLKPENFLFANKSEDSPLKVIDFGLSVFFKPDRTFTEVNGSAYYMAPEVLRRSYGEQVDVWSAGVIL
YILLCGVPPFWGDNDEKTVTAILQGGINFQREPWPVKVSPHAKDLVSKMLDPPDSTRLTAKVELEHPWLKNADRAPNVSLGEIIVRSRLMQFSAMNKFKKKA
LGVVAKNLPVEEMDKYTQMFHKMDKDNSGNLTLEDLKLGLQINGHPVPETEIEMLLEAGDIDGNGTLDCDEFVTVLLHIKMSNDEYLPKAFKFFDKDGN
GFIEMBELMDALGDELGPTEQVVKDIIRDIDTDKGRISYQEFESMMISGSDWRNASHRYSKANFSSLSRKLCKGNS*

>LOC_Os10g39420 Org_Osativa peptide: LOC_Os10g39420.1 CAMK_CAMK_like.8 - CAMK includes
calcium/calmodulin depeident protein kinases, expressed (PAC:33099225)
MKNSCQNGTYGNVQNSNRQFASRYVDGNDTDCYSGSSRASLAGALRQGLNLKPSVLGKPTPNVRELYTLGRELGGQFGKTYLCTEISTGCQYA
CGTILKSNLRCSDIEDVREIQIMHHLGSGQNNIVTIKDTYEDQAVHIVLMELCAGGELFSLQYQKRGHYSERKAAELIKIIVGIIETCHSHGVHRDLKP
ENFLLLDADDEFVSKAIDFGLSVFFRPGQVFRREVVGSPYYIAPEVLEKRYGPEADIWTAGVILYVLLTGVPVPPFWADTQSGIYEKVLDRIDFKSNRPRI
SDSAKDLIKKMLCPYPSERLKAHEVLKHPWICDNGVATNRALDPSVLPRLKQFSAMNRLKLSLQIIAERLSEEEIIVGLREMFKAMDTKNRSVVTFGELK
GLKRYSSVFKDTEINDLEAADDTTSTINWEEFIAAAVSNLKIIEKHLMAAFTYFDKDGSGFITVDKLGKACMERNMEDTFLIEMILEVDQNNDDGQIDY
AEFVTMMQSNFGLGWQTVESLNLVALREAPQVY*

>LOC_Os11g04170 Org_Osativa peptide: LOC_Os11g04170.1 CAMK_CAMK_like.42 - CAMK includes
calcium/calmodulin depeident protein kinases, expressed (PAC:33163826)
MGQCCTGGGKAVAGDEAEPGTSKAAAPPSTSSKNGSAKQPCSPAAKAAATEAAAAAASSKKPAGIEVLERPMEEVRTTYSIGKELGRGQFGVTHLC
THKATGEKLACKTIAKRKLANKEDVDDVREVVQIMHHLGSGQNNIVDLRGAYEDKHNHVLVLMELCAGGELFDRIIARGHYTERAAAAALLRAIVGIVHTCHS
MGVIHRDLKPENFLLLSKGDAPLKDFTGLSVFFKEGEVFRDIVGSAYYIAPEVLEKRYGPEADIWSIGVMLYIFLAGVPPFWAEESENAIFTAILRGQI
DLASEPWPKISSGAKDLVRKMLNINPKERLTAQVQLNHPWIKEDGDAPDVPLDNVVLNRLKQFRAMNQFKKAALRIAGCLSEEEIKGLKEMFKNIDKN
SGTITLLEELKNGLAKGQTKFSDNETEQLEMAAADADGNGIIDYEEFVTATVHMNMKDREEHLYTAFQYFDKDNSGYITKEELEQALKEQGLYDANEIKDVI
TDADSNNDGRIDYSEFVAMMRKSGSCAEATNPKKKRRDLVL*

>LOC_Os11g07040 Org_Osativa peptide: LOC_Os11g07040.1 CAMK_CAMK_like.43 - CAMK includes
calcium/calmodulin depeident protein kinases, expressed (PAC:33164500)
MOPDPGSGSGDGNANAKALAPPVTAAGGRPVSVLPKHTANVRDHYRIGKKGLOGOGFTTYLVCVDKASGGFEACKSIPKRKLLCREDYEDVWREIOIM

HLSEHPNVVRIRGAYEDALFVHIVMELCAGGELFDRIIVAKGHYTERAAQLIRTIVAVVEGCHSLGVMHRDLKPENFLFASAAEDAPLKATDFGLSMFYK
PGDKFSDVVGSPYYVAPEVLQKCYGPESDVWSAGVILYILLCGVPPFWAETEAGIFRQILRGKLDSESEWPWSISDSAKDLVRNMLCRDPTKRLTAHEVL
CHPWIVDDAVAPDKPIDSAVLSRLKHFSA MNKLLKLMALRVIAESLSEEEIGGLKELFKMIDTDDSGTITFDELKEGLKRVGSELTEHEIQALMEADIDN
SGTIDYGEFIAATLHMNKLREENLVSAFSFFDKDGS GFITIDELSQACREFGLDLHLEDMIKDQNDGQIDYSEFTAMMRKGNAGGAGRRTMRNSL
QLNLGEILNPSNS*

>LOC_Os12g03970 Org_Osativa peptide: LOC_Os12g03970.1 CAMK_CAMK_like.44 - CAMK includes
calcium/calmodulin depe dent protein kinases, expressed (PAC:33153859)
MGQCCCTGGGKAVAGDEAEPGTSKAAPP SRGTSSKNGSAKQQPCSPA AKAATEAAAASSSKKPAGPIGEVLERPMEEVRTTYSIGKELGRGQFGVTHLC
THKATGEKLACKTIAKRKLANKEDVDDVREVEQIMHHLSGQPNIVDLRGAYEDKHNVHLMELCAGGELFDRIIARGHYTERAAAAALLRAIVGIVHTCHS
MGVIHRDLKPENFLLLSKGGDAPLKATDFGLSVFFKEGEVFRDIVGSAYYIAPEVLKRKYGPEADIWSIGVMYIIFLAGVPPFWAESENAFIAAILRGQI
DLASEFPWKISSGAKDLVRKMLNINPKERLTAFQVLNHPWIKEDGADPVDLNVVLNRLKQFRAMNQFKKAALRIIAGCLSEEEIKGLKEMFKNIDKDN
SGTITLLEELKNGLAKQGTKFSDNEIEQLMEAADADGNGIIDYEEFVTATVHMNMKDREEHLYTAFQYFDKDNSGYITKEELEQALKEQGLYDANEIKDVI
TDADSNNDGRIDYSEFVAMMRKSGCAEATNPKKRRDLVL*

>LOC_Os12g07230 Org_Osativa peptide: LOC_Os12g07230.1 CAMK_CAMK_like.45 - CAMK includes
calcium/calmodulin depe dent protein kinases, expressed (PAC:33152950)
MQPDPQPHGRGREKAAGAGPRLPPVPTAPSVGRPASVLPKHTANVRDHYRIGKKGQGGFQGTYYLVCVGKPDGGEYACKSIPKRKLLCREDYEDVWREIQI
MHHLSEHPNVVRIRGAYEDALFVHIVMELCAGGELFDRIIVAKGHYTERAAALLIRTIVGVVEGCHSLGVMHRDLKPENFLFASTAEDAPLKATDFGLSVF
YKPGDKFSDVVGSPYYVAPEVLQKIYGP EADVWSAGVILYILLCGVPPFWAETESGIFRQILRGKLDLESDPWPWSISDSAKDLVRNMLIRDPTKRFTAHE
VLCHPWIVDDAVAPDKPIDSAVLSRLKHFSA MNKLLKLMALRVIAESLSEEEIGGLKELFKMIDTNSGTITYDELKNGLKRKRVGSDLMPEPIQALMDAAD
DNSGTIDYGEFLAATLHMNKLREENLVSAFTFFDKDGS GFITIDELSQACEQFGLSDVHLEDMIKDQNDGQIDYSEFAAMMRKGNAGGANAGGVTS
TGGTGRRTMRNSLRVNLGDILKPEN*

>LOC_Os12g12860 Org_Osativa peptide: LOC_Os12g12860.1 CAMK_CAMK_like.46 - CAMK includes
calcium/calmodulin depe dent protein kinases, expressed (PAC:33151749)
MGNCCVSRPSGADKRRRCGSSTAPHTRGGRRVIGAA NMRLSTVSSVSDAARAVMSNEPATVLGNSGSSGNGGVMAAEEMLRRYEIGEELGRGEFGVTRR
CRDVAITGERLACKSISKRKLSSVDVEDVRREVAIMRSLPAHANVVRLEAFEDADAVHLVMEVCEGELFDRIIVARGHYTERAAAVMRTIMDVVQHCH
KNGVMHRDLKPENFLYANASENSPLKVIDFGLSVCFKPGARFNEIVGSPYMAPEVLKRN YGQEIDIWSAGVILYILLCGVPPFWAETDEGIAQAIIRSH
IDFQREPWPVKVSDNAKDLVRRMLDPNPYTRLTAAQQVLEHPWIQNASAAPNIPLGEAVRSRLKQFTVMNKFKKKALLVVAEYLPTEELDAIRELFNMLDTK
KKGHLTLEELRKGLQVIGHNIHDTDVDMLMEAADIDGNGILDCKEFVTVSIHLKKIRSDEHLPKVFSFFDKNGSGYIEIEELKEALSPRGDQKSIDDIFL
DVDIDDKGKISYEEFELMMSAGMDWRNASRQYSRAVYNTLSRKIFKEVSLKLDHSGPLVAAGK*

>LOC_Os12g30150 Org_Osativa peptide: LOC_Os12g30150.1 CAMK_CAMK_like.47 - CAMK includes
calcium/calmodulin depe dent protein kinases, expressed (PAC:33154342)
MGNVCIGPRRNFAKNGLLGILRPRHAAPSSPSQPTTTSRISIPVVLPSAPSSKPPPTQTAPPVPVVI SEPPPPQPPPEQPAAPSQPPPPQEQSPPPPPA
SSNTTQQPPPPQQRQSSRAKPAHIKRISAGLQVESVLRKRTENLKD KYS LGRKLGQGGF GTTYLCVDKANGGEYACKSIAKRKLLTDEDVEDVRREIQ
IMHHLAGHPNIISIRGAYEDAVAVHVMELCAGGELFDRIIVRKGHYTERQAAGLARVIVAVVESCHSLGVMHRDLKPENFLFVGNEEDAPLKTI DFGLSM
FFRPGEVFTDVVGSPYYVAPEVLKKS YGQEADVWSAGVILYILLCGVPPFWAETE QGIFEQVLHGTLDFESDPWPVNVDGAKDLLRKVLVRDPKKRLTAH
EVLCHPWLQMSG SAPDKPLDSAVLSRLRQFSAMNKLKLMALRVIAENLSEEEIAGLKEMFKMMDTNSGQINYEELKAGLERVGANMKESEIYQLMQAAD
IDNSGTIDYGEFIAATLHLNKVEREDHLYAAFQYFDKDGSGYITSDELQACDEFGIEDVRLEDMIGEVDQDNDGRIDYNEFVAMMQKTTTGFGKKGHN
FSGFRDALKSHS*

>Mapoly0004s0215 Org_Mpolymorpha peptide: Mapoly0004s0215.1.p (1 of 3) PTHR24349:SF81 - CALCIUM-
DEPENDENT PROTEIN KINASE 20 (PAC:33015907)
MTKSGSIRYKVPNSILQRETENPKDLFIIGRRLGAGQFGTYSCTEKATGKEYACKVIPKRKLLLKEDAEDVRREIQIMHLLSGHPNIVDIKAYEDTGN
VYVMVMELCAGGELFDRIITQRGHYSEAQASAAIRAI LEAIEICHELGVFHRDLKPENFLADKDEDAPLKVIDFGLSTYFKIDEVFTDIVGSPYYIAPEVL
LRNYGPEADVWSAGVILYILLSGIPFWAENEDAI FKLILTS D VVFMSETWKSISLPAKD LIQKMLIRNPLKRPTAREALMHPW IQEDGVAPDVMPDPIV
QCRLKKFSAMNKLKMAIRVIAENLSEEEIAGLKEIFKMVDTNSSTITFEELKIALRRFGSVLKDSEIHDLLDAADV DQNGIIDYGEFIAATISLNKVS
QQENLHIAFQYFDRDNGSYITKDELQACVEHHLKDVQVDMIKELDKDNDGRIDYNEFSAMFTRVN SGLSRRASRNSLSTFGTC*

>Mapoly0007s0233 Org_Mpolymorpha peptide: Mapoly0007s0233.1.p (1 of 1) PF00069//PF13499 - Protein
kinase domain (Pkinase) // EF-hand domain pair (EF-hand_7) (PAC:33022332)
MGNTCLGSSVGKNGFFQGVTHPNSTYTPWGRQNSFTSQGNSGTSPANRRSSEPNSAIRSKDLNENSSSNLVSHQESSFDTP IYPFATQHRPPVANHIPGG
AAAQPGKGPQSAANHRPSHTT VTVADPVNPGDPMARRAQPVSVVPGQSLTHSVLQRTTEPLKELFTLGRKLGQGGF GTTYLCIEKSTGREYACKSIAKRK
LISQEDVEDVRREIQIMHLLSGHPNIVMIKAYEDSSSVHLMELCAGGELFDRIIQRGHYSEAKAAALTRTIVGVQACHSLGVMHRDLKPENFLLANR
HEDAPLKATDFGLSVFFKPEEVFTDVVGSPYYVAPEVLKRKYGPEADVWSAGVILYILLSGVPPFWAETE QGIFEQVLRGDIDFMSDPWP TISESAKDLI
RKMLHPNPAKRLKAHQVLSHPW IQEAGVAPDRPIDPAVQSR LKQFSAMNKLKLMALRVIAESLSEEEIAGLKEMFKMMDTNSGTITFEELKAGLKR VGS
DLMESEIHELMEAADVDRGDAIDYGEFIAATINLNKIEREENLFAAFSYFDKDKSGYITVDELQACVDHNLGDVRIDEMIREVDQDNDGRIDYNEFVTM
MRKGNNGGIGRHTMRNSLRSASLSDVLMEEVQQRMVNTHVDPR AAGHRDNVNGGRK*

>Mapoly0017s0021 Org_Mpolymorpha peptide: Mapoly0017s0021.1.p (1 of 2) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:33005537)
MGNCCACGSPKPHPKSQKSNVYSGDGYP SKVLVFKDVKGQENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRKLRTAVDVEDVRREVAVMH
HLPSPHNIVTLRGVYQDDAAVHLMELCEGGELFDRIIARGHYSEREA AVTRTIVEVVQVCHKHRVMHRDLKPENFLFANKENNSPLK AIDFGLSCFFT
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETE QGVALAILRGVLD FSRDPWPVKVSDNAKSLVRHMLEADPKSRYTAQQVL
QHPWLQNAKAPNAALGDAVRARL KQFSAMNKLK KALRI IAEHLSGEEIEGLRDMFQMMDTNSGAITFEELKAGLQKIGSQLAESEVRLMDAADVDG
NGTLDYGEFVAAS IHLQRMNDNEHLQKAFAHFDRNGSGYIDMDELRDALGDDLGPNDTDV IQDIMHEVDTDKDQGISYEEFASMMRTGT DWRKASRHYSR
ELFNSLSTRLFRDGSFQAGNYSSREKR*

>Mapoly0017s0021 Org_Mpolymorpha peptide: Mapoly0017s0021.2.p (1 of 2) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:33005538)
MGNCCACGSPKPHPKSQKSNVYSGDGYP SKVLVFKDVKGQENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRKLRTAVDVEDVRREVAVMH

HLPSHPNIVTLRGVYQDDAAVHLMELCEGEGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFANKENNSPLKAI DFGLS CFFT
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETE QGVALAILRGVLD FSRDPWPKVSDNAKSLVRHMLEADPKSRYTAQQVL
 QHPWLQNAKKAPNAALGDVAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLMDAADVDG
 NGTLDYGEFVAASIIHLQRM DNEEHLQKAFAHFDRNGSGYIDMDEL RDALGDDLGPNDTDV IQDIMHEVDTDKDGQISYEEFASMMRTGT DWRKASRHYSR
 ELFNSLSTRLFRDGSFQAGNYSREKR*

>Mapoly0017s0021 Org_Mpolymorpha peptide: Mapoly0017s0021.3.p (1 of 2) PTHR24349:SF167 - CALCIUM-
 DEPENDENT PROTEIN KINASE 10-RELATED (PAC:33005539)
 MGNCACGSPKPHPKSQKSNVYSGDGYPSKVLVFKDVKQGENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRLRTAVDVEDVRREVAVMH
 HLPSHPNIVTLRGVYQDDAAVHLMELCEGEGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFANKENNSPLKAI DFGLS CFFT
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETE QGVALAILRGVLD FSRDPWPKVSDNAKSLVRHMLEADPKSRYTAQQVL
 QHPWLQNAKKAPNAALGDVAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLMDAADVDG
 NGTLDYGEFVAASIIHLQRM DNEEHLQKAFAHFDRNGSGYIDMDEL RDALGDDLGPNDTDV IQDIMHEVDTDKDGQISYEEFASMMRTGT DWRKASRHYSR
 ELFNSLSTRLFRDGSFQAGNYSREKR*

>Mapoly0089s0009 Org_Mpolymorpha peptide: Mapoly0089s0009.1.p (1 of 1) PTHR24349:SF95 - CALCIUM-
 DEPENDENT PROTEIN KINASE 3 (PAC:33014564)
 MGNCVGGHSDRKNGLNPNEPAPTNVQRGTGAPQGTGGAGTAGVSAHGSTPAPMGGISAKQKPTLTGNVLRPLEDVRSIYTLGRELGRGQFGVTHLCTH
 KVTGELLACKSIAKRKLTKNDDEDVVRREVQIMHHLEGQKNIVELKAYEDKHNHVLVLMELCAGGELFDRIIQRGHYSERAAAAALCRTIVQVVTCHSLG
 VMHRDLKPENFLANKKEDAPLKATDFGLSVFFKPGEVFTDQVIFRKIQGRVDYNSYPWPSISASAKDLVRRMLDMNPKTRITALEVLNHPWVAVDGVAPTE
 TSDPWSLQKAKDLVKSMLKQNPKE RLTAHEVLSHPWISVDGEAPDKPLDNVLSRLKQFTAMNKLK LKALKVAESLSEEEIMGLKEMFKSMDTDNSG
 TITFEELKDG LQKQGSNLAESEVRQLMAAADVDNGTIDYLEFITATMHLNKEIEDHLYAAAFQHFDDQSSGFTIMEELEQALIKHGMGDPDTLKEIIRE
 VTDHDGRINRYDEFVAMMRKGTGPHGQEGHRRSISNMAPVGAPRQH HHHK*

>Mapoly0214s0015 Org_Mpolymorpha peptide: Mapoly0214s0015.1.p (1 of 3) PTHR24349:SF81 - CALCIUM-
 DEPENDENT PROTEIN KINASE 20 (PAC:33016405)
 MAPTRPPAMKMTGNPIADSVLQRKTEDVNEVYTLGHKLQGGQFGVTFYFCQEKATGQTYACKSIAKRKLVLQDDVEDVRREIQIMHHLSGHPNVVTIKDA
 YEDETHVHLMELCAGGELFDRIIVKKNYSEAAAALSTRITVGVIAACHSLNMHRDLKPENFLMANKTEESPLKTTDFGLSVFFKPGETFTNLVGSPPY
 IAEVLNKLKGPEADVWAGVILYILLSGVPPFWGETDQVIFRKIQGRVDYNSYPWPSISASAKDLVRRMLDMNPKTRITALEVLNHPWVAVDGVAPTE
 PFDPAVQTRLKQFSAMNKLKKMALRVIAESLSAEETAGLKEMFKAMDADNSGNITFDELKGG LKRVGSKLSESEI HDLMEAADVDQDGTIDYGEFIAATV
 SLSKVEKEENLFAAFSYFDKDKSGYITVDELQACIDHNLGEVRIEEMLEIDQNNDGRIDYNEFVKMMRMGR LNI*

>MapolyY_A0006 Org_Mpolymorpha peptide: MapolyY_A0006.1.p (1 of 2) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:33010283)
 MGNCACGSPKPHPKSQKSNVYSGDGYPSKVLVFKDVKQGENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRLRTAVDVEDVRREVAVMH
 HLPSHPNIVTLRGVYQDDAAVHLMELCEGEGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFASKDANSPLKAI DFGLS CFFT
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETE QGVALAILRGVLD FSRDPWPKVSDNAKSLVRHMLEADPKCRYTAQQVL
 QHPWLQNAKKAPNTALGDVAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLMDAADVDG
 NGTLDYGEFVAASIIHLQRM DNEEHLQKAFAHFDRNGSGYIDMDELREALGDDLGPNDTDV IQDIMHEVDTDKDGQISYEEFASMMRTGT DWRKASRHYSR
 ELFNSLSTRLFRDGS LQAGNYSREKR*

>MapolyY_A0006 Org_Mpolymorpha peptide: MapolyY_A0006.2.p (1 of 2) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:33010284)
 MGNCACGSPKPHPKSQKSNVYSGDGYPSKVLVFKDVKQGENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRLRTAVDVEDVRREVAVMH
 HLPSHPNIVTLRGVYQDDAAVHLMELCEGEGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFASKDANSPLKAI DFGLS CFFT
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETE QGVALAILRGVLD FSRDPWPKVSDNAKSLVRHMLEADPKCRYTAQQVL
 GHPWLQNAKKAPNTALGDVAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLMDAADVDG
 NGTLDYGEFVAASIIHLQRM DNEEHLQKAFAHFDRNGSGYIDMDELREALGDDLGPNDTDV IQDIMHEVDTDKDGQISYEEFASMMRTGT DWRKASRHYSR
 ELFNSLSTRLFRDGS LQAGNYSREKR*

>Medtr0028s0170 Org_Mtruncatula peptide: Medtr0028s0170.1 (1 of 3) PTHR24349:SF131 - CALCIUM-DEPENDENT
 PROTEIN KINASE 17-RELATED (PAC:31092213)
 MGNCSSQGGDTPADNPAVADKGETNTNQDNEPSTNPITTPPTSKPPQSTAPPSSKPSKPAAVGPVLQRP MEDVRATYSIGKELGRGQFGVTHLCTHKVT
 KEQFACKTIAKRKLVNKEDIEDVVRREVQIMHHLTGQANIVELKAYEDKQSVHLMELCAGGELFDRIIAKGHYTERAAASLMRTIVQIIHTLHSMGVIIH
 RDLKPENFLLLNKDENAPLKATDFGLSVFFKEGEMFKDIVGSAYYIAPEVLKRRYGP EVDIWSIGVMLYILLSGVPPFWAESEHGIFNAILRGHIDFTSD
 PWPSISPAAKDLVRKMLNSDPKQRLTA FEVLNHPWIKEDGEAPDKPIDNAVLNRLKQFRAMNQFKKVALRV IAGCLSEEEIMGLKEMFKGMDTDNSGTIT
 VEELKQGLAKQGTKLSEQEVKQLMDAADADNGTIDYDEFITATMHHMNMNREEHLYTAFQYFDKDNSGFTITTEELDQALREYNMHDGRDIKEILQEVDG
 DNDGRINRYDEFAAMMRKGNPEAHTKKRRDSFVSH*

>Medtrlg026190 Org_Mtruncatula peptide: Medtrlg026190.1 (1 of 7) PTHR24349:SF89 - CALCIUM-DEPENDENT
 PROTEIN KINASE 29 (PAC:31099703)
 MGHCFTKPHDNRPVPSIDYGTNSQPPQRNPQPRYPHPIIAKSDPTSYSASSSNANASDHHQPILGRPYIDMKTLYSIGKELGRGQFGVVTYLC TENAT
 GRNYACKSISRRLTRKKEIEDVKREIMILQDLSGQPNIVEFKGAYEDRESVHLMELCLGGELFDRIITAKGSYSEREAASIFKQIMNVVHACHFM
 VMHRDLKPENFLLLASKDHPKATDFGLSVFIEEGKVYKELVGSAYYVAPEVLKRSYKKEID IWSAGIILYILLSGVPPFWAETEKGIFQAILEGKLD
 LESAPWPSISVAAKDLIRKMLSYPDKKRITASDALEHPWMKEGGEASDKPLDNV LIRMKQFRAMNKMKKLALKVAENLSDEEIKGLKQMFNNIDTDRS
 GTITYEELKSGLSKLSKLESEIKQLMDAADVDKNGTIDYHEFITATINRHKLEREENLFKAFQYFDKDNSGYVTREELRQALAEYQMGEATIDEVID
 DVDTDNDGRINRYQEFATMMRKGTLDNDDKEKPR*

>Medtrlg041150 Org_Mtruncatula peptide: Medtrlg041150.1 (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
 PROTEIN KINASE 1-RELATED (PAC:31095901)
 MGNTCVGSPSISKNGI IQSFSAI IWRSQPPDAEGSVSNRGNEDNEPESPLPVQNKPP EQUITMPKPEIKQEAKSEPESEKEKKHRRPSVKRSSSAG
 LRVDVSLQRETGNFKEFYSLGKKLQGGQGTFTFLCIEKATGYQYACKSIAKRKLVTDEDEDVRREIQIMHHLAGHPNVISIKGAYEDAMAVHVMELCA
 GGELFDRIIQRGHYTERKAAELIRITVGVVEACHSLGVMHRDLKPENFLFVNQQEDSLLKTI DFGLSVFFMPGDTFIDVVGSPYYVAPEVLKRYGPEAD

VWSAGVILYILLSGVPPFFWAESEQGIFEQVLRGDLDFVSDPWPAPSESASAKDLVRKMLVRDPKRRMTAHQVLCHPWIQVDGVAPDKPLDSAVLSRLKQFSA
MNKLKMLIVIAESLSEELAGLKEMFKMIDTNSGQITFEELKVGLKKVGANLKESEIYDLMQAADVDNSGTIDYGEFIAATLHINKIEREDHLFAAF
SYFDKDGSGYITQEELQQACDEFKIDVRLEEEIIEIDEDNDGRIDYNEFAAMMQKGNLPMVGKKGLENNFSIRFKEALKL*

>Medtr1g041150 Org_Mtruncatula peptide: Medtr1g041150.2 (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:31095900)
MGNTCVGPSISKNGIIQSFAAIWRSQPPDAEGSVSNRGSVNEGRTDNEPESPLPVQNKPEQITMPKPEIKQEAKSEPESEKEKKKRRPSVKRSSSAG
LRVDSVLQRETGNFKEFYSLGKKLGQGGFTTFLCIEKATGYQYACKSIAKRKLVTDEDEDVRREIQIMHHLAGHPNVISIKGAYEDAMAVHVMELCA
GGELFDRIIQRGHYTERKAAELIRTVGVVEACHSLGVMHRDLKPNFNFVNQQEDSLLKTIIDFGLSVFFMPGDTFIDVVGSPYYVAPEVLKKRYGPEAD
VWSAGVILYILLSGVPPFFWAESEQGIFEQVLRGDLDFVSDPWPAPSESASAKDLVRKMLVRDPKRRMTAHQVLCHPWIQVDGVAPDKPLDSAVLSRLKQFSA
MNKLKMLIVIAESLSEELAGLKEMFKMIDTNSGQITFEELKVGLKKVGANLKESEIYDLMQAADVDNSGTIDYGEFIAATLHINKIEREDHLFAAF
SYFDKDGSGYITQEELQQACDEFKIDVRLEEEIIEIDEDNDGRIDYNEFAAMMQKGNLPMVGKKGLENNFSIRFKEALKL*

>Medtr1g052530 Org_Mtruncatula peptide: Medtr1g052530.1 (1 of 1) PTHR24349:SF126 - CALCIUM-DEPENDENT
PROTEIN KINASE 32 (PAC:31094145)
MGNCCTNPITKLRRKEKPKKHGPTTKNKTNIKNTLVVLKKPTGREILQQYELGRELGRGEFGITYLCKDRETGEELACKSISKDKLRTAIDIEDVRRE
VEIMRHLPKHPNIVTLKDTYEDDDNVHLVMECEGGEFDRIVAKGHYTERAAATVVKTIQVQVMCHHEGVMHRDLKPNFNFANKKETSPKKAIDFGL
SITFKPGDKFNEIVGSPYYMAPEVLKRNYPGEIDIWSAGVILYILLCGIPPFWAETEQQIAQAIIRSVIDFKKEPWPVKVSDNAKDLIKKMLDPDPKRRLT
AQEVLDPHVLQNAKTAPNVSIGETVRARLMQFVSMNKLKKTALRIADHLSVEEVAGIKEGFQVMDTENKGKINLDELVRGLLKGHIPEGDVQILMEA
GDVDKDGFLDYGEFVAISHLRKISHDEHLQRAQFFDKNESGFIELEELRNALADEVDTNSEEVINAIMHDVDTDKDGKISYEEFATMMKAGTDWRKAS
RQYSRERFTSLSIKLMKEGSELELNEGR*

>Medtr1g052530 Org_Mtruncatula peptide: Medtr1g052530.2 (1 of 1) PTHR24349:SF126 - CALCIUM-DEPENDENT
PROTEIN KINASE 32 (PAC:31094146)
MGNCCTNPITKLRRKEKPKKHGPTTKNKTNIKNTLVVLKKPTGREILQQYELGRELGRGEFGITYLCKDRETGEELACKSISKDKLRTAIDIEDVRRE
VEIMRHLPKHPNIVTLKDTYEDDDNVHLVMECEGGEFDRIVAKGHYTERAAATVVKTIQVQVMCHHEGVMHRDLKPNFNFANKKETSPKKAIDFGL
SITFKPGDKFNEIVGSPYYMAPEVLKRNYPGEIDIWSAGVILYILLCGIPPFWAETEQQIAQAIIRSVIDFKKEPWPVKVSDNAKDLIKKMLDPDPKRRLT
AQEVLDPHVLQNAKTAPNVSIGETVRARLMQFVSMNKLKKTALRIADHLSVEEVAGIKEGFQVMDTENKGKINLDELVRGLLKGHIPEGDVQILMEA
VSIFPLSGIFFFYLFHN*

>Medtr1g054865 Org_Mtruncatula peptide: Medtr1g054865.1 (1 of 1) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:31098861)
MGNNCVGPNLGNNGGLQSVSAVWKTRPPEARLPNNAEDKNKTPTTNPENAVTGSSKPESCAGGKVSEHVSQSTPPEQVKIAAAEIKPLEHEKPVKAA
ASSAVAGGGGGVAAATAGAGGAGEGDADKPKKPTHVKRLSSIGLQVESVLGRKTENIKDFYSLGRKLGGQGGFTTFLCMAKGTNKEFACKSIAKRKLTTQ
EDVEDVRREIRIMHHLAGHPNVIQIVGAYEDAVAVHVMELCAGGELFDRIIQRGHYSERKASELTRILGVVQACHSLGVMHRDLKPNFNFVSHDEES
ALKTIIDFGLSVFFRPGETFTDVVGSPYYVAPEVLKRNYPGECDVWSAGVILYILLSGVPPFWDETEQGIQFEQVLKGELDFISDPWPSISESADLVRML
IRDPKKRMTAHEVLCHPWVQVGGVAPDKPLDSAVLSRLKQFSAMNKLKKAIRVIAENLSEEEIAGLKEMFKMIDTNSGQISLEELKNGLERVGSVLKD
SEINWLMQAADVDNSGTIDYGEFIAAMLHLNKVQKEDHLFAAFNYFDKDGSGYITKDELQQACNQFGLQEDHLDIIREADRNDGRIDYSEFVAMMQDT
DFGKKGL*

>Medtr1g055255 Org_Mtruncatula peptide: Medtr1g055255.1 (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:31096757)
MGNNCVGTRTFFSKDESSSRATFPSPSCWSRSKSDSAHKTSPTKPKESVQNNPPVMKIEKEDEKPPQQHHHKKPRQKPTNEAVVATPAKPKRPHNVK
RLASAGLKADSVLQKRTVSLKEFYTLGPKLGQGGFTTFLCVEKSTGKEYACKSIMKRKLLTEDEDVRREIQIMHHLAGSSNVISIKEASEDAVAVHV
VMECAGGELFDRIVERGHYTERKAAKLARTIVGVIQSCHSGLGVMHRDLKPNFNFVNQQEEESPLKAIDFGLSCFFKPGDIFNDVVGSPYYVAPEVLKRR
YGPEADVWSAGVILYILLCGVPPFWGESEQDIFEAILNSDLDFSSDPWPSISESADLVRKMLVRDPKRLTAFDVLRRHPWILIDGAAPDKPLDSAVLSR
MKQFTAMNKLKMLALRVIAENLSEEEIAGLKEMFKMIDTNSGHITFEELKVGLKRFGANLKESEIYDLKMAADVNDNSGTIDYGEFIAATLHLNKVDRED
HLHAAFSYFDKDGSGYITKDELQKACEEFGFRDVPLEEMIREVDQNDGRIDYNEFVAMMRGNAEMGKRGRKSGSSSISIGFREALPVC*

>Medtr1g096490 Org_Mtruncatula peptide: Medtr1g096490.1 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:31095859)
MQKHNLGSSKSSSKCTAVLPYQTPRLRDHYLLGKKLGQGGFTTYLCTHKSTGKLYACKSIPKRKLLCKEDYDDVWREIQIMHHLSEHPNVVQIQGTIED
SVFVHVLVMECAGGELFDKIIQKGHYSEKAAKLMKTIVGVVETCHSLGVMHRDLKPNFNFDPGEDAEMKATDFGLSVFYKPGQTFHDVVGSPYYIAP
ELLCKIYGPQVDVWSAGVILYILLSGVPPFWAETESGIFRQILHGLDLESEPEWPTISESADLVRKMLERDPKQIRISAHEVLCHPWILDTPADPQLD
SAVLTRLKHFSAMNKLKMLALRVIAERLSEEEIIGLKLKELFKMIDTNSGTITYEELKDGKLQVGSNLMSEIISLMEASADIDNNGTIDYGEFLAATLHLN
KMEREENLVAFAFYFDKDGSGYITIDELQQACKDFGLGVEHLDDMIKEIQDNDGRIDYGEFVAMMKGGDDQVGRSRTKKGNINFNIAADAFGVKEESS*

>Medtr3g051770 Org_Mtruncatula peptide: Medtr3g051770.1 (1 of 7) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:31058617)
MGCLLSKDKDSEPEHNNGGYRYGEHNNRNNHEQVNTSRTAPTSSYQPQIPTKPSISAPSPKPLIKQDSNTILGKGLVDVKQFYTLGKELGRGQFGVTFL
CTENSTGLLYACKSISKRLVSKSDREDIKREIQIMQHLGSGPNIVEFKGAYEDRNSVHVMELCAGGELFDRIIAKGHYSEKAAASICRQIVNVNICH
FMGMHRDLKPNFNFLLASKDENALLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRCCKGEIDIWSAGVILYILLSGVPPFWAETEKGIFDAILEGH
IDFESEFPWKISDSADLVRKMLIQEPKKRITAAQVLEHPWIKDGNASDKPIDSAVLSRMKQFRAMNKLKLLKLVIAENMSEEEIRGLKAMFTNMDTND
SGTITYEELKAGLQRLGSKLSEAENVKQLMEEAADVDGNGTIDCIEFITATMHRHKLERDDHLYKAFQYFDKSSSGFITRDELETAMKEYGMGDATIKI
SEVDTIISEVDTDHGRINYEFCAMMRSGNQQVVKLF*

>Medtr3g098070 Org_Mtruncatula peptide: Medtr3g098070.1 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:31057225)
MSKSNNTNTTPPKPTWVLPVVTENLREVYTLGRKLGGQGGFTTYLCTHKSTGKLYACKSISKKLLCKEDYDDVWREIQIMHHLSENPNVVRHGTYES
FSVHVLVMECEGGEFDRIVQKGHYSERQAALIRTIIVEVEACHSLGVMHRDLKPNFNFDSVDEDALKTIDFGLSVFYKPGEIFSDVVGSPYYVAPE
VLHKKHYGPEADVWSAGVILYILLSGVPPFWAETDQGIQFQKGLDFRSEFPWPGISDSADLIRKMLDRNPKTRFTAHQVLCHPWIVDDNIAPDKPLDS
AVLSRLKQFSAMNKLKMLALRVIAERLSEEEIIGLKLKELFRMLDADNSGTITLLEELKEGLKRVGSELMSEIISLMEASADIDNNGTIDYGEFLAATLHLN
LREENLLSAFYSYFDKDCSGYITIDEIQACKEFGLDDVHIDEMVKEIQDNDGQIDYGEFAAMMRKNGGGIGRRTMTSTLNFRLALGITNGNSN*

>Medtr3g098090 Org_Mtruncatula peptide: Medtr3g098090.1 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:31060081)
MSKSNIPDKTTPPTTKTTLVPRVTKNLHEVYTLGRKLGGQGFGITYHCTHNSGTGRYACKSISKKKLLCKEDYDDAWREIQIMHHLSEHPNVVRIRETY
EDSFVHLVMEICEGEGELFDRIQVKGHYSERQAALKIKTIVEVVEACHSLGVMHRDLKPENFLFDSVDEDAVLKTIIDFGLSVFYKPGEIFSDISGSPYYV
APEVLHKKYGEADVWSAGVILYILLSGRLPFCADTENGIFRQICRGRNLNFGQSEWPWEISYSADKLRKMLDRNPRTFRTAHQVLCHPWIVDDNIAPDKP
LDSAVLSRLKQFSAMNKLKMLALHVIKRLNEEEIGGLKELFRMLDADNSGTITLDELKEGLQVRGSELMESEIKDLMDAADIDNNGTLDYGEFIAATVH
LNKLEREENLSAFSYFDKDGSGYITIDEIQAACEKFGLDDVHIDEMVKEIDQDNDGQIDYGEFAAMMRKGNNGIGRRTMSSTLDSRDALEIIGNGSN*
>Medtr4g066660 Org_Mtruncatula peptide: Medtr4g066660.1 (1 of 2) PTHR24349:SF160 - CALCIUM-DEPENDENT
PROTEIN KINASE 24 (PAC:31111529)
MGSCVSTQKGKHGRKSKDHINTKHKINDQNHEPNTPTTRSSSVTGRSSSVTSRQLNVVNTNPSPGNIFDKYELGKELGRGEFGVTHRCVELKTGEAFAC
KKIAKTKLRTEIDIQDVRREVQIMRHLPEHPNIVAFREAYEDRDVYLVMEICEGEGELFDRIQVKGHYTERAAANVAKTILEVCKVCHEHGVVHRDLKPE
NFLFADGSEAAASKAIDFGLSTFYVNGDRFNEIVGSPYYMAPEVLRNRYGPEIDIWSTGVILYILLCGVPPFWAETEEAIAQAIIRGNVDFTRDPWPVKVS
EEAKYLVRKMLDPNPFSRITVQEVLDHWSIQNREHGKNSVSLGDQVRSRIKQFSLMNRFKKKVLRVVDNLDPDEQIDGFRKMFDMMDKDKNGHLLTFFELKD
GFAEIGNVIPPDLQMLMDAADFDGNGTLNCEEFTMSVHMRLGNDEHLEAFNFFDKNKSQYVEFDELKDALSNDGSDDDQVIRDILNDVDLDKDG
SFEEFKAMMKTGGDWKMASRQYSKAFNLALSFMRFKDKSTGVATN*
>Medtr4g107490 Org_Mtruncatula peptide: Medtr4g107490.1 (1 of 2) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:31106321)
MGNCNTCINKDAIESTGKAKTSSTTESNSNHGRRRTKPKPKSNPYTEQSLTPGATIRVLKESNPNRNRINDKYILGRELGRGEFGITYLCTDKETKQELA
CKSISKRKRLTAVDDVEDVRREVAIMSTLPEHPNVVKLKATYEDDENVHLMELCEGEGELFDRIQVARGHYSERAAAHVARTIAEVVRMCHVNGVMHRDLK
ENFLFANKKENSVLKAIDFGLSVFFKPGERFSEIVGSPYYMAPEVLRNRYGPEVDIWSAGVILYILLCGVPPFWAETEQQVALAILRGVIDFKREPWPQI
SDSAKSLVRQMLEPDPKKRLTAEQVLEHPWLQNAKKASNVPLGDIVRTRKQFSLMNRFKKRALRVIAEHLSELEEVEIKDMFTLMDTDKDGRIITYEELK
AGLRKVGSQLAEPEIKLLMDVADVDGNGVLDYGEFVAVTIHLQRMENDEHFRKAFKFFDKDESQYIELSELEAALVDDLGETDTNVLNEIMREVDTDKDG
RISYEEFVAMMKTGTDWRKASRQYSRERFKSLINLMKDGSLQLHDEISGQAVV*
>Medtr4g132040 Org_Mtruncatula peptide: Medtr4g132040.1 (1 of 7) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:31115236)
MGCYTSKPEVDKFAFPHRGYAAITADDDTTYRYVTVSAYSNQIQIITTPPKLDSLASEPVTAPPNPKPSPTAQNVKTVQKTQKTILEKPYEDIKKLYTFGKE
LSRGKFGITYFCTENSTGQNYACRSILKRLVSKADKEDIKREIQILQHLSGQPNIVKFKGAYEDSLSIHLVLEHCAYGELFDTINAHPHGYSERVVASL
CRCIVNVVHTCHCMGMVHRDLNPNENFLFSTKDKALTLKAVDFRFSVFIEEGKIYNDMVGSGCYVAPEVLLRSYGKEIDIWSAGIILYILLSGGPPFPSPGT
DKGLNNAVLEGELDLLSEPWPSSISDSAKDLVKKMLTPDPKKRITSQVLEHTWMRDGGEASDKPIDISVLSRMKQFRAINTFTKLGLKVAENLAEVKG
LKETFENMDTDSSGTITYEELKTGLAQIGSELSEAEENQMLKAADVVDGKGSIDYLEFISATMHRRLERDENIHKAFQYFDKDNSSGHITREELETALT
KHGISDEAKIKEIVTEVYTDNDGKINYDEFCAMMRSGMPHQGLF*
>Medtr4g132070 Org_Mtruncatula peptide: Medtr4g132070.1 (1 of 7) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:31108323)
MGCHGSKEKKHAKDEFTARQRSSPARPTAPPSPAGVDSNFRYINVPVQVQSSSTPSSNPKPSAITTQKPVQKQVDTTILGKPYEDIKKFYTLGKELGRG
QFGITYFCTENSTGLNYACKSILKRLVSKADREDIKREIQILQHLSGQPNIVEFKGAFEDRFSVHLVMELCAGGELFDRIIAQGHYSERAAASICRDVV
KVVHICHFMGVLHRDLKPNENFLFSTKDKALTLKAVDFRFSVFIEEGKVYRDMVGSAYYVAPEVLRNRYGKEIDIWSAGIILYILLSGVPPFWAETKEGIF
NAILEGELDFVSEPWPSSISDSAKDLVRKMLTPDPKKRITSTEVLHHPWMREGGEASDKPIDSAVLSRMKQFRAMNKFKKLALKVAENLSEEEIKGLKAM
FANMDTDSSGTITYEELKTGLARIGSRLSEAEVQLMEAADVDGNGSIDYLEFISATMHRRLERDEHLYKAFQYFDKDNSSGHITREELETAMTKHGMGD
EATIKEIIEVVDTDNDGRINYEFCAMMRSGMPHQGLF*
>Medtr5g009830 Org_Mtruncatula peptide: Medtr5g009830.1 (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:31086214)
MGNRISSKHKPSSDSQTRSKSEPSHSTPTSFHPPNRTPKQSTHTPTPSSSPLGRVLGKPMEDVRSTYTFGRELGRGQFGVYTLVTHKLTKEQFACKSIAT
RKLIIRDDLDIRREVQIMHHLTGHNRNIVELKGAYEDRHSVNLIMELCAGGELFDRIISKGHYSERAAELCRQIVTVVHNCHTMGMVHRDLKPENFLFL
SKHENSPLKATDFGLSVFFKPEDVFKDLVGSAYYVAPEVLRNRYGPEADIWSAGIILYILLSGVPPFWAENEQGFDAILRGHLDFASDPWPKISSIAKD
LIKKMLRADPKERISAVEVLDHSMWKEDGASDKPLDIAVLTRMKQFRAMNKLKKVALKVAENLSEEEIIGLKEMFKSMDTDNSGTITFEELKAGLPKLG
TKISESEVRQLMEAADVDGNGTIDYIEFITATMHLNRMEREDHLYKAFYFDNDKSGYITKEELESALTKNYMGDEKTIKEIIDEVDSNDGRINYEYFV
AMMRKGNPDLITNKRK*
>Medtr5g009830 Org_Mtruncatula peptide: Medtr5g009830.2 (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:31086213)
MGNRISSKHKPSSDSQTRSKSEPSHSTPTSFHPPNRTPKQSTHTPTPSSSPLGRVLGKPMEDVRSTYTFGRELGRGQFGVYTLVTHKLTKEQFACKSIAT
RKLIIRDDLDIRREVQIMHHLTGHNRNIVELKGAYEDRHSVNLIMELCAGGELFDRIISKGHYSERAAELCRQIVTVVHNCHTMGMVHRDLKPENFLFL
SKHENSPLKATDFGLSVFFKPEDVFKDLVGSAYYVAPEVLRNRYGPEADIWSAGIILYILLSGVPPFWAENEQGFDAILRGHLDFASDPWPKISSIAKD
LIKKMLRADPKERISAVEVLDHSMWKEDGASDKPLDIAVLTRMKQFRAMNKLKKVALKVAENLSEEEIIGLKEMFKSMDTDNSGTITFEELKAGLPKLG
TKISESEVRQLMEAADVDGNGTIDYIEFITATMHLNRMEREDHLYKAFYFDNDKSGYITKEELESALTKNYMGDEKTIKEIIDEVDSNDGRINYEYFV
AMMRKGNPDLITNKRK*
>Medtr5g009830 Org_Mtruncatula peptide: Medtr5g009830.3 (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:31086215)
MGNRISSKHKPSSDSQTRSKSEPSHSTPTSFHPPNRTPKQSTHTPTPSSSPLGRVLGKPMEDVRSTYTFGRELGRGQFGVYTLVTHKLTKEQFACKSIAT
RKLIIRDDLDIRREVQIMHHLTGHNRNIVELKGAYEDRHSVNLIMELCAGGELFDRIISKGHYSERAAELCRQIVTVVHNCHTMGMVHRDLKPENFLFL
SKHENSPLKATDFGLSVFFKPEDVFKDLVGSAYYVAPEVLRNRYGPEADIWSAGIILYILLSGVPPFWAENEQGFDAILRGHLDFASDPWPKISSIAKD
LIKKMLRADPKERISAVEVLDHSMWKEDGASDKPLDIAVLTRMKQFRAMNKLKKVALKVAENLSEEEIIGLKEMFKSMDTDNSGTITFEELKAGLPKLG
TKISESEVRQLMEAVRFLHHYLSVTVYYNLYF*
>Medtr5g089320 Org_Mtruncatula peptide: Medtr5g089320.1 (1 of 3) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:31086627)
MGNCSSGGTEDPEDKGENNQNNNDANGDSSATTPPPWSKSPQPSKPSKPSAIGPVLGRPMEDVKATYSMGKELGRGQFGVTHLCTHKTGKQYACKTIA

LSKDKNEDIEDVRRREVQIMHHLTGQPNIVELIGAFEDKQSVLHVMELCAGGELFDRIIAKGYHTERAASLLRTIIVQIVHTCHSMGVIHRLDKPENFLLLSKDENSEPLKATDFGLSVFYKQGDQFKDIVGSAYYIAPDVLKRKYGPEVDIWSVGVMLYILLCGVPPFWAESENGIFNAILRGHVDSSDPWPSISPSAKDLVRKMLNSDPKQRITAYEVLNHPWIKEDGEAPDTPLDNAVLNRLKQFRAMNQFKKVALKVIASCLSEEEIMGLKQMFKGMDTDNSGTITIEELKQGLAKQGTRLSETEVKQLMEAADADNGNGIIDYDEFITATMHMNRNLNREEHVYTAFFQFDKDNSGYITIEELEQALHEYNMHDGRDIKEIIEIVDADNDGRINYDEVFVAMMGKNPEANTKKRRDSTLY*

>Medtr5g092810 Org_Mtruncatula peptide: Medtr5g092810.1 (1 of 1) PF00069//PF13499//PF13833 - Protein kinase domain (Pkinase) // EF-hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) (PAC:31086500)

MGGCLSKKESKPDHRHVGVSIGIHNNHHNNHHNNHHNNHKNHEPYVNQSKTPSQQPYQSPNKHAPRSPKPIVQRPNNTAILGKQFEDVKQIYITLKGELGRGQFGVTYLCFTENSTGLKYACKSISKRKLVSKSDKEDIKREIQIMQHMSGQPNIVEFEKGAYEDKNSVHVVMELCAGGELFDRIIAKGYSERAAASICRQIVNVVHICHFMGMVHRDLKPENFLLSSKDDKATIKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRKRYGKETDIWSAGVILYILLCGVPPFWAETEKGIFDAIILQGHIDFESRPWPSISNSAKDLVSRMLMQDPKKRITASQVLDHPWLKEGGNASDKPIDSAVLSRMKQFRAMNKLKALKLVIAENLSSEIEIQLKMAFTNMTDTKSGTITYTEELRAGLQLRGLSKLTAEVRLKLEMAADVNGNGTIDYIEFITATMHRHRLERDEHLYKAFQYFDKDNSGGFITRDELETAMKEYGMGDEETITREIIESEVTDNDGRINYEELFTMMRSEAGVQQQGLF*

>Medtr5g099240 Org_Mtruncatula peptide: Medtr5g099240.1 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT PROTEIN KINASE 6 (PAC:31089325)

MGNTCRGSLKGKQYIQEGYTQPVHDHSSKRTIISDNNNNNNNNDSNSDHHNHHRNNNNKPLNPPPPPSFNFKNDAAMRRGPDNQTYVVLGHKTPNIRDLYTLGRKLGQGGQFGTTFLAIDNSTSIEYACKSISKRKLVSKSDKEDIKREIQIMHHLAGHKNIVTIKAYEDALYVHVMELCSGGELFDRIIQRGHYTERKAAELTRIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVGVSPPYVAPEVLLKHGYPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSEPWPLISDSGKDLIRKMLCSRPSDRLTAHEVLCHPWICENGVAADRSLDPAVLSRLKQFSAMNKLKMLARVIAESLSEEEIAGLREMFQTMDDTNSGAIITFDELKAGLRRYGSTLKDIERDLMEAADVNSGTIDYGEFIAATVHLNKLEREHLVAAAFQYFDKDNSGGYITVDELQQACTIONHMTDVFLEDIIEKVDQDNDGRIDYGEFVAMMQKGNVIGIRRTMRNSLNLMSRDAPSAH*

>Medtr5g099240 Org_Mtruncatula peptide: Medtr5g099240.2 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT PROTEIN KINASE 6 (PAC:31089328)

MRRGPDNQTYVVLGHKTPNIRDLYTLGRKLQGGQFGTTFLAIDNSTSIEYACKSISKRKLVSKSDKEDIKREIQIMHHLAGHKNIVTIKAYEDALYVHVMELCSGGELFDRIIQRGHYTERKAAELTRIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVGVSPPYVAPEVLLKHGYPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSEPWPLISDSGKDLIRKMLCSRPSDRLTAHEVLCHPWICENGVAADRSLDPAVLSRLKQFSAMNKLKMLARVIAESLSEEEIAGLREMFQTMDDTNSGAIITFDELKAGLRRYGSTLKDIERDLMEAADVNSGTIDYGEFIAATVHLNKLEREHLVAAAFQYFDKDGSGYITVDELQQACTIONHMTDVFLEDIIEKVDQDNDGRIDYGEFVAMMQKGNVIGIRRTMRNSLNLMSRDAPSAH*

>Medtr5g099240 Org_Mtruncatula peptide: Medtr5g099240.3 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT PROTEIN KINASE 6 (PAC:31089327)

MRRGPDNQTYVVLGHKTPNIRDLYTLGRKLQGGQFGTTFLAIDNSTSIEYACKSISKRKLVSKSDKEDIKREIQIMHHLAGHKNIVTIKAYEDALYVHVMELCSGGELFDRIIQRGHYTERKAAELTRIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVGVSPPYVAPEVLLKHGYPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSEPWPLISDSGKDLIRKMLCSRPSDRLTAHEVLCHPWICENGVAADRSLDPAVLSRLKQFSAMNKLKMLARVIAESLSEEEIAGLREMFQTMDDTNSGAIITFDELKAGLRRYGSTLKDIERDLMEAADVNSGTIDYGEFIAATVHLNKLEREHLVAAAFQYFDKDGSGYITVDELQQACTIONHMTDVFLEDIIEKVDQDNDGRIDYGEFVAMMQKGNVIGIRRTMRNSLNLMSRDAPSAH*

>Medtr5g099240 Org_Mtruncatula peptide: Medtr5g099240.4 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT PROTEIN KINASE 6 (PAC:31089326)

MRRGPDNQTYVVLGHKTPNIRDLYTLGRKLQGGQFGTTFLAIDNSTSIEYACKSISKRKLVSKSDKEDIKREIQIMHHLAGHKNIVTIKAYEDALYVHVMELCSGGELFDRIIQRGHYTERKAAELTRIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVGVSPPYVAPEVLLKHGYPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSEPWPLISDSGKDLIRKMLCSRPSDRLTAHEVLCHPWICENGVAADRSLDPAVLSRLKQFSAMNKLKMLARVIAESLSEEEIAGLREMFQTMDDTNSGAIITFDELKAGLRRYGSTLKDIERDLMEAADVNSGTIDYGEFIAATVHLNKLEREHLVAAAFQYFDKDGSGYITVDELQQACTIONHMTDVFLEDIIEKVDQDNDGRIDYGEFVAMMQKGNVIGIRRTMRNSLNLMSRDAPSAH*

>Medtr7g068710 Org_Mtruncatula peptide: Medtr7g068710.1 (1 of 1) PTHR24349//PTHR24349:SF145 - SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:31078445)

MGNCRCSPAAVAREDEVKSSFSNHDHPKRTETTANKSKSPVTVLAATKTSNDMEDRYLIDRELGRGEFGVTYLCIDRDTRELLACKSISKRLRTAVDVDDVRREVAIMRHLPKSSSIVTLREACEDDNAVHLMELCEGGELFDRIIVARGHYTERAAAARTIVEVVQLCHKHGVHRLDKPENFLFANKKENSPLKAI

DFGLSIFFKPGEKFSEIVGSPYYMAPEVLKRNYPGPEIDIWSAGVILYILLCGVPPFWAESEQVAQAILRGLIDFKREPWPSISESAKSLVKQMLEPDPKLRLTAQVLDHLPWLINAKKAPNVSLGDTVRSRLKQFSMMNRFRKALRVIAIDFLSNEEVEDIKEMFKKMDTDNDGIVSIEELKVGFRNHQSQLAESEVQMFIEADVNNKGELDYGGEYVAISVHLRKLMDGNEHLHKAFFYFDKDGNGYIEPEELRNALMEDGTDGTDVANDIFQEVDTDKDGKISYDEFVAMMKTGTDWRKASRHSYSRGRFNSLSLKLMDGSLQLNND*

>Medtr7g091890 Org_Mtruncatula peptide: Medtr7g091890.1 (1 of 1) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN KINASE 14 (PAC:31078915)

MGNCATPAVAGEEITNKKKKKGKKENPFATDYAYNNNTTSKLTVLKDPTGNEIETRYELGRELGRGEFGVTYLCETKETREELACKSISKKKLRTAIDIEDVRRVEIMRHMMPKHNNIVTLKDTYEDDNAVHLMELCEGGELFDRIIVARGHYTERAAAARTIVEVVQMKCHKHGMHRDLKPENFLFANKKETAAALKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYPGPEVDIWSAGVILYILLCGVPPFWAETEQQVAQAIIRSVVDFKRDWPVKVSDNAKDLVKKMLNPD

KRLTAQEVLDHPWLINAKKAPNVSLGETVRLRLKQFSVMNKLKRALRVIAEHLVSEEAAGLKEGFNLMDTTNRGKINIDELRGLHLKLGHQVDPDSLQILMEAGDIDRDEGLDYGEYVAISVHLRKLMDGNEHLHKAFFYFDKDGNGYIEPEELRNALMEDGTDGTDVANDIFQEVDTDKDGKISYDEFVAMMKTGTDWRKASRHSYSRGRFNSLSLKLMDGSLQLNND*

>Medtr7g091890 Org_Mtruncatula peptide: Medtr7g091890.2 (1 of 1) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN KINASE 14 (PAC:31078916)

MGNCATPAVAGEEITNKKKKKGKKENPFATDYAYNNNTTSKLTVLKDPTGNEIETRYELGRELGRGEFGVTYLCETKETREELACKSISKKKLRTAIDIEDVRRVEIMRHMMPKHNNIVTLKDTYEDDNAVHLMELCEGGELFDRIIVARGHYTERAAAARTIVEVVQMKCHKHGMHRDLKPENFLFANKKETAAALKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYPGPEVDIWSAGVILYILLCGVPPFWAETEQQVAQAIIRSVVDFKRDWPVKVSDNAKDLVKKMLNPD

PKRLTAQEVLDHLPWLINAKKAPNVSLGETVRLRLKQFSVMNKLKRALRVIAEHLVSEEAAGLKEGFNLMDTTNRGKINIDELRGLHLKLGHQVDPDSLQILMEAGDIDRDEGLDYGEYVAISVHLRKLMDGNEHLHKAFFYFDKDGNGYIEPEELRNALMEDGTDGTDVANDIFQEVDTDKDGKISYDEFVAMMKTGTDWRKASRHSYSRGRFNSLSLKLMDGSLQLNND*

QILMEAVSFSTTCLCLDSILHICIYVFC*

>Medtr7g106710 Org_Mtruncatula peptide: Medtr7g106710.1 (1 of 1) PF07714//PF13499//PF13833 - Protein tyrosine kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) (PAC:31082859)

MGNNCVGPRTTYEHESFQTSFWWPWSLSWSYPINQQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNASDRQTSISQEDAEFVTQLKEKATPTKT MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGFGTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVREIEIMHHLVGIPNVISIK GAYEDPVVVYIVMELCEGGEFLDRIIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA YYVAPEVIEECYGPADVWSAGVYIIYLLCGTPPFYGELEDRIFDEVHLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP DRPLDSATLSRLKQFSAMNKLKKMALRVIAKNLSEEEISGLKESFKTIDTNTGQITFEKLKVGLKKFGANLSESEIFDLMQAADIDNNGMIDYGEFIAA TLHLNKVDKEDHLVAAFSYFDKDGNGYITQDELQQVCKEFGMKDVFHEEMIREADQNNNDGQIDYNEFVAMMQRGADLENNSVKCSTSFNIGLGKTKTLS IC*

>Medtr7g106710 Org_Mtruncatula peptide: Medtr7g106710.2 (1 of 1) PF07714//PF13499//PF13833 - Protein tyrosine kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) (PAC:31082860)

MGNNCVGPRTTYEHESFQTSFWWPWSLSWSYPINQQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNASDRQTSISQEDAEFVTQLKEKATPTKT MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGFGTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVREIEIMHHLVGIPNVISIK GAYEDPVVVYIVMELCEGGEFLDRIIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA YYVAPEVIEECYGPADVWSAGVYIIYLLCGTPPFYGELEDRIFDEVHLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP DRPLDSATLSRLKQFSAMNKLKKMALRVIAKNLSEEEISGLKESFKTIDTNTGQITFEKLKVGLKKFGANLSESEIFDLMQAADIDNNGMIDYGEFIAA TLHLNKVDKEDHLVAAFSYFDKDGNGYITQDELQQVCKEFGMKDVFHEEMIREADQNNNVSTYYNVMCFHFRTE*

>Medtr7g106710 Org_Mtruncatula peptide: Medtr7g106710.3 (1 of 1) PF07714//PF13499//PF13833 - Protein tyrosine kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) (PAC:31082864)

MGNNCVGPRTTYEHESFQTSFWWPWSLSWSYPINQQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNASDRQTSISQEDAEFVTQLKEKATPTKT MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGFGTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVREIEIMHHLVGIPNVISIK GAYEDPVVVYIVMELCEGGEFLDRIIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA YYVAPEVIEECYGPADVWSAGVYIIYLLCGTPPFYGELEDRIFDEVHLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP DRPLDSATLSRLKQFSAMNKLKKMALRVIAKNLSEEEISGLKESFKTIDTNTGQITFEKLKVGLKKFGANLSESEIFDLMQAVSIKSKIIVNSLNVTTQQ TLLLLL*

>Medtr7g106710 Org_Mtruncatula peptide: Medtr7g106710.4 (1 of 1) PF07714//PF13499//PF13833 - Protein tyrosine kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) (PAC:31082861)

MGNNCVGPRTTYEHESFQTSFWWPWSLSWSYPINQQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNASDRQTSISQEDAEFVTQLKEKATPTKT MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGFGTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVREIEIMHHLVGIPNVISIK GAYEDPVVVYIVMELCEGGEFLDRIIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA YYVAPEVIEECYGPADVWSAGVYIIYLLCGTPPFYGELEDRIFDEVHLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP DRPLDSATLSRLKQFSAMNKLKKMALRVIAKNLSEEEISGLKESFKTIDTNTGQITFEKLKVGLKKFGANLSESEIFDLMQAVSIKSKIIVNSLNVTTQQ TLLLLL*

>Medtr7g106710 Org_Mtruncatula peptide: Medtr7g106710.5 (1 of 1) PF07714//PF13499//PF13833 - Protein tyrosine kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) (PAC:31082863)

MGNNCVGPRTTYEHESFQTSFWWPWSLSWSYPINQQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNASDRQTSISQEDAEFVTQLKEKATPTKT MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGFGTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVREIEIMHHLVGIPNVISIK GAYEDPVVVYIVMELCEGGEFLDRIIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA YYVAPEVIEECYGPADVWSAGVYIIYLLCGTPPFYGELEDRIFDEVHLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP DRPLDSATLSRLKQFSAMNKLKKMALRVSTFSIT*

>Medtr7g106710 Org_Mtruncatula peptide: Medtr7g106710.6 (1 of 1) PF07714//PF13499//PF13833 - Protein tyrosine kinase (Pkinase_Tyr) // EF-hand domain pair (EF-hand_7) // EF-hand domain pair (EF-hand_8) (PAC:31082862)

MGNNCVGPRTTYEHESFQTSFWWPWSLSWSYPINQQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNASDRQTSISQEDAEFVTQLKEKATPTKT MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGFGTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVREIEIMHHLVGIPNVISIK GAYEDPVVVYIVMELCEGGEFLDRIIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA YYVAPEVIEECYGPADVWSAGVYIIYLLCGTPPFYGELEDRIFDEVHLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP DRPLDSATLSRLKQFSAMNKLKKMALRVSTFSIT*

>Medtr8g095440 Org_Mtruncatula peptide: Medtr8g095440.1 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT PROTEIN KINASE 11-RELATED (PAC:31073956)

MAKENPTPTIALKPVTWVLPYRTEKVTEIYRMGRKLGQGFQGTYYLCTHKSTNKKFACKSIPKRKLFCCKEDYEDVWREIQIMHHLSEHPHVRIEGTYED STAVHIVMELCEGGEFLDRIVKKGHYSERQAAGLIKTIEVVESCHSLGVMHRDLKPENFLFDTVDEDAKLKATDFGLSVFYKPGESFSDVVGSPYYVAP EVLRKLYGPESDVWSAGVILYILLSGVPPFWAETEPGIFRQILLGKLDQSEWPWPSISDSAKDLIRKMLDQNPRTLTAHEVLRHPWIVDDNIAPDKPID SAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTSSSGTITFDELKDGKLRVGSSELMESEIQDLMDAADVDKSGTIDYGEFIAATVHLN KLEREENLLSAFAYFDKASGYITIDEISQACKDFGLDDIHIDEMIKEIDQDNDGQIDYSEFAAMMRKNGGGIGRTRMNTLNLRDALGLVNGSNQVID GYL*

>Medtr8g095440 Org_Mtruncatula peptide: Medtr8g095440.2 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT PROTEIN KINASE 11-RELATED (PAC:31073957)

MAKENPTPTIALKPVTWVLPYRTEKVTEIYRMGRKLGQGFQGTYYLCTHKSTNKKFACKSIPKRKLFCCKEDYEDVWREIQIMHHLSEHPHVRIEGTYED STAVHIVMELCEGGEFLDRIVKKGHYSEROAAGLIKTIEVVESCHSLGVMHRDLKPENFLFDTVDEDAKLKATDFGLSVFYKPGESFSDVVGSPYYVAP

EVLRLKLYGPESDVWSAGVILYILLSGVPPFWAETEPGIFRQILLGKLDQFQSEPWPSISDSAKDLIRKMLDQNPRTRLTAHEVLRHPWIVDDNIAPDKPID
SAVLSRLKQFSAMNKLKLMALRVIAERLSEEEIGGLKELFKMIDTSSGTTTFDELKDGKLRVGSSELMSESIQDLMDAVSVFLWEDNSFFMQALNLTQS
SLP*

>Medtr8g099095 Org_Mtruncatula peptide: Medtr8g099095.1 (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:31073428)
MGGNCSTGAGAGINTTTTTPHSDPPPKNAPTILPQNFTPSPPQPLPTTTTLGRILNRPMDVRSIFIFGRELGRGQFGVTYLVTHKVTKEQFACKSIATR
KLVNRDDIDVVRREVQIMHHLTGHRNIVELKGAYEDKHSVNLVLMELCAGGELFDRIILKGHYSERAAANLCRQIVTVVHNCHTMGMVHRDLKPNENFLFLG
KEENSPLKATDFGLSVFFKPGDVFKDLVGSAYYVAPEVLRKSYGPETDIWSAGIILYILLSGVPPFWAENEQGIFDAILRGQIDFASDPWPSISSAKDL
VKKMLRNDAKERISAVEVLNHPWMRVGDGASDKPLDIAVLSRMKQFRAMNKLKVALKVAIENLSEEEIIGLKEMFKSMDTDNSGTITFEELKAGLPKLG
SKMSESEVRQLMEAADVNGTIDYIEFITATMHMNRMEREDHLYKAFFEYDQDKSGYITKEELESALKKYNMGDENTIKEIIAEVDTNDARINIDEFV
AMMRKGNPDITHRRRK*

>Pp3c11_25550 Org_Ppatens peptide: Pp3c11_25550V3.1.p (1 of 1) PF00069//PF13202//PF13499 - Protein
kinase domain (Pkinase) // EF hand (EF-hand_5) // EF-hand domain pair (EF-hand_7) (PAC:32958204)
MADFEVLVGFQEHVPLPALQATDDLEKLYSLGKKLGEGQFGTYYLCTERATGLQFACKCIPKRKLISSEEIEDVGREVEVMYHLSGHPNIVTLKGAYE
DATNVYLVLMELCEGGELFDRIIERGTYTEAEARLRTITVSVEACHKSGVVHRDLKPNENFLFKTKEDDSVLKAADFGSARFFEPGDVFTDIVGSPYYVA
PEVLDRLHYGPEADIWSAGVMLYILLSGAPFFWAETVQGIFEKVMEGEPPTFTADPWPNISEVAKDLIRKMLDPNPEKRLKAHEVLNHPWIREDGVAPKKP
IASLVQFRMKQFAAMNKLKLAIRIIAETLSEEEIANLKEIFTEMDSNDGAISFEELKAGLLRVGTSLKDAELFDLMDAADVDHDMIDCGEFLAATLS
LNHIELEENLMAAFQYLDKSGSGYITDELLAVCFEFHMEVDRLDLHDVSIAGDGSIDYKMFVMTMRKCNNGMGHQNLRCTLGITDVLTLLEEQY*

>Pp3c11_25550 Org_Ppatens peptide: Pp3c11_25550V3.2.p (1 of 1) PF00069//PF13202//PF13499 - Protein
kinase domain (Pkinase) // EF hand (EF-hand_5) // EF-hand domain pair (EF-hand_7) (PAC:32958205)
MADFEVLVGFQEHVPLPALQATDDLEKLYSLGKKLGEGQFGTYYLCTERATGLQFACKCIPKRKLISSEEIEDVGREVEVMYHLSGHPNIVTLKGAYE
DATNVYLVLMELCEGGELFDRIIERGTYTEAEARLRTITVSVEACHKSGVVHRDLKPNENFLFKTKEDDSVLKAADFGSARFFEPGDVFTDIVGSPYYVA
PEVLDRLHYGPEADIWSAGVMLYILLSGAPFFWAETVQGIFEKVMEGEPPTFTADPWPNISEVAKDLIRKMLDPNPEKRLKAHEVLNHPWIREDGVAPKKP
IASLVQFRMKQFAAMNKLKLAIRIIAETLSEEEIANLKEIFTEMDSNDGAISFEELKAGLLRVGTSLKDAELFDLMDAADVDHDMIDCGEFLAATLS
LNHIELEENLMAAFQYLDKSGSGYITDELLAVCFEFHMEVDRLDLHDVSIAGDGSIDYKMFVMTMRKCNNGMGHQNLRCTLGITDVLTLLEEQY*

>Pp3c11_4640 Org_Ppatens peptide: Pp3c11_4640V3.1.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32959137)
MGNCVCGSTTKPKKQRPNPFAQDGYQTNLQILKNQPKSRILDKYNLGRLEGRGEFGITYLCTDKETGEVFACKSISKKKLRTAVDVEDVRREVAIMKHL
EHPNIVTLKGAYEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVHRDLKPNENFLFANKNENSPLKAIDFGLSVFFKPG
RFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQGVQAAILRGILDFKRDWPVKVSDSAKSLVRHMLEPDPKARYSAQQVLDHP
WLQNAKKNPNVPLDAVRSRLKQFSAMNKLKRALQVIAEHLGGEEIDGLKEIFEKLDSDKTGTITFEKLKMGLEIGSQLTEHEVRMLMEAADVNGTLD
DYGEFVAATVHLQRLDDDEHLRRAFDFFDVDRSGYIETEELREAVGEPLNGSPSETDVVQAILEVDIDKDGRISEYEEFATMMRRGTDWRKASRQYSRDR
FNLSMLRLLRDGS LNPDKIVAVR*

>Pp3c11_4640 Org_Ppatens peptide: Pp3c11_4640V3.2.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32959139)
MKHLEHPNIVTLKGAYEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVHRDLKPNENFLFANKNENSPLKAIDFGLSVF
FKPGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQGVQAAILRGILDFKRDWPVKVSDSAKSLVRHMLEPDPKARYSAQQ
VLDHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKRALQVIAEHLGGEEIDGLKEIFEKLDSDKTGTITFEKLKMGLEIGSQLTEHEVRMLMEAADV
NGTLDYGEFVAATVHLQRLDDDEHLRRAFDFFDVDRSGYIETEELREAVGEPLNGSPSETDVVQAILEVDIDKDGRISEYEEFATMMRRGTDWRKASRQ
YSRDRFNLSMLRLLRDGS LNPDKIVAVR*

>Pp3c11_4640 Org_Ppatens peptide: Pp3c11_4640V3.3.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32959138)
MKHLEHPNIVTLKGAYEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVHRDLKPNENFLFANKNENSPLKAIDFGLSVF
FKPGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQGVQAAILRGILDFKRDWPVKVSDSAKSLVRHMLEPDPKARYSAQQ
VLDHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKRALQVIAEHLGGEEIDGLKEIFEKLDSDKTGTITFEKLKMGLEIGSQLTEHEVRMLMEAADV
NGTLDYGEFVAATVHLQRLDDDEHLRRAFDFFDVDRSGYIETEELREAVGEPLNGSPSETDVVQAILEVDIDKDGRISEYEEFATMMRRGTDWRKASRQ
YSRDRFNLSMLRLLRDGS LNPDKIVAVRFCAGFFGLFFRCLLKDHCH*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.1.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956551)
MGNCVCGSSTKKSRRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
HLPHHPHIVTLEGAYEDDVAHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVHRDLKPNENFLFANTNENAPLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQGVQAAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLEIGSQLTEHEVRMLMEAADVEGN
GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDSGSGYIETEELREAVGEAMTELSSEPDVVQAILEVDLKDGRISYEEFVMMRRGTDWRKASRQYS
RDRFNLSMLRLLRDGS LNPPSYSSMSMR*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.2.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956552)
MGNCVCGSSTKKSRRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
HLPHHPHIVTLEGAYEDDVAHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVHRDLKPNENFLFANTNENAPLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQGVQAAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLEIGSQLTEHEVRMLMEAADVEGN
GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDSGSGYIETEELREAVGEAMTELSSEPDVVQAILEVDLKDGRISYEEFVMMRRGTDWRKASRQYS
RDRFNLSMLRLLRDGS LNPPSYSSMSMR*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.3.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956553)

MGNCCVGSSTKKSRRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
 HLPHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL
 DHPWLQNAKKPNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVEGN
 GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDDVVQAILSEVDLDKDGRISEYEEFVMMRRGTDWRKASRQYS
 RDRFNSLSMRLLRDGSLNPPSYSMSSMR*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.4.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:32956554)

MGNCCVGSSTKKSRRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
 HLPHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL
 DHPWLQNAKKPNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVEGN
 GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDDVVQAILSEVDLDKDGRISEYEEFVMMRRGTDWRKASRQYS
 RDRFNSLSMRLLRDGSLNPPSYSMSSMR*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.5.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:32956558)

MKHLPHHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVF
 FKPERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQ
 VLDHPWLQNAKKPNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVE
 GNGTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDDVVQAILSEVDLDKDGRISEYEEFVMMRRGTDWRKASRQ
 YSRDRFNSLSMRLLRDGSLNPPSYSMSSMR*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.6.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:32956555)

MGNCCVGSSTKKSRRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
 HLPHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL
 DHPWLQNAKKPNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVEGN
 GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDDVVQAILSEVDLDKDGRISEYEEFVMMRRGTDWRKASRQYS
 RDRFNSLSMRLLRDGSLNPPSYSMSSMR*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.7.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:32956556)

MGNCCVGSSTKKSRRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
 HLPHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL
 DHPWLQNAKKPNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVEGN
 GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDDVVQAILSEVDLDKDGRISEYEEFVMMRRGTDWRKASRQYS
 RDRFNSLSMRLLRDGSLNPPSYSMSSMR*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.8.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:32956559)

MKHLPHHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVF
 FKPERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQ
 VLDHPWLQNAKKPNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVE
 GNGTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDDVVQAILSEVDLDKDGRISEYEEFVMMRRGTDWRKASRQ
 YSRDRFNSLSMRLLRDGSLNPPSYSMSSMR*

>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.9.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:32956557)

MGNCCVGSSTKKSRRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
 HLPHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL
 DHPWLQNAKKPNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVEGN
 GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDDVVQAILSEVDLDKDGRISEYEEFVMMRRGTDWRKASRQYS
 RDRFNSLSMRLLRDGSLNPPSYSMSSMR*

>Pp3c11_5820 Org_Ppatens peptide: Pp3c11_5820V3.1.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:32957965)

MGNCCVGSSTKKSRRARRANLFAHRRYGNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMKH
 LPHHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL
 HPWLQNAKKPNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVEGN
 TLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDDVVQAILSEVDLDKDGRISEYEEFVMMRRGTDWRKASRQYS
 DRFNSLSMRLLRDGSLNPPSYSMSSMR*

>Pp3c11_5820 Org_Ppatens peptide: Pp3c11_5820V3.2.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
 PROTEIN KINASE 10-RELATED (PAC:32957966)

MGNCCVGSSTKKSRRARRANLFAHRRYGNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMKH
 LPHHPHPIVTLLEGAYEDDVAHVLMELCEGGEFLDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
 PGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVL

HPWLQNAKKNPVPLDAVRSLRKQFSAMNKLKKRALQVIAEHLGGEIDGLKEMFEKLDSDKTGTITFEKLKMGLEIGSQLTEHEVRMLMEAADVEGNG
 TLDYGEFVAATVHLQRLDDDEHLRAAFDVFDDVSGSYIETEELREAVGEAMTELSSEPDVQAILSEVDLDKDGRISEYEEFAVMMRRGTDWKASRQYSR
 DRFNSLSMRLLRDGSLNPPSYSSMSMR*

>Pp3c12_190 Org_Ppatens peptide: Pp3c12_190V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
 KINASE 20 (PAC:32975193)
 MGNTECVGAAGYFQGFSAIALGGRSSRSNSERSPTASKIDSDRKVEVDTPATQQNPQRQNHIPSVDTADQQQFKEVIEAMKKGREIKSVSGQSLTHSVL
 QRKTENLRDLTYLGGKLGQGGFTTYLCIEKATNKEYACKSIKRLKISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDR
 IIQRGQYSEAKAAVLTTRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAAKLTDFGLSVFFKPGEVFRDVGSPYYVAPEVLRKNYGPEADVWSAGVI
 LYILLSGVPPFWAETEQQGIFEQVLKSELDFASDPWPKISDSAKDLIRKMLNPQASKRLKAHQVLCWPICEDGVAPDRPIDSAVQSRCLKHFSAMNKLKKI
 AIRVIAESLSEEEIAGLKEMFKMMDTNSGSIYSDELKAGLKKVGSILKEEDIRQLMDAADVDGNGTIDYGEFLAATLHLNKKIERDENMLAAFSYLDKDN
 SGYLTIDELQHALLQFMGDISVDELLHEVDQNNNDGQIDYAEFVTMMRKGNPGAAGRSSFRNSQSLSLNDVLMVG*

>Pp3c12_190 Org_Ppatens peptide: Pp3c12_190V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
 KINASE 20 (PAC:32975194)
 MGNTECVGAAGYFQGFSAIALGGRSSRSNSERSPTASKIDSDRKVEVDTPATQQNPQRQNHIPSVDTADQQQFKEVIEAMKKGREIKSVSGQSLTHSVL
 QRKTENLRDLTYLGGKLGQGGFTTYLCIEKATNKEYACKSIKRLKISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDR
 IIQRGQYSEAKAAVLTTRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAAKLTDFGLSVFFKPGEVFRDVGSPYYVAPEVLRKNYGPEADVWSAGVI
 LYILLSGVPPFWAETEQQGIFEQVLKSELDFASDPWPKISDSAKDLIRKMLNPQASKRLKAHQVLCWPICEDGVAPDRPIDSAVQSRCLKHFSAMNKLKKI
 AIRVIAESLSEEEIAGLKEMFKMMDTNSGSIYSDELKAGLKKVGSILKEEDIRQLMDAADVDGNGTIDYGEFLAATLHLNKKIERDENMLAAFSYLDKDN
 SGYLTIDELQHALLQFMGDISVDELLHEVDQNNNDGQIDYAEFVTMMRKGNPGAAGRSSFRNSQSLSLNDVLMVG*

>Pp3c12_21850 Org_Ppatens peptide: Pp3c12_21850V3.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT
 PROTEIN KINASE 3 (PAC:32973633)
 MGNISGRPRKNRGHTKGMNLGRPTDPRQKNESERPMYEGSTQRSSAVASSYGGGTQHKQDGGSTRPATGTGSHAEGGHAARPSSGATPSEPPGMSAPM
 PRPRPTSYSANGVLGKPLVDIRQTYSLGRELGRGQFGVYTLCTHKTGTTEILACKSIKRLKLTTEKEDVEDVKREVQIMHHLSGTPNIVDLKGVYEDRHSVH
 LVMELCAGGELFDRIIAKGHYSERAAADLCRIVNVVHRCHTLGVFHRDLKPENFLLSSEAEDAQLKATDFGLSTFFKPGEVFHDIVGSAYYVAPEVLR
 NYGPEADVWSAGVIVYILLCGVPPFWAETEQQGIFDAVLRGHIDFVSDPWPKISSGAKDLVRKMLNMNVKERLTAYQVLNHPWMEEGGDASDTPDNAVLT
 RLKNFSTANKMKKLALKVIKLNSEEEIVGLRELKFSMDTNSGMVTFEELKDGLLRQGSGLRESIDIRELMEAADVDGNGKIDFNEFISATMHHMNKLEME
 DHLFAAFSHFDTDGSGYITIDELQEAEMKNGMGDPQTIQEIINEVDTRDGRIDYDEFVAMMRKGNPITEDGGKHRHR*

>Pp3c12_21850 Org_Ppatens peptide: Pp3c12_21850V3.2.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT
 PROTEIN KINASE 3 (PAC:32973634)
 MGNISGRPRKNRGHTKGMNLGRPTDPRQKNESERPMYEGSTQRSSAVASSYGGGTQHKQDGGSTRPATGTGSHAEGGHAARPSSGATPSEPPGMSAPM
 PRPRPTSYSANGVLGKPLVDIRQTYSLGRELGRGQFGVYTLCTHKTGTTEILACKSIKRLKLTTEKEDVEDVKREVQIMHHLSGTPNIVDLKGVYEDRHSVH
 LVMELCAGGELFDRIIAKGHYSERAAADLCRIVNVVHRCHTLGVFHRDLKPENFLLSSEAEDAQLKATDFGLSTFFKPGEVFHDIVGSAYYVAPEVLR
 NYGPEADVWSAGVIVYILLCGVPPFWAETEQQGIFDAVLRGHIDFVSDPWPKISSGAKDLVRKMLNMNVKERLTAYQVLNHPWMEEGGDASDTPDNAVLT
 RLKNFSTANKMKKLALKVIKLNSEEEIVGLRELKFSMDTNSGMVTFEELKDGLLRQGSGLRESIDIRELMEAADVDGNGKIDFNEFISATMHHMNKLEME
 DHLFAAFSHFDTDGSGYITIDELQEAEMKNGMGDPQTIQEIINEVDTRDGRIDYDEFVAMMRKGNPITEDGGKHRHR*

>Pp3c12_21880 Org_Ppatens peptide: Pp3c12_21880V3.1.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
 PROTEIN KINASE 5 (PAC:32974473)
 MGNSSGRPRDRSRKSGGGSGGSSQGSYPNREGSYPRGSGHGGSTQPRGCNQQGSTQPRGNSQQGSTQPRGSGHGNAGGYRQAPKYTPPVKPKPVAPGF
 LGKPLSDILNSYTLGKELGRGEFGVYTTCTHKDNEVYACKTIAKRKLTHKDDIEDVKREVQIMHHLSGTLNIVTLKAVFEDKHNHILVMELCAGGELFD
 RIVAKKCYSERAAADLCRIVNVVHRCHSLGVFHRDLKPENFLFTSMAEDAPLKATDFGLSTFFKPGERFQDLVGTAYYIAPEVLRKDYGPEADVWSAGV
 ILYILLCGVPPFWAETEKGIFDAIMRGTLDFTSDPWPRISSDAKVLVKGMLNPDVNARLTAQQVLDHHPWMKEDGASNAPLDNAVLTRLKNFSAANKMKKL
 ALKVIAQNLSSEEEIAGLRQLFKSIDVNSGTVTLLLEKEGLIKQGSKFESDIKLMESADLDGNGKIDFNEFISATMHHMNKLEKEDHLFAAFHHFDRDN
 SGYITVFELQQALEENGVDYDTIQEIIDEVDTDNDGRIDYDEFVAMMRKGNPGAEEGEGKHNHRHRY*

>Pp3c12_21880 Org_Ppatens peptide: Pp3c12_21880V3.2.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
 PROTEIN KINASE 5 (PAC:32974474)
 MGNSSGRPRDRSRKSGGGSGGSSQGSYPNREGSYPRGSGHGGSTQPRGCNQQGSTQPRGNSQQGSTQPRGSGHGNAGGYRQAPKYTPPVKPKPVAPGF
 LGKPLSDILNSYTLGKELGRGEFGVYTTCTHKDNEVYACKTIAKRKLTHKDDIEDVKREVQIMHHLSGTLNIVTLKAVFEDKHNHILVMELCAGGELFD
 RIVAKKCYSERAAADLCRIVNVVHRCHSLGVFHRDLKPENFLFTSMAEDAPLKATDFGLSTFFKPGERFQDLVGTAYYIAPEVLRKDYGPEADVWSAGV
 ILYILLCGVPPFWAETEKGIFDAIMRGTLDFTSDPWPRISSDAKVLVKGMLNPDVNARLTAQQVLDHHPWMKEDGASNAPLDNAVLTRLKNFSAANKMKKL
 ALKVIAQNLSSEEEIAGLRQLFKSIDVNSGTVTLLLEKEGLIKQGSKFESDIKLMESADLDGNGKIDFNEFISATMHHMNKLEKEDHLFAAFHHFDRDN
 SGYITVFELQQALEENGVDYDTIQEIIDEVDTDNDGRIDYDEFVAMMRKGNPGAEEGEGKHNHRHRY*

>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
 KINASE 20 (PAC:32905868)
 MGNTECIGAAGYFQGFSAIAIALGGRSFTSNSEISPSAKADGDRHKAGGDSTATQQKAPRQNYIPSVETDQQEFRDVIAMRKGREIEPVPGQSLTHSVLQ
 RKTENLRDLTYLGGKLGQGGFTTYLCIEKATNKEYACKSIKRLKISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDR
 IYQRGHYSEAKAAIIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAAKLTDFGLSVFFKPGEIFRVDVVGSPYYVAPEVLRKNYGPEADVWSAGVIL
 ILLCGVPPFWAETEKGIFDAQVLKSELDFATDPWPKISDSAKDLIRKMLNPEASKRMKAHVLCWPICEDGVAPDRPIDSAVQSRCLKHFSAMNKLKKIA
 IRVIAESLSEEEIAGLKEMFKMMDADNSGSIYSDELKAGLKKVGSILKEEDMRQLMDAADVDGNGTIDYGEFLAATLHLNKKIERDENMLAAFSYLDKDKS
 GYLTVDVQHALAEFRMGDISVDELLREVDQNNNDGRIDYAEFVAMMRKGNTPGAGRSSLRNSQSLSLNDVLMVG*

>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
 KINASE 20 (PAC:32905869)
 MGNTECIGAAGYFQGFSAIAIALGGRSFTSNSEISPSAKADGDRHKAGGDSTATQQKAPRQNYIPSVETDQQEFRDVIAMRKGREIEPVPGQSLTHSVLQ
 RKTENLRDLTYLGGKLGQGGFTTYLCIEKATNKEYACKSIKRLKISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDR
 IYQRGHYSEAKAAIIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAAKLTDFGLSVFFKPGEIFRVDVVGSPYYVAPEVLRKNYGPEADVWSAGVIL
 ILLCGVPPFWAETEKGIFDAQVLKSELDFATDPWPKISDSAKDLIRKMLNPEASKRMKAHVLCWPICEDGVAPDRPIDSAVQSRCLKHFSAMNKLKKIA

IRVIAESLSEEEIAGLKEMFKMMDADNSGSI SYEELKEGLKKVGSILKEEDMRQLMDAADVDGNGTIDYGEFLAATLHLNKKIERDENMLAAFSYLDKDKS
GYLTVDDEVQHAAEFMRGDLSDVDELLREVDQNNDRIDYAEFVAMMRKGNTEGGAGRSSLRNSQSLSLNDVLMVG*

>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32905870)

MGNTCIGAAGYFQGFSAAIAGLGRSFTSNSEISPSAKADGRHKAGGDSTATQQKAPRQNYIPSV EATDQQEFRDVI EAMRKGREIEPVPGQSLTHSVLQ
RKTEENLRDLYTLGKKLGQGGFGTTYLCIEKATSKEYACKSI AKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIK GAYEDPASVHLMELCAGGELFDRI
IQRGHYSEAKAAIIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEIFR DVGVSPPYVAPEVLRKNYGP EADVWSAGVIL
YILLCGVPPFWAETEQQGIFEQVLKSELDFATDPWPKISDSAKDLIRKMLNPEASKRMKAHHVLC HPWICEDGVAPDRPIDSAVQSR LKHFSAMNKLKKIA
IRVIAESLSEEEIAGLKEMFKMMDADNSGSI SYEELKEGLKKVGSILKEEDMRQLMDAADVDGNGTIDYGEFLAATLHLNKKIERDENMLAAFSYLDKDKS
GYLTVDDEVQHAAEFMRGDLSDVDELLREVDQNNDRIDYAEFVAMMRKGNTEGGAGRSSLRNSQSLSLNDVLMVG*

>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.4.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32905871)

MGNTCIGAAGYFQGFSAAIAGLGRSFTSNSEISPSAKADGRHKAGGDSTATQQKAPRQNYIPSV EATDQQEFRDVI EAMRKGREIEPVPGQSLTHSVLQ
RKTEENLRDLYTLGKKLGQGGFGTTYLCIEKATSKEYACKSI AKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIK GAYEDPASVHLMELCAGGELFDRI
IQRGHYSEAKAAIIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEIFR DVGVSPPYVAPEVLRKNYGP EADVWSAGVIL
YILLCGVPPFWAETEQQGIFEQVLKSELDFATDPWPKISDSAKDLIRKMLNPEASKRMKAHHVLC HPWICEDGVAPDRPIDSAVQSR LKHFSAMNKLKKIA
IRVIAESLSEEEIAGLKEMFKMMDADNSGSI SYEELKEGLKKVGSILKEEDMRQLMDAADVDGNGTIDYGEFLAATLHLNKKIERDENMLAAFSYLDKDKS
GYLTVDDEVQHAAEFMRGDLSDVDELLREVDQNNDRIDYAEFVAMMRKGNTEGGAGRSSLRNSQSLSLNDVLMVG*

>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.5.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32905872)

MGNTCIGAAGYFQGFSAAIAGLGRSFTSNSEISPSAKADGRHKAGGDSTATQQKAPRQNYIPSV EATDQQEFRDVI EAMRKGREIEPVPGQSLTHSVLQ
RKTEENLRDLYTLGKKLGQGGFGTTYLCIEKATSKEYACKSI AKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIK GAYEDPASVHLMELCAGGELFDRI
IQRGHYSEAKAAIIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEIFR DVGVSPPYVAPEVLRKNYGP EADVWSAGVIL
YILLCGVPPFWAETEQQGIFEQVLKSELDFATDPWPKISDSAKDLIRKMLNPEASKRMKAHHVLC HPWICEDGVAPDRPIDSAVQSR LKHFSAMNKLKKIA
IRVIAESLSEEEIAGLKEMFKMMDADNSGSI SYEELKEGLKKVGSILKEEDMRQLMDAADVDGNGTIDYGEFLAATLHLNKKIERDENMLAAFSYLDKDKS
GYLTVDDEVQHAAEFMRGDLSDVDELLREVDQNNDRIDYAEFVAMMRKGNTEGGAGRSSLRNSQSLSLNDVLMVG*

>Pp3c20_12010 Org_Ppatens peptide: Pp3c20_12010V3.1.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32946771)

MAKSPPPNSIQMSAVLDHRGSNVIPHDLISSLDRESNLVNLKVGYNKAELELSPGSSCSPDNTPRVAVEKKPEVKYTTQNSKQVEGVIIQAIKASDNKDQ
KKGKLTVCVLQHVTEVDVRDVTYTLGKKLGAGNFGITYLCTEKSTGDDYACKTISKKKLKSDDVADVRKELQIMHHLSGHPNIVAIKGAFED EASVHFVME
LCAGGELFTRITEKGHYSEAAAAAMRTIVSVIETCHILGVIHRDLKPENFLLLNKREDSPLKATDFGLSTFFKPGEVCKDVVGS AFYVAPEVLR RRYGP
ESDIWSAGVILYILLSGVPPFWADTEDGIFAEVLKAKVDFDTPWPKISKDAKDLIRKILNPDVKARLTASEVL AHPWVREKGVASTKPM DSSVQNRLKR
FAAMNMKKLAVRVIAQSMSEEEIAGLRNIFKIMDVGSGTITFEELKQGLQKVGSNMREADVRLMDAADVDKNGTIDYGEFLAATINMNKVEREENML
AAFRYLDKDNNGYITGEELQNACAEFNMGMENLEDLMRDVDLDNDGRIDYQEFVAMMRKGTGTAPPQRGARMEPSFGFSAALQL*

>Pp3c20_12010 Org_Ppatens peptide: Pp3c20_12010V3.2.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32946772)

MNPQQSLCSSLFIRGLSLSQSSCSPDNTPRVAVEKKPEVKYTTQNSKQVEGVIIQAIKASDNKDQKKGKLTVCVLQHVTEVDVRDVTYTLGKKLGAGNFGI
TYLCTEKSTGDDYACKTISKKKLKSDDVADVRKELQIMHHLSGHPNIVAIKGAFED EASVHFVME LCAGGELFTRITEKGHYSEAAAAAMRTIVSVIE
TCHILGVIHRDLKPENFLLLNKREDSPLKATDFGLSTFFKPGEVCKDVVGS AFYVAPEVLR RRYGPESDIWSAGVILYILLSGVPPFWADTEDGIFAEVL
KAKVDFDTPWPKISKDAKDLIRKILNPDVKARLTASEVL AHPWVREKGVASTKPM DSSVQNRLKRFAAMNMKKLAVRVIAQSMSEEEIAGLRNIFKIM
DVGSGTITFEELKQGLQKVGSNMREADVRLMDAADVDKNGTIDYGEFLAATINMNKVEREENMLA AFRYLDKDNNGYITGEELQNACAEFNMGMENLE
DLMRVDLDNDGRIDYQEFVAMMRKGTGTAPPQRGARMEPSFGFSAALQL*

>Pp3c20_4100 Org_Ppatens peptide: Pp3c20_4100V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32945505)

MGNTCVGAASKAGFFFPQEGGSPSPSVTPKGTQPEEPAKPNNPSPPEERRKSGAGVEQEARAE LKPQLSLTIQAPAVIRIAPT VYPSAANRRQENC VVP
AMRRAGLNLIPLGSLFTHSVLQRQTENLKDLYRLERKLGQGGFGTTYLCVEKATGREYACKSI AKRKLISQEDVDVDRRELHIMHHLSGHPNIVTIK GAYE
DQMAVHLMELCAGGELFDRI IQRGHYSEAAAE LCRVIVGVVETCHSLGVMHRDLKPENFLLS DQSEGAALKTDFGLSVFFKPGEVFTDVVGS PYYVA
PEVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLKSELDFVSEPWPSISDSAKDLIRRM LDPNAKRRLKAHQVLSHPWIGEEGVAPDRPM
DPAVQSR LKQFSAMNKLKKVAIRVIAELLSEEEIAGLRMFKIMIDTHSGTITFEELKSGLERVGSNLVSEIRQLMDAADVDQNGTIDYGEFLAATLHL
NKIEREENLFAAFSWLDKDNNGYITVDELQQA CSKYNMGETSIEDLIREVDQDNDGRIDYNEFVTMMRKNGAVGR TTRLNLSLS DALMNPQ*

>Pp3c20_4100 Org_Ppatens peptide: Pp3c20_4100V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32945506)

MGNTCVGAASKAGFFFPQEGGSPSPSVTPKGTQPEEPAKPNNPSPPEERRKSGAGVEQEARAE LKPQLSLTIQAPAVIRIAPT VYPSAANRRQENC VVP
AMRRAGLNLIPLGSLFTHSVLQRQTENLKDLYRLERKLGQGGFGTTYLCVEKATGREYACKSI AKRKLISQEDVDVDRRELHIMHHLSGHPNIVTIK GAYE
DQMAVHLMELCAGGELFDRI IQRGHYSEAAAE LCRVIVGVVETCHSLGVMHRDLKPENFLLS DQSEGAALKTDFGLSVFFKPGEVFTDVVGS PYYVA
PEVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLKSELDFVSEPWPSISDSAKDLIRRM LDPNAKRRLKAHQVLSHPWIGEEGVAPDRPM
DPAVQSR LKQFSAMNKLKKVAIRVIAELLSEEEIAGLRMFKIMIDTHSGTITFEELKSGLERVGSNLVSEIRQLMDAADVDQNGTIDYGEFLAATLHL
NKIEREENLFAAFSWLDKDNNGYITVDELQQA CSKYNMGETSIEDLIREVDQDNDGRIDYNEFVTMMRKNGAVGR TTRLNLSLS DALMNPQ*

>Pp3c20_4170 Org_Ppatens peptide: Pp3c20_4170V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32948019)

MGNTCVGAASKAGFFFPQEGGSPSPSVTPKGTQPEEPAKPNNPSPPEERRKSGAGVEQEARAE LKPQLSLTIQAPAVIRIAPT VYPSAANRRQENC VVP
AMRRAGLNLIPLGSLFTHSVLQRQTENLKDLYRLGRKLGQGGFGTTYLCVEKATGREYACKSI AKRKLISQEDVDVDRRELHIMHHLSGHPNIVTIK GAYE
DQMAVHLMELCAGGELFDRI IQRGHYSEAAAE LCRVIVGVVETCHSLGVMHRDLKPENFLLS DQSEGAALKTDFGLSVFFKPGEVFTDVVGS PYYVA
PEVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLKSELDFVSEPWPSISDSAKDLIRRM LDPNAKRRLKAHQVLSHPWIGEEGVAPDRPM
DPAVQSR LKQFSAMNKLKKVAIRVIAELLSEEEIAGLRMFKIMIDTHSGTITFEELKSGLERVGSNLVSEIRQLMDAADVDQNGTIDYGEFLAATLHL

NKIEREENLFAAFSWLDKDNSGYLTVDELQQACSKYNMGETSIEDLIREVDQDNDGRIDYNEFVMMMRKNGGAVGRTTLRNSLSLSDALMNPQ*

>Pp3c20_4170 Org_Ppatens peptide: Pp3c20_4170V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32948021)

MRRAGLNLIPLGLSFTHSVLQRQNTENLKDLYTLGRKLGQGGQFGTTYLCVEKATGREYACKSIAKRKLISQEDVDDVRRELHIMHLSGHPNIVTIKAYEDQMAVHLMELCAGGELFDRIIQRGHYSEAQAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDQSEGAALKTTDFGLSVFFKPGEVFTDVGSPYYVAP

EVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLKGLDFVSEPPWPSISDSAKDLIRRLDPNAKRRLKAHQVLSHPWIGEEGVAPDRPMD

PAVQSRKQFSAMNKLKKVAIRVIAEELLSEEEIAGLREMFKIMIDTHSGTITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLN

KIEREENLFAAFSWLDKDNSGYLTVDELQQACSKYNMGETSIEDLIREVDQDNDGRIDYNEFVMMMRKNGGAVGRTTLRNSLSLSDALMNPQ*

>Pp3c20_4170 Org_Ppatens peptide: Pp3c20_4170V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32948020)

MGNTCVGAASKAGFFFPQERGSFSPSVTPKGTQPEEPAKPNNPSPPEERRKSGAGVEQEARAELKPQLSLTIQAPAVIRIAPTVPYPSAANRRQENCVPV

AMRRAGLNLIPLGLSFTHSVLQRQNTENLKDLYTLGRKLGQGGQFGTTYLCVEKATGREYACKSIAKRKLISQEDVDDVRRELHIMHLSGHPNIVTIKAYE

DQMAVHLMELCAGGELFDRIIQRGHYSEAQAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDQSEGAALKTTDFGLSVFFKPGEVFTDVGSPYYVA

PEVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLKGLDFVSEPPWPSISDSAKDLIRRLDPNAKRRLKAHQVLSHPWIGEEGVAPDRPM

DPAVQSRKQFSAMNKLKKVAIRVIAEELLSEEEIAGLREMFKIMIDTHSGTITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHL

NKIEREENLFAAFSWLDKDNSGYLTVDELQQACSKYNMGETSIEDLIREVDQDNDGRIDYNEFVMMMRKNGGAVGRTTLRNSLSLSDALMNPQ*

>Pp3c23_18880 Org_Ppatens peptide: Pp3c23_18880V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32950805)

MRRGVNLVPGQSFTHSVLQRQNTENLKDLYTLGRKLGQGGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHLSGHPNIVTIKAYEDQ

VSVHLMELCAGGELFDRIIQRGHYSEAQAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVGSPYYVAPE

VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLGELDFVSEPPWPSISDSAKDLIRRLDPNAKRRLKAHQVLSHPWIREAGVAPDRPMDP

AVQSRKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKIMIDTHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK

IEREENLFAAFSWLDKDHSGYLTVDLQHCSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKNGTGVGRATLRNSLSLSDALMHTN*

>Pp3c23_18880 Org_Ppatens peptide: Pp3c23_18880V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32950806)

MRRGVNLVPGQSFTHSVLQRQNTENLKDLYTLGRKLGQGGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHLSGHPNIVTIKAYEDQ

VSVHLMELCAGGELFDRIIQRGHYSEAQAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVGSPYYVAPE

VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLGELDFVSEPPWPSISDSAKDLIRRLDPNAKRRLKAHQVLSHPWIREAGVAPDRPMDP

AVQSRKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKIMIDTHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK

IEREENLFAAFSWLDKDHSGYLTVDLQHCSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKNGTGVGRATLRNSLSLSDALMHTN*

>Pp3c23_18880 Org_Ppatens peptide: Pp3c23_18880V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32950804)

MRRGVNLVPGQSFTHSVLQRQNTENLKDLYTLGRKLGQGGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHLSGHPNIVTIKAYEDQ

VSVHLMELCAGGELFDRIIQRGHYSEAQAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVGSPYYVAPE

VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLGELDFVSEPPWPSISDSAKDLIRRLDPNAKRRLKAHQVLSHPWIREAGVAPDRPMDP

AVQSRKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKIMIDTHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK

IEREENLFAAFSWLDKDHSGYLTVDLQHCSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKNGTGVGRATLRNSLRMGNGKATAAVDGSERGA

SAAMSVQRCGGVDSIRENAARNSKGVGGEGGRVCWLSGRGLETMPRLGTGVGVHEVKNGLERAAEQGVG*

>Pp3c23_18930 Org_Ppatens peptide: Pp3c23_18930V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32950555)

MRRGVNLVPGQSFTHSVLQRQNTENLKDLYTLGRKLGQGGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHLSGHPNIVTIKAYEDQ

VSVHLMELCAGGELFDRIIQRGHYSEAQAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVGSPYYVAPE

VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLGELDFVSEPPWPSISDSAKDLIRRLDPNAKRRLKAHQVLSHPWIREAGVAPDRPMDP

AVQSRKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKIMIDTHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK

IEREENLFAAFSWLDKDHSGYLTVDLQHCSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKNGTGVGRATLRNSLSLSDALMHTN*

>Pp3c23_18930 Org_Ppatens peptide: Pp3c23_18930V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32950556)

MRRGVNLVPGQSFTHSVLQRQNTENLKDLYTLGRKLGQGGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHLSGHPNIVTIKAYEDQ

VSVHLMELCAGGELFDRIIQRGHYSEAQAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVGSPYYVAPE

VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLGELDFVSEPPWPSISDSAKDLIRRLDPNAKRRLKAHQVLSHPWIREAGVAPDRPMDP

AVQSRKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKIMIDTHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK

IEREENLFAAFSWLDKDHSGYLTVDLQHCSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKNGTGVGRATLRNSLSLSDALMHTN*

>Pp3c23_18930 Org_Ppatens peptide: Pp3c23_18930V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32950557)

MRRGVNLVPGQSFTHSVLQRQNTENLKDLYTLGRKLGQGGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHLSGHPNIVTIKAYEDQ

VSVHLMELCAGGELFDRIIQRGHYSEAQAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVGSPYYVAPE

VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQQGIFEQVLGELDFVSEPPWPSISDSAKDLIRRLDPNAKRRLKAHQVLSHPWIREAGVAPDRPMDP

AVQSRKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKIMIDTHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK

IEREENLFAAFSWLDKDHSGYLTVDLQHCSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKNGTGVGRATLRNSLSLSDALMHTN*

>Pp3c3_37890 Org_Ppatens peptide: Pp3c3_37890V3.1.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED PROTEIN KINASE 5 (PAC:32944916)

MGNTSSRGSRKSTRQVNQGVGSQDTREKNDVSNPKTRQGGSVGANNYGKPPSSGAQAGERSTSAPAALPRPKPASRSVSGVLGKPLSDIRQSYILGREL

RGQVGHVRLCTDKMTNEAYACKSIAKRKLTSKEDIEDVKREVQIMHLSGTPNIVVLKDVFEKHSVHLMELCAGGELFDRIIAKGYHERAAADMCRV

IVNVVHCHSLGVFHRDLKPENFLLASKAEDAPLKATDFGLSTFFKPGDVQDIVGSAYVVAPEVLKRSYGPEADVWSAGVILYILLCGVPPFWAETEQQ

IFDAVLKGHIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQQVLNHPWMKEDGAPDVLDNAVLTRLKNFSAANKMKKALKVIAESLSEEEIVGLR

EMFKSIDTNSGTVTFEELKEGLLKQGSKLNESDIRKLMEAADVDGNGKIDFNEFISATMHMNKTEKEDHLWAAFMHFDTDNSGYITIDELQEAMEKNGM
 GDPETIQEIIESEVDTDNDGRIDYDEFVAMMRKGNPGAENGGTVNKP RHR*

>Pp3c3_37890 Org_Ppatens peptide: Pp3c3_37890V3.2.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
 PROTEIN KINASE 5 (PAC:32944917)

MGNSTSSRGSRKSTRQVNQGVGSQDTREKNDVSNPKTRQGGSVGANNYGGKPSGQAQAGERSTSAPAALPRPKPASRSVSGVLGKPLSDIRQSYIILGREL
 RGQFGVYTLCTDKMTNEAYACKSIAKRKLTSKEDIEDVKREVQIMHHLSGTPNIVLKDVFEDKHSVHLMELCAGGELFDRIIAKGHYSERAAADMCRV
 IVNVVHRCHSLGVFHRDLKPENFLASKAEDAPLKATDFGLSTFFKPGDVFQDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYIILCGVPPFWAETEQQ
 IFDAVLKGHIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQQVLNHPWMKEDGADPVDPLDNAVLTRLNKNSAANKMKKALKVIAESLSEEEIVGLR
 EMFKSIDTNSGTVTFEELKEGLLKQGSKLNESDIRKLMEAADVDGNGKIDFNEFISATMHMNKTEKEDHLWAAFMHFDTDNSGYITIDELQEAMEKNGM
 GDPETIQEIIESEVDTDNDGRIDYDEFVAMMRKGNPGAENGGTVNKP RHR*

>Pp3c3_37890 Org_Ppatens peptide: Pp3c3_37890V3.4.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
 PROTEIN KINASE 5 (PAC:32944918)

MGNSTSSRGSRKSTRQVNQGVGSQDTREKNDVSNPKTRQGGSVGANNYGGKPSGQAQAGERSTSAPAALPRPKPASRSVSGVLGKPLSDIRQSYIILGREL
 RGQFGVYTLCTDKMTNEAYACKSIAKRKLTSKEDIEDVKREVQIMHHLSGTPNIVLKDVFEDKHSVHLMELCAGGELFDRIIAKGHYSERAAADMCRV
 IVNVVHRCHSLGVFHRDLKPENFLASKAEDAPLKATDFGLSTFFKPGDVFQDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYIILCGVPPFWAETEQQ
 IFDAVLKGHIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQQVLNHPWMKEDGADPVDPLDNAVLTRLNKNSAANKMKKALKVIAESLSEEEIVGLR
 EMFKSIDTNSGTVTFEELKEGLLKQGSKLNESDIRKLMEAADVDGNGKIDFNEFISATMHMNKTEKEDHLWAAFMHFDTDNSGYITIDELQEAMEKNGM
 GDPETIQEIIESEVDTDNDGRIDYDEFVAMMRKGNPGAENGGTVNKP RHR*

>Pp3c3_37890 Org_Ppatens peptide: Pp3c3_37890V3.5.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
 PROTEIN KINASE 5 (PAC:32944919)

MGNSTSSRGSRKSTRQVNQGVGSQDTREKNDVSNPKTRQGGSVGANNYGGKPSGQAQAGERSTSAPAALPRPKPASRSVSGVLGKPLSDIRQSYIILGREL
 RGQFGVYTLCTDKMTNEAYACKSIAKRKLTSKEDIEDVKREVQIMHHLSGTPNIVLKDVFEDKHSVHLMELCAGGELFDRIIAKGHYSERAAADMCRV
 IVNVVHRCHSLGVFHRDLKPENFLASKAEDAPLKATDFGLSTFFKPGDVFQDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYIILCGVPPFWAETEQQ
 IFDAVLKGHIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQQVLNHPWMKEDGADPVDPLDNAVLTRLNKNSAANKMKKALKVIAESLSEEEIVGLR
 EMFKSIDTNSGTVTFEELKEGLLKQGSKLNESDIRKLMEAADVDGNGKIDFNEFISATMHMNKTEKEDHLWAAFMHFDTDNSGYITIDELQEAMEKNGM
 GDPETIQEIIESEVDTDNDGRIDYDEFVAMMRKGNPGAENGGTVNKP RHR*

>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.1.p (1 of 5) PTHR24349//PTHR24349:SF135 -
 SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919729)

MAAPRPRSVSNVGLGKPLVDIRQYISLKGELGRGQFGVYTLCTHKETGEKLACKSIAKRKLIKEDIEDVKREVQIMHHLSGTPNIVDLKGVEYDRHSV
 HLMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPENFLASKDEADPLQATDFGLSTFFKLGVEVFRDIVGSAYYVAPEVLK
 RNYGPEADVWSAGVIVYIILCGVPPFWAEESEQGIFDAVLKGHIDFESEPWPRISGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVL
 DRLKNFSAANKMKKALKVIANSLSEEEIVGLRELKFSMDTDNSGMVTFEELKQGLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEK
 EDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEI IREVDTDNDGKIDYDEFVAMMRKGNPDTEDGVMVPPRHR*

>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.2.p (1 of 5) PTHR24349//PTHR24349:SF135 -
 SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919722)

MGNVSGRQSKNRGQGGMSQEGSADTRFKSESERPRAEQSNQRSSATSSSRGASTHPNQGSARPASTGSAHTGSAHNASTHNNQGGSTRPASTGSTHTG
 SSHNASTHSNQGGSTRPASTGSSHGSESGHSARPSSGTAPAERPRVPMAPRPRSVSNVGLGKPLVDIRQYISLKGELGRGQFGVYTLCTHKETGEKLAC
 KSIKRKLIKEDIEDVKREVQIMHHLSGTPNIVDLKGVEYDRHSVHLMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPE
 NLFASKDEADPLQATDFGLSTFFKLGVEVFRDIVGSAYYVAPEVLKRNYPGPEADVWSAGVIVYIILCGVPPFWAEESEQGIFDAVLKGHIDFESEPWPRIS
 SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLNKNSAANKMKKALKVIANSLSEEEIVGLRELKFSMDTDNSGMVTFEELKQ
 GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEI IREVDTDNDGKI
 DYDEFVAMMRKGNPDTEDGVMVPPRHR*

>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.3.p (1 of 5) PTHR24349//PTHR24349:SF135 -
 SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919723)

MGNVSGRQSKNRGQGGMSQEGSADTRFKSESERPRAEQSNQRSSATSSSRGASTHPNQGSARPASTGSAHTGSAHNASTHNNQGGSTRPASTGSTHTG
 SSHNASTHSNQGGSTRPASTGSSHGSESGHSARPSSGTAPAERPRVPMAPRPRSVSNVGLGKPLVDIRQYISLKGELGRGQFGVYTLCTHKETGEKLAC
 KSIKRKLIKEDIEDVKREVQIMHHLSGTPNIVDLKGVEYDRHSVHLMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPE
 NLFASKDEADPLQATDFGLSTFFKLGVEVFRDIVGSAYYVAPEVLKRNYPGPEADVWSAGVIVYIILCGVPPFWAEESEQGIFDAVLKGHIDFESEPWPRIS
 SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLNKNSAANKMKKALKVIANSLSEEEIVGLRELKFSMDTDNSGMVTFEELKQ
 GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEI IREVDTDNDGKI
 DYDEFVAMMRKGNPDTEDGVMVPPRHR*

>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.4.p (1 of 5) PTHR24349//PTHR24349:SF135 -
 SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919724)

MGNVSGRQSKNRGQGGMSQEGSADTRFKSESERPRAEQSNQRSSATSSSRGASTHPNQGSARPASTGSAHTGSAHNASTHNNQGGSTRPASTGSTHTG
 SSHNASTHSNQGGSTRPASTGSSHGSESGHSARPSSGTAPAERPRVPMAPRPRSVSNVGLGKPLVDIRQYISLKGELGRGQFGVYTLCTHKETGEKLAC
 KSIKRKLIKEDIEDVKREVQIMHHLSGTPNIVDLKGVEYDRHSVHLMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPE
 NLFASKDEADPLQATDFGLSTFFKLGVEVFRDIVGSAYYVAPEVLKRNYPGPEADVWSAGVIVYIILCGVPPFWAEESEQGIFDAVLKGHIDFESEPWPRIS
 SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLNKNSAANKMKKALKVIANSLSEEEIVGLRELKFSMDTDNSGMVTFEELKQ
 GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEI IREVDTDNDGKI
 DYDEFVAMMRKGNPDTEDGVMVPPRHR*

>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.5.p (1 of 5) PTHR24349//PTHR24349:SF135 -
 SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919725)

MGNVSGRQSKNRGQGGMSQEGSADTRFKSESERPRAEQSNQRSSATSSSRGASTHPNQGSARPASTGSAHTGSAHNASTHNNQGGSTRPASTGSTHTG
 SSHNASTHSNQGGSTRPASTGSSHGSESGHSARPSSGTAPAERPRVPMAPRPRSVSNVGLGKPLVDIRQYISLKGELGRGQFGVYTLCTHKETGEKLAC
 KSIKRKLIKEDIEDVKREVQIMHHLSGTPNIVDLKGVEYDRHSVHLMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPE

NFLFASKDEDAFLQATDFGLSTFFKLGVEVFRDIVGSAYYVAPEVLKRNYPGEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEWPWRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLNKNSAANKMKKLALKVIANSLSSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEGDMVVPVPRHR*

>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.6.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919726)

MGNVSGRQSKNRGQQGMSQEGSADTRFKSESERPRAEQSNQRSSATSSSRGASTHPNQGSARPASTGSAHTGSAHNASTHNNQGGSTRPASTGSTHTG
SSHNASTHSNQGGSTRPASTGSSHGSESGHSARPPSGTAPAERPRVPMAPRPRSVSNVGVGLKPLVDIRQTYSLGKELGRGQFGVITYLCTHKETGEKLAC
KSIARKKLIKEDIEDVKREVQIMHHLSTGTPNIVDLKGVYEDRHSVHLMELCAGGELFDRIIAKGHYSERAAADLCRIVNVVHRCBSLGVFHRDLKPE
NFLFASKDEDAFLQATDFGLSTFFKLGVEVFRDIVGSAYYVAPEVLKRNYPGEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEWPWRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLNKNSAANKMKKLALKVIANSLSSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEGDMVVPVPRHR*

>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.7.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919727)

MGNVSGRQSKNRGQQGMSQEGSADTRFKSESERPRAEQSNQRSSATSSSRGASTHPNQGSARPASTGSAHTGSAHNASTHNNQGGSTRPASTGSTHTG
SSHNASTHSNQGGSTRPASTGSSHGSESGHSARPPSGTAPAERPRVPMAPRPRSVSNVGVGLKPLVDIRQTYSLGKELGRGQFGVITYLCTHKETGEKLAC
KSIARKKLIKEDIEDVKREVQIMHHLSTGTPNIVDLKGVYEDRHSVHLMELCAGGELFDRIIAKGHYSERAAADLCRIVNVVHRCBSLGVFHRDLKPE
NFLFASKDEDAFLQATDFGLSTFFKLGVEVFRDIVGSAYYVAPEVLKRNYPGEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEWPWRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLNKNSAANKMKKLALKVIANSLSSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEGDMVVPVPRHR*

>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.8.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919728)

MGNVSGRQSKNRGQQGMSQEGSADTRFKSESERPRAEQSNQRSSATSSSRGASTHPNQGSARPASTGSAHTGSAHNASTHNNQGGSTRPASTGSTHTG
SSHNASTHSNQGGSTRPASTGSSHGSESGHSARPPSGTAPAERPRVPMAPRPRSVSNVGVGLKPLVDIRQTYSLGKELGRGQFGVITYLCTHKETGEKLAC
KSIARKKLIKEDIEDVKREVQIMHHLSTGTPNIVDLKGVYEDRHSVHLMELCAGGELFDRIIAKGHYSERAAADLCRIVNVVHRCBSLGVFHRDLKPE
NFLFASKDEDAFLQATDFGLSTFFKLGVEVFRDIVGSAYYVAPEVLKRNYPGEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEWPWRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLNKNSAANKMKKLALKVIANSLSSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEGDMVVPVPRHR*

>Pp3c6_50 Org_Ppatens peptide: Pp3c6_50V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32978421)

MAEVALLNPLEQIHDFAVLQHKSEVDKDIYTLGKKLGEGQFGITYLCTEKATGLKYACKCIPKRKLISEEEIENVGREIEVVMYHLAGHPNIVAIAKAYED
ETMVYLVLMELCEGGELFDRIIERGTYTEAKAADLRTIVGVVEACHNSGVVHRDLKPENFLFQTKHEDSMLKAADFSSRRFFEPGDVFTTEIVGSPFYVAP
EVLDRHYGPEADIWSAGVILYILLSGVPPFWAETVQGFEEVMKGEPPSFAADPWPNISEGAKDLIRQMLNPDPRKRLTAAEVLKHPWIREDGVASNKPI
ASLVQFRLKQFSAMNKLKLAIRIIAEKLSEEEIACLKEIFSEMMDRDKGAI SFEEELKEGLLKAGTTLDPEIFDLMDAADIDQDGIIDYGEFLAATLSL
NHIELEENLFAAFQYFDKDGSGHITMDEVLA VCREFNMEVDLIEDLLHEVDVDHGTIDYKMFVTMMRKNGGGVGHQTLRCTLGITDVLADHMT*

>Pp3c6_50 Org_Ppatens peptide: Pp3c6_50V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32978422)

MAEVALLNPLEQIHDFAVLQHKSEVDKDIYTLGKKLGEGQFGITYLCTEKATGLKYACKCIPKRKLISEEEIENVGREIEVVMYHLAGHPNIVAIAKAYED
ETMVYLVLMELCEGGELFDRIIERGTYTEAKAADLRTIVGVVEACHNSGVVHRDLKPENFLFQTKHEDSMLKAADFSSRRFFEPGDVFTTEIVGSPFYVAP
EVLDRHYGPEADIWSAGVILYILLSGVPPFWAETVQGFEEVMKGEPPSFAADPWPNISEGAKDLIRQMLNPDPRKRLTAAEVLKHPWIREDGVASNKPI
ASLVQFRLKQFSAMNKLKLAIRIIAEKLSEEEIACLKEIFSEMMDRDKGAI SFEEELKEGLLKAGTTLDPEIFDLMDAADIDQDGIIDYGEFLAATLSL
NHIELEENLFAAFQYFDKDGSGHITMDEVLA VCREFNMEVDLIEDLLHEVDVDHGTIDYKMFVTMMRKNGGGVGHQTLRCTLGITDVLADHMT*

>Pp3c6_50 Org_Ppatens peptide: Pp3c6_50V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32978423)

MAEVALLNPLEQIHDFAVLQHKSEVDKDIYTLGKKLGEGQFGITYLCTEKATGLKYACKCIPKRKLISEEEIENVGREIEVVMYHLAGHPNIVAIAKAYED
ETMVYLVLMELCEGGELFDRIIERGTYTEAKAADLRTIVGVVEACHNSGVVHRDLKPENFLFQTKHEDSMLKAADFSSRRFFEPGDVFTTEIVGSPFYVAP
EVLDRHYGPEADIWSAGVILYILLSGVPPFWAETVQGFEEVMKGEPPSFAADPWPNISEGAKDLIRQMLNPDPRKRLTAAEVLKHPWIREDGVASNKPI
ASLVQFRLKQFSAMNKLKLAIRIIAEKLSEEEIACLKEIFSEMMDRDKGAI SFEEELKEGLLKAGTTLDPEIFDLMDAADIDQDGIIDYGEFLAATLSL
NHIELEENLFAAFQYFDKDGSGHITMDEVLA VCREFNMEVDLIEDLLHEVDVDHGTIDYKMFVTMMRKNGGGVGHQTLRCTLGITDVLADHMT*

>Pp3c7_22440 Org_Ppatens peptide: Pp3c7_22440V3.1.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925272)

MGNCCAGSATKKPKQRPNPFAQDGYQANSQILKNQPKAKILDYILGRELGRGEFGITYLCTDKETGETLACKSISKKKLRTAVDVEDVRREVAIMKHL
EHPNIVTLNGAFEDDNAVLHLMELCEGGELFDRIIARGHYTERGAQVTRTIVEVVQACHIQGVHRDLKPENFLFANKNENSVLKAIDFGLSVFVKPGE
KFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGVLDKFDKRDWPVKVSDSAKSLVRRMLEPDPKARYNAQQVLDHP
WLQNAKKNPNVPLDTPRSRLKQFSAMNKLKRALQVIAESLGGEEEMNGLKEMFEKLDSDNAGVITFEKLMGLIEIGSQLTEHEVRMLMGAADV DNGAL
DYGEFVAAAVHLQRLGDDEYLKAFDVFVDGSGYIETEELRVAVGEPLNGSPSESDDVQGILLEVVDVDKGRISYEESAMMRRTDWRKASRQYSRDR
FNSLSMRLVREGSLNPDKSAVVR*

>Pp3c7_22440 Org_Ppatens peptide: Pp3c7_22440V3.2.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925273)

MGNCCAGSATKKPKQRPNPFAQDGYQANSQILKNQPKAKILDYILGRELGRGEFGITYLCTDKETGETLACKSISKKKLRTAVDVEDVRREVAIMKHL
EHPNIVTLNGAFEDDNAVLHLMELCEGGELFDRIIARGHYTERGAQVTRTIVEVVQACHIQGVHRDLKPENFLFANKNENSVLKAIDFGLSVFVKPGE
KFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGVLDKFDKRDWPVKVSDSAKSLVRRMLEPDPKARYNAQQVLDHP

WLQNAKKNPNVPLD TVRSRLKQFSAMNKLKKRALQVIAESLGG EEMNGLKEMFEKLDSDNAGVITFEKLMGLIEIGSQLTEHEVRMLMGAADV DGNAL
DYGEFVAAA VHLQRLGDDEYLRKAFD VFDV DSGSYIETEELRVAVGEPLNGSPSESDVVQGILLEV DVDKDGRI SYEEFSAMMR RGT DWRKASRQYSRDR
FNSLSMRLVREGSLNPDKSAVVR*

>Pp3c7_22440 Org_Ppatens peptide: Pp3c7_22440V3.3.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925274)
MGNCCAGSATKKPKQRPNPF AQDGYQANSQILKNQPKAKILD KYILGRELGRGEFGITYLCTDKETGETLACKSISKKKLRTAVDVEDVRREVAIMKHLP
EHPNIVTLNGAFEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHIQGV IHRDLKPENFLFANKNENSVLK AIDFGLSVFFKPG E
KFSEIVGSPYYMAPEVLKRN YGPEVDVWSAGVILYILLCGVPPFWAETE QGVAQAILRGVLD FKRDPWPKVSDS AKSLVR RMLEPDPKARYNAQQVLDHP
WLQNAKKNPNVPLD TVRSRLKQFSAMNKLKKRALQVIAESLGG EEMNGLKEMFEKLDSDNAGVITFEKLMGLIEIGSQLTEHEVRMLMGAADV DGNAL
DYGEFVAAA VHLQRLGDDEYLRKAFD VFDV DSGSYIETEELRVAVGEPLNGSPSESDVVQGILLEV DVDKDGRI SYEEFSAMMR RGT DWRKASRQYSRDR
FNSLSMRLVREGSLNPDKSAVVR*

>Pp3c7_22440 Org_Ppatens peptide: Pp3c7_22440V3.4.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925275)
MGNCCAGSATKKPKQRPNPF AQDGYQANSQILKNQPKAKILD KYILGRELGRGEFGITYLCTDKETGETLACKSISKKKLRTAVDVEDVRREVAIMKHLP
EHPNIVTLNGAFEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHIQGV IHRDLKPENFLFANKNENSVLK AIDFGLSVFFKPG E
KFSEIVGSPYYMAPEVLKRN YGPEVDVWSAGVILYILLCGVPPFWAETE QGVAQAILRGVLD FKRDPWPKVSDS AKSLVR RMLEPDPKARYNAQQVLDHP
WLQNAKKNPNVPLD TVRSRLKQFSAMNKLKKRALQVIAESLGG EEMNGLKEMFEKLDSDNAGVITFEKLMGLIEIGSQLTEHEVRMLMGAADV DGNAL
DYGEFVAAA VHLQRLGDDEYLRKAFD VFDV DSGSYIETEELRVAVGEPLNGSPSESDVVQGILLEV DVDKDGRI SYEEFSAMMR RGT DWRKASRQYSRDR
FNSLSMRLVREGSLNPDKSAVVR*

>Pp3c7_22710 Org_Ppatens peptide: Pp3c7_22710V3.1.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925774)
MGNCCVGSSTKKSRQERRTNPFAPQDGFQSTNQILKNQPKARILD KYVLGRELGRGEFGITYLCTDKETQDV FACKSISKKKLRTAVDVEDVRREFAIMK
HLPEHPHVVT LKGAYEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGV MHRDLKPENFLFANKDEN S PLKAIDFGLSVFFK
PGEKFSEIVGSPYYMAPEVLKRN YGPEVDVWSAGVILYILLCGVPPFWAETE QGVAQAILRGVLD FKRDPWPKVSDS AKSVVR HMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLD TVRSRLKQFSAMNKLKKRALQVIAEHLGG EEIDGLKEMFEKLDSDNTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVDGN
RTL DYG E FVAATVHLQRLDDDDHLRRAFDVFDVNESG FIEVEELREAVGESLMGSSSES D VVQAILSEVDLDKDGRI SYEEFAMMR RGT DWRKASRQYS
RDRFNSLSTRLLRDGSLNPPSSYSTR*

>Pp3c7_22710 Org_Ppatens peptide: Pp3c7_22710V3.2.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925775)
MGNCCVGSSTKKSRQERRTNPFAPQDGFQSTNQILKNQPKARILD KYVLGRELGRGEFGITYLCTDKETQDV FACKSISKKKLRTAVDVEDVRREFAIMK
HLPEHPHVVT LKGAYEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGV MHRDLKPENFLFANKDEN S PLKAIDFGLSVFFK
PGEKFSEIVGSPYYMAPEVLKRN YGPEVDVWSAGVILYILLCGVPPFWAETE QGVAQAILRGVLD FKRDPWPKVSDS AKSVVR HMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLD TVRSRLKQFSAMNKLKKRALQVIAEHLGG EEIDGLKEMFEKLDSDNTGTITFEKLMGLIEIGSQLTEHEVRMLMEAADVDGN
RTL DYG E FVAATVHLQRLDDDDHLRRAFDVFDVNESG FIEVEELREAVGESLMGSSSES D VVQAILSEVDLDKDGRI SYEEFAMMR RGT DWRKASRQYS
RDRFNSLSTRLLRDGSLNPPSSYSTR*

>Pp3c7_25180 Org_Ppatens peptide: Pp3c7_25180V3.1.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32925156)
MGNCCVGSSTKKSRKERRPNPFAQGDYHTNLQILKNQPKARILD KYVLGRELGRGEFGITYLCTDKETQEI FACKSISKKKLRTAVDVEDVRREVAIMKH
LPEHPHVVT LKGAYEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGV MHRDLKPENFLFANKDEN S PLKAIDFGLSVFFK
GEKFSEIVGSPYYMAPEVLKRN YGPEVDVWSAGVILYILLCGVPPFWAETE QGVAQAILRGLLDFKRDPWPKVSDS AKSLVR HMLEPDPKARYNAQQVL
HPWLQNAKKNPNVPLD TVRSRLKQFSAMNKLKKRALQVIAERLGG EEIDGLKEILEKLDIDNMGVITFEKLMGLIEIGSQLTEHEVRMLMEAADVDGN
TL DYG E FVAAA VHLQRLDDDEHLRKAFDVFDVNESG FIEVEELREAVGESLTGSPSESDVVQGILSEVDLDKDGRI SYEEFATMMRRGT DWRKASRQYSR
DRFNSLSMRLLRDGS LNPPSSYSMR*

>Pp3c7_25180 Org_Ppatens peptide: Pp3c7_25180V3.2.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32925157)
MGNCCVGSSTKKSRKERRPNPFAQGDYHTNLQILKNQPKARILD KYVLGRELGRGEFGITYLCTDKETQEI FACKSISKKKLRTAVDVEDVRREVAIMKH
LPEHPHVVT LKGAYEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGV MHRDLKPENFLFANKDEN S PLKAIDFGLSVFFK
GEKFSEIVGSPYYMAPEVLKRN YGPEVDVWSAGVILYILLCGVPPFWAETE QGVAQAILRGLLDFKRDPWPKVSDS AKSLVR HMLEPDPKARYNAQQVL
HPWLQNAKKNPNVPLD TVRSRLKQFSAMNKLKKRALQVIAERLGG EEIDGLKEILEKLDIDNMGVITFEKLMGLIEIGSQLTEHEVRMLMEAADVDGN
TL DYG E FVAAA VHLQRLDDDEHLRKAFDVFDVNESG FIEVEELREAVGESLTGSPSESDVVQGILSEVDLDKDGRI SYEEFATMMRRGT DWRKASRQYSR
DRFNSLSMRLLRDGS LNPPSSYSMR*

>Pp3c7_25180 Org_Ppatens peptide: Pp3c7_25180V3.3.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32925158)
MKHLPEHPHVVT LKGAYEDDNAVHLMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGV MHRDLKPENFLFANKDEN S PLKAIDFGLSVF
FKPGEKFSEIVGSPYYMAPEVLKRN YGPEVDVWSAGVILYILLCGVPPFWAETE QGVAQAILRGLLDFKRDPWPKVSDS AKSLVR HMLEPDPKARYNAQQ
VLDHPWLQNAKKNPNVPLD TVRSRLKQFSAMNKLKKRALQVIAERLGG EEIDGLKEILEKLDIDNMGVITFEKLMGLIEIGSQLTEHEVRMLMEAADVD
GNTL DYG E FVAAA VHLQRLDDDEHLRKAFDVFDVNESG FIEVEELREAVGESLTGSPSESDVVQGILSEVDLDKDGRI SYEEFATMMRRGT DWRKASRQYSR
YSRDRFNSLSMRLLRDGS LNPPSSYSMR*

>Pp3c8_690 Org_Ppatens peptide: Pp3c8_690V3.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN
KINASE 3 (PAC:32965098)
MGNTSARPRDGRKKH KASQGNDSVQPKSHQGS SHGDSGHPGSGSHRGSGSYGGSQSRHVPKMKSSSTGILGKPLRDIK LHYTLGRELGRGQFGV TYLCTDKET
GISYACKTIAKRKLTNKDDIEDVKREVQIMHHLSGTPNIVELKDV FEDKQNVNLMELCAGGELFDRIIAKGHYSERDAADMC RIVTVTVHRCHSLGVFH
RDLKPENFL LASKDKNA PLKATDFGLS IFFKPGDEFH DIVGSAYYVAPEVLKRSYGP EADVWSAGVIVYILLCGVPPFWAETEKEIFD T IMRGHIDFKSD
PWP KISDEAKDLVKMLNSV NKERLTAQEV LNHPWMQRDGVDPVPLDN AVLTRLRNFSAANKMKK LALKVIADNLSEEEIVGLREL FKSIDT DNSGTVTI
DELKKG LLLKQGTRLT EADVRLKMEAADVDGNGKIDFNEFISATMHMNKTQKEDHLHA AFQHFD T DNSGYIT IYELQEAMEKQGMGPETLQE I INEVDTD

HDGRIDYDEFVAMMRKGNPGTEDGGNLKSPRHRW*

>Pp3c8_690 Org_Ppatens peptide: Pp3c8_690V3.2.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE 3 (PAC:32965100)

MGNTSARPRDGRKHKASQGNDVSQPKSHQGSSHGDSGHPGGSHRGSGYGGQSQRHVPKMKSSSTGILGKPLRDIKLYHTLGRGLRGQFGVYTLCTDKETGISYACKTIAKRKLTNKDDIEDVKREVQIMHHLSTGPNIVELKDVFEKQNVNLMELCAGGELFDRIIAKGHYSERDAADMCRVIVTVVHRCHSLGVFHRDLKPENFLLASKDKNAPLKTDFGLSIFFKPGDEFHDIIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEKEIFDITMRGHIDFKSDPWPKISDEAKDLVKKMLNSNVKERLTAQEVLNHPWMQRDGVDPDVLDNAVLTRLNFSANKMKKLALKVIADNLSEEEIVGLRELFKSIDTDNSGTVTIDELKKGLLKQGTRLTEADVRLKMEAADVDGNGKIDFNEFISATMHMKNKTQKEDHLHAAFQHFDTDNSGYITIYELQEAMEKQGMGPETLQEIINEVDTDHDGRIDYDEFVAMMRKGNPGTEDGGNLKSPRHRW*

>Pp3c8_690 Org_Ppatens peptide: Pp3c8_690V3.3.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE 3 (PAC:32965100)

MGNTSARPRDGRKHKASQGNDVSQPKSHQGSSHGDSGHPGGSHRGSGYGGQSQRHVPKMKSSSTGILGKPLRDIKLYHTLGRGLRGQFGVYTLCTDKETGISYACKTIAKRKLTNKDDIEDVKREVQIMHHLSTGPNIVELKDVFEKQNVNLMELCAGGELFDRIIAKGHYSERDAADMCRVIVTVVHRCHSLGVFHRDLKPENFLLASKDKNAPLKTDFGLSIFFKPGDEFHDIIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEKEIFDITMRGHIDFKSDPWPKISDEAKDLVKKMLNSNVKERLTAQEVLNHPWMQRDGVDPDVLDNAVLTRLNFSANKMKKLALKVIADNLSEEEIVGLRELFKSIDTDNSGTVTIDELKKGLLKQGTRLTEADVRLKMEAADVDGNGKIDFNEFISATMHMKNKTQKEDHLHAAFQHFDTDNSGYITIYELQEAMEKQGMGPETLQEIINEVDTDHDGRIDYDEFVAMMRKGNPGTEDGGNLKSPRHRW*

>Pp3c8_690 Org_Ppatens peptide: Pp3c8_690V3.4.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE 3 (PAC:32965101)

MGNTSARPRDGRKHKASQGNDVSQPKSHQGSSHGDSGHPGGSHRGSGYGGQSQRHVPKMKSSSTGILGKPLRDIKLYHTLGRGLRGQFGVYTLCTDKETGISYACKTIAKRKLTNKDDIEDVKREVQIMHHLSTGPNIVELKDVFEKQNVNLMELCAGGELFDRIIAKGHYSERDAADMCRVIVTVVHRCHSLGVFHRDLKPENFLLASKDKNAPLKTDFGLSIFFKPGDEFHDIIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEKEIFDITMRGHIDFKSDPWPKISDEAKDLVKKMLNSNVKERLTAQEVLNHPWMQRDGVDPDVLDNAVLTRLNFSANKMKKLALKVIADNLSEEEIVGLRELFKSIDTDNSGTVTIDELKKGLLKQGTRLTEADVRLKMEAADVDGNGKIDFNEFISATMHMKNKTQKEDHLHAAFQHFDTDNSGYITIYELQEAMEKQGMGPETLQEIINEVDTDHDGRIDYDEFVAMMRKGNPGTEDGGNLKSPRHRW*

>Pp3c9_21410 Org_Ppatens peptide: Pp3c9_21410V3.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE 3 (PAC:32913788)

MGNQCVGAIGGPYKQEKAAHHVHGHRDGGVGRGVGHGQGGQNNQHYRQNVQERGVEITTTTRTAPPVTMPKPRPVNVAAGTVLGKPLSDVRSVYTLGKELGRGQFGVYIYACTNIKTGEHLACKSIKRKLISKEDIEDVRREVQIMHHLSTGPNIVELKGVFEDKHHVHIVMELCAGGELFDRIIAKGHYSERAAAAALCRTIIVSVVHRCHSLNVFHRDLKPENFLLANKAENSSSLKATDFGLSVFFKPGEVFHEIVGSAYYVAPEVLRNRYGPEADVWSAGVIVYILLCGVPPFWAEESEQGIFDAVLKGYIDFKSDPWPKVSAADKLVSKMLKQDPKERLTAQEVLPKPMKEDGDAPDEPLDNAVLTRLKNFSSANKMKKLALQVIAQSLSEDEIMGLKEMFKAMDTDNSGTITFDELKEGLHRQGSKLVESDVKKLMEAADVDGNGKIDFSEFISATMHMKNKEKEDHLAEAFQHFDTDGSGYITVEELQEAMAKNGMDPETINEIIREVDTDNDGRIDYDEFVAMMRKGNVPMQMTTRRHR*

>Pp3c9_21410 Org_Ppatens peptide: Pp3c9_21410V3.2.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE 3 (PAC:32913789)

MGNQCVGAIGGPYKQEKAAHHVHGHRDGGVGRGVGHGQGGQNNQHYRQNVQERGVEITTTTRTAPPVTMPKPRPVNVAAGTVLGKPLSDVRSVYTLGKELGRGQFGVYIYACTNIKTGEHLACKSIKRKLISKEDIEDVRREVQIMHHLSTGPNIVELKGVFEDKHHVHIVMELCAGGELFDRIIAKGHYSERAAAAALCRTIIVSVVHRCHSLNVFHRDLKPENFLLANKAENSSSLKATDFGLSVFFKPGEVFHEIVGSAYYVAPEVLRNRYGPEADVWSAGVIVYILLCGVPPFWAEESEQGIFDAVLKGYIDFKSDPWPKVSAADKLVSKMLKQDPKERLTAQEVLPKPMKEDGDAPDEPLDNAVLTRLKNFSSANKMKKLALQVIAQSLSEDEIMGLKEMFKAMDTDNSGTITFDELKEGLHRQGSKLVESDVKKLMEAADVDGNGKIDFSEFISATMHMKNKEKEDHLAEAFQHFDTDGSGYITVEELQEAMAKNGMDPETINEIIREVDTDNDGRIDYDEFVAMMRKGNVPMQMTTRRHR*

>Sphfalx0012s0095 Org_Sfallax peptide: Sphfalx0012s0095.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32627609)

MGNCCLGFSAPESRKERKPNPFAQDGESQQAASAAVHILKNQPKSRISDKYVMGELGRGEFGVYTLCTDIENNNGGGRGEKYACKSISKRLRTAIDVEDVRREVAIMNHLPPQHPNIVKLKAAAYEDEHAVHLMELCEGGELFDRIIARGHYTERAAAVVTRTIVEVVQVCHQHGVMHRDLKPENFLFANKKEVSPKLAIDFGLSVFFKPGKEKFEIVGSPYYMAPEVLKRNRYGPEIDVWSAGVILYILLCGVPPFWAETEQQGVAQAILRGTLDFKRPWPVLVSDAAKSLVHHMLEPDPPTARFNAQQVLDHPWLQNAKTNPNIPLDVAVRSRLKQFSAMNKLKKALQVIAELIGSEEIQKLQDMFETMDTDKNGAITLEELKNGLVQIGSQLTEGEVQQLM DAADV DNGNTLDYGEFVAATIHQLRLDNDHLLKQAFTHFDTRSGYIEVEELRVAIGNDSAAAASVINGILEEVDTDKDRISYDEFSAMMRRTDWRKASRQYSRDLFNSLSMRLLRNGTVNPNANQSER*

>Sphfalx0019s0046 Org_Sfallax peptide: Sphfalx0019s0046.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32600007)

MGNCCVGASSAAPKPKKEKSNPFAQDGYQVSGNQILKNQPKVSIADKYMLGRELGRGEFGITYLCTVDKESQEVYACKSISKRLRTAVDVEDVRREVAIMGHLPKHPNIVTLKAYEDDQAVHLMELCEGGELFDRIIARGHYTERAAAVVTRTIVEVVQLCHIKGVMHRDLKPENFLFANSNENSPLKAIDFGLSVFFKPGERFSEIVGSPYYMAPEVLKRNRYGPEVDVWSAGVILYILLSGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSETAKSLVRHMLEPDPKARYNAQQVLDHPWLQNAKKNNSVPLDAVRSRLKQFAAMNKLKRKALQIAEHLDGDEIDGLRDMFQMMDTDNMGAITFEKLKAGLIQIGSHLTAEVRMLMDAADVDGNGTLDYGEFVAATIHQLRLDNDHLLKFAQFDANGSGYIEMDELRAAIGDHLVSDMSVINAILEEVDTDKDRISYDEFAAMMRRTDWRKASRQYSRDRFNSLSVRLFRDGSVNPMPKSR*

>Sphfalx0022s0143 Org_Sfallax peptide: Sphfalx0022s0143.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE 3 (PAC:32616043)

MGNQCGSGSDSPNSDKTYTSPHVATHNSHTSSAPSSAAPAAAHNSHDSNMAHKVPPALILPMPKPHSNFPTIGHVLGRPLEDVQTYTLGRELGRGQFGVYTLCTHNSREVFAKSIKRKLTKEDIEDVKREVQIMHHLSTGPNIVELKGVYEDRHSVHLMELCAGGELFDRIIAKGHYSERAAASLCRTIIVKVVQACHSLGVMHRDLKPENFLLADKSENAAVKATDFGLSVFFKPSQVFTDIIVGSAYYVAPEVLRNRYGPEADVWSAGVILYILLCGVPPYWAETEQQGIFDAVLGEVDFRSDPWPDISGAKDLVKKMLQDQPKLRITAHQVNLNHEWVEDRGKAPDKPLDSAVLTRMKQFSAMNKMKLALKVIASLSSEDEIMGLKEMFKSLDNTDNGSTITFEELKEGLQKQSGSKLAESVQQLMQAADV DNGNTIEFNEFITATMHLNMEKEDHMYVAFQHFDTDHSGYITMDELEQAMTKHNMGDEDTIKDIIREVDTDNDGRINYDEFVAMMRKGTGPGDGPKKHRQVNRQT*

>Sphfalx0034s0077 Org_Sfallax peptide: Sphfalx0034s0077.1.p (1 of 5) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32628748)
MRRYEAAARVLMGLQSPASVLRQQTENLWDLYSGLRKLGQGFQGTYYLCEISTQKEFACKSIAKRKLISREDVEDVRRELHIMHHLSGHPNIVTIEGAY
EDASSVHLVLMELCAGGELFDRIIQRGHYSEAKAAQLTRTIVGVVEACHSLGVMHRDLKPENFLFSNHTEDAALKTTDFGLSVFFKPGVEFTDVVGSPPYYV
APEVLKRHYGPEADVMSAGVILYILLSGVPPFWAETEQQGIFDQVMKGDLDVSDPWPNISESAKDLICKMLNPNPARRLTAHQVLCHPWIREEGVAPDMP
IDSAVQSRKQFSAMNRLKKIAIRVIAESLSEEEIVGLKEMFKMMDTDGSGSISFEELKEGLRKVGSNLMEEDVRQLMDAADVDHNGTIDYGEFLAATLN
LNKIEREENVFAAFSYLDKDKSGYLTDELQQACIDLHMGDMCVEDMIREVDQDNDGRIDYNEFVTMMRKGNNGIGRSSSLRNSLSWSLSLHLMAG*
>Sphfalx0034s0079 Org_Sfallax peptide: Sphfalx0034s0079.1.p (1 of 5) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32628931)
MGNVCMGVSWSKYIQMIPSAFISTPSPASTSQTTDNSNNNSNNGKLEAELEKITQHSPLANYIPSVNEANHPQQVTELINAMVKKTEVKIVPGQSFT
ASVLQRQTENLRDLTYLGRKLGGQGFVYTLCEKSTGKEFACKSIAKRKLISMEDVEDVRRELHIMHHLSGHPNIVNIKAYEDVTSVHLVLMELCAGGE
LFDRIIQRGHYSEAKAAELTRTIVGVVEACHSLGVMHRDLKPENFLFSNHSEDAALKTTDFGLSVFFKPGEIFTDVVGSPPYYVAPEVLKRHYGPEADVMS
AGVILYILLSGVPPFWAETEQQGIFEQVLKSELDFVSDPWPKISESAKDLRLKMLNPNVAKRLKSHQVLCHPWIREGDAVDRPIDPAVQTRLKQFSAMNK
LKKIAIRVIAESLSEEEIAGLKEMFLMMDSDGSGAISFEELKEGLKKGVSNLMEADIRQLMDAADVDHNGTIDYGEFLAATLNLNKIEREENLYAAFSYL
DKDKSGYLTDELQQACNDLHMGDMCVEDLIREVDQDNDGRIDYNEFVTMMRKGNNGVGRSSSLRNLNSWGLSDALMGA*
>Sphfalx0038s0118 Org_Sfallax peptide: Sphfalx0038s0118.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE 3 (PAC:32603542)
MGNQCGGNSHTSSGKADAAFTSHHPQTSSAPASGYGNHNNNTHTPVPVPPVTPAIPRQSRPAIGHVLGRPLEDVRKTYTLGRELGRGQGFVYTLCTHN
ETGEVFACKSIAKRKLITKEDFDVVKREVQIMHHLSGHENIVELKGAYEDKQSVHLVLMELCAGGELFDRIIKRGHYSERAAASLCRTIVKVQICHSLGV
MHRDLKPENFLANKAENAALKATDFGLSVFFKPGSEVFTDIVGSAYYVAPEVLRRNYGPEADVMSAGVILYILLCGVPPFWAETEQQGIFDAVLRGELDLK
SDPWPPEISSGAKDLIKMLQDDPKCRLTAHEVLTHDVKEDGEAPDKPLDSAVLSRLKQFSAMNKLKMKALKVIAESLSEDEIMGLKEMFKSMDTDNSGT
ITFEELKTGLAKQGSKLLESEVRQLMQAADVDGNGTIEFNEFITATMHLNKMKEKDHLIAAFQHFDTDSHGYITIDELEQAMMKNNMGERGTIKDIIREV
DTDHDGRINYDEFVAMMRKMPGLDSHRKSMRGNTR*
>Sphfalx0040s0092 Org_Sfallax peptide: Sphfalx0040s0092.1.p (1 of 5) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20 (PAC:32624088)
MNNYGSEMRVLPQGSITASVLRHTENLRDLIYLGRKLGGQGFVYTHCTEKATGLHFACKSIAKRKLISREDVEDVRREIHIMHHLSGHPNIVTIKAY
EDATSVHLVLMELCAGGELFDRIIQRGHYSEAKAAELTRTIVGVVETCHSLGVMHRDLKPENFLANQREDAPLKTDFGLSVFFKPGEIFTDVVGSPPYYV
APEVLRRHYGPEADVMSAGVILYILLSGVPPFWAETEQQGIFEQVLKSELDFVSDPWPKISDDAKDLIQMLNPHIESRLKAHQVLCHPWIREEGVASDRP
IDPAVQSRKQFSAMNKLKKIAIRVIAESLSEEEIAGLKEMFKMMDTDGSGAISFEELKEGLRKVGSNLKEADVRELMDAADVDHNGTIDYGEFLAATLN
LNKIEREENLYSAFSYLDKDKSGYLTDELQAAITDFHMGDISIDMIREVDQDNDGRIDYNEFVTMMRNNGGVGRALTALRNSLSGLSDTNA*
>Sphfalx0048s0038 Org_Sfallax peptide: Sphfalx0048s0038.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32612500)
MGNCCVGSSAASRRNSRKERTNPFSEHGYQVSGNQILKTPKVGADKFTLGSELGRGEFGITYLCVDKDTQEVYACKSISKRKLRTAIDVEDVRREVA
IMGHLPFHNGNIVTLKAYEDDQAVHLVLMELCEGGELEFDRIIARGHYTERAAAGVTRTIVEVQVQLCHIKGVMHRDLKPENFLFANKSENSPLKAIIDFGLSI
FFKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVMSAGVILYILLCGVPPFWAETEQQGVAQAILRGILDFKREPWPVKVSDIAKALVRHMLEPDPKARYNAQ
QVLDHPWLQHAKRNSNVPLDAVRSRLKQFAAMNKLKKKALQIIAEHLEGEDEVEGLRDMFQMMMDTDNSGAIITFEKLKAGLIQIGSHLTEADVQMLMDAADV
DNGTLDYGEFVAATIHQLRLDNDLHKAFAQFDANSSGYIEMEELRTAIGDHLVSDGMSVINAILEEVDTRDRGCISFEDEFAAMMRRTDWRKASRQY
SRDRFNSLSIKLFRDGSINPNYSK*
>Sphfalx0049s0049 Org_Sfallax peptide: Sphfalx0049s0049.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32617816)
MGNCCGSSGANSRKRERNPFPAQDGYHVSNGQILVNQPKASIVDKYTLGAELGRGEFGITYSCVDKDTQEVYACKSISKRKLRTAVDVEDVRREVAIMG
HLPQHPNIVSLKAYEDDEAVHLVLMELCEGGELEFDRIIARGHYTERAAAGVTRTIVEVQVQLCHIQGVMHRDLKPENFLFANKTEDSLLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEIDVMSAGVILYILLCGVPPFWAETEQQGVAQAILRGNLDFRREPWPVKVSDSAKSLVRHMLEPDPKERYNAQQVL
DHPWLQNAKKNNSNVPLDAVRSRLKQFAAMNKLKKKALQIIAEHLEGEDEIEGLRDMFQMMMDTDNSGAIITFEKLKAGLIQIGSHLTEAEVQLMDAADVDSN
GSLDYGEFVAATIHQLRLDNDLHKAFTHFANNSGYIEMQELRAAIGDNLVADEMSSVINGILEEVDTRDRGRISFEFEAAMMRRTDWRKASRQYSRD
RFNSLSMKLFRDGSINPNYSR*
>Sphfalx0049s0049 Org_Sfallax peptide: Sphfalx0049s0049.2.p (1 of 8) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32617817)
MGNCCGSSGANSRKRERNPFPAQDGYHVSNGQILVNQPKASIVDKYTLGAELGRGEFGITYSCVDKDTQEVYACKSISKRKLRTAVDVEDVRREVAIMG
HLPQHPNIVSLKAYEDDEAVHLVLMELCEGGELEFDRIIARGHYTERAAAGVTRTIVEVQVQLCHIQGVMHRDLKPENFLFANKTEDSLLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEIDVMSAGVILYILLCGVPPFWAETEQQGVAQAILRGNLDFRREPWPVKVSDSAKSLVRHMLEPDPKERYNAQQVL
DHPWLQNAKKNNSNVPLDAVRSRLKQFAAMNKLKKKALQIIAEHLEGEDEIEGLRDMFQMMMDTDNSGAIITFEKLKAGLIQIGSHLTEAEVQLMDAADVDSN
GSLDYGEFVAATIHQLRLDNDLHKAFTHFANNSGYIEMQELRAAIGDNLVADEMSSVINGILEEVDTRDRGRISFEFEAAMMRRTDWRKASRQYSRD
RFNSLSMKLFRDGSINPNYSR*
>Sphfalx0049s0049 Org_Sfallax peptide: Sphfalx0049s0049.3.p (1 of 8) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32617818)
MGNCCGSSGANSRKRERNPFPAQDGYHVSNGQILVNQPKASIVDKYTLGAELGRGEFGITYSCVDKDTQEVYACKSISKRKLRTAVDVEDVRREVAIMG
HLPQHPNIVSLKAYEDDEAVHLVLMELCEGGELEFDRIIARGHYTERAAAGVTRTIVEVQVQLCHIQGVMHRDLKPENFLFANKTEDSLLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEIDVMSAGVILYILLCGVPPFWAETEQQGVAQAILRGNLDFRREPWPVKVSDSAKSLVRHMLEPDPKERYNAQQVL
DHPWLQNAKKNNSNVPLDAVRSRLKQFAAMNKLKKKALQIIAEHLEGEDEIEGLRDMFQMMMDTDNSGAIITFEKLKAGLIQIGSHLTEAEVQLMDAADVDSN
GSLDYGEFVAATIHQLRLDNDLHKAFTHFANNSGYIEMQELRAAIGDNLVADEMSSVINGILEEVDTRDRGRISFEFEAAMMRRTDWRKASRQYSRD
RFNSLSMKLFRDGSINPNYSR*
>Sphfalx0073s0063 Org_Sfallax peptide: Sphfalx0073s0063.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32615718)
MGNCCAPGGATAGPKHRKKPKRPNPYAQDGYYPQSGNLIILKNQELRNLRDEYGLGREVGRGEFGITYMCTHKATQAVYACKSISKSLRTPVDVEDVR

REVAIMQHMPSPHPIVTLRAAYEDENAVHLVLMELCEGGELFDRIIERVHYTERAAAGVTRTIVEVVQACHKEGVMHRDLKPENFLFANKKENSPLKAIDF
GLSVFFKPGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQVAQAILRGVLDKREPWPEVSDSAKSLVRHMLEPDPKLR
YTAQQVLDHPWLLNARKNPNVPLDAVRSLKQFSAMNKLKKKALQVIAEHLGGEEIEGLKEMFQMMDDTDRGAIITFENLKAGLLRIGSHLTEAEVRLLE
AADLDGNGTLDYGEFVAATIHQLRLDNDEHLHKAFFNFDDVSGSYIEMDELREALGQDMVNESDVIKIDILQEVDIDKDGRIISYEEFAAMMRRTDWRKA
SRQYSRDRFNSLSTRLFRDGTSTNPPNFSKQNER*

>Sphfalx0095s0016 Org_Sfallax peptide: Sphfalx0095s0016.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:32601305)

MGNQCIGSSRTSNDKIETPFPTPYNPHTSSAPAVHSNNHSSSNTQNAHPPPVASPVPRPRVSPNVGHVLRPLEDNQTYTLGRELGRGQFGITYLCTDN
NTGAVFACKSIARKRLMTKEDFEDVKREVQIMHHLSGHENIVELKGVYEDKHFNVLVLMELCAGGELFDRIIQRGHYSERAAASLRTIVKVVQICHSLGV
MHRDLKPENFLADKSENSALKATDFGLSVFFKPESEVFTDIVGSAYYVAPEVLRKRYGPEADVWSGVVILYILLCGVPPFWAETEQQGIFDAVLQGDIDFR
SDPWEISPAAKDLVKMLRHDPKHRLTAHEVLTHHWIKEDGEAPDKPLDSAVLRLKQFSAMNKMMLKALKVIAESLSEDEIMGLKEMFKCMDTDSNGT
ITFEELKEGLQKQSGSLAESEVRQLMQAADVDGNGTIEFNEFITATMHLNKMKEEHLYVAFQHFDTDHSGYITIDELEQAMTRNNMGDDATIRDIKEV
DTDHDGRINYDEFFAMMRKGTGMDVQRKSMRGNRTR*

>Sphfalx0112s0037 Org_Sfallax peptide: Sphfalx0112s0037.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32630832)

MGNCCVGISAASQSKKDRKPNPFAQDGGGAYPASAAAQILKNQSKCKITDKYALGKELGRGEFGITYLCTDIESGDKDACKSISKRLRTAVDVEDVRR
EVAIMHHLKPKHPNIVKLKGEYEDEQAVHLVLMELCEGGELFDRIIARGHYTERAAAVVTRTIVEVVQVCHQHGMHRDLKPENFLFANKKENSPLKAIDFG
LSVFFKPGKFKCEIVGSPYYMAPEVLKRNYPGEIDVWSAGVILYILLCGVPPFWAETEQQVAQAILRGILDFKRDWPVVSDSAQSLVRHMLEPDPKARY
NAQQVLDHPWLQNAKKNSTPLDAVRSLKQFSAMNKLKKKALQVIAEILGGEVEEKLDMFMDMDTDRSGAITFEKLLTGLIQGSLTEGEVQLMDV
ADVVDGNGTLDYGEFVAATVHLQRFNDNDHLHKAFTHFDADGSGYIEVEELRVAIGDDPSSDAETSIVISSILEEVDTDKDGRIISYDEFAAMMRRTDWRK
ASRQYSRDRFNSLSTLLRNGSVTPAAVQNTKI*

>Sphfalx0133s0014 Org_Sfallax peptide: Sphfalx0133s0014.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32631140)

MGNCCSGPAPPPTSPNNRKKHRRANPYAQDGYCQPGSGNLILKKQEKTDLRKEYGLGREVGGRGEFGITYMCTHKTTQAVYACKSISKSLRTPVDVEDVR
REVAIMQHMPHPIVTLRAAYEDDDAVHLVLMELCEGGELFDRIIARGHYTERAAAGVTRTIVEVVQVCHQHGMHRDLKPENFLFANKKENSPLKAIDF
GLSVFFKPGERFSEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQVAQAILRGKLDKREPWPEVSDSAKSLVRHMLEPDPKLR
YSAQQVLDHPWLVNNSKKNPNVPLDAVRSLKQFSAMNKLKKKALQVIAEHLGGQIEGLKDMFQMMDDTKRGVITFDNLKAGLLHIGSQLTEGEVRLLE
AADVDGNGTLDYGEFVAATVHLQRFNDNDHLHKAFTHFDADGSGYIEVEELRVAIGDDPSSDAETSIVISSILEEVDTDKDGRIISYDEFAAMMRRTDWRK
SRQYSRDRFNSLSTLLRNGSVTPAAVQNTKI*

>Sphfalx0159s0028 Org_Sfallax peptide: Sphfalx0159s0028.1.p (1 of 5) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32627846)

MISKGNLSKAGNKYDKDKEQVAGIVYALKEGASKKLKPGENLTSSVLQRPTDNLKSLYILGKKLGQGGFGITYLCTEKATGKEYACKTIAKRKLICQAD
VDDVREIHHMHLHSGHPNIVTIKAGYEDASAVHLVLMELCAGGELFERIVKKGHYSEAKASELARTVVDVVEACHSLGMHRDLKPENFLFANKKENSPLKAIDF
KATDFGLSIFPKPGETFKDVGVSPPYVAPEVLRKHYGIEADISWAGVILYILLCGVPPFWADNEQGFIVSVSKAEFDLESEKPNISESAKDLIRKMLNP
SRVRLKAHEVLSPHWIHEEGVAPDKPMDSAVQSRKQFSAMNKLKKLAIRVIAESMSEEEIVGLKEMFKTIDTSSGAISFEELKEGLRKGVSNLTEAD
IRDLMSADIDQNGTIDYGEFLAATLHMKNINREENLFAAFKFLDKNSGYITIDELQQACIQNMGDIPIEDLIRDVDQDNDGRLDYHEFVAMMRKGNE
DASQTRTDSLFEEAIKPTKPKAKLPMDNLDWMG*

>Sphfalx0202s0012 Org_Sfallax peptide: Sphfalx0202s0012.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32627879)

MGNCCVGSSSSRSASRSRKRKPNPFAQDGYQISAVQILKNQSKRSITDKYVLGGELGRGEFGITYLCTDMENGCGEKYACKSISKRLRTAVDVEDVR
REVAIMHHLQHPHPIVTLRAAYEDDHAVHLVLMELCEGGELFDRIIARGHYTERAAAVITRTIVEVVQVCHQHGMHRDLKPENFLFANKKEASPLKAIDF
GLSVFFKPGKFKFYEIVGSPYYMAPEVLKRNYPGEIDVWSAGIILYILLCGVPPFWAETEQQVAQAILRGALDFKRDWPVVSDSAQSLVRHMLEPDPPTAR
FDAQQVLDHPWLQNTKKNPNVPLDAVRSLKQFSAMNKLKKKALQVIAEILGGEIEKLRDMFEMIDSDKDGAITFEELKNGLIQIGSQLTEAEVRQLMD
AADVDGNGALNYGEFVAATIHQLRLDNDHLRKAFAHFDTDGSGFIEEMEELRVAIGDDSTSAETSIVINGILEEVDTDKDGCIISYDEFAAMMRRTDWRKA
SRQYSRDRFNSLSVRLFRDGSVNPANESKR*

>Thecc1EG001677 Org_Tcacao peptide: Thecc1EG001677t1 Calcium-dependent protein kinase 2 (79%T)
(PAC:27436851)

MSKTSSTGTPSRVLPYTPPSLADHYSLGKTLGQGGFGTTLCTHKPTGQQYACKSIPKRKLICQEDYEDVWREIQIMHHLSEHPHVVRIRGTIEDQLSVH
LVLMELCEGGELFDRIIVKKGHYSEREAALKIKTIVGVVETCHSLGVMHRDLKPENFLFDTVDEDAALKATDFGLSVFYKPGESFCDVVGSPYYVAPEVLRK
HYGPEADVWSAGVILYILLSGVPPFWAETEMGIFRQILQKIDFDSEPPWPAISESAKDLIRKMLDRNPKGRILTAYQVLCHPWIVDDTIAPDKPLDSAVLS
RLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTSSGTITFEELKDGLKRVGSELMSESEIKDLMDAADIDNSGTIDYGEFLAATVHLNKLRE
ENLVSFAFAFDKDGSGYITIDELQQACKEFGLSDVHLDEMIKEIDQDNDGQIDYGEFAAMMRTGNGGIGRRTMRRTINLGDALAVMANGSKKIE*

>Thecc1EG001677 Org_Tcacao peptide: Thecc1EG001677t2 Calcium-dependent protein kinase 2 (79%T)
(PAC:27436852)

MSKTSSTGTPSRVLPYTPPSLADHYSLGKTLGQGGFGTTLCTHKPTGQQYACKSIPKRKLICQEDYEDVWREIQIMHHLSEHPHVVRIRGTIEDQLSVH
LVLMELCEGGELFDRIIVKKGHYSEREAALKIKTIVGVVETCHSLGVMHRDLKPENFLFDTVDEDAALKATDFGLSVFYKPGESFCDVVGSPYYVAPEVLRK
HYGPEADVWSAGVILYILLSGVPPFWAETEMGIFRQILQKIDFDSEPPWPAISESAKDLIRKMLDRNPKGRILTAYQVLCHPWIVDDTIAPDKPLDSAVLS
RLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTSSGTITFEELKDGLKRVGSELMSESEIKDLMDAADIDNSGTIDYGEFLAATVHLNKLRE
ENLVSFAFAFDKDGSGYITIDELQQACKEFGLSDVHLDEMIKEIDQDNDGQIDYGEFAAMMRTGNGGIGRRTMRRTINLGDALAVMANGSKKIE*

>Thecc1EG007580 Org_Tcacao peptide: Thecc1EG007580t1 Calmodulin-domain protein kinase 5 (84%T)
(PAC:27464444)

MGNTRGSGFKGLYQGYSPEDHSSKRNNSTSSDRNSDYSPTSLSNAQQLIAQEFSEKTTKKDTHLALISPTKKDNIMRRGIDNQAYYVLGHKTPNIRDLY
TLGRKLGGQFGTTLCLIEISTGIEYACKSISKRLISKEDVEDVREIQIMHHLGAKHNIVTIKAGYEDSLYHIVHLMELCSGGELFDRIIQRGHYSERK
AAELTKIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLLKHYGPEADVWTAAGVILYILLSGVPPF
WAETQQGIFDAVLKGHIDFSDPWLISDSAKDLIRKMLCSRPSERLTAHEVLCHPWICENGVAAPDRALDPAVLRLKQFSAMNKLKKMALRVIAESLSE

EEIAGLREMFTTMDTNSGAITFDELKAGLRRYGSTLKDTEIRDLMDAADVDNSGTIDYGEFIAATVHLNKLEREEHLVAAFQYFDKDGSGYITVDELQQ
 ACAEHNMTDVLLEDIIREVDQDNDGRIDYGEFVAMMQKNAGIGRRTMRNSLNMSMRDAPGA*
 >Thecc1EG007580 Org_Tcacao peptide: Thecc1EG007580t2 Calmodulin-domain protein kinase 5 (84%T)
 (PAC:27464445)
 MGNTRCRGSFKGKLYQGYSQPEDHSSKRNTSSDRNSDYSPTSLSNAQQLIAQEFSEKTTKKDTHLALISPTKKDNIMRRGIDNQAYYVLGHKTPNIRDLY
 TLGRKLGQGGFGTTLICIEISTGIEYACKSISKRLISKEDVEDVRREIQIMHHLAGHKNIIVTIKAYEDSLYVHIVMELCSGGELFDRIIQRGHYSERK
 AAELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPPYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPF
 WAETQQGIFDAVLKGHIDFSDPWLISDSAKDLIRKMLCSRPSERLTAHEVLCHPWICENGVAAPDRALDPAVLRLKQFSAMNKLKKMALRVIAESLSE
 EEIAGLREMFTTMDTNSGAITFDELKAGLRRYGSTLKDTEIRDLMDAADVDNSGTIDYGEFIAATVHLNKLEREEHLVAAFQYFDKDGSGYITVDELQQ
 ACAEHNMTDVLLEDIIREVDQDNDGRIDYGEFVAMMQKNAGIGRRTMRNSLNMSMRDAPGA*
 >Thecc1EG013784 Org_Tcacao peptide: Thecc1EG013784t1 Calcium-dependent protein kinase 30 (83%T)
 (PAC:27449469)
 MGNCNACVRPDDSPESKPNRSEHSQRGKKKTRERKPNPYAEKVPSPAPIRVLKDVIPLSHRTRIGDKYIILGRELGRGEFGITYLCTDRETREALACKSIS
 KRKLRTAVDIEDVRREVAIMSTLPEHPNIVKLKATYEDNENVHLMELCEGGELFDRIVARGHYTERAAANVAKTIAEVVRMCHENGVMHRDLKPENFLF
 ANKKEHAPLKAIDFGLSVFFKPGERFSEIVGSPYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQQVALAILRGVIDDFKREFPWPQVSES
 SLVRQMLEPDPKKRLTAQQVLEHSLWLNQAKKAPNVLPGDIVRTRLKQFSVMNRFKKKALRVIAEHLVSVEEVIVIRMFTLMDTDNDGKVSYEELKAGLRK
 VGSQLAPEPIKMLMEVADVDGNGVLDYGEFVAVTIHLQKMENDEHFRRAFMFDFDKDGSGYIELDELQEAALADESGEADVLDNDIMREVDTDKDGCSISYD
 EFMAMKAGTDWRKASRQYSRERFKSLSLNLMKDGSLQLHDAVTGQAVAV*
 >Thecc1EG013784 Org_Tcacao peptide: Thecc1EG013784t2 Calcium-dependent protein kinase 30 (83%T)
 (PAC:27449470)
 MGNCNACVRPDDSPESKPNRSEHSQRGKKKTRERKPNPYAEKVPSPAPIRVLKDVIPLSHRTRIGDKYIILGRELGRGEFGITYLCTDRETREALACKSIS
 KRKLRTAVDIEDVRREVAIMSTLPEHPNIVKLKATYEDNENVHLMELCEGGELFDRIVARGHYTERAAANVAKTIAEVVRMCHENGVMHRDLKPENFLF
 ANKKEHAPLKAIDFGLSVFFKPGERFSEIVGSPYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQQVALAILRGVIDDFKREFPWPQVSES
 SLVRQMLEPDPKKRLTAQQVLEHSLWLNQAKKAPNVLPGDIVRTRLKQFSVMNRFKKKALRVIAEHLVSVEEVIVIRMFTLMDTDNDGKVSYEELKAGLRK
 VGSQLAPEPIKMLMEVWVNSCLHRI*
 >Thecc1EG016367 Org_Tcacao peptide: Thecc1EG016367t1 Calcium-dependent protein kinase 6 (81%P)
 (PAC:27449549)
 MGNCNGHPSADNQFRPDSDSGGGPHNGINIKAGSPPPRQQHSTTHHSSAASNHRLATPTTPPIGRVLGRPMEDVRSNYVFGRELGRGQFGITYLVTHK
 ETKQQFACKSIATRKLINRDDIEDVRREVQIMHHLTGHRNIVELKGAYEDRHSVNLIMELCAGGELFDRILAKGHYSEREAANLCRQIVMVVNCHSMGV
 MHRDLKPENFLFLSKDEDSPLKATDFGLSVFFKRGDVFKDLVGSAYVAPEVLRRLRYGPEADIWSAGVILYILLSGVPPFYGETEQSIFDSILRGNIDFS
 SDPWPSVSSSAKDLVRKMLLDDPKERLSASEVLNHPWMREDGDASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGT
 ITYEELKAGLPKLGTLKSESEVRQMLEAADVDGNGTIDYIEFITATMHHNMRMEREEHLYTAFQYFDKDNDSGYITMEELEQALRKYNMGDEKTIKEIIAEV
 DTDGRGRINYDEFVAMMRKGNPDVLGNRRRK*
 >Thecc1EG016367 Org_Tcacao peptide: Thecc1EG016367t2 Calcium-dependent protein kinase 6 (81%P)
 (PAC:27449550)
 MGNCNGHPSADNQFRPDSDSGGGPHNGINIKAGSPPPRQQHSTTHHSSAASNHRLATPTTPPIGRVLGRPMEDVRSNYVFGRELGRGQFGITYLVTHK
 ETKQQFACKSIATRKLINRDDIEDVRREVQIMHHLTGHRNIVELKGAYEDRHSVNLIMELCAGGELFDRILAKGHYSEREAANLCRQIVMVVNCHSMGV
 MHRDLKPENFLFLSKDEDSPLKATDFGLSVFFKRGDVFKDLVGSAYVAPEVLRRLRYGPEADIWSAGVILYILLSGVPPFYGETEQSIFDSILRGNIDFS
 SDPWPSVSSSAKDLVRKMLLDDPKERLSASEVLNHPWMREDGDASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGT
 ITYEELKAGLPKLGTLKSESEVRQMLEAADVDGNGTIDYIEFITATMHHNMRMEREEHLYTAFQYFTTWDRIVLAF*
 >Thecc1EG020113 Org_Tcacao peptide: Thecc1EG020113t1 Calcium-dependent protein kinase 24 (69%T)
 (PAC:27455265)
 MGSCISTPSRLVGVVSKSYNTSKTKRKLHASFDEAARKSMNLRVNTGKVLKDSSGDNILERYELGKELGRGEFGVTHQCFDLVTGEAYACKKISKAK
 LRSEIDVEDVRREVEIMRHLKPHNIVTFREAFEDKEAVYLVLMELCHGGELFDRIVAKGHYTERAAATAIKTILEIVKVCHEHGVHRLDKPENFLLADE
 SETAPIKAIIDFGLSIFYEPGQRFSIDVGSPPYMAPEVLRRLRYGPEVDIWSIGVILYILLCGVPPFWADTEEGIAHAIIKGDIDFERDPWPVKVSEAKDLV
 RSMOLDPNPYSRMTVQEVFEHPWIQNLHAPNVNLGENVRTRIKQFSFMSKFKKKVLRVAVAGNLPNEQTDIAVQIFRMMDTDENGHLSFEELRDGLQKIGH
 CVADPDVQLLMDAADIDGNGTSLCEEFVTMAVHLKRMSNDEHLSQAFHHFDKNQSGYIEFEELQEALLHDDLGPNEQVIRDIHVDVLDKDGRISEYEEF
 KAMMLTGMDWKMASRQYSRALLNAVSIIKILKQSGQLR*
 >Thecc1EG021684 Org_Tcacao peptide: Thecc1EG021684t1 Calcium-dependent protein kinase 13 (85%T)
 (PAC:27420927)
 MGNCRCSPAAREVDVKSNSFAHDHARKDSVSKQKPPITVNGVPKENIEEKYLVDRRELGRGEFGVTYLCIDRGTRRELLACKSISKRLRTAVDIEDVRR
 EVAIMKHLKPNSSIVSLKEACEDDNAVHLMELCEGGELFDRIVARGHYTERAAAVTRTIVEVQVLCCHKHGVHRLDKPENFLFANKKENSPLKAIDFG
 LSIFFKPGERFSEIVGSPYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAEESEQGVAQAILRGLIDFKRDPWPNISESASLVRQMLEPDPKRLRL
 TAKQVLGSKISSVLCGLVYVSWEGAGWGLGVQHPWLQNAKAPNVLPGDVVKSRRLKQFSMMNRFRKALRVIAEFLSIEEVEDIKEMFKKMDTDNDGI
 VSIEELKAGFRNFGSHLASEVQMLIEAVDANGKGTLDYGEFLAVSLHLQRIANDEHLRKAFSYFDKDGNGYIEPDELRLDSLMEDGADDCTNVANDIFQE
 VDTDKDGRISYDEFTAMMKTGTDWRKASRHSRGRFNSLSMKMLKDGSLNLGNE*
 >Thecc1EG021684 Org_Tcacao peptide: Thecc1EG021684t2 Calcium-dependent protein kinase 13 (85%T)
 (PAC:27420928)
 MGNCRCSPAAREVDVKSNSFAHDHARKDSVSKQKPPITVNGVPKENIEEKYLVDRRELGRGEFGVTYLCIDRGTRRELLACKSISKRLRTAVDIEDVRR
 EVAIMKHLKPNSSIVSLKEACEDDNAVHLMELCEGGELFDRIVARGHYTERAAAVTRTIVEVQVLCCHKHGVHRLDKPENFLFANKKENSPLKAIDFG
 LSIFFKPGERFSEIVGSPYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAEESEQGVAQAILRGLIDFKRDPWPNISESASLVRQMLEPDPKRLRL
 TAKQVLEHPWLQNAKAPNVLPGDVVKSRRLKQFSMMNRFRKALRVIAEFLSIEEVEDIKEMFKKMDTDNDGIVSIEELKAGFRNFGSHLASEVQMLIE
 AVDANGKGTLDYGEFLAVSLHLQRIANDEHLRKAFSYFDKDGNGYIEPDELRLDSLMEDGADDCTNVANDIFQEVDTDKDGRISYDEFTAMMKTGTDWRKA
 SRHSRGRFNSLSMKMLKDGSLNLGNE*
 >Thecc1EG023099 Org_Tcacao peptide: Thecc1EG023099t1 Calcium dependent protein kinase 1 (68%T)

(PAC:27421427)
 MGNSCITLRKDGFLQTISNSIWWSRPAEVLGNEDEKKGIGNEAHSESTEAQVQNPPEEMKIVKEETGREQQGKSQEEETQRRQSSAPQRNLNSKPSQLAGF
 NKEETKVEPGKPRKPHNVKQSCAGLQVDSVLQTKTGHLKEYYNLGRKLGHGQFGTTFLCVEKSGKEACKSIAKRKLTTQDDVDDVREIQQIMHHMAG
 HPNVLSIKGAYEDSVAVHVMELCAGGELFDRIVKRGHYTERKAAELARTIVGVVEACHSMGMVHRDLKPENFLFVNEEEDSPLKAI DFGLSIFFKPGDI
 LSDVVGSPYYVAPEVLKRKYGPEADVWSAGV IYIILLSGVPPFWGETEQEIFDEVHLGDLDFTSDFWPSISDSAKDLVRKMLVRDAKKRITAYEVL RHPW
 VQVDGVAPDKPLDSIVLSRMKQFSAMNKLKMLALRVIAQRLSEEEIAGLKEIFKMDITDNSGQITYEELKAGLKKFGANLAESEFHALMQAADVNSGTI
 DYEEFIAATLHLNKIEREDHLFAAFSYFDRDGSYITQDELQKACQEFGEIDISLDEMIQEVDDQNDGRIDYNEFVAMMQGNPEFGMKGPQGKGSIGF
 REALPVC*

>Thecc1EG024724 Org_Tcacao peptide: Thecc1EG024724t1 Calcium-dependent protein kinase 19 (81%T)
 (PAC:27422680)
 MGNCATPSTGSHEKKNKGKKQNPFSDIDYQGHQNGGHHKLSVLKDPDTGTEIEQSYELGRELGRGEFGITYLCTDKVTGDTFACKSISKKKLRTAVDID
 DVRREVEIMKHLPKPHNIVSLKDTYEDDNAVHLMELCEGGELFDRIVARGHYTERAAAVVTKTIVEVVQMCHKHGMVHRDLKPENFLFANKKETAALKA
 IDFGLSVFFKPGERFTEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAIIRSFIDFKRDPWPKVSDNAKDLVRKMLNPDP
 KQRLTAQEVLDHPWLQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSEVEVAGIKEVFQLMGTGNRGKINIDELRVGLHKLGHITPDADLQ
 ILMEAGDVDRDGYLDYGEFVAISVHLRKMGNDEHLKKAFFEDRNQSGFIEIEELRDALADEVTNSEEVISAIMHDVDTDKDGRISYDEFAAMMKAGTD
 WRKASRQYSRERFNSLSLKLMDRGSLSQSNNEPR*

>Thecc1EG030220 Org_Tcacao peptide: Thecc1EG030220t1 Calcium-dependent protein kinase 21 (76%T)
 (PAC:27441153)
 MGCCGSKHKLSEPDYKDYRSGMPPSRPVQPASQPQPVQTKMSVQPIQAPQMRQPPIAPPLKPSPASSRPVQGGQETILGKPLEDIKQYYTLGKELGRGQ
 FGITYLCTENSTGNTYACKSILKRLKLNKQDREDIKKEVQIMQHLSGQPNIVEFRGAYEDRQSVHLMELCAGGELFDRITAQGHYSERAAAAICRSVNV
 VVHICHFMGMVHRDLKPENFLSSKDEGAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRSSYGKEIDIWSAGIILYILLSGVPPFWAETEKGIFD
 AITEGELHFESQPWPSISESAKDLIRKMLTMDPKKRLTSAQVLEHPWMREGGEASDKPIDSAVLSRLKQFRAMNKLKKLALKVIENLSEEEIKGLKAMF
 TNMDTDKSGTITYEELKAGLARLGSKLSEAEVKQLMQAADVDGNGTIDYIEFISATMHRYLRLERDEHLYKAFQYFDKDNDSGYITKDELETAMKEYGMGDE
 ASIREVISEVDTDNDGKINYEECTMMRSGTQQTGKPF*

>Thecc1EG030220 Org_Tcacao peptide: Thecc1EG030220t2 Calcium-dependent protein kinase 21 (76%T)
 (PAC:27441154)
 MGCCGSKHKLSEPDYKDYRSGMPPSRPVQPASQPQPVQTKMSVQPIQAPQMRQPPIAPPLKPSPASSRPVQGGQETILGKPLEDIKQYYTLGKELGRGQ
 FGITYLCTENSTGNTYACKSILKRLKLNKQDREDIKKEVQIMQHLSGQPNIVEFRGAYEDRQSVHLMELCAGGELFDRITAQGHYSERAAAAICRSVNV
 VVHICHFMGMVHRDLKPENFLSSKDEGAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRSSYGKEIDIWSAGIILYILLSGVPPFWAETEKGIFD
 AITEGELHFESQPWPSISESAKDLIRKMLTMDPKKRLTSAQVLEHPWMREGGEASDKPIDSAVLSRLKQFRAMNKLKKLALKVIENLSEEEIKGLKAMF
 TNMDTDKSGTITYEELKAGLARLGSKLSEAEVKQLMQAADVDGNGTIDYIEFISATMHRYLRLERDEHLYKAFQYFDKDNSTSQRMN*

>Thecc1EG030220 Org_Tcacao peptide: Thecc1EG030220t3 Calcium-dependent protein kinase 21 (76%T)
 (PAC:27441155)
 MGCCGSKHKLSEPDYKDYRSGMPPSRPVQPASQPQPVQTKMSVQPIQAPQMRQPPIAPPLKPSPASSRPVQGGQETILGKPLEDIKQYYTLGKELGRGQ
 FGITYLCTENSTGNTYACKSILKRLKLNKQDREDIKKEVQIMQHLSGQPNIVEFRGAYEDRQSVHLMELCAGGELFDRITAQGHYSERAAAAICRSVNV
 VVHICHFMGMVHRDLKPENFLSSKDEGAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRSSYGKEIDIWSAGIILYILLSGVPPFWAETEKGIFD
 AITEGELHFESQPWPSISESAKDLIRKMLTMDPKKRLTSAQVLEHPWMREGGEASDKPIDSAVLSRLKQFRAMNKLKKLALKVIENLSEEEIKGLKAMF
 TNMDTDKSGTITYEELKAGLARLGSKLSEAEVKQLMQAADVDGNGTIDYIEFISATMHRYLRLERDEHLYKAFQYFDKDNDSG*

>Thecc1EG030876 Org_Tcacao peptide: Thecc1EG030876t1 Calmodulin-domain protein kinase 9 (74%T)
 (PAC:27445147)
 MGGCLTKSKEPKPKHNGYRSGATTVAHVHQRYQEFPVRPAPVQPQFHFIPEKPGAQTWPWKVPAPAPSPKPAAPRVDTILGKPYEDIRMRYTIGKELGKGQF
 GVTYLCTENSTGKQYACKTISKRLVTKNDKEDMKREIQIMQHLSGQPNIVEFKGAYEDKQSVHLMELCAGGELFDRITAKGHYSERAAASICRAIVNV
 VHACHFMGMVHRDLKPENFLSSKDENALLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRSSYGKEIDVWSAGVMLYILLSGVPPFWAETEKGIFDA
 ILEGEIDFESQWPWPSISDSAKELVCRMLTQDPKKRITSQVLEHPWIREGGSASDKPLDSAVLSRMKQFRMRNKLKQLALKVIENLSTEEIQGLKQMF
 NIDTNSGTITYDELKNGLARLGSKLSEAEVQQLMEAADVDGNGSIDYIEFITATMHRHRLERDEHLYKAFQHFQDKDNDSGYITRDELETAMKEYGMGDND
 TIKEIISEVDTDNDGKINYEFRDMMRSGTQQGQLF*

>Thecc1EG030876 Org_Tcacao peptide: Thecc1EG030876t2 Calmodulin-domain protein kinase 9 (74%T)
 (PAC:27445148)
 MGGCLTKSKEPKPKHNGYRSGATTVAHVHQRYQEFPVRPAPVQPQFHFIPEKPGAQTWPWKVPAPAPSPKPAAPRVDTILGKPYEDIRMRYTIGKELGKGQF
 GVTYLCTENSTGKQYACKTISKRLVTKNDKEDMKREIQIMQHLSGQPNIVEFKGAYEDKQSVHLMELCAGGELFDRITAKGHYSERAAASICRAIVNV
 VHACHFMGMVHRDLKPENFLSSKDENALLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRSSYGKEIDVWSAGVMLYILLSGVPPFWAETEKGIFDA
 ILEGEIDFESQWPWPSISDSAKELVCRMLTQDPKKRITSQVLEHPWIREGGSASDKPLDSAVLSRMKQFRMRNKLKQLALKVGHCRKSFY*

>Thecc1EG034289 Org_Tcacao peptide: Thecc1EG034289t1 Calcium-dependent protein kinase 29 (68%T)
 (PAC:27459424)
 MGLCQSGQFCLRKSGTHEIPISSSSDSSPRPYQPLPKAAREEFNPPRQKPASENQNPSSSQIGSILLKPYVDITTFYDLDELGRGRFGITYLCTEKATG
 RKYACKSISRRLKSDKYIKVVRREILILQHLTGQPNIVEFKGAYEDRHNHLHLMELCSGGELFDRITAKGTYSERQAASIGRQIVKVVDCHFMGMVHR
 DLKPENFLLVSKDENSPIKATGFGLSVFIEEGKWRDLVGSAYYVAPEVFNRYKYGKEIDVWSAGVILYILLSGVPPFWGETEELKAVLEGNLDLKSQF
 WPSISDAADLLRKMALRDPQRITASQALEHPWMKEGGDTSKPKVGSVLSRLKQFRVMNKLKKLALKVIENLSEEEVKGLKYMNFNFDTDGSGTIT
 LEELRVGLARLGSKLTAETQQLMDAADVDKNGIVDYIEFITATMHRHRLEREDNIIYKAFQFFDKDNDSGFITRDEL RHAMTEYMGDEATIDEVIEDVDI
 DKDGRINYEFEVAMMRGTQDGDGKDR*

>Thecc1EG034291 Org_Tcacao peptide: Thecc1EG034291t1 Calcium-dependent protein kinase 29 (71%T)
 (PAC:27458029)
 MGLCQSLGFLCRKSGTHEIPISSSSESSPRPGEFIPWPQQALENQNPSSSQIGSILRKPYVDITTFYDLDELGRGQFGITYLCTEKATGRKYACKSI
 SRGKLKSDKDREDVREILILQHLTGQPNIVKFKGAYEDRHNHLHLMELCSGGELFDRITAKGTYSERQAASIGRQIVNVVHVCHFMGMVHRDLKPENFL
 LVSKDENSPIKATDFGLSVFIEEDRWYKDLVGSAYYVAPEVFNRYKYGKEIDVWSAGVILYILLSGVPPFWGETEQEIFKAVIEGNLDLKSQWPWPSISDGA

KDLLSKMLARDPKKRITAAQALEHPWIKEGGDASDKPMSAVLSRLRQFRVMNKLKLLKLVIAETLSSEEEVKGLKQMFNNIDTDGSGTITIEELRVGL
ARLGSKLTEAEIQQLMDAADVDRSGSIDYIEFITATMPRHRLEREDNIYKAFQFFDKDNSGFITRDELQAMTEYGMGDEATIDEVIEDVDTDKDGRINY
EEFVAMMRGTQDGR*

>Thecc1EG036367 Org_Tcacao peptide: Thecc1EG036367t1 Calcium-dependent protein kinase 2 (81%P)
(PAC:27458877)

MGWNGMEWLIPWNQTKLLRTIRRSPIQLQAYNKKQKKEEENNSKQEGRKKVKEKEIPSEIFSAMNKKTNSSSSSTTTKPAAGTVLPYQTPRLRDHYLLGK
KLGQGGQFGTTYQCTHKATGTYACKSIPKRKLLCREDYDDVWREIQIMHHLSEHPSVVQIKGTYESVVFVHLMELCAGGELFDRIVAKGHYSEREAVKL
IKTIVGVVEACHSLGVMHRDLKPENFLFDSPADDAILKATDFGLSIFYKPGQYFSDVVGSPYYVAPEVLCKYYGPEVDIWSAGVILYILLSGVPPFWAET
ESGIFRQILHGKIDFASEPWPSPISDSAKDLIRKMLERDPRQRISAHEVLCHPWIVDDRVPDKPLDSAVLSRLKQFSAMNKLKLMALRVIAERLSEEEIG
GLKELFKMIDTNSGTITFQELKDGLKKVGSSELMSESEIKSLMEAADIDNSGTIDYGEFLAATLHINKMEREENLVAAFFFDKDGSGYITIDELQNACKE
FGLGDVHLDDEMIKEIDQDNDGRIDYGEFTAMMRKGDGIGRSRTMRSLNFTIADAFGVKDPSTSDSN*

>Thecc1EG036367 Org_Tcacao peptide: Thecc1EG036367t2 Calcium-dependent protein kinase 2 (81%P)
(PAC:27458879)

MNKKTNSSSSSTTTKPAAGTVLPYQTPRLRDHYLLGKLLGQGGQFGTTYQCTHKATGTYACKSIPKRKLLCREDYDDVWREIQIMHHLSEHPSVVQIKGT
YESVVFVHLMELCAGGELFDRIVAKGHYSEREAVKLKTIKTVGVVEACHSLGVMHRDLKPENFLFDSPADDAILKATDFGLSIFYKPGQYFSDVVGSPYY
VAPEVLCKYYGPEVDIWSAGVILYILLSGVPPFWAETESGIFRQILHGKIDFASEPWPSPISDSAKDLIRKMLERDPRQRISAHEVLCHPWIVDDRVPDK
PLDSAVLSRLKQFSAMNKLKLMALRVIAERLSEEEIGGLKELFKMIDTNSGTITFQELKDGLKKVGSSELMSESEIKSLMEAVNIPS*

>Thecc1EG036367 Org_Tcacao peptide: Thecc1EG036367t3 Calcium-dependent protein kinase 2 (81%P)
(PAC:27458878)

MNKKTNSSSSSTTTKPAAGTVLPYQTPRLRDHYLLGKLLGQGGQFGTTYQCTHKATGTYACKSIPKRKLLCREDYDDVWREIQIMHHLSEHPSVVQIKGT
YESVVFVHLMELCAGGELFDRIVAKGHYSEREAVKLKTIKTVGVVEACHSLGVMHRDLKPENFLFDSPADDAILKATDFGLSIFYKPGQYFSDVVGSPYY
VAPEVLCKYYGPEVDIWSAGVILYILLSGVPPFWAETESGIFRQILHGKIDFASEPWPSPISDSAKDLIRKMLERDPRQRISAHEVLCHPWIVDDRVPDK
PLDSAVLSRLKQFSAMNKLKLMALRVIAERLSEEEIGGLKELFKMIDTNSGTITFQELKDGLKKVGSSELMSESEIKSLMEAADIDNSGTIDYGEFLAATL
HINKMEREENLVAAFFFDKDGSGYITIDELQNACKEFGLGDVHLDDEMIKEIDQDNDGRIDYGEFT

>Thecc1EG036367 Org_Tcacao peptide: Thecc1EG036367t4 Calcium-dependent protein kinase 2 (81%P)
(PAC:27458880)

MNKKTNSSSSSTTTKPAAGTVLPYQTPRLRDHYLLGKLLGQGGQFGTTYQCTHKATGTYACKSIPKRKLLCREDYDDVWREIQIMHHLSEHPSVVQIKGT
YESVVFVHLMELCAGGELFDRIVAKGHYSEREAVKLKTIKTVGVVEACHSLGVMHRDLKPENFLFDSPADDAILKATDFGLSIFYKPGQYFSDVVGSPYY
VAPEVLCKYYGPEVDIWSAGVILYILLSGVPPFWAETESGIFRQILHGKIDFASEPWPSPISDSAKDLIRKMLERDPRQRISAHEVLCHPWIVDDRVPDK
PLDSAVLSRLKQFSAMNKLKLMALRVIAERLSEEEIGGLKELFKMIDTNSGTITFQELKDGLKKVGSSELMSESEIKSLMEAVNIPS*

>Thecc1EG040717 Org_Tcacao peptide: Thecc1EG040717t1 Calcium-dependent protein kinase 19 (87%T)
(PAC:27430665)

MGNCCATPGSPVQSNKKGKNKNKANPFFGDDYAVTNGSATTFKLRLVLEKPTGHDISAQYDLGRELGRGEFGVITYLCTDVSSGDKFACKSISKKKLRTAVD
IEDVRRREVQIMKHLPKHPNIVSLKDYEDDDAVHIVMELCEGGELFDRIVARGHYTERAAAGVMRTIVEVVQMCHKHGMHRDLKPENFLFANKKETAPL
KAIDFGLSVFFFKPGERFNEIVGSPYYMAPEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAIIRSVIDFKRDPWPKVSDNAKDLVRKMLNP
DPKQRLTAQEVLEHPWLQNAKKAPNVPLGETVKARLKQFSVMNKLKRALRVIAEHLSEEVAGIKEAFKMMMDTRKQKINLDELRLMGLQKLGQQIPDAD
LQILMEAADVDGDTLNYGEFVAVSVHLKKMANDEHLHKAFAFFDLNKSYLEIEDLRDALNDEVDTSSSEVIDAIMHDVDTDKDGRISYEEFVAMMKAG
TDWRKASRQYSRERFNSLSLKLMDGSLQLAN*

>Thecc1EG040717 Org_Tcacao peptide: Thecc1EG040717t2 Calcium-dependent protein kinase 19 (87%T)
(PAC:27430666)

MELCEGGELFDRIVARGHYTERAAAGVMRTIVEVVQMCHKHGMHRDLKPENFLFANKKETAPLKAIDFGLSVFFFKPGERFNEIVGSPYYMAPEVLKRN
YGEVDVWSAGVILYILLCGVPPFWAETEQQGVAQAIIRSVIDFKRDPWPKVSDNAKDLVRKMLNPDPKQRLTAQEVLEHPWLQNAKKAPNVPLGETVKARL
KQFSVMNKLKRALRVIAEHLSEEVAGIKEAFKMMMDTRKQKINLDELRLMGLQKLGQQIPDADLQILMEAADVDGDTLNYGEFVAVSVHLKKMANDEH
LHKAFAFFDLNKSYLEIEDLRDALNDEVDTSSSEVIDAIMHDVDTDKDGRISYEEFVAMMKAGTDWRKASRQYSRE

>Thecc1EG040893 Org_Tcacao peptide: Thecc1EG040893t1 Calcium-dependent protein kinase 17 (83%T)
(PAC:27426008)

MGNCCSRGNPAGAPNTNEKGATPDNNGNNPSSSLQDSSANNPPRHSQSPSPGASSKPSKPNPIGPVLGRPMEDIKSTYTIGKELGRGQFGVTHLCTN
KATGEQFACKTIAKRKLNVKEDIEDVRRREVQIMHHLTGQPNIVELKAYEDKHSVHLMELCAGGELFDRIIAKGHYTERAAASLLRTIVQIVHTCHSMG
VIHRDLKPENFLLLNKDENSPLKATDFGLSVFYKPGEVFKDIVGSAIYIAPEVLKRRYGEADIIWSIGVMLYIILLSGVPPFWAESEHGIFNAILRGHIDF
TSDPWPSISHQAKDLVRKMLNSDPKQRLTAIQVLSHPWIKEDGEAPDTPLDNAVLRRLKQFKAMNKFKKVALRVIAAGCLSEEEIMGLKEMFRGMDTNSG
TITLEELKQGLAKQGTGLSEYEVKQLEMAADADNGTIDYDEFITATMMHMRMDREDHLYHAFQHFDDKNSGYITTEELEQVLRREYGMHDGRDIKEILSE
VDSNDGRINIDEFVAMMRKGNPETNPKKRDDVFV*

>Thecc1EG044380 Org_Tcacao peptide: Thecc1EG044380t1 Calcium dependent protein kinase 1 (82%T)
(PAC:27442713)

MGNSCVGPISISKNFFQSVSAAMWRSRIPDDSVSHNTGETGSEVASKEPESPLPVQNKPPQVTPMPKPKETKPKENKPKETNPEKSPKPSPHMKRVSSAGLR
TESVLQRKTGNFKEYSLGRKLGGQFGTTFLCVEKATGKEYACKSIAKRKLVTDDVEDVREIQIMHHLAGHPNVISIKGAYEDAVAVHLMELCAGG
ELFDRIVQRGHYTERKAAALTRTIVGVVEACHSLGVMHRDLKPENFLFVNQQEDSLKTIIDFGLSIFFKPGKEFTDVVGSPYYVAPEVLKRRYGEADVW
SAGVILYIILLSGVPPFWAESEQGIQVVLHGDLDFFESDPWPSISESAKDLVRMLVRDPRRRLTAHEVLCHPWIQIDGVAPDKALDSAVLSRMKQFSAMN
KLKLMALRVIAESLSEEEIAGLKEMFKMIDTNSGQITFEELKAGLKRVGANLKESEIYDLMKAADVNDNSGTIDYGEFVAATLHNLKIEREDHLFAAFSY
FDKDGSGYITPDELQACEEFGIEDVRLEEMIREVDQDNDGRIDYNEFVAMMQKNLASNVAGAGKKGLQNSFSIGFREALKL*

Note that the below sequence corresponds to the representative gene model and not the queried gene model.

>AT1G08650.1 | Symbols:PPCK1,ATPPCK1 | phosphoenolpyruvate carboxylase kinase 1,PHOSPHOENOLPYRUVATE
CARBOXYLASE KINASE 1 | Chr1:2752206-2753232 FORWARD LENGTH=284
MTCSQTLGNNTNKYQICEEIGRGRFGTVSRVYAPATGDFACKTIDKASLSDDLDRACLDNEPKLMALLSYHPNIVQIHDLIDTSTLSIFMELVHPSV

SIYDRLVSSGTFEPQTASFAKQILQALSHCHRYGVVHRDIKPENILVDLRNDTVKICDFGSGIWLGEGETTEGVVGTPIYYVAPEVLMGYSYGEKVDLWS
AGVVLTYMLAGTTPFFYGETAEIEFAVLRGNLRFPTKIFRGVSSMAKDFLRKLICKDASRRFSAEQALRHPWIQRAGETEERFI
>AT1G35670.1 | Symbols:ATCPK2,ATCPK11,CDPK2,CPK11 | calcium-dependent protein kinase 2 |
Chr1:13205456-13208058 FORWARD LENGTH=495
METKPNRRPSNTVLPYQTPRLRDHYLLGKKLGQGGFTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFV
HIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTIILGVVEACHSLGVMHRDLKPNFLFDSFKDDAKLKATDFGLSVFYKPGQYLYDVVGSPIYYVAPEVLK
KCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDKFSDPWPTISEAAKDLYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVL
SRLKQFSQMNKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMER
EENLVAAFSYFDKDGSGYITIDELQSACTEFGLCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTMMKNLNFNIADAFGVDGEKSD
>AT1G50700.1 | Symbols:CPK33 | calcium-dependent protein kinase 33 | Chr1:18782214-18784385 FORWARD
LENGTH=521
MGNCIAKKYGLVMKPPQNGERSVEIENRRRSTHQDPSKISTGTNPPPPWRNPAKHSGAAAILEKPYEDVKLFYTLSELGRGQFVYTLCTEKSTGKRFA
CKSISKKKLVTKGDKEDMRREIQIMQHLSGQPNIVEFKGAYEDEKAVNLVMELCAGGELFDRILAKGHYSERAAASVCRQIVNVNICHFMGMVHRDLKP
ENFLSSKDEKALIKATDFGLSVFIEGRVYKDIVGSAYVVAPEVLKRRYKKEIDIWSAGIILYILLSGVPPFWAETEGKIFDAILEGEIDFESQWPSSI
SNSAKDLVRMLTQDPKRRISAAEVLKHPWLREGGEASDKPIDSAVLSRMKQFRAMNKLKLLKLVIAENIDTEEIQGLKAMFANIDTNSGTITFEELK
EGLAKLGSRLTEAEVKQLMDAADVDGNGSIDYIEFITATMHRHRLESNENVYKAFQHFDDKDGSGYITTDELEAALKEYGMGDDATIKEILSDVDADNDGR
INDEFECAMMRSGNPQQPRLF
>AT1G74740.1 | Symbols:ATCPK30,CPK30,CDPK1A | CALCIUM-DEPENDENT PROTEIN KINASE 1A,calcium-dependent
protein kinase 30 | Chr1:28080199-28082476 REVERSE LENGTH=541
MGNCIACVKFDPDPSKNPKKKPPRGRQRNPYDDPDGLRTHAPLRVIMSHQSQISDKYILGRELGRGEFGITYLCTDRETREALACKSISKRLRTAVD
VEDVRREVTIMSTLPEHPNVVVKLKYEDNENNVHLMELCEGGELFDRIVARGHYTERAAATVARTIAEVVMCHVNGVMHRDLKPNFLFANKKENSAL
KAIDFGLSVLFKPGERFTEIVGSPYYMAPEVLKRYNGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVLDKFRDPWSQISESAKSLVKQMLEP
DSTKRLTAQQVLDHPWIQNAKKAPNVPLGDIVRSRLKQFSMMNRLKKKALRVIAEHLISQIEVEVIRNMFTLMDDNDGKISYLELRAGLRKVGSQLGEPE
IKLLMEVADVNGGCLDYGEFVAVIHLQKMEDEHFRQAFMFDDKDGSGYIESEELREALTDELGEPDNSVIIIDIMREVDTDKDGKINYDEFVMMKAG
TDWRKASRQYSRERFKSLSLNLMKDGSMHLHDALTGQSIIV
>AT1G76040.2 | Symbols:CPK29 | calcium-dependent protein kinase 29 | Chr1:28537743-28540448 FORWARD
LENGTH=561
MLQNQHKTTKNQRNKNIGTKYFLRKKIMGFCFSKFGKSQTHEIPISSSSDSSPPHHYQPLPKPTVSQGGTSNPTSNPQPKPKPAPPPPPSTSSGSQIGPI
LNRPMIDLSALYDLHKLGRGQFGITYKCTDKSNGREYACKSISKRLIRKDIEDVRREVMILQHLTGPQNVIEFRGAYEDKDNHLVMELCSSGGEFLD
RIIKKGSYSEKAAANIFRQIVNVVHVCHFMGVVHRDLKPNFLLVSNEDSPIKATDFGLSVFIEEGKVYRDIVGSAYVVAPEVLHRYNGKEIDVWSAGV
MLYILLSGVPPFWGETEKTIFEAILGKLDLETSPWPTISESAKDLIRKMLIRDPKKRITAAEALEHPWMTDTKISDKPINSALVLRMKQFRAMNKLKLL
ALKVIAENLSEEEIKGLKQTFKNMMDTDESGTITFDELNRGLHRLGSKLSEIEIKQLEMAADVDSKGTIDYIEFVATMHRHRLEKEENLIEAFKYFDKDR
SGFITRDELKHSMTYGMGDDATIDEVINDVDTNDGRINYEYFVAMMRKGTDSDPKLR
>AT2G17290.1 | Symbols:CPK6,ATCDPK3,ATCPK6 | ARABIDOPSIS THALIANA CALCIUM-DEPENDENT PROTEIN KINASE
6,ARABIDOPSIS THALIANA CALMODULIN-DOMAIN PROTEIN KINASE 3,calcium dependent protein kinase 6 |
Chr2:7517005-7519239 FORWARD LENGTH=544
MGNSCRGSFKDKIEGNHSRPEENSKSTTTTVSSVHSPTTDQDFSKQNTNPALVIPVKEPIMRRNVNDSYVVLGHKTPNIRDLYTLRKLGGQGGFTTY
LCTDIATGVYACKSISKRLISKEDVEDVRREIQIMHHLAGHKNIVTIKAYEDPLYVHIVMELCAGGELFDRIIHRGHYSERKAAELTKIIVGVVEAC
HSLGVMHRDLKPNFLLVNKDDDFSLKAIDFGLSVFFKPGQIFKDVVGSPIYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKG
YIDFDTDPWPVISDSAKDLIRKMLCSSPSERLTAHEVLRHPWICENGVAAPDRALDPAVLRLKQFSAMNKLKMKALKVIAESLSEEEIAGLRAMFEAMDT
DMSGAITFDELKAGLRRYGTSLKDTIEIRDLMEAADVNSGTIDYSEFIAATIHNLKLEREEHLVSAFYFDKDGSGYITIDELQQSCIEHGMDTVFLEDI
IKEVDQDNDGRIDYEEFVAMMQKGNAGVGRRTMKNSLNIEMRDV
>AT2G31500.1 | Symbols:CPK24 | calcium-dependent protein kinase 24 | Chr2:13414016-13416324 FORWARD
LENGTH=582
MGSCVSSPLKGSFPGKRPVRRHSSNSRTSSVPRFDSSTNLRRILFQPPSRVLPEPIGDGIHLKYDLGKELGRGEFGVTHECIEISTRERFACKRISKE
KLRTIEDVEDVRREVEIMRCLPKHPNIVSFKEAFEDKDAVYLVMEICEGGELFDRIVSRGHYTERAAASVAKTILEVVKVCHEHGVHRLDLKPNFLFSN
GTETAQLKAIDFGLSIFFKPAQRFEIVGSPYYMAPEVLRNRYGPEIDVWSAGVILYILLCGVPPFWAETEEGIAHAIVRGNIIDFERDPWPKVSHEAKEL
VKNMLDANPYSLRTVQEVLEHPWIRNAERAPNVNLGDNVTRKIQQLFLMNRFKKKVLRIVADNLPNEEIAAIVQMFQTMDDTKNGHLLTFEELRDGLKKIG
QVVPDGDVVKMLMDAADTDGNGMGLSCDEFVTLISHLKRMGCDEHLQEAFFKYFDKNGNGFIELDELKVALCDDKLGHANGNDQWIKDIFFDVLDNKDGRISF
DEFKAMMKSGTDWKMASRQYSRALLNALSIMKFEDFGDNGPKSHSMEFPPIARKRAKLLDAPKNKSMELQISKTYKPSGLRN
>AT2G35890.1 | Symbols:CPK25 | calcium-dependent protein kinase 25 | Chr2:15067175-15069136 REVERSE
LENGTH=520
MGNVVHVMVNNCVDTKSNSVWRPTDLIMDHPLKPQLQDKPPQMLMNKDDDKTKLNDTHGDPKLLLEGKEKPAQKQTSQGGGGRKCSDEEYKKRAIACANS
KRKAHNVRRLMSAGLQAESVLKTKTGHLEKEYNLGSKLGHGQGGFTTFVCEKGTGEEYACKSIPKRKLENEEDVEDVRREIEIMKHLGQPNVISIKGAY
EDSVAVHVMVMELCRGGELFDRIVERGHYSERKAAHLAKVILGVVQTCCHSLGVMHRDLKPNFLFVNDDSDSLKAIIDFGLSMFLKPGENFTDVVGSPIYI
APEVLNKNYGPEADIWSAGVMIYVLLSGSAPFWGETEEEIFNEVLEGELDLSDPWPQVSESADLIRKMLERNPIQRLTAQQVLCHPWIRDEGNAPDTP
LDTTVLSRLKKFSATDKLKKMALRVIAERLSEEEIHELRETFKTDISGKSGRVTYKELKNGLERFNTNLDSNLSLMQIPTDVHLEDTVDYNEFIEAIV
RLRQIQEEEEANDRLESSTKV
>AT2G41860.1 | Symbols:CPK14 | calcium-dependent protein kinase 14 | Chr2:17467646-17469786 REVERSE
LENGTH=530
MGNCCTAGSLIQDKQKKGFKLPNPFNSNEYGNHHDGLKLIVLKEPTGHEIKQKYKLGRELGRGEFGVTYLCETIETGEIFACKSILKKKLKTSIDIEDVK
REVEIMRQMPHEHPNIVTLKETIEDDKAVHLVMELCAGGELFDRIVARGHYTERAAASVIKTIIEVVQMCHKHGMHRDLKPNFLFANKKETASLKAIDF
GLSVFFKPGERFNEIVGSPYYMAPEVLRNRYGQEIWDIWSAGVILYILLCGVPPFWAETEHGVAKAILKSVIDFKRDPWPKVSDNAKDLIKMLHPDPRR
LTAQQVLDHPWIFNGKNASVSLGETVRARLKQFSVMNKLKRALRVIAEHLSEETSCIKERFQVMDTSNRGKITITELGIGLQKLGIIVVPQDDIQILM
DAGVDKDGGLDVNEFVAISVHIRKLGNDHLKKAFTFFDKNKSGYIEIEELRDALADDVDTTSEEVVEAILDVDTNKGKISYDEFATMMKTGTDRK

ASRQYSRDLFKCLSLKLMQDGSLSQNGDTK
>AT2G46700.1 | Symbols:CRK3,ATCRK3 | CDPK-related kinase 3 | Chr2:19182968-19186430 REVERSE LENGTH=595
MGQCYGKVNQSKQNGEEANTTTTYVVSVDGNQIQPLTPVNYGRAKNTPARSSNPSPWPSFPFHGSASPLSPGVSPSPARTSTPRRFFRRFPFPPSPAKHI
KASLIKRLGVKPKKEGPIPEERGTEPEQSLDKSFGYGKNGFAGYELGKEVGRGHFGHTCSGRGKKGDIKDHPIAVKIIISKAKMTTAAIEIDVVRREVKLLKS
LSGHKYLKYYDACEDANNVYIVMELCDGGELLDRLILARGGKYPEDDAKAIIVVQILTVVSFCHLQGVVHRDLKPENFLFTSSREDSDLKLIDFGLSDFIR
PDERLNDIVGSAYYVAPEVLHRSYSLEADIWSIGVITYILLCGSRPFWARTESGIFRTVLRTEPNYDDVPWPSCSSEGKDFVKRLNLDYRKRMASAVQAL
THPWLRRDSRVIPLDILYIKLVKAYLHATPLRRAALKALAKALTENELVYLRAQFMLLGPNGKDGVSLENFKTALMQNATDAMRESRVPEILHTMESLAY
RKMYFEFCAAISIHQLEAVDAWEEIATAGFQHFETEGNRVITIEELARELNVGASAYGHLRDWVRSSDGKLSYLGFTKFLHGVTLRAAHARPR
>AT3G10660.1 | Symbols:ATCPK2,CPK2 | calmodulin-domain protein kinase cdpk isoform 2 | Chr3:3331599-3334268 REVERSE LENGTH=646
MGNACVGPNISGNGLQTVTAAMWRPRIGAEQASSSSHGNGQVSKEAASEPATDQVQNKPEPITMPSSKTNPETKLPDLEIQPEEKKEKVLAEETKQK
VVPEESKQEVPPPEESKREVVVQPESAKPETKSESKPETTKPETTSETKPKETKAEPQKPKHMRVSSAGLRTESVLQRKTENFKEFYSLGRKLGGQGFQTT
FLCLEKGTGNEYACKSISKRLKLTDEDDVEDVRREIQIMHHLAGHPNVISIKGAYEDVVAHVLMELCSGGELFDRIIQRGHYTERKAAELARTIVGVLEA
CHSLGVMHRDLKPENFLFVSREEDSLKTIIDFGLSMFFKPEDEVFTDVVGSFYVAPEVLKRYGPESDVWSAGVIVYILLSGVPPFWAETEQQGIFEQVLH
GDLDFSSDPWPSISSESAKDLVRKMLVRDPKRRRLTAHQVLCHPWQIDGVAPDKPLDSAVLSRMKQFSAMNKKFKMALRVAESLSEEEIAGLQKMFKID
ADNSGQITFEELKAGLKRVGANLKESEILDMQAADVDNSGTIDYKEFIAATLHLNKKIEREDHLFAAFSYFDKDESGFITPDELQQACEEFGVEDARIEE
MMRDVDQDKDGRIDYNEFVAMMQKGSIMGGPVKMGLENSISISLKH
>AT3G20410.1 | Symbols:CPK9 | calmodulin-domain protein kinase 9 | Chr3:7116388-7118824 FORWARD LENGTH=541
MGNCFAKNHGLMKPQQNGNTTRSVEVGVTNQDPPSYTPQARTTQQPEKPGSVNSQPPPWAAAAAPGLSPKTTTKSNSILENAFEDVKLFYTLGKELGRG
QFGVTYLCTENSTGKKYACKSISKKLVTAKDKDMRREIQIMQHLGSGPNIVEFKGAYEDEKAVNLVLMELCAGGELFDRIIAKGHYTERAAASVCRQIV
NVVKICHFMGLVHRDLKPENFLSSKDEKALIKATDFGLSVFIEEGKVYRDIWGSAYYVAPEVLRRLRYGKEVDIWSAGIILYILLSGVPPFWAETKEGIF
DAILEGHIDFESQPWPSISSAKDLVRRMLTADPKRRISAADVLQHPWLREGGEASDKPIDSAVLSRMKQFRAMNKLKALKVAENIDTEEIQGLKAM
FANIDTNSGTITYEELKEGLAKLGSKLTEAEVKQLMDAADVDNGNSIDYIEFITATMHRHRLESNENLYKAFQHFQDKDSSGYITIDELESALKEYGMGD
DATIKEVLSDDVSDNDGRINYEFCAMMRSGNPQQQPRLF
>AT3G51850.1 | Symbols:CPK13 | calcium-dependent protein kinase 13 | Chr3:19232667-19235526 FORWARD LENGTH=528
MGNCCRSAPAAREVDKSNYSGHDAAGGKKSAPIRVLSDVPKENIEDRYLLDRELGRGEFGVITYLCIERSSRDLLACKSISKRLRTAVDIEDVK
REVAIMKHLPKSSIVTLKEACEDDNAVHLMELCEGGELFDRIIVARGHYTERAAAGVTKTIVEVVQLCHKHGVHRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGKEFSEIVGSPYYMAPEVLKRNYPGEIDIWSAGVILYILLCGVPPFWAEESEQVQAAILRGVIDFKREPWPNISETAKNLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKAPNVPLGDVVKSRLKQFSVMNRFRKALRVIAEFLSTEEVEDIKVMFNKMDTDNDGIVSIEELKAGLRDFTQLAESEVQMLI
EAVDTKGKGTLDYGEFVAVSLHLQKVANDEHLRKAFFSYFDKDGNGYILPQELCDALKEDGGDDCVDVANDIFQEVDTDKDGRISYEEFAAMMKTGTDRK
ASRHSYRGRFNSLSIKLMKDGSLNLGNE
>AT3G57530.1 | Symbols:ATCPK32,CPK32,CDPK32 | calcium-dependent protein kinase 32 | Chr3:21296898-21299351 REVERSE LENGTH=538
MGNCCGTAGSLAQNDNKPKKGRKKQNPFSIDYGLHHGGGDDGGRPLKLIVLNDPTGREIESKYTLGRELGRGEFGVITYLCTDKETDDVFACKSILKKKL
TAVDIEDVRREVEIMRHMPEHPNVVTLKETYEDEHAVHLMELCEGGELFDRIIVARGHYTERAAAVTKTIVEVVQVCHKHGMHRDLKPENFLFGNKKE
TAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYPGEVDIWSAGVILYILLCGVPPFWAETEQQVQAIIIRSVLDFRRDPWPKVSENAKDLIRK
MLDPPQKRRLTAQQVLDPWLQNAKTAPNVSLGETVVRARLKQFTVMNKLKRALRVIAEHLSDDEASGIREGFQIMDTSQRGKINIDELKIGLQKLGHAI
PQDDLIQILMDAGDIDRDGYLDCDEFIAISVHLRMGNDEHLKKAFAFFDQNNNGYIEIEELREALSDELGTSEEVDVAIIRDVDTDKDGRISSYEEFVTMM
KTGTDWRKASRQYSRERFNSISLKLMDQASLQVNGDTR
>AT4G04695.1 | Symbols:CPK31 | calcium-dependent protein kinase 31 | Chr4:2381634-2383996 REVERSE LENGTH=484
MGCYSSKNLKQSKRTILEKPFVDIGKVYILGDELQGGQFGITRCKVEKTSKGTIYACKTILKTNLKSREDEEAVKREIRIMKHLSGEPNIVEFKKAYEDRD
SVHIVMEYCGGELFKKIEALSKDGKSYSEKEAVEIIRPIVNVVNCHYMGVMHRDLKPENFLSTDKNATVKAIDFGCSVFIEEGEVHRKFAGSAYYI
APEVLQGGYKGEADIWSAGIILYILLCGKPPFVTEPEAQMFSEIKSAKIDVDSESWKFIDVKAHLVNRMLNRNPKERISAAEVLGHPWMKDGEASDKPI
DGVVLSRLKQFRDMNKLKVALKVAANLSEEEIKGLKTLFTNIDTDKSGTITLLEELKTLGLTRLSNLSKTEVEQLMEAADVDNGTIDIDEFISATMHR
YRLDRDDHVYQAFQHFQDKDNDGHITKEELEMAMKEHGVGDEVSIKQIITEVDTDNDGKINFEFRTMMRSGSSLPQRELLPIK
>AT4G04700.1 | Symbols:CPK27 | calcium-dependent protein kinase 27 | Chr4:2385276-2387986 REVERSE LENGTH=485
MGCFSKELQQSKRTILEKPLVDITKIYILGEELGRGNFGLTRCKVEKSTGKTIFACKTILKTKLKDEECEEEDVKREIRIMKQLSGEPNIVEFKNAYEDKD
SVHIVMEYCGGELYDKILALYDVGKSYSEKEAAGIIRSVNVVNCHYMGVMHRDLKPENFLSTNDDNATVKVIDFGCSVFIEEGKVYQDLAGSDYYI
APEVLQGGYKGEADIWSAGIILYILLCGKSPFVKEPEGQMFNEIKSLEIDYSEEPWPLRDSRAIHLVLRMLDRNPKERISAAEVLGHPWMKEGEASDKPI
DGVVLSRLKFRDANKFKKVVLFKIAANLSEEEIKGLKTLFTNIDTDKSGNITLLEELKTLGLTRLSNLSKTEVEQLMEAADMDNGTIDIDEFISATMHR
YKLDREDEHVYKAFQHFQDKDNDGHITKEELEMAMKEDGAGDEGSIKQIADADTDNDGKINFEFRTMMRTESSLQPEGELLPIN
>AT4G04710.1 | Symbols:CPK22 | calcium-dependent protein kinase 22 | Chr4:2390497-2392887 REVERSE LENGTH=498
MGNCCGSKPLTASDIVSDQKQETILGKPLEDIKKHYSFGDELGKNGFTTYLCKENSTGKSYACKSIPKRTLSSEEEKEAVKTEIQIMDHVSGQPNIVQI
KGSYEDNNSIHIVMELCGGGELFDKIDALVKSHSYSEKDAAGIFRSIVNAVVKICHSLDVVHRDLKPENFLFSSKDENAMLKAIDFGCSVYIKEGKTFER
VVGSKYYIAPEVLEGSYGKEIDIWSAGVILYILLSGVPPFGTGIESIIVSTLCIVDAEIKECRDLFESQPWPLISFKAKHLIGKMLTKKPKERISAADVL
EHPWMKSEAPDKPIDNVVLSRMKQFRAMNKLKALKVIAEGLSEEEIKGLKTFMENMDMDKSGSITYEELKMGMLNRHGSKLSETVEVKQLEAAADV DNG
TIDYIEFISATMHRRLERDEHLYKAFQYFDKDGSGHITKEEVEIAMKEHGMGDEANAKDLISEFDKNNDGKIDYEEFTMMRNGILQPGQKLVIHI
>AT4G04720.1 | Symbols:AtCPK21,CPK21 | calcium-dependent protein kinase 21 | Chr4:2394817-2397631 REVERSE LENGTH=531
MGCFSKSKHRKTQNDGGEKSIPINPVQTHVPEHRKPQTPTPKPMTQPIHQQISTPSSNPVSVRDPDTILGKPFEDIRKFYSLGKELGRGQFGITYMCKEI

GTGNTYACKSILKRKLISKQDKEDVKREIQIMQYLSGQPNIVEIKGAYEDRQSIHLVMELCAGGELFDRIIAQGHYSERAAAGIIRSIVNVVQICHFMGV
VHRDLKPENFLSSKEENAMLKATDFGLSVFIEEGKVYRDI VGSAYYVAPEVLRSSYGEKIDISAGVILYILLSGVPPFWAENEKGIFDEVIKGEIDFV
FSPWPSISESAKDLVRKMLTKDPKRRITAAQVLEHPWIKGGEAPDKPIDSAVLSRMKQFRAMNKLKKLALKVIAESLSEEEIKGLKTMFANIDTDKSGTI
TYEELKTGLTRLGSRSLSETEVKQLMEAADVDGNGTIDYYEFISATMHRYKLDREHVYKAFQHFDKDNSGHITRDELESAMKEYGMGDEASIKEVISEVD
TDNDGRINFEEFCAMMRSGSTQPPQKGLLPFH
>AT4G04740.2 | Symbols:CPK23,ATCPK23 | calcium-dependent protein kinase 23 | Chr4:2404883-2408493
REVERSE LENGTH=533
MGCFFSSKHKRKTQNDGGERSIPIIPVQTHIVDQVPDHRKPQIPSPSIPISVRDPETILGKPFEDIRKFYSLGRELGRGGLGITYMCKEIGTGNİYACKSI
LKRKLISELGREDVKTEIQIMQHLSGQPNVVEIKGSYEDRHSVHLVMELCAGGELFDRIIAQGHYSERAAAGTIKSIVDVVQICHNGVIHRDLKPENFL
FSSKEENAMLKVTD FGLSAFIEEGKIYKDVVGSPPYVAPEVLRQSYGKEIDIWSAGVILYILLCGVPPFWADNEEGVFVEILKCKIDFVREPWPSPISDSA
KDLVEKMLTEDPKRRITAAQVLEHPWIKGGEAPDKPIDSVLSRMKQFRAMNKLKKLALKVSAVLSSEEEIKGLKTLFANMDTNRSGTITYEQLQTGLSR
LRSRLSETEVQQLVEASDV DNGTIDYYEFISATMHRYKLHHDHVKAFQHLDKDKNGHITRDELESAMKEYGMGDEASIKEVISEVDTDNALSPVEIM
REVALEIGVPVNTFKQNNVQEDGLYLPVLNNAA
>AT4G09570.1 | Symbols:CPK4,ATCPK4 | calcium-dependent protein kinase 4 | Chr4:6049560-6052184 FORWARD
LENGTH=501
MEKPNPRRPSNSVLPYETPRLRDHYLLGKKLGQGGFTTYLCTEKKSSSANYACKSIPKRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTIEDSVFVH
IVMEVCEGGELFDRI VSKGCFSEERAAKLIKILGVVEACHSLGMHRDLKPENFLFDSPSDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKK
CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGIKDFKSDPWTPTISEGAKDLIYKMLDRSPKKRISAHEALCHFWIDHAAADPKPLDPAVLS
RLKQFSQMNKIKKMLARVIAERLSEEEIGLKLKELFKMIDTNSGTITFEELKAGLRVGSSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHINKMERE
ENLVVAFSYFDKDGSGYITIDELQQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDVGRSRTMRNNLNFNIAEAFGVEDTSSTAKSDDSP
K
>AT4G21940.2 | Symbols:CPK15 | calcium-dependent protein kinase 15 | Chr4:11640847-11643487 FORWARD
LENGTH=561
MGCFFSSKHNTESDIINGSVQSSIPTNQPENHVSRDVLKPQKPPSPQIPTTTQSNHHHQESKPVNQIEKKHVLTOPLKPIVRETETILGKPFEEIRK
LYTLGKELGRGQFGITYTCKENSTGNTYACKSILKRKLTRKQDIDDVKREIQIMQYLSGQENIVEIKGAYEDRQSIHLVMELCGGSELFDRIIAQGHYSE
KAAAGVIRSVLNVVQICHFMGVHRLDLKPENFLLASTDENAMLKATDFGLSVFIEEGKVYRDI VGSAYYVAPEVLRSSYGEKIDISAGIILYILLCGVP
PFWSETEKGIFNEIITKGEIDFDSQPWPSISESAKDLVRKLLTKDPKQRI SAAQALEHPWIRGGEAPDKPIDSAVLSRMKQFRAMNKLKKLALKVIAESLS
EEEIKGLKTMFANMDTDKSGTITYEELKNGLAKLGSKLTAEEVKQLMEAADVDGNGTIDYIEFISATMHRYRFRDRDEHVFKAFQYFDKDNSGFI TMDLE
SAMKEYGMGDEASIKEVIAEVDTDNDGRINYEFCAMMRSGITLPPQGGKILPPCKRVADLN
>AT4G23650.1 | Symbols:CDPK6,AtCDPK6,CPK3 | Calcium dependent protein kinase 3,calcium-dependent
protein kinase 6 | Chr4:12324967-12327415 REVERSE LENGTH=529
MGHRHSKSKSSDPPPPSSSSSSSGNVVHHVKPAGERRGSSSGSGTGVSSSGSGTGGSRSTTSTQQNGRILGRPMEEVRRTYEFGRGLRGQFGVTVTLVTHKET
KQQVACKSIPTRRLVHKDDIEDVRREVQIMHHLSGHRNIVDLKAYEDRHSVNLIMELCEGGELFDRIISKGLYSERAAADLCRQMVVMVHSCSMGMVMH
RDLKPENFLFLSKDENSPLKATDFGLSVFFKPGDKFDLVGSAYYVAPEVLKRNYPGPEADIWSAGVILYILLSGVPPFWGENETGIFDAILQQGQDFDAD
PWPALSDGAKDLVRKMLKYDPKDRLTAAEVLNHPWIREDGEASDKPLDNAVLSRMKQFRAMNKLKKMALKVIAENLSEEEIIGLKEMFKSLD TDNNGIVT
LEELRTGLPKLGSKISEAEIRQLMEAADMDGGSIDYLEFISATMHMNRIEREDHLYTAFQFFDNDNSGYITMEELELAMKKYNMGDDKSIKEIIAEVDT
DRDGKINYEFEFVAMMKGNPELVPNRRRM
>AT4G35310.1 | Symbols:CPK5,ATCPK5 | calmodulin-domain protein kinase 5 | Chr4:16802436-16804628
FORWARD LENGTH=556
MGNSCRGSFKDKLDEGDNNKPEDYSKTSTTNLSSNSDHSNPAADIIAQEFKSDNNNNNSKDPALVIPLREPIMRRNPDNQAYYVLGHKTPNIRDIYTL
RKLGGQFGTTYLCTEIASGVYACKSISKRLISKEDVEDVRREIQIMHHLAGHGSIVTIKAYEDSLYVHIVMELCAGGELFDRIIQRGHYSERKAAE
LTKIILGVVEACHSLGMHRDLKPENFLVNKDDDFSLKAIDFGLSVFFKPGQIFTDVVVGSPPYVAPEVLLKRYGPEADVWTAGVILYILLSGVPPFWAE
TQQGIFDAVLKGYIDFESDPWPVISDSADKLIRRLSSKPAERLTAHEVLRHPWICENGVPADRALDPAVLSRLKQFSAMNKLKKMALKVIAESLSEEEI
AGLREMFQAMDTDNSGAI TFDLKA GLRKYGSTLKDTEIHDLMDAADV DNSGTIDYSEFIAATIHNLKLEREEHLVAAFQYFDKDGSGFITIDELQQACV
EHGMADVLEDDI I KEVDQNNDGKIDYGEFVEMMQGNAGVGRRTMRNSLNISMRDA
>AT4G38230.2 | Symbols:CPK26,ATCPK26 | ARABIDOPSIS THALIANA CALCIUM-DEPENDENT PROTEIN KINASE
26,calcium-dependent protein kinase 26 | Chr4:17928994-17931101 REVERSE LENGTH=514
MGLALFSSDGKLIWKGSTQTGKRRPQEEATMKHSGGNQACYVLGQKTPSIRDLYSLGHKLGGQFGTTYMCKEISTGREYACKSITKRKLISKEDVEDVR
REIQIMHHLAGYKNIVTIKAYEDPLYVHIVMELCSGGELFDRIIQRGHYSERKAAELIKIIVGVVEACHSLGMHRDLKPENFLVNKDDDFSLKAIDF
GLSVFFKPGQIFEDVVGSPYYVAPEVLLKHYPGPEADVWTAGVILYILVSGVPPFWAETQQGIFDAVLKGHIDFSDPWPPLISDSAKNLIRGMLCSRPSER
LTAHQVLRHPWICENGVPADRALDPAVLSRLKQFSAMNKLQMALRVIAESLSEEEIAGLKEMFKAMDTDNSGAI TFDLKA GLRKYGSTLKDTEIRDL
EAADIDKSGTIDYGEFIAATIHNLKLEREEHLLSAFRYFDKDGSGYITIDELQHACAEQMSDVFLIEDVKEVDQDNDGRIDYGEFVAMMQKGI VGRTRM
KSINMSIRNNAVSQ
>AT5G04870.1 | Symbols:ATCPK1,CPK1 | calcium dependent protein kinase 1 | Chr5:1417015-1419877 REVERSE
LENGTH=610
MGNTCVGPSRNGFLQSVSAAMWRPRDGDSDASMSNGDIASEAVSGELSRSLSDDEVQNKPPQVMTMPKPGTDVETKDREIRTESKPETLEEISLESKPETK
QETKSETKPESKPDPAKPKPKPKMKRVSSAGLRTESVLQKRTENKFEYSLGRKLGGQFGTTFLCVEKTGKEFACKSI AKRLLTDDEDVEDVRREIQ
IMHHLAGHPNVISIKGAYEDVVAVHLVMECCAGGELFDRIIQRGHYTERKAAELTRTIVGVVEACHSLGMHRDLKPENFLVSKHEDSLLKTIDFGLSM
FFKPDVDVTDVVGSPPYVAPEVLRKRYGPEADVWSAGVIVYILLSGVPPFWAETEQQGIFQVVLHGDLDFSSDPWPSISESAKDLVRKMLVRDPKKRLTAH
QVLCHPWVQDVGAPDKPLDSAVLSRMKQFSAMNKFKKMALRVIAESLSEEEIAGLKEMFNMDADKSGQITFEELKAGLRVGANLKESEILDMQAAD
VDNSGTIDYKEFIAATLHLNKIEREDHLFAAFTYFDKDGSGYITPDELQQACEEFVGVEDVRIEELMRDQDNDGRIDYNEFVAMMQKSGITGGPVKMGL
EKSFSIALKL
>AT5G12180.1 | Symbols:CPK17 | calcium-dependent protein kinase 17 | Chr5:3937136-3939323 FORWARD
LENGTH=528
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CKTIAKRKLNVNKEDIEDVRREVQIMHHLTGQPNIVELKGAYEDKHSVHLMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIVHTCHSMGVIHRDLKP
ENFLLLNKDENSPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLRRKYGPEADIWSIGVMYIILLCGVPPFWAESENGIFNAILRGHVDFSSDPWPSI
SPQAKDLVKKMLNSDPKQRLTAAQVLNHPWIKEDGEAPDVLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDSSTITLLEELR
QGLAQGTRLSEYEVQQLMEAADADNGTIDYGEFIAATMHINRLDREEHLYSAFQHFDDKNSGYITMEELEQALREFGMNDGRDIKEIIEVDGDNDGR
INYDEFVAMMRKGNPDPIPKKRRELSFK
>AT5G12480.1 | Symbols:CPK7 | calmodulin-domain protein kinase 7 | Chr5:4047817-4050035 REVERSE
LENGTH=535
MGNCCGNPSSATNQSKQGKPKNNPNFYSEYATTDRSAGFGLSVLKDPTGHDISLQYDLGREVGRGEFGITYLCTDKETGEKYACKSISKKKLRTAVD
IEDVRREVEIMKHMPPKHPNVVSLKDSFEDDDAVHIVMELCEGGELFDRIIVARGHYTERAAAAVMKTIVEVVQICHKQGMHRDLKPENFLFANKKETSAL
KAIDFGLSVFFKPGEQFNEIVGSPYYMAPEVLRNRYGPEIDVWSAGVILYIILLCGVPPFWAEQGVQAIIRSVIDFKRDPWPRVSDSAKDLVRKMLEP
DPKKRLTAAQVLEHTWILNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSSVEEAAGIKEAFEMMDVNKRGINLEELKYGLQKAGQQIADTD
LQILMEATDVGDDGTLYNSEFVAVSVHLKKMANDEHLHKAFFDQNSGYIEIDELREALNDELNTSSSEEVIAAIMQDVTDDKGRISYEEFVAMMKA
GTDWRKASRQYSRERFNSLSLKLMDGSLQLEGET
>AT5G19360.1 | Symbols:CPK34,AtCPK34 | calcium-dependent protein kinase 34 | Chr5:6521716-6523780
REVERSE LENGTH=523
MGNCCSHGRSDSDNKEEPRPENGSGGVGAEEASVRASKHPPASPPATKQGPVIGPVLGRPMEDVKSSYTLGKELGRGQFGVTHLCTQKATGLQFACKTIA
KRKLNVNKEDIEDVRREVQIMHHLTGQPNIVELKGAYEDKHSVHLMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIHTCHSMGVIHRDLKPENFLL
LSKDENSPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLRNRYGPEADIWSIGVMYIILLCGVPPFWAESENGIFNAILSGQVDFSSDPWVISQAK
DLVRKMLNSDPKQRLTAAQVLNHPWIKEDGEAPDVLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDSSTITLLEELRQGLAK
QGTRLSEYEVQQLMEAADADNGTIDYGEFIAATMHINRLDREEHLYSAFQHFDDKNSGYITTEELEQALREFGMNDGRDIKEIIEVDGDNDGRINYYE
FVAMMRKGNPDNPNKKRRELSFK
>AT5G19450.1 | Symbols:CPK8,CDPK19 | calcium-dependent protein kinase 19 | Chr5:6558672-6561471
REVERSE LENGTH=533
MGNCCASPGETSGSKGPKIKSNPFYSEAYTTNGSGTGFKLSVLKDPDTHGDISLMDLGREVGRGEFGITYLCTDIKTGEKYACKSISKKKLRTAVDIE
DVRREVEIMKHMPPRHPNIVSLKDAFEDDDAVHIVMELCEGGELFDRIIVARGHYTERAAAAVMKTILEVVQICHKHGMHRDLKPENFLFANKKETSALKA
IDFGLSVFFKPGEGFNEIVGSPYYMAPEVLRNRYGPEVDIWSAGVILYIILLCGVPPFWAEQGVQAIIRSVIDFKRDPWPRVSETAKDLVRKMLEPDP
KKRLSAAQVLEHSWIQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSSVEEVAGIKEAFEMMDSKKTGKINLEELKFLHKLGGQQIPDIDL
QILMEAADVDGDDGTLYNGEFVAVSVHLKKMANDEHLHKAFFDQNSDYIEIEELREALNDEVDNTSEEVVAAIMQDVTDDKGRISYEEFAAMMKAGT
DWRKASRQYSRERFNSLSLKLMDREGSLQLEGEN
>AT5G23580.1 | Symbols:ATCDPK9,CPK12,CDPK9,ATCPK12 | calmodulin-like domain protein kinase
9,ARABIDOPSIS THALIANA CALMODULIN-LIKE DOMAIN PROTEIN KINASE 9,CALCIUM-DEPENDENT PROTEIN KINASE 12 |
Chr5:7950388-7952433 REVERSE LENGTH=490
MANKPRTRWVLPYKTKNVEDNYFLGQVLGGQFGTTFCLTHKQTGQKLACKSIPKRKLLCQEDYDDVLREIQIMHHLSEYPNVVRIESAYEDTKNVHLVM
ELCEGGELFDRIIVKRGHYSEREAALKTIIVGVVEACHSLGVVHRDLKPENFLFSSSDEDASLKSTDFGLSVFCTPGEAFSELVGSAYYVAPEVLHKKHYG
PECDVWSAGVILYIILLCGVPPFWAESEIGIFRKILQGKLEFEINPWSISSESADLIKKMLESNPKKRLTAHQVLCHPWIVDDKVAPDKPLDCAVVSRLK
KFSAMNKLKMLALRVIAERLSEEEIGGLKELFKMIDTDKSGTITFEELKDSMRVGSSELMESEIQELLRAADVDESGETIDYGEFLAATIHNLKLEREENL
VAAFSFFDKDASGYITIEELQQAWEFGINDSNLDEMIKDIDQDNDGQIDYGEFVAMMRKGNNGTGGGIGRRTMRNSLNFGTTLPDSESMNV