# 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 [$Ca^{2+}$] 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 ~ 3 µM of free $Ca^{2+}$ (30) while CPK5 only requires ~100 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 [$Ca^{2+}$]. 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, $CPK28^{S228A}$, $CPK28^{S318A}$

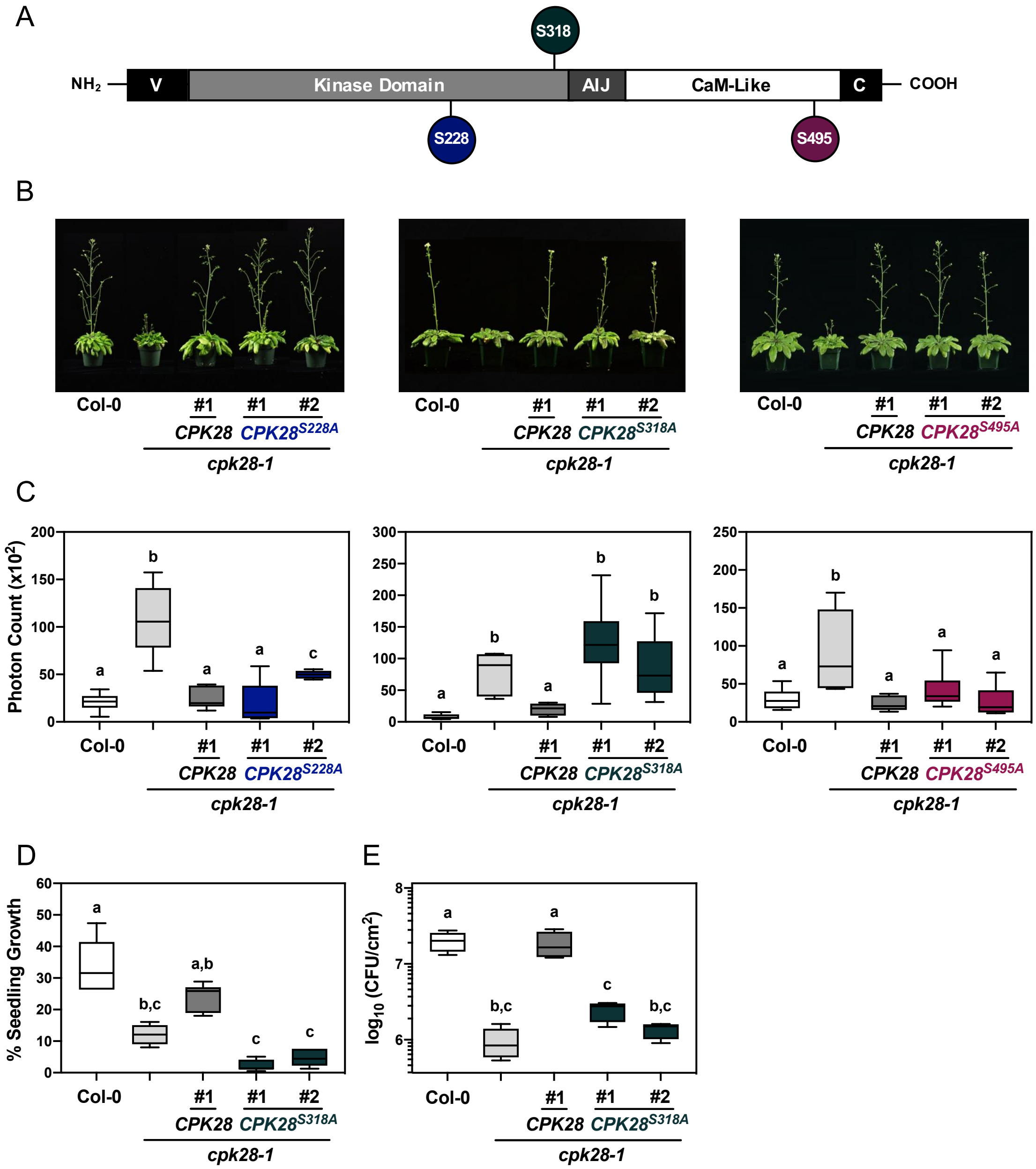

**Figure 1. Ser318 phosphorylation differentially regulates CPK28 function in immune homeostasis.** *(A)* Domain structure of CPK28 and position of tested autophosphorylation sites. V= amino-terminal variable domain; AIJ= autoinhibitory junction; C= carboxyl-terminal variable domain. *(B)* Stem elongation 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 cm$^2$ 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 $Ca^{2+}$-dependent autophosphorylation site by conducting autophosphorylation assays with increasing levels of $CaCl_2$ (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-$His_6$-$CPK28^{D188A}$ as a substrate for $His_6$-CPK28 (Fig 2B). $His_6$-CPK28 could trans-phosphorylate MBP-$His_6$-$CPK28^{D188A}$, 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 $Ca^{2+}$ expected to occur under resting conditions *in vivo.*

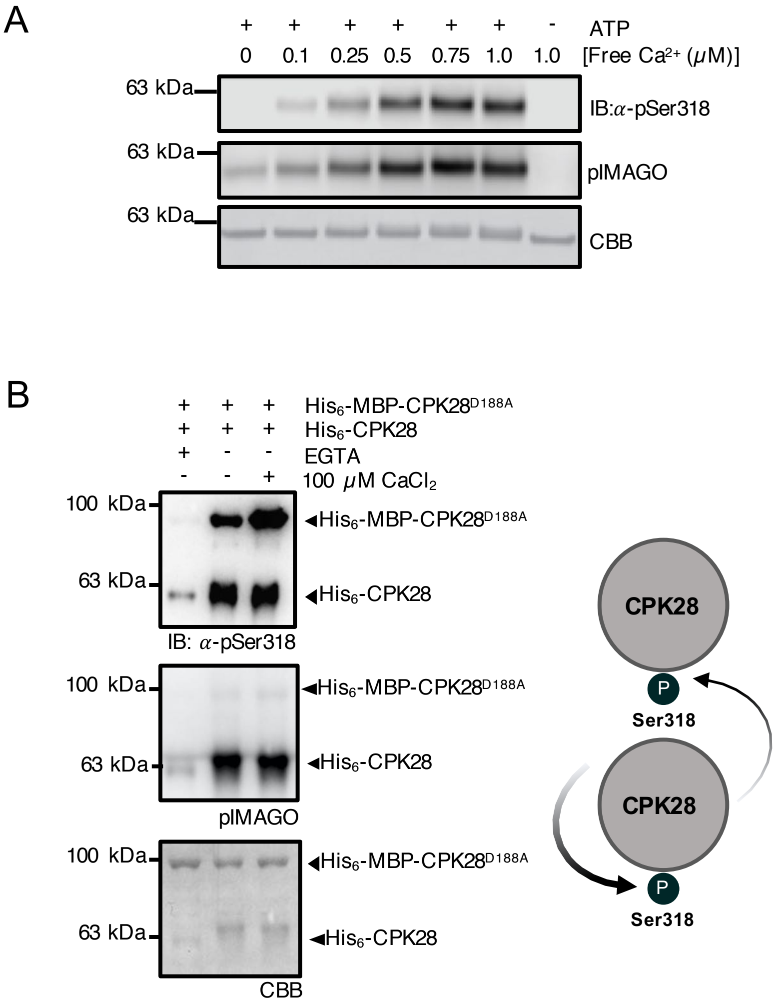

**Figure 2. CPK28 undergoes intra- and inter-molecular autophosphorylation at Ser318.** *(A)* $\text{His}_6$-CPK28 autophosphorylation under increasing $\text{Ca}^{2+}$ concentrations. *(B) In vitro* kinase assays using recombinant $\text{His}_6$-CPK28, $\text{His}_6$-$\text{CPK28}^{\text{S318A}}$, or $\text{His}_6$-$\text{CPK28}^{\text{D188A}}$ and $\text{His}_6$-MBP-$\text{CPK28}^{\text{D188A}}$. 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 [$Ca^{2+}$], 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 $His_6$-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 $His_6$-CPK28$^{D188A/S318A}$ compared to $His_6$-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

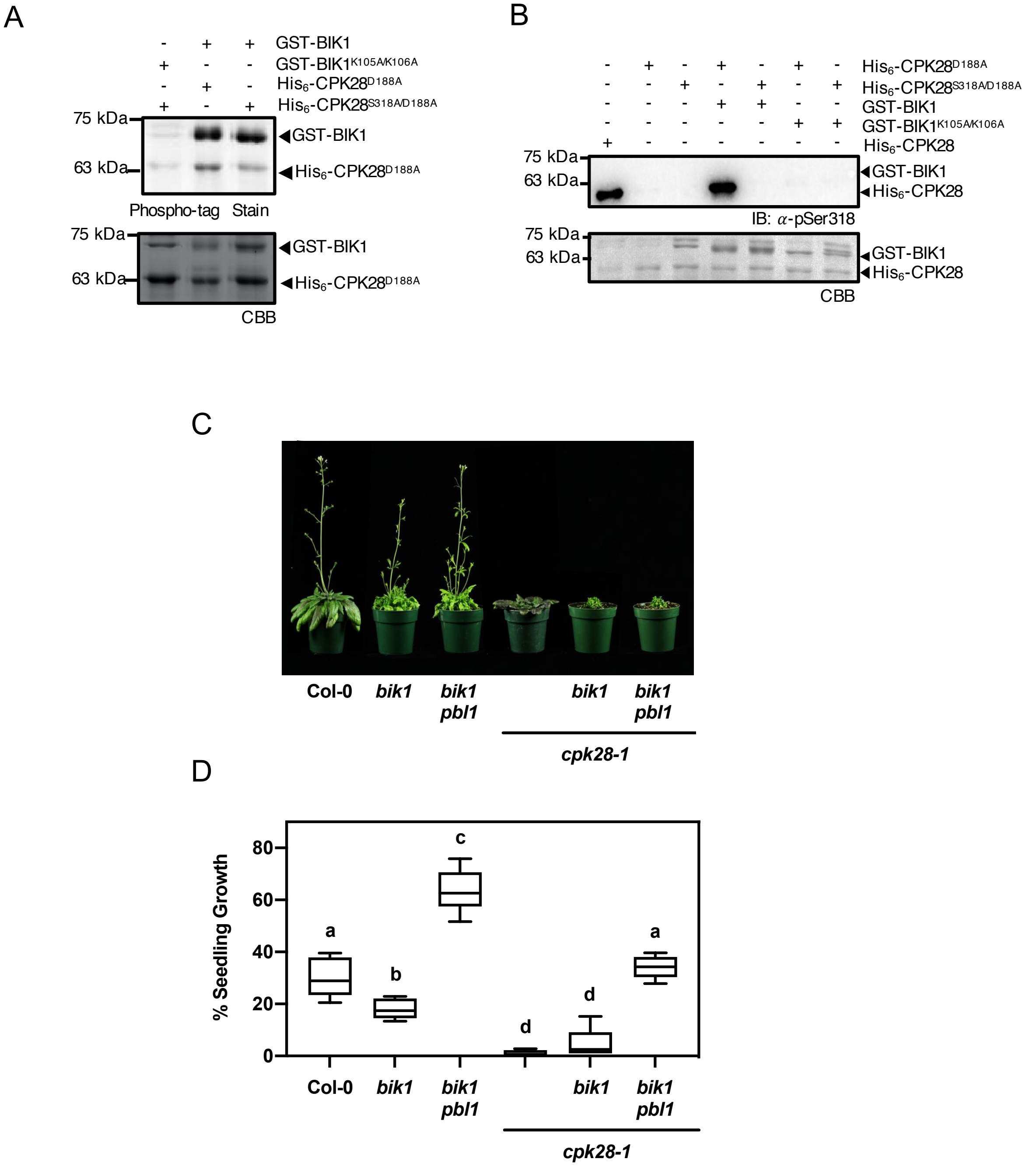

**Figure 3. BIK1 transphosphorylates CPK28 at Ser318 and is required for CPK28-dependent immune signaling.** *(A)* Phospho-tag gel stain and *(B)* Western blot analysis ($\alpha$-pSer318) of *in vitro* kinase assay using recombinant GST-BIK1 or GST-BIK1$^{K105A/K106A}$ and His$_6$-CPK28$^{D188A}$ or His$_6$-CPK28$^{S318A/D188A}$. In order to visualize both Ser318 autophosphorylation and GST-BIK1 transphosphorylation, 500 ng of His$_6$-CPK28 and and 2 $\mu$g of His$_6$-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 Ca$^{2+}$-responsiveness

We previously reported on the phosphorylation-dependent Ca$^{2+}$-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 Ca$^{2+}$-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 $\mu$M $CaCl_2$. 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 $His_6$-CPK28 and $His_6$-$CPK28^{S318A}$ 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 $His_6$-CPK28 and $His_6$-$CPK28^{S318A}$ showed low levels of autophosphorylation in chelation experiments (Fig 4A), confirming their $Ca^{2+}$-dependence. $His_6$-CPK28 was highly active

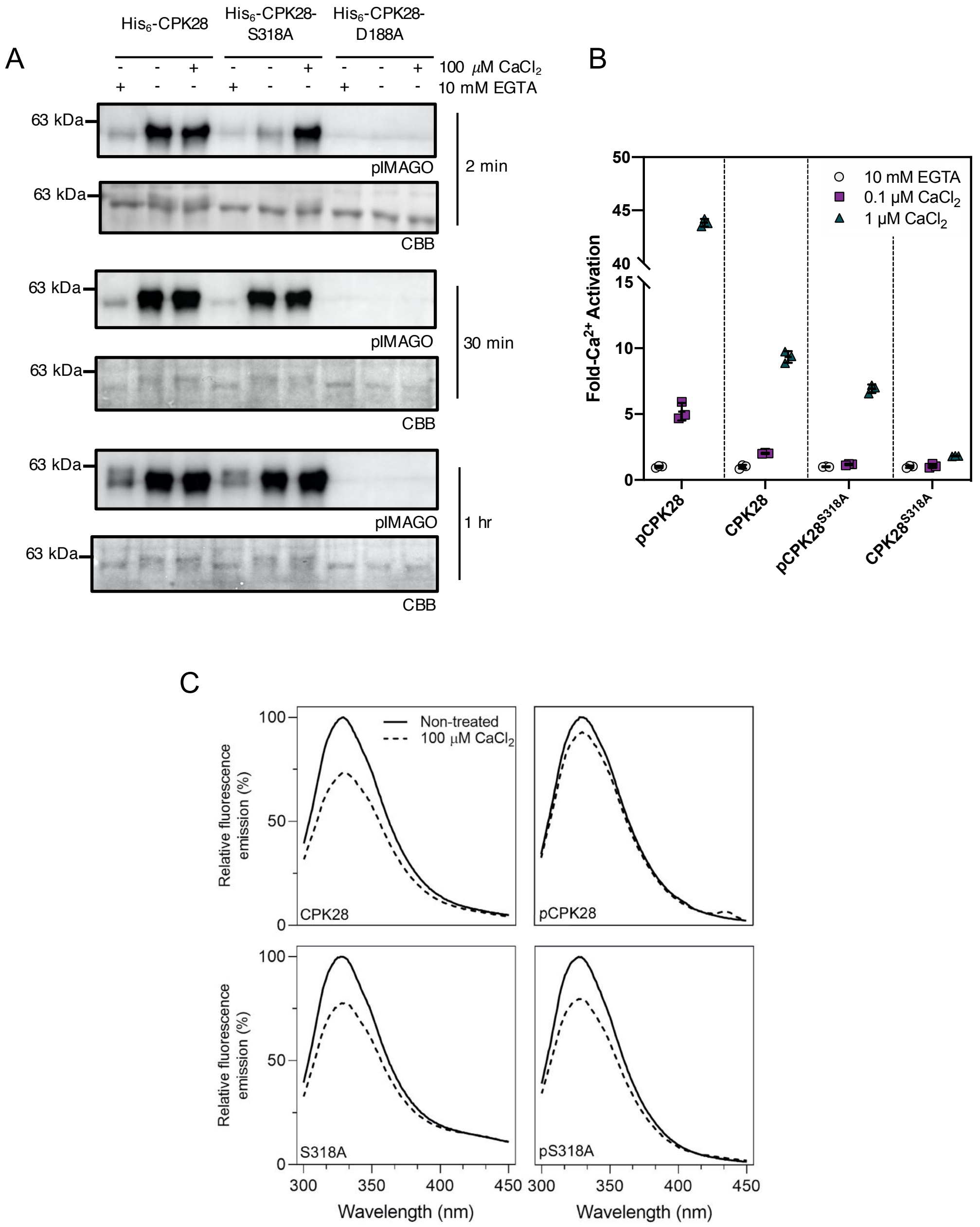

**Figure 4. Phosphorylation at Ser318 primes CPK28 Ca$^{2+}$-responsiveness.** *(A)* Autophosphorylation of recombinant His$_6$-CPK28 or His$_6$-CPK28$^{S318A}$ without Ca$^{2+}$ (+10 mM EGTA), at background Ca$^{2+}$ (-EGTA, -CaCl$_2$), or with the addition of 100 µM CaCl$_2$ for 1-30 min as indicated. Kinase dead His$_6$-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 µM 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, $His_6$-CPK28$^{S318A}$ displayed dramatically reduced autophosphorylation activity compared to wild-type protein (Fig 4A). However, when assays were conducted in the presence of excess $Ca^{2+}$, $His_6$-CPK28 and $His_6$-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), $His_6$-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 $His_6$-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 $His_6$-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, $His_6$-CPK38$^{S318A}$ was substantially less active at physiological $Ca^{2+}$, having negligible activity at 0.1 $\mu$M $Ca^{2+}$ (relative to EGTA-treated protein) regardless of its overall phosphorylation status and only ~2 and 7-fold activation for dephosphorylated and phosphorylated $His_6$-CPK28$^{S318A}$, respectively, at 1.0 $\mu$M $Ca^{2+}$. 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 $His_6$-CPK28 and $His_6$-CPK28$^{S318A}$ (Fig 4C), Trp fluorescence emission decreased following the addition of 100 $\mu$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 $His_6$-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 $His_6$-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

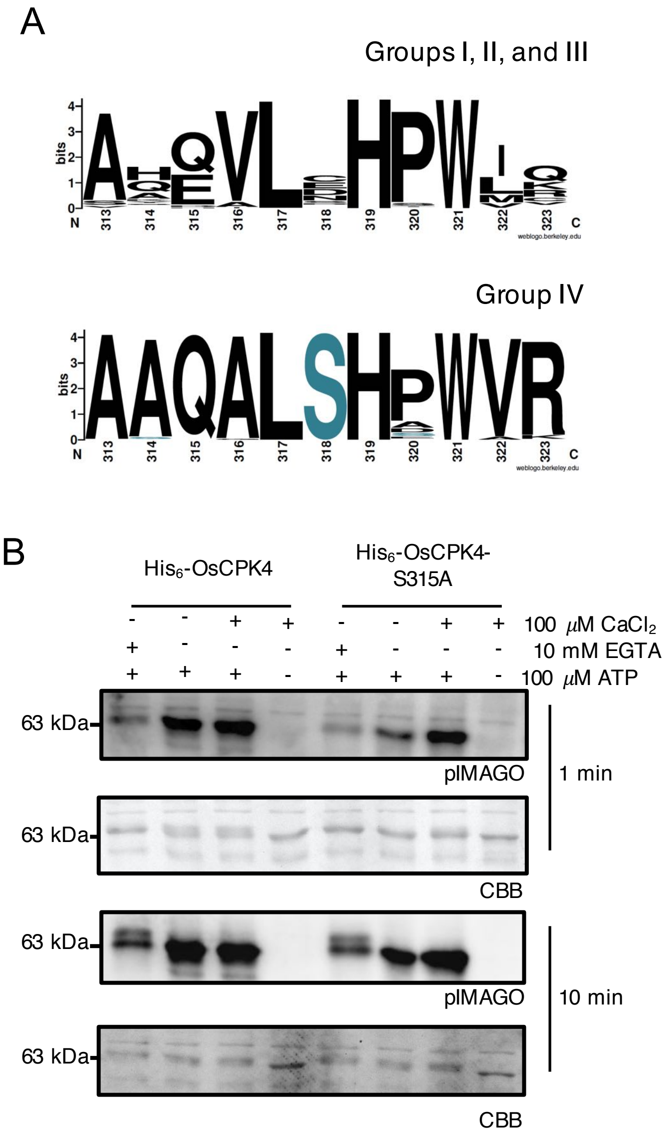

**Figure 5. Ser318 is a conserved feature of group IV CDPKs.** *(A)* Amino acid consensus at position 318 (AtCPK28) across CDPK subgroups. Sequences were retrieved from Phytozome and aligned as described in the Experimental Procedures. Logos were generated using WebLogo (97). *(B)* Autophosphorylation of recombinant His$_6$-OsCPK4 and His$_6$-OsCPK4$^{S315A}$. Reactions were carried out in the absence of Ca$^{2+}$ (+10 mM EGTA), in the presence of background Ca$^{2+}$(-EGTA, -CaCl$_2$), or with the addition of 100 $\mu$M CaCl$_2$ 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 His$_6$-OsCPK4 and His$_6$-OsCPK4$^{S315A}$ produced in LamP-expressing *E. coli* cells, as described above. His$_6$-OsCPK4 displayed a clear requirement for Ca$^{2+}$ with a marked decrease in overall phosphorylation in the presence of 10 mM EGTA (Fig 5B). While wild-type His$_6$-OsCPK4 displayed high levels of autophosphorylation at basal [Ca$^{2+}$], His$_6$-OsCPK4$^{S315A}$ was comparatively less active (Fig 5B). The addition of 100 µM CaCl$_2$ did not further activate His$_6$-OsCPK4 but did restore His$_6$-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 Ca$^{2+}$ sensitivities (27), however the biophysical properties underlying Ca$^{2+}$ sensitivity are not fully understood. Analysis of protein sequences from Arabidopsis indicates that CDPKs with little or no requirement for Ca$^{2+}$ possess one or more degenerated EF-hand motifs (37, 69). However, some CDPKs with the ability to bind Ca$^{2+}$ 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 Ca$^{2+}$ 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

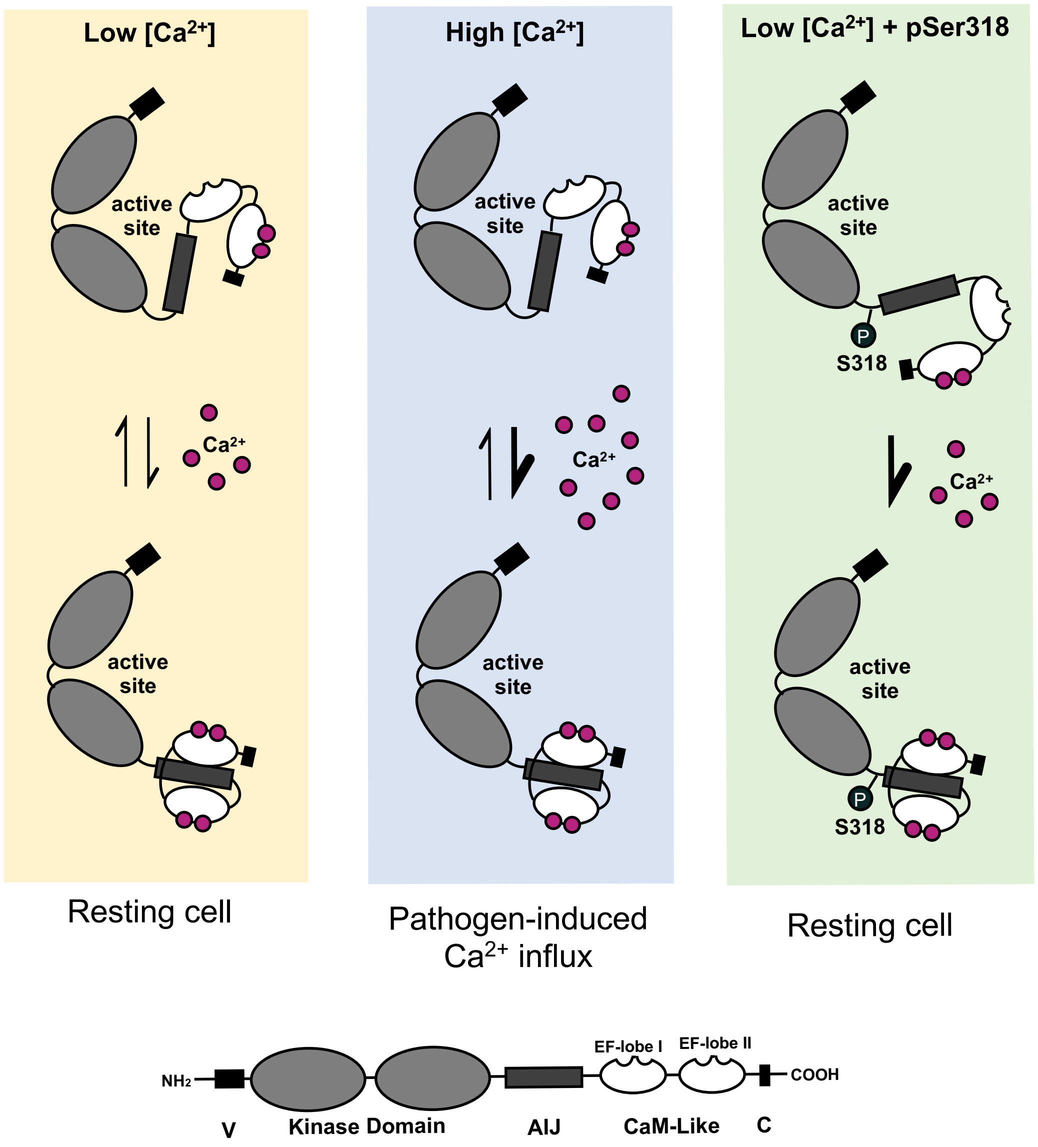

**Figure 6. Model for CPK28 activation.** Proposed mechanism of $Ca^{2+}$-sensitivity priming of CPK28 by phosphorylation of Ser318. In a resting cell, CPK28 transitions between active and inactive conformations, binding and releasing $Ca^{2+}$ from the amino-terminal EF-hand lobe of the calmodulin (CaM)-like domain. $Ca^{2+}$ elevation during signaling events shifts this equilibrium towards the activated state via $Ca^{2+}$-induced conformational changes. When Ser318 is phosphorylated, the transition of CPK28 from an inactive to an active state occurs at lower $Ca^{2+}$ 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 $Ca^{2+}$ 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 $Ca^{2+}$ as stress-induced signals. In support of this hypothesis, prolonged exposure to low levels of $Ca^{2+}$ 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 $Ca^{2+}$ 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 $\mu E\ m^2\ s^{-1}$) 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 $\mu E\ m^2\ s^{-1}$), 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 µE $m^2$ $s^{-1}$ 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). $T_1$ plants were selected on MS agar plates containing 50 µg/mL hygromycin. Only lines displaying a 3:1 segregation ratio on selective media in the $T_2$ 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:His$_6$-CPK28* construct in pET28a+ (EMD Biosciences), and the *pT7:MBP-His$_6$-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:His$_6$-OsCPK4* and *pET100:His$_6$-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 needless 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 ($NH_2$-CKDPRARLTAAQAL**pS**HAWV-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-Burtani (LB) broth at 37 °C to an $OD_{600}$ 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. $His_6$-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 $MgCl_2$. 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 $OD_{600}$ 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 $N_2$ and stored at -80 °C until use.

### *In vitro* autophosphorylation assays

Autophosphorylation assays were conducted by incubating 5 µg of purified $His_6$-CPK28/$His_6$-OsCPK4 or mutant variants in a 50 µL reaction containing 25 mM Tris-HCl (pH7.5), 10 mM DTT, 100 µM ATP, and 100 µM $CaCl_2$ 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 µg of $His_6$-MBP-CPK28 or $His_6$-MBP-CPK28$^{D188A}$ and 4 µg of $His_6$-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 µg of purified GST-BIK1 or GST-BIK1$^{K105A/K106A}$ and 4 µg of

$His_6$-CPK28$^{D188A}$ or $His_6$-CPK28$^{D188A/S318A}$ in a 20 µL total reaction volume of 25 mM Tris-HCl (pH 7.5), 10 mM $MgCl_2$, 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.

### $Ca^{2+}$-activation assays

Analysis of CPK28 peptide kinase activity was carried out as exactly as previously described (53) using the ACSM+1 peptide ($NH_2$-NNLRLSMGKR-$COO^-$) as substrate. Briefly, reactions contained 40 mM Tris-HCl, pH 7.5, 1 mM DTT, 10 mM $MgCl_2$, 100 µM ATP, 0.1 µCi/µl [γ-$^{32}$P]ATP (150 cpm/pmol), 500 ng purified of $His_6$-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-$^{32}$P]ATP mixture. Reactions contained combinations of $CaCl_2$, or EGTA as indicated in the appropriate figures. For experiments at physiological $Ca^{2+}$, final free $Ca^{2+}$ concentrations were achieved by buffering $CaCl_2$ with EGTA, calculated using the online WEBMAXC Extended calculator (102). Final reaction volumes were 40 µl. After addition of the ATP/[γ-$^{32}$P]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 $^{32}$P was assessed by liquid scintillation counting.

## Intrinsic Trp fluorescence measurements

Intrinsic Trp fluorescence of recombinant purified dephosphorylated or hyperphosphorylated His$_6$-CPK28 or His$_6$-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 Ca$^{2+}$ levels (‘non-treated’) and after the titration of 100 $\mu$M CaCl$_2$ 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 $\mu$M CaCl$_2$. 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. moellendorffi, A. trichopoda, O. sativa, A. thaliana, V. vinifera, R. comunis, 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 | EDGRI**S**INEFR |
| KF169738 | (BnaCDPK18) | QDIVG**S**AYYVA | AAQAL**S**HSWVR | EDGRI**S**IHEFR |
| Bradi3g02600 | (BdCDPK17) | RDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGRI**S**LSEFR |
| GRMZM2G157068 | (ZmCDPK22) | HDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGKI**S**LSEFR |
| GRMZM2G053868 | (ZmCDPK40) | HDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGKI**S**LSEFR |
| Os02g0126400 | (OsCDPK4) | HDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGRI**S**LSEFR |
| AT2G17890.1 | (AtCPK16) | HDIVG**S**AYYVA | AAQAL**S**HPWVR | NDGKI**S**LQEFR |
| GRMZM2G365035 | (ZmCDPk33) | RDIVG**S**AYYVA | AAQAL**S**HDWVR | KDGKI**S**LDEFR |
| Bradi1g52567 | (BdCDPK07) | RDIVG**S**AYYVA | AAQAL**S**HEWVR | KDGKI**S**LDEFR |
| Os07g0409900 | (OsCPK18) | RDIVG**S**AYYVA | AAQAL**S**HEWVR | RDGKI**S**LDEFR |
| AT5G66210.2 | (AtCPK28) | HDIVG**S**AYYVA | AAQAL**S**HAWVR | RDGKI**S**LHEFR |
| JX122909 | (BnaCDPK28) | HDIVG**S**AYYVA | ASQAL**S**HAWVR | RDGKI**S**LHEFR |
| Solyc02g083850.2.1 | (SlCDPK28) | QDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGKI**S**LSEFR |
| Solyc03g033540.2.1 | (SlCDPK29) | QDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGKI**S**ISEFR |
| VIT_04s0023g03420 | (VvCPK3) | QDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGRI**S**LAEFR |
| Glyma02g05440 | (GmCPK3) | HDIVG**S**AYYVA | AAQGL**S**HPWVR | KDGKI**S**LPEFR |
| Glyma16g23870 | (GmCPK31) | HDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGKI**S**LPEFR |
| Glyma11g08180 | (GmCPK24) | QDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGKI**S**LPEFR |
| Glyma01g37100 | (GmCPK1) | QDIVG**S**AYYVA | AAQAL**S**HPWVR | KDGKI**S**LPEFR |
| Smo164119 | (SmCPK28) | HDIVG**S**AYYVA | AAQAL**S**HPWVR | GDGRI**S**LREFQ |
| Contig_10120 | (MpCPK28) | QDVVG**S**AYYVA | ASQAL**S**HPWAR | GDGRI**S**LPEFQ |
| Smo92726 | (SmCPK18) | HDVVG**S**AYYVA | AAQAL**S**HPWVR | GDGRI**S**LAEFQ |
| Pp1s83_172V6 | | RDVVG**S**AYYVA | AAQAL**S**HPWVK | KDGRI**S**LSEFQ |
| Pp1s370_37V6 | | GDVVG**S**AYYVA | AAQAL**S**HPWVK | GDKRI**S**LPEFQ |
| Pp1s83_8V6 | | QDVVG**S**AYYVA | AAQAL**S**HPWAK | GDGRI**S**LPEFQ |
| Pp1s199_57V6 | | HDVVG**S**AYYVA | AAQAL**S**HPWAK | GDGKI**S**LSEFQ |
| | | *:******** | **:*.****.: | * :**: **: |

**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.

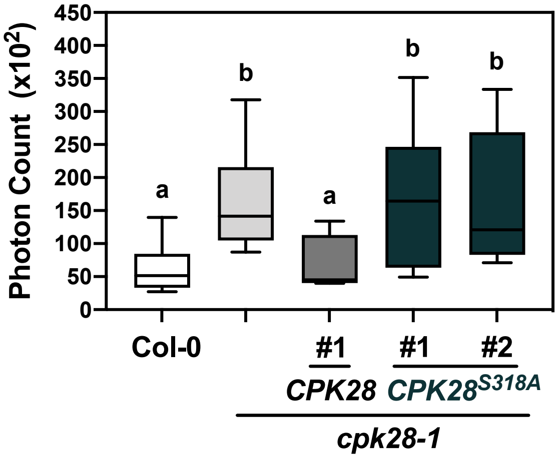

**Figure S2. CPK28$^{S318A}$ does not complement *cpk28-1* in response to elf18 treatment.** Oxidative bursts of Col-0, *cpk28-1*, *cpk28-1/pCPK28:CPK28-FLAG*, and *cpk28-1/pCPK28:CPK28*$^{S318A}$*-FLAG* lines following continual growth in elf18 (100 nM) for 12 days (n=6). Values are presented as boxplots 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.

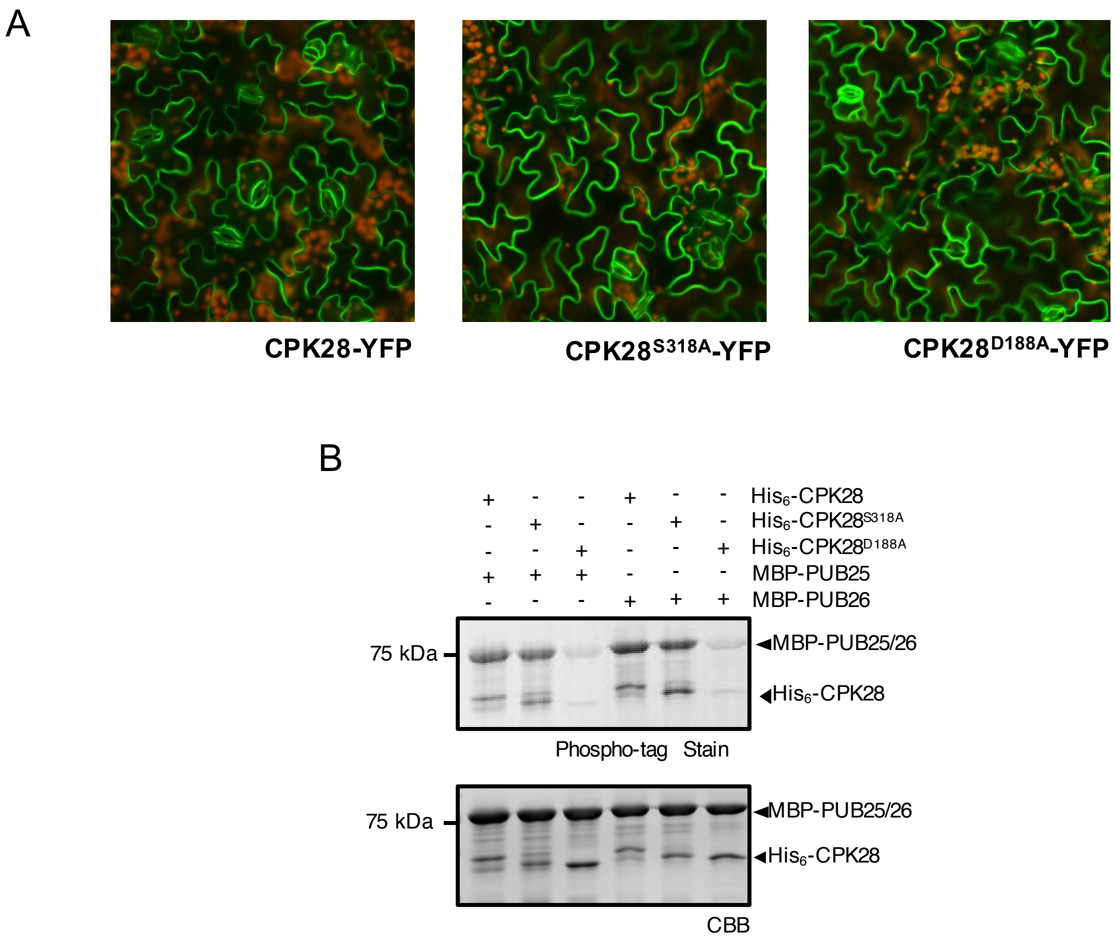

**Figure S3. CPK28$^{S318A}$ localizes to the plasma membrane and phosphorylates PUB25 and PUB26.** *(A)* Subcellular localization of CPK28-YFP, CPK28$^{S318A}$-YFP, and CPK28$^{D188A}$-YFP stably expressed under the CaMV *35S* promoter in *cpk28-1* mutants. Imaging was performed using a LSM 710 (Zeiss) 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 His$_6$-CPK28, His$_6$-CPK28$^{S318A}$, or His$_6$-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.

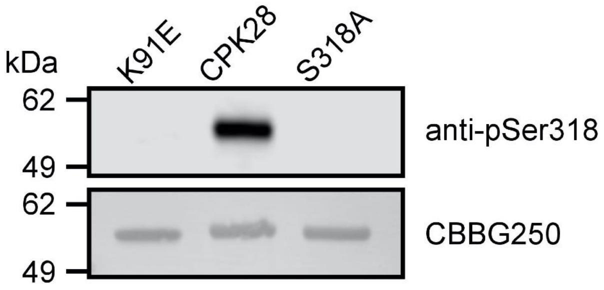

**Figure S4. Specificity of the $\alpha$-pSer318 antibody.** Specificity of the CPK28 pSer318 antibody was determined by immunoblotting against wildtype (CPK28), kinase-dead (CPK28$^{K91E}$), or CPK28$^{S318A}$ . 200 ng of *in situ* phosphorylated purified recombinant protein was separated by gel electrophoresis and blotted to a PVDF membrane before probing with 2 $\mu$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.

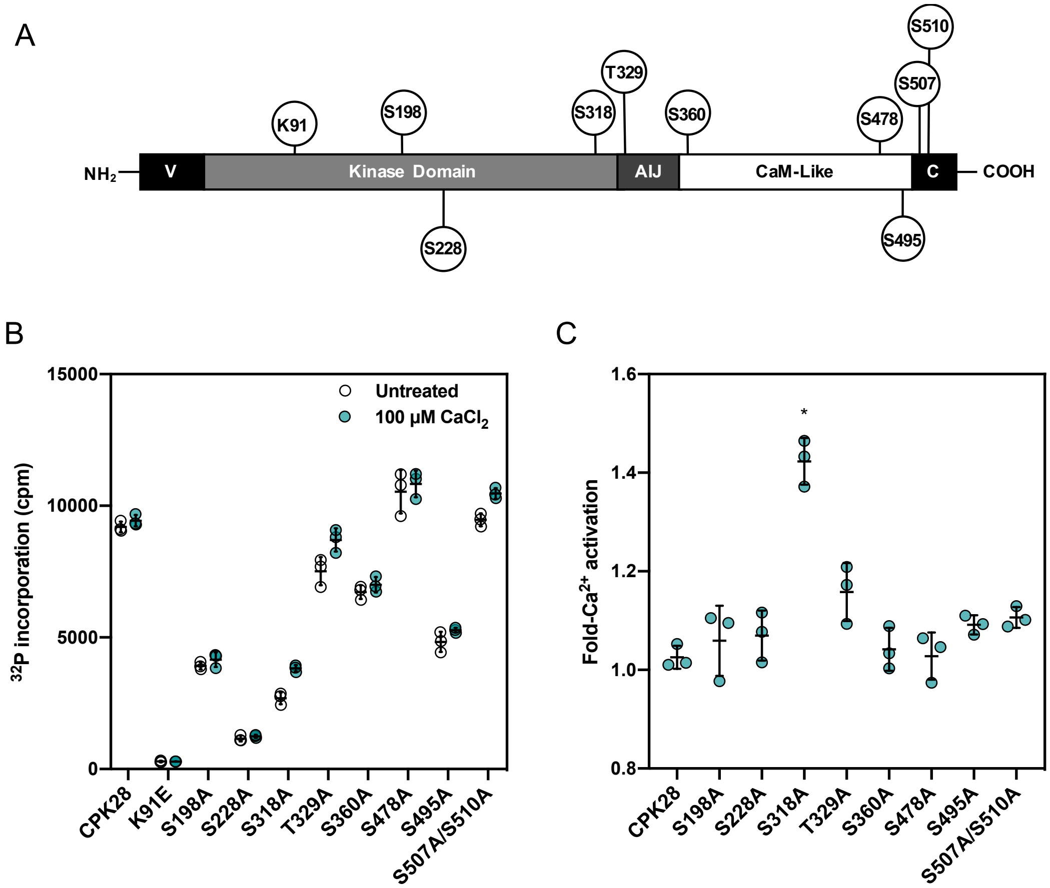

**Figure S5. Ser318 phosphorylation uniquely primes CPK28 for Ca$^{2+}$-activation.** *(A)* Position of tested phosphorylation sites across CPK28 protein domains. *(B)* Biochemical screen of CPK28 phospho-null mutants for Ca$^{2+}$ activation of peptide kinase activity using the ACSM+1 peptide as substrate. Activity was assessed using *in situ* phosphorylated purified recombinant proteins at either background (open circles) or 100 *µ*M CaCl$_2$ (teal circles) and is shown as $^{32}$P 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 Ca$^{2+}$ 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 Ca$^{2+}$ (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.

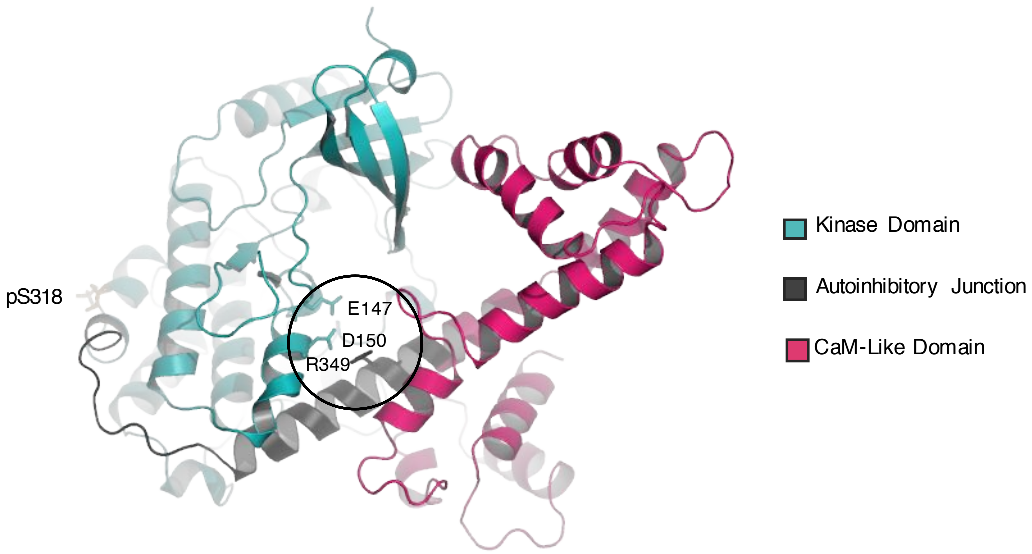

**Figure S6. Structural modeling of CPK28.** A model for CPK28 was generated using the PHYRE2.0 Protein Recognition Server (104) with inactive TgCDPK1 (iTgCDPK1; 3KU2) as a template (95% confidence score). Phosphorylated Ser318 is indicated in orange. The residues in the autoinhibitory triad that stabilizes 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 |
|---|---|
| *cpk28-1* | Matschi et al., 2012 |
| *bik1* | Zhang et al., 2010 |
| *bik1 pbl1* | Zhang et al., 2010 |
| *cpk28-1 bik1 pbl1* | This study |
| *cpk28-1/pCPK28:CPK28-FLAG* line #1 | This study |
| *cpk28-1/pCPK28:CPK28-S228A-FLAG* line #3 | This study |
| *cpk28-1/pCPK28:CPK28-S228A-FLAG* line #6 | This study |
| *cpk28-1/pCPK28:CPK28-S318A-FLAG* line #1 | This study |
| *cpk28-1/pCPK28:CPK28-S318A-FLAG* line #2 | This study |
| *cpk28-1/pCPK28:CPK28-S495A-FLAG* line #1 | This study |
| *cpk28-1/pCPK28:CPK28-S495A-FLAG* line #2 | This study |
| *cpk28-1/pCPK28:CPK28-S318D-FLAG* line #2 | This study |
| *cpk28-1/pCPK28:CPK28-S318D-FLAG* line #3 | This study |
| *cpk28-1/35S:CPK28-YFP* | Matschi et al., 2012 |
| *cpk28-1/35S:CPK28-D188A-YFP* | Matschi et al., 2012 |
| *cpk28-1/35S:CPK28-S318A-YFP* | Matschi et al., 2012 |

**Constructs**

| Construct name | Primers used (5'-3') or Reference |
|---|---|
| pRZ949-pCPK28:CPK28-FLAG | Promoter: FW: 5'-atcgGGTACCgggcgacgaggaagaccaactc-3' RV: 5'-atcgCCATGGggctctgatgaatcgagaaag-3' |
| | CDS cloning: FW: 5'-actgCCATGGGTGTCTGTTTCTCCGCCATTAG-3' RV: 5'-atcgGGATCCCTACTTATCATCATCATCCTTGTAATCTCGAAGATTCCTGTGACC-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'-CATTGTTGGTgcgCCTATTATGTG-3' RV: 5'-TCATGGAACCTTTTCCCTG-3' |
| pET28a(+)-T7:His6-CPK28-S228A | FW: 5'-CATTGTTGGTgcgCCTATTATGTG-3' RV: 5'-TCATGGAACCTTTTCCCTG-3' |
| pRZ949-pCPK28:CPK28-S318A-FLAG | FW: 5'-GCTGCACAAGCACTAGCACATGCGTGGGTTAGAGAAGGCGGGAATGC-3' RV: 5'-GCATTCCCGCCTTCTCTAACCCACGCATGTGCTAGTGCTTGTGCAGC-3' |
| pET28a(+)-T7:His6-CPK28-S318A | FW: 5'-GCTGCACAAGCACTAGCACATGCGTGGGTTAGAGAAGGCGGGAATGC-3' RV: 5'-GCATTCCCGCCTTCTCTAACCCACGCATGTGCTAGTGCTTGTGCAGC-3' |
| pRZ949-pCPK28:CPK28-S495A-FLAG | FW: 5'-GAGATGGGAAAATAGCCCTGCATGAGTTCA-3' RV: 5'-TGAACTCATGCAGGGCTATTTTCCCATCTC-3' |
| pET28a(+)-T7:His6-CPK28-S495A | FW: 5'-GAGATGGGAAAATAGCCCTGCATGAGTTCA-3' RV: 5'-TGAACTCATGCAGGGCTATTTTCCCATCTC-3' |
| pET28a(+)-T7:His6-CPK28-D188A | FW: 5'-GTCTTGTACATAGAGCTATGAAACCAGAGA-3' RV: 5'-TCTCTGGTTTCATAGCTCTATGTACAAGAC-3' |
| pRZ949-pCPK28:CPK28-S318D-FLAG | FW: 5'-ACAAGCACTAgacCATGCGTGGGTTAGAGAAGG-3' RV: 5'-GCAGCAGTTAGCCGTGC-3' |
| pET28a(+)-T7:His6-CPK28-S198A | FW: 5'-GAAACCAGAGAACTTTTTGTTCAAAGCAGCTCAACTAGATTCGCCTCTAAAGG -3' RV: 5'-CCTTTAGAGGCGAATCTAGTTGAGCTGCTTTGAACAAAAAGTTCTCTGGTTTC-3' |
| pET28a(+)-T7:His6-CPK28-T329A | FW: 5'-GGGTTAGAGAAGGCGGGAATGCTGCTGATATCCCTGTCGACATTTCAGTTC-3' RV: 5'-GAACTGAAATGTCGACAGGGATATCAGCAGCATTCCCGCCTTCTCTAACCC-3' |
| pET28a(+)-T7:His6-CPK28-S360A | FW: 5'-CAATTTGCTTTAAGGGCGCTTGCTGCCACACTTGACGAGGCAGAGATCTC-3' RV: 5'-GAGATCTCTGCCTCGTCAAGTGTGGCAGCAAGCGCCCTTAAAGCAAATTG-3' |
| pET28a(+)-T7:His6-CPK28-S478A | FW: 5'-GAATGCACACGGGGTTAAGAGGAGCAATAGATCCACTGCTGGATGAAGC-3' RV: 5'-GCTTCATCCAGCAGTGGATCTATTGCTCCTCTTAACCCCGTGTGCATTC-3' |
| pET28a(+)-T7:His6-CPK28-S507A/S510A | FW: 5'-GTTCAGGAGACTTCTAAGAACAGCGGCCATAAGTGCACAGAGAGCACCAAGCCC-3' RV: 5'-GGGCTTGGTGCTCTCTGTGCACTTATGGCCGCTGTTCTTAGAAGTCTCCTGA |
| pMAL-c2x:MBP-PUB25 | FW: 5'-AATCTCTAGAATGCCTAGGAATATAGAACC-3' RV: 5'-GATTCTGCAGTCAAAAAGGGACCACTTGG-3' |
| pMAL-c2x:MBP-PUB26 | FW: 5'-AATCTCTAGAATGCCGGGGAATTTAGAGCC-3' RV: 5'-GATTCTGCAGTCAAAACGGCGCCACTTCGC-3' |
| pGex6.1-T7:GST-BIK1 | FW:5'-TCGAGCGGCCGCATCGTGACATGGGTTCTTGCTTCAGTTC-3' RV:5'-GCGAGGCAGATCGTCAGTCACACAAGGTGCCTGCCAAAAG-3' |
| pGex6.1-T7:GST-BIK1-K105A/K106A | FW:5'-TCGAGCGGCCGCATCGTGACATGGGTTCTTGCTTCAGTTC-3' RV:5'-GCGAGGCAGATCGTCAGTCACACAAGGTGCCTGCCAAAAG-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)
MGICFSADKSEKAEKEKNKKHGDHAAKDQVKNKEQRSKNQSAHVVPLGKRTNFGYGRDFQAKYKLGKLLGHGQFGYTYAATKIGSGENVAVKRIEKKKML
LPISVEDVRREVRILQLLSGHENVVQFYASFEDDDYVYIVMELCEGGELLDRILSKKNGCYSEKDAAELVRQMLKVVARCHLHGVVHRDLKPENFLFKSQ
RDNTPLKATDFGLSDFIRPGRRFHDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGKRPFWDKTEAGIFNEVLKKKPEFRIKPWPSISANAKDFV
KRLLVKDPRARPTAAQALSHPWVREGGCAPDFPLDIIVLSNMREFVKFSRLKQFAFRALATTLEPEEIHNLRDQFNIIDVDGSGTITLEEIRQALLKDRP
WTLKESKVLEIVQAMDANMDGFIDFDEFVAATLHVRQLEELDSEKWQLRTKCAFDKFDKDGDGFISPDEIKEYTGLKGSLDTLLDEADADGDGRISLREF
QKLLRQASLGSRTNHHHIQPHLKHPKLLEMHAPSPKISEESSQ*
>29830.t000004 Org_Rcommunis peptide: 29830.m001387 calcium-dependent protein kinase, putative
(PAC:16810129)
MGACFSTIKVSGSSSNNTATTTTTVGGHHYQRKEIAGNPQRISTATKTNKQTKNNNNNNNENNNNESRQQKQQSQQQQQKVKEKQTLRRPGGVIPCGKRT
DFGYAKDFDKRYSIGKLLGHGQFGYTYVATDKANGDRVAVKKIEKNKMVLPIAVEDVKREVKILQELAGHENVVHFYNAFEDDSFVYIVMELCEGGELLD
RILLKKDSRYTEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKDDSPLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLKRRSGPESDVWSI
GVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPSISSSAKDFVKKLLVKDPRVRLTAAQALSHPWVREGGNASEIPIDISVLNNMRQFVKYSRF
KQFALRALASTLDDEELSDLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFSEFVAAALHVHQLEEHNSEKWQHRSQ
AAFEKFDIDKDGFITSEELRMHTGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASISSRNAPSPSGHRNSRKM
>92726 Org_Smoellendorffii peptide: 92726 (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE
16-RELATED (PAC:15420653)
MGVCFSVPKRRKQDPATGNAKSRVRPAGHNRKNNAIPLGLRTNFGYGRDFKSKYRIGKLLGHGQFGYTYSAVELMTGDKVAVKRIEKKKMLLPISIEDVK
REVKILDALSGHENVVQFHAAFEDDEFVYIVMELCEGGELLDRILAKKEGRYTEKDAAVIVRQMLRVVARCHLNGVVHRDLKPENFLFKSQQDDSLLRAV
DFGLSDFIRPGKRFHDVVGSAYYVAPEVLKRKSGPESDVWSVGVITYILLCGRRPFWDKTEAGIFNEVLKRKPDLRERPWPSIGSSAKDFVRKLLVKDPR
ARLTAAQALSHPWVREGGDALEIPLDISVLSNMREFVKYSRLKQLAFRALATTLDPEDIAALRDQFDAIDADKSGSISLEEMKQALAKDRPWDLKESMVM
EILQAMDCNCDGLVDFEEFVAATLHVHQLEDMGSDKWQKRSKAAFDQFDVDGDGYITSEELKQYTGLKGSLGTLLEEGDIDGDGRISLAEFQKLLRQASL
GSRN*
>Aco015726 Org_Acomosus peptide: Aco015726.1 calcium-dependent protein kinase 28 (PAC:33034109)
MGNCYSNSSKVRGSSSGRGGRGGGGGAANAGGANHERRPPEEREREKEKGKERKGVVPCGKRTDFGYDKDFESRYAIGKLLGHGQFGYTFVATDKANGDK
VAVKRIDKNKMVLPVAVEDVRREVKILKALKGHENVVHFFNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLHGLVHR
DMKPENFLLKSTKEDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRNP
WPSISDSAKDFVQRLLVKDPRARLTAAQALSHPWVREGGNASDIPLDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADLRDQFNAIDVDKNGTISL
EEMKHALAKDLPWRMREPRVLEILEAIDSNTDGLVDFDEFVAATLHVHQLVELDSEKWQSLSQAAFDQFDVDRDGYITPDELRMHSGLKGSIDPLLEEAD
IDKDGKISLDEFRRLLKTASMSSRNIPNHSAVRNTSKS*
>Aco027228 Org_Acomosus peptide: Aco027228.1 calcium-dependent protein kinase 28 (PAC:33049140)
MFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKKPWPTISASAKDFIIKLLVKNPRARLTAAQALSHP
WVREGGDASEIPVDISVLSNMREFVMYSRMKQFALRALASTLDEEELSDLKDQFDAIDVDKNGSISLEEMRHALAKDLPWRLRGPRVLEILQAIDSNTDG
LVDFKEFVTATLHVHQMAEHDSEKWHLRCQAAFDKFDLDGDGYITPEELRLHTGLKGSIEPLLEEADIDKDGKISLYEFRKLLRTASMSNLPSPTGVRNP
HQL*
>AHYPO_018869 Org_Ahypochondriacus peptide: AHYPO_018869-RA (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:32834481)
MGSCLSTTKVNGSNSNSTTTTTTNNALTVIKNQRKEPAKSVANTAPKNDGSHQKQTQKRNEIEGNGKNHKNNNNNNVGMFKHREKTSSRRQGAIPCGKRT
DFGYDKDFEYKYTIGKLLGHGQFGYTYVATDKSNGDRVAVKKIDKSKMVLPIAVEDVKREVKILKALAGHENVVQFHNAFEDENYVYIVMELCEGGELLD
RILAKKDSRYTEKDAAVVVRQMLKVAAQCHLNGLVHRDMKPENFLFKSPKEDSALKATDFGLSDFIKPGRKFTDIVGSAYYVAPEVLKRKSGPESDVLRN
KPDFRRKPWPTISNDAKDFVKKLLVKDPRARYTAAQALSHPWVREGGNALDIPIDISVLRNMRQFVKYSRMKQFALRALASTLNEEELADLRDQFDAIDV
DKSGTISLEEMRQALAKDLPWNNTDGLVDFTEFVAATLHVHQLQEHDNEKWQQLSQAAFEKFDVDKDGFITPEELKLHTGLKGSVDPLLEEADIDKDGKI
SLSEFRRLLRSASISSRKIASPTCRKNSRRL*
>AL3G50930 Org_Alyrata peptide: AL3G50930.t1 (1 of 1) PF13202//PF14531 - EF hand (EF-hand_5) // Kinase-
like (Kinase-like) (PAC:35941968)
MGLCFSSGHNRSSRNPNHHPPLTVAKTRPPQSPCSFMAVTIQKDHRTQPRRNAAAKKTPTRQTPPHGRGREKVISNNGRRHGEAIPYGKRIDFGYAKDFD
HRYTIGNLLGHGQFGYTYVATDKKTDDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGGELLDRILARKDSR
YSERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVISYILLC
GRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKFSRLKQFALRALA
TTLDEEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFGEFVAAALHVNQLEEHDSEKWQQRSRAAFEKFDID
GDGFITAEELRMHTGLKGSIEPLLEEADIDNDGKISLQEFRRLLRTASIKSRNVRSPPGYLISRKV*
>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)
MGLCFSSPKATRRGTSRRNPNLHSPTQGKASNKNKKKTKKSKNKIQWRHGGGIPYGKRIDFGYAKDFDNRYIIGRLLGHGQFGFTYVATDNNNGNRVAVK
RIEKAKMTQPIEVEDVKREVKILQALGGHENVVGFHNAFEDNNYIYIVMELCEGGELLDRILAKKDSRYTEKDAAVVVRQMLKVAAECHLRGLVHRDMKP
ENFLFKSTEEGSSLKATDFGLSDFIKPGMKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTQDGIFNEVMRKKPDFREVPWPTI
SNGAKDFVKKLLVKEPRARLTAAQALSHPWVKEGGEASEVPIDISVLNNMRQFVKFSRLKQIALRALATTIDEDELDDLRDQFDAIDIDKNGSISLEEMR
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QALAKDVPWKLKDARVAEILQAIDSNTDGLVDFTEFVVAALHVNQLEEHDSEKWQQRSRAAFDKFDIDGDGFITPEELRLQTGLKGSIEPLLEEADIDKD
GRISINEFRRLLRSASLKSRNVKSPPGYQLSQKM*
>AL8G45320 Org_Alyrata peptide: AL8G45320.t1 (1 of 3) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN KINASE
16-RELATED (PAC:35949817)
MGVCFSAIRVTGASSSRPSSQTNNPKSKAAPSPIDTKRRTGSIPCGKRTDFGYAKDFHDHYTIGKLLGHGQFGYTYVAIHKPNGDRVAVKRLDKTKMVLP
IAVEDVKREVQILIALSGHENVVQFYNAFEDDDYVYIVMELCEGGELLDRILSKKGNRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMKPENFLFKSAQL
DSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRKKPDFSRKPWLTISDSAKDFVKK
LLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEEMRQALAKDLPWK
LKDSRVAEILEAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDEADIDRDGKISLHEFRR
LLRTASISSQRAPSPQGHRNPR*
>Aqcoe1G376400 Org_Acoerulea peptide: Aqcoe1G376400.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:33079349)
MGICFSTSNTKVTGGTSNTTTTTTNATTTTTTTINNNVNNNQRESIKPSSTTIHHVPSQQRPYESHRNRSQHQQSQLHQRQHSRRPSSGVFPCGKRTDFG
YLKDFDDKYSIGKLLGHGQFGYTFVATDKINGDRVAVKRIEKNKMILPIAVEDVKREVKILRALTGHENVVQFHNAFEDSEYVYIVMELCEGGELLDRIL
SRKDSRYTEKDAAIIVRQMLKVAAECHLHGLVHRDMKPENFLFKSSKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRKSGPESDVWSIGVI
TYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPSIGNSAKDFVQKLLVKDPRARLTAAQALSHPWVREGGDASEIPVDISVLSNMRQFVKYSRLKQF
ALRALASTLNEEELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKMKEPRVLEIVEAIDSNTDGFVDFSEFVAATLHVHQLEEHDTDKWQVRSQAAF
EKFDVDRDGFITPEELKMHTGLKGSIDPLLEEADVDKDGKISLSEFRRLLRTASMSSRNVPTPAGFRNSRKLP*
>Aqcoe5G209900 Org_Acoerulea peptide: Aqcoe5G209900.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:33089879)
MGLCLSTTSNKNRKKRDNQQQSQSNNNNNKKKITQKKKPQQQQLQQEKKKSNLNRSSVGKRTDFGYEKDFDEKYSIGKLLGHGQFGYTFVATDKSNGDRV
AVKRIDKKKMTLPIAVEDVKREVKIFQALTGHENVVQFYNAFEDDSYVYIVMELCEGGELLDRILAKKDKRYSEKDAAIIVRQMLKVAAECHLHGLVHRD
LKPENFLFKSTKDDSPLKATDFGLSDFIKPGRKFKDIVGSAYYVAPEVLKRQSGPESDVWSIGVITYILLCGRRPFWNKTEDGIFKEVLKNKPDFHRKPW
PSISNSAKDFVQKLLVKDPRVRLTAAQALSHPWVREGGDASDIPVDILVLSNMRKFVKYSRFKQFALRALASTLNEEELSVLRDQFDAIDVDKSGCISFD
EMKQALEKDLPWKIKEPRVLEILQAIDSNTDGHIDFSEFVAATLHVHQLEEHDSQKWHLLSQAAFEKFDVDGDGFITSEELRMHTGLKGSIVPLLEEADI
DKDGKINLLEFRKLLRTASMTSPNVPSPSGVGNSKRS*
>Araha.1084s0035 Org_Ahalleri peptide: Araha.1084s0035.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:28844220)
MARESDAPSVTGIAKEIISFVVTFHPHWEKFNSKKSNEPVYVKKGNASTKRRTGSIPCGKRTDFGYAKDFHDHYTIGKLLGHGQFGYTYVAIHKPNGDRV
AVKRLDKTRMVLPIAVEDVKREVQILIALSGHENVVQFYNAFEDDDYVYIVMELCEGGELLDRILSKKGNRYSEKDAAVVVRQMLKVAGECHLHGLVHRD
MKPENFLFKSAQLDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRKKPDFSRKPW
LTISDSAKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLE
EMRQALAKDLPWKLKDSRVAEILEAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDEADI
DRDGKISLHEFRRLLRTASISSQRAPSPQGHRNPR*
>Araha.13406s0005 Org_Ahalleri peptide: Araha.13406s0005.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:28853710)
GRGREKVISNNGRRHGEAIPYGKRIDFGYAKDFDHRYTIGNLLGHGQFGYTYVATDKKTDDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVR
FYNAFEDKNSVYIVMELCEGGELLDRILARKDSRYSERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSPLKATDFGLSDFIKPGKKFHDI
VGSAYYVAPEVLKRRSGPESDVWSIGVISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLALATTLDEEELADLRDQFDAID
VDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFGEFVAAALHVNQLEEHDSEKWQERSRAAFEKFDIDGDGYITAEELRMHTGLKGS
IEPLLEEADIDNDGKISLQEFRRLLRTASIKSRNVRSPPGYLISRKV*
>AT2G17890 Org_Athaliana peptide: AT2G17890.1 calcium-dependent protein kinase 16 (PAC:19642660)
MGLCFSSAAKSSGHNRSSRNPHPHPPLTVVKSRPPRSPCSFMAVTIQKDHRTQPRRNATAKKTPTRHTPPHGKVREKVISNNGRRHGETIPYGKRVDFGY
AKDFDHRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGGELLDRILA
RKDSRYSERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVIS
YILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKFSRLKQFA
LRALATTLDEEELADLRDQFDAIDVDKNGVISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFGEFVAAALHVNQLEEHDSEKWQQRSRAAFE
KFDIDGDGFITAEELRMHTGLKGSIEPLLEEADIDNDGKISLQEFRRLLRTASIKSRNVRSPPGYLISRKV*
>AT4G36070 Org_Athaliana peptide: AT4G36070.2 calcium-dependent protein kinase 18 (PAC:19645425)
MGLCFSSPKATRRGTGSRNPNPDSPTQGKASEKVSNKNKKNTKKIQLRHQGGIPYGKRIDFGYAKDFDNRYTIGKLLGHGQFGFTYVATDNNNGNRVAVK
RIDKAKMTQPIEVEDVKREVKILQALGGHENVVGFHNAFEDKTYIYIVMELCDGGELLDRILAKKDSRYTEKDAAVVVRQMLKVAAECHLRGLVHRDMKP
ENFLFKSTEEGSSLKATDFGLSDFIKPGVKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTQDGIFNEVMRKKPDFREVPWPTI
SNGAKDFVKKLLVKEPRARLTAAQALSHSWVKEGGEASEVPIDISVLNNMRQFVKFSRLKQIALRALAKTINEDELDDLRDQFDAIDIDKNGSISLEEMR
QALAKDVPWKLKDARVAEILQANDSNTDGLVDFTEFVVAALHVNQLEEHDSEKWQQRSRAAFDKFDIDGDGFITPEELRLQTGLKGSIEPLLEEADVDED
GRISINEFRRLLRSASLKSKNVKSPPGTEHIICHNLLDGICIEDTEERTSAVRFEYVSQVL*
>AT5G66210 Org_Athaliana peptide: AT5G66210.2 calcium-dependent protein kinase 28 (PAC:19666939)
MGVCFSAIRVTGASSSRRSSQTKSKAAPTPIDTKASTKRRTGSIPCGKRTDFGYSKDFHDHYTIGKLLGHGQFGYTYVAIHRPNGDRVAVKRLDKSKMVL
PIAVEDVKREVQILIALSGHENVVQFHNAFEDDDYVYIVMELCEGGELLDRILSKKGNRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMKPENFLFKSAQ
LDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFSRKPWATISDSAKDFVK
KLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEEMRQALAKDLPW
KLKDSRVAEILEAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDLDKDGYITPEELRMHTGLRGSIDPLLDEADIDRDGKISLHEFR
RLLRTASISSQRAPSPAGHRNLR*
>Bol012461 Org_Boleraceacapitata peptide: Bol012461 (1 of 2) PF13202//PF13499//PF14531 - EF hand (EF-
hand_5) // EF-hand domain pair (EF-hand_7)  // Kinase-like (Kinase-like) (PAC:37347443)
MGLCFSSAKVSGRRNHSPRSPNPNPLTVAKHRPPQTPCSFLAVTIQKDHRTQPRRSPATTKKTPPQTQTQTRQTPPHGKGREKGGNNNNNNNTNKGKRHG
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EAIPYGKRVDFGYAKDFDNRYTIGKLLGYGQFGYTYVATDKKTGDRVAVKKIDKAKMRIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIAME
LCEGGELLDRILAKKESRYSERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRS
GPESDVWSIGVISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTVSNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNM
RQFVKFSRLKQFALRALATTLDEEESADLRDQFDAIDVDKNGAISLDEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFEEFVAAALHVNQLEEHD
SEKWQQRSRAAFEKFDIDGDGFITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLLRTASIKSRNVRNPPGYLVSRKV*
>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)
MGLCFSSPKTTGHGTNHPNPNTPTDIPKPQPQAKGREKVCNKNKKKTKNNKIQWRHVGGNPFGKRIDFGYARDFDNRYIIGKLLGHGQFGFTYAATDNNN
GDRVAVKRLDKAKMTQPIEIEDVKREVKILQALGGHENVVGFHNVFEDKSYVYIVMELCEGGELLDRILSKKDSRYTEKDAAVVVRQMLKVAAECHLRGL
VHRDMKPENFLFKSTGEDSSLKATDFGLSDFIKPGMKFKDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTQNGIFNEVMRKEPDFK
TNPWPTISDGAKDFVKKLLVKEPRARLTAAQALSHSWVREGGEASEIPLDISVLENMRQFVKFSRLKQIALKALATTIDEDELDDLRDQFDAIDIDKNGS
ISLEEMRQALAKDLPWKLKDARVAEILQAIDSNTDGLVDFTEFVVATLHVNQLEEHDSDKWEQRSRAAFEKFDVDRDGFITPEELRLQTGLKGSIEPLLE
EADVDEDGRISIHEFRRLLRSASLKPRTVKSPPGYQLSRKM*
>Bol019292 Org_Boleraceacapitata peptide: Bol019292 (1 of 1) PF13499//PF14531 - EF-hand domain pair
(EF-hand_7) // Kinase-like (Kinase-like) (PAC:37350374)
MGLCFSDIRVTGTSSSSSRRSSSQTNNNNNNKKNPKSNKTRPPPPENNNDKPSTTTTKRRTGSVPCGKRTEFGYAKDFHDQYSIGKLLGHGQFGYTYVAI
HKSNGDRVAVKRLDKSKMVLPVAVEDVKREVQILKALSGHENVVQFYNAFDDDDYVYIVMELCEGGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECH
LHGLVHRDMKPENFLFKSAKLDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNK
PDFRRKPWSTISDSAKDFIKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVD
KNGVISLEEMRQALAKDLPWKLKESRVAEILEAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDIDKDGYITPEELRMHTGLRGSID
PLLDEADIDRDGKISLHEFRRLLRTASISSPRVPSTAGHRIPR*
>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)
MGVCFSAIRVTGASSSRQTNNNNKAHKKGCKKPPENKPSTTTTTNAKRRATGSVPCGKRTDFGYAKDFHEQYTIGKLLGHGQFGYTYVAIDKANGDRVAV
KRLDKSKMVLPIAVEDVKREVEILKALSGHENVVQFYNAFDDDDYVYIVMELCEGGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMK
PENFLFKSTQLDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRRKPWST
ISESAKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDALAKDLPWKLKD
SRVAEILQAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDEADIDRDGKISLHEFRRLLR
TASISSQRVVSPGGRHRNPR*
>Bol041462 Org_Boleraceacapitata peptide: Bol041462 (1 of 1) PF13202//PF13833//PF14531 - EF hand (EF-
hand_5) // EF-hand domain pair (EF-hand_8)  // Kinase-like (Kinase-like) (PAC:37361599)
MGLCFSSAKVSGRQHRSPRSPNPPHHPLAVAKPRAPQTPCSFLAVTIQKDHKAQPRRNAATTTNKKTPPQTQTRQTPTHGKVREKAKRHGEKIPYGKRVD
FGYAKDFDNRYTIGKLLGHGQFGYTYVATDKRTGDRVAVKKIDKAKMTRPIAVEDVRREVKILQALTGHENVVRFYNAFEDKNSVYIAMELCEGGELLDR
ILSKKDSHYTERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSVLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIG
VISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDATEIPIDISVLSNMRQFVKFSRLK
QFALRALATTLDEEELADLRDQFGAMDADKNGAISLDEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFEEFVAAALHVNQLEEHDSEKWQQRSRA
AFEKFDIDGDGFITAEELRMHTGLKGSIEPLLEEADIDHDGKISLHEFRRLLKTASIKSRNVRNPPGYLISRKA*
>Bostr.0568s0032 Org_Bstricta peptide: Bostr.0568s0032.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:30669325)
MGLCLSSIRVTGASSSRRSSQTNNHNHKGCKKAVPNPKDIDTKRRTDSSIPCGKRTDFGYAKDFHDQYSIGKLLGHGQFGYTYVAIDKANGDRVAVKRLD
KSKMVLPIAVEDVKREVQILKALSGHENVVQFYNAFEDDNYVYIAMELCEGGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMKPENF
LFKSAKLDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRRKPWSTISDS
AKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEEMRQAL
AKDLPWKLKDSRVAEILQAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDEADIDRDGKI
SLHEFRRLLRTASISSQRVSSPSGHRNPR*
>Bostr.18351s0257 Org_Bstricta peptide: Bostr.18351s0257.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:30676600)
MGLCFSSAAKASGHNHSRRNPIPHPPLTVAKPRPPQTPCSFMAVTIQKDHRTQPRRNAAKKTPTWQTPPHGRERDKVSSNNNNNNNNGRRHGEAIPYGKR
IDFGYAKDFDHRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGGELL
DRILARKDSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWS
IGVISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKFSR
LKQFALRALATTLDEEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFTEFVAAALHVNQLEEHDSEKWQQRS
RAAFEKFDIDGDGYITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLLRTASIKSRNVRSPPGYLISRKV*
>Bradi1g52567 Org_Bdistachyon peptide: Bradi1g52567.1.p (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32792415)
MGLCSSSSAASPADPAGGNGNKEKGRKGSGSRGIVACGKRTDFGYDKDFEARYTIGKLLGHGQFGYTFAAVDRYSDERVAVKRIDKNKMVLPVAVEDVKR
EVKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSSKEGSPLKATD
FGLSDFIRAGKQFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWTNITPSAKDFVQKLLVKDPRA
RLTAAQALSHEWVREGGQASEIPLDISVLHNMRQFVKYSRFKQFALRALASTLNSEELSDLRDQFNAIDIDKSGTISLEELKQALAKDVPWRLKGPRVLE
IVEAIDSNTDGLVDFEEFVAATLHVHQLVEHDSEKWKSLSQAAFDKFDVDGDGYITSDELRMNTGLKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMS
SRNATPKSVSKSYRFA*
>Bradi3g02600 Org_Bdistachyon peptide: Bradi3g02600.2.p CAMK_CAMK_like.26 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed, subfamily CAMK_like(CAMK_1) (PAC:32812227)
MGGCFSTNTPATPAAERRRRRRRRQRAASPEKGSGGGAEGVARVVEFGYERDFEGRYEVGRLLGHGQFGYTFAATDRGSGDRVAVKRIDKAKMNRPVAVE
DVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTKEDSPL
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KATDFGLSDFINPGKKFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWPSISTSAKDFVKRLLVK
NPRARLTAAQALSHPWVREGGDASEIPVDISVLYNMRQFVKYSRFKQFALRALASTVNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLPWRLKGP
RVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGLRCQAAFSKFDLDGDGYITPDELRMHTGLKGSIEPLLEEADIDKDGRISLSEFRKLLRT
ASMSNLPSPTGVPNPQAL*
>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)
MGLCFSSAKVSGRRNHSPRSPNPNPLTVAKHRPPQTPCSFLAVTIQKDHRTQPRRSPATTKKTPPQTQTQTRQTPPHGKGREKAGNNNNNNNKGKRHGEA
IPYGKRVDFGYAKDFDNRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIAMELC
EGGELLDRILAKKESRYSERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTDEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGP
ESDVWSIGVISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTVSNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQ
FVKFSRLKQFALRALATTLDEEESADLRDQFDAIDVDKNGAISLDEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFEEFVAAALHVNQLEEHDSE
KWQQRSRAAFEKFDIDGDGFITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLLRTASIKSRNVRNPPGYLVSRKV*
>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)
MGLCFSSAKVSGRQHRSPRSPNPPHHPLTVAKPKPPQTPCSFLAVTIQKDHKAQQRRNAATTTNKKTPPTRQTPTHGKAREKAKRHGEKIPYGKRVDFGY
AKDFDNRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTLPIAVEDVRREVKILQALTGHENVVRFYNAFEDKNSVYIAMELCEGGELLDRILA
KKDSHYTERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEDSALKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVIS
YILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDATEIPIDISVLSNMRQFVKFSRLKQFA
LRALATTLDEEELADLRDQFGAMDADKNGAISLDEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFEEFVAAALHVNQLEEHDSEKWQQRSRAAFE
KFDIDGDGFITAEELRMHTGLKGSIEPLLEEADIDHDGKISLHEFRRLLKTASIKSRNVRNPPGYLISRKT*
>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)
MGVCFSAIRVTGASSSRQTNNNKAHKGCKKPPENKPSTNTKRRATGSVPCGKRTDFGYAKDFHEQYTIGKLLGHGQFGYTYVAIDKSNGDRVAVKRLDKS
KMVLPIAVEDVKREVEILKALSGHENVVQFYNAFDDDDYVYIVMELCEGGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVHRDMKPENFLF
KSTQLDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRRKPWSTISDSAK
DFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEEMRQALAK
DLPWKLKDSRVAEILQAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDEADIDRDGKISL
HEFRRLLRTASISSQRVISPAGHRNPR*
>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)
MGVCFSAIRVTGTSSSRRSSSQTNNNNKKNPKSNNKTPPPENNNNKPSTTTTKRRTGSVPCGKRTEFGYAKDFHEQYSIGKLLGHGQFGYTYVAIHKSNG
DRVAVKRLDKSKMVLPVAVEDVKREVQILKALSGHENVVQFYNAFDDDDYVYIVMELCEGGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLV
HRDMKPENFLFKSAKLDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRR
KPWSTISDSAKDFIKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVI
SLEEMRQALAKDLPWKLKESRVAEILEAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDE
ADIDRDGKISLHEFRRLLRTASISSPRVASTAGHRIPR*
>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)
MGLCFSSPKATRHGTNHPNPNPPPDIPKPQSQGKGREKVCNQNKKKTTKNNKIQWRHVGGTLFGKRIDFGYARDFDNRYTIGKLLGHGQFGFTYAATDNN
NEDRVAVKRIDKAKMTQPIEIEDVKREVKILQALGGHENVVGFHNVFEDKNYVYIVMELCEGGELLDRILSKKDSRYTEKDAAVVVRQMLKVAAECHLRG
LVHRDMKPENFLFKSTEENSSLKATDFGLSDFIKPGMKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTQNGIFNEVMRKKPDF
ETTPWPTISDGAKDFVKKLLVKEPRARLTAAQALSHSWVREGGEASEIPIDISVLENMRQFVKFSRLKQIALKALATTIDEDELDDLRDQFDAIDIDKNG
SISLEEMRQALAKDLPWKLKDARVAEILQAIDSNTDGLVDFTEFVVATLHVNQLEEHDSDKWEQRSRAAFEKFDVDRDGFITPEELRLQTGLKGSIEPLL
EEADIDEDGRISIHEFRRLLRSASLKPRTVKSPPGYQLSRKM*
>Brast04G317700 Org_Bstacei peptide: Brast04G317700.1.p (1 of 1) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32863370)
MGGCFSTSASATPAAERRRRRRQQRAASPEKGSGGAEGVAPRVVEFGYERDFEGRYEVGRLLGHGQFGYTFAATDRGSGDRVAVKRIDKAKMNRPVAVED
VKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTKEDSPLK
ATDFGLSDFIKPGKKFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWPSISTSAKDFVKRLLVKN
PRARLTAAQALSHPWVREGGDASEIPVDISVLYNMRQFVKYSRFKQFALRALASTVNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLPWRLKGPR
VLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGLRCQAAFSKFDLDGDGYITPDELRMVQHTGLKGSIEPLLEEADIDKDGKISLSEFRKLLR
TASMSNLPSPTGVPNPQAL*
>Brast06G146700 Org_Bstacei peptide: Brast06G146700.1.p (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32852110)
MGLCSSSSAARPADPAGSNGNKEKGRKGSGGRGLVACGKRTDFGYDKDFEARYTIGKLLGHGQFGYTFAAVDRYSDERVAVKRIDKNKMVLPVAVEDVKR
EVKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSSKEGSPLKATD
FGLSDFIRAGKQFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWTNITPSAKDFVQKLLVKDPRA
RLTAAQALSHEWVREGGQASEIPLDISVLHNMRQFVKYSRFKQFALRALASTLNSEELSDLHDQFNAIDIDKSGTISLEELKQALAKDVPWRLKGPRVLE
IVEAIDSNTDGLVDFEEFVAATLHVHQLVEHDSEKWKSLSQAAFDKFDVDGDGYITSDELRMNSGLKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMS
SRNATPKSVSKS*
>Cagra.10427s0030 Org_Cgrandiflora peptide: Cagra.10427s0030.1.p (1 of 3) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:28917453)
MGVCFSAIRVTGASSSRRSSQTTTNHNRTKGCQKKKKAASPCPNPKAIDAKRSRTGSIPCGKRTDFGYPKDFHDQYSIGKLLGHGQFGYTYVAIDKSNGD
RVAVKRLDKSKMVLPIAVEDVKREVQILQALSGHENVVQFHNAFEDDDYVYIAMELCEGGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVH
RDMKPENFLFKSDKLDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLKNKPDFRRK
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PWSTISDSAKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVIS
LEEMRQALAKDLPWKLKDSRVSEILQAIDSNTDGLVEFTEFVAAALHVHQLEEHDSEKWQQRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDEA
DIDRDGKISLHEFRRLLRTASISSQRVSSPSGRHRNPR*
>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)
MGLCCSSPKATRHGTSPRNPNGHSPTQGKANEKVSNKNGKKTKNKNKIQRRQGGRTPYGKRIDFGYAKDFDNRYTIGKLLGHGQFGFTYVATDNNNGNSV
AVKRIDKAKMSLPIEVEDVKREVKILQALGGHENVVGFHNAFDDKNYVYIVMELCEGGELLDRILGKKDSRYTEKDAAVVVRQMLKVAAECHLRGLVHRD
MKPENFLFKSTEEDSSLKATDFGLSDFIKPGTKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTQDGIFNEVMRKKPDFKTVPW
PTISNSAKDFVKKLLVKEPCARLTAAQALSHPWVREGGEASEIPIDISVLNNMRQFVKFSRLKQIALRALATTIDEDELDDLRDQFDAIDIDKNGSISLE
EMRQALAKDVPWKLKDARVAEILQAIDSNTDGLVDFTEFVVATLHVNQLEEHDSEKWQQRSRAAFDKFDIDRDGFITPEELRLQTGLKGSIEPLLEEADV
DEDGRLSIHEFRRLLRSASIKSRNTKSPPGYQLSRKM*
>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)
MGLCFSSAAKATGHNRSGRNPVPHPPLTVAKHRPPQSPCSFMAVTIQKDHHRTQPRRKKTPTRQTPPHGRGREKVISNNNNNNNKRHGEAVIIPYGKRVD
FGYAKDFDHRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGGELLDR
ILARKDSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTDEDSALKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIG
VISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKFSRLK
QFALRALATTLDEEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFSEFVAAALHVNQLEEHDSEKWQQRSRA
AFEKFDIDGDGYITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLLRTASIKSRNVRSPPGYLISRKV*
>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)
MGLCCSSPKATRHGTSPRNPNGHSLTQGKANEKVSNKNGKKTKNKNKIQRRRGGRTPYGKRIDFGYAKDFDNRYTIGKLLGHGQFGFTYVATDNNNGNSV
AVKRIDKAKMSLPIEVEDVKREVKILQALGGHENVVGFHNAFDDKNYVYIVMELCEGGELLDRILGKKDSRYTEKDAAVVVRQMLKVAAECHLRGLVHRD
MKPENFLFKSTEEDSSLKATDFGLSDFIKPGTKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTQDGIFNEVMRKKPDFKTVPW
PTISNSAKDFVKKLLVKEPCARLTAAQALSHPWVREGGEASEIPIDISVLNNMRQFVKFSRLKQIALRALATTIDEDELDDLRDQFDAIDIDKNGSISLE
EMRQALAKDVPWKLKDARVAEILQAIDSNTDGLVDFTEFVVATLHVNQLEEHDSEKWQQRSRAAFDKFDIDRDGFITPEELRLQTGLKGSIEPLLEEADV
DEDGRLSIHEFRRLLRSASIKSRNIKSPPGYQLFRKM*
>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)
MGLCFSSAAKATGHNRSGRNPVPHPPPPLTVAKHRPPQSPCSFMAVTIQKDHHRTQPRRKKTPTRQTPPHGRGREKVISNNNNNNKRHGEAVIIPYGKRV
DFGYAKDFDHRYTIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGGELLD
RILARKDSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTDEDSALKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSI
GVISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKFSRL
KQFALRALATTLDEEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFSEFVAAALHVNQLEEHDSEKWQQRSR
AAFEKFDIDGDGYITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLLRTASIKSRNVRSPPGYLISRKV*
>Carubv10028399m.g Org_Crubella peptide: Carubv10028399m (1 of 3) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:20911700)
MGVCFSAIRVTGASSSRRSSQTTTNHNRTKGCQKKKKAASPCPNPKAIDAKRSRTGSIPCGKRTDFGYPKDFHDQYSIGKLLGHGQFGYTYVAIDKSNGD
RVAVKRLDKSKMVLPIAVEDVKREVQILQALSGHENVVQFHNAFEDDDYVYIAMELCEGGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVH
RDMKPENFLFKSDKLDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLKNKPDFRRK
PWSTISDSAKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVIS
LEEMRQALAKDLPWKLKDSRVSEILQAIDSNTDGLVEFTEFVAAALHVHQLEEHDSEKWQQRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDEA
DIDRDGKISLHEFRRLLRTASISSQRVSSPSGRHRNPR*
>Ciclev10025251m.g Org_Cclementina peptide: Ciclev10025251m (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:20800576)
MGICLSTTKVSGSNSGSNNNNANHHRNANKEEAKRRHNRHARNDTTHKHQHQHQERAKNYQQLKTKQHQKTNSRRQTGVIPCGKRTDFGYDKDFDRRYTI
GKLLGHGQFGYTYVATDKANGDRVAVKKIEKNKMILPIAVEDVKREVKILQALAGHENVVKFYNAFEDDNYVYIAMELCEGGELLDRILAKMISITLTSA
WFLAIRKDSRYTEKDAAVVVRQMLRVAAECHLHGLVHRDMKPENFLFKSAKEDSSLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLKRKSGPESDVWS
IGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPSISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKYSR
LKQFALRALASTLDDEELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDCNTDGLVDFSEFVAATLHVHQLEEHDSEKWHLRS
QAAFEKFDIDRDGFITPEELRMHTGLKGSIDPLLEEADIDKDGRISLSEFRRLLRTASISSRNVPPSPSGHRNPRKL*
>DCAR_016603 Org_Dcarota peptide: DCAR_016603 hypothetical protein (PAC:36076972)
MGSCFSTKKITGSSSNTTNTNTHVKKPASSATSTSATTKLTYRNNNNKNKNKNDNDHRNQQLIRHRDKASSRKQNGVIPCGKRTDFGYDKDFDLRYSIGK
LLGHGQFGYTYVAVDRSNGDRVAVKKIDKNKMILPIAVEDVKREVRILKALSGHENVVQFYNAFEDDSYVYIAMELCEGGELLDRILAKKSSRYTEKDAA
RVVRQMLKVAAECHLHGLVHRDMKPENFLFKSPKDDSALKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWD
KTEDGIFKEVLRNKPDFRRKPWPTISNGAKDFVKKLLVKEPRARYTAAQALSHPWVREGGNALEIPLDISVLYNMRQFVKYSRLKQFALRALASTLDEEE
LADLRDQFHAIDVDKNGAISLEEMRQALAKDIPWKVKESRVLEILQAMDSNTDGLVDFHEFVAATLHVHQLEEHNSEKWQQISHAAFEKFDVDKDGYITA
EELKMHTGLRGSIDPLLEEADIDKDGKISLSEFRKLLRTASMGTRNVNSPAAHRGSRRQ*
>DCAR_021501 Org_Dcarota peptide: DCAR_021501 hypothetical protein (PAC:36084600)
MGKLLGHGQYGYTYVATDNSNGDRVAVKKIDKNKMILPIAVEGVKREVRIMKALSGHENVVQFHNSFEDDSYVYIAMELCEGGELLDRILAKKSSRYTEK
DAAAVARQMLKVAAECHLHGLVHRDMKPENFLFKSPEEDSTLKVTDFGLSDFIRPGNKFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRP
FWDETEDGIFKEVLRKKPDFCRKPWPTISDDAKDFVNKLLVKEPRARYTAAQALSHPWVREGGNALEIPLDISVLYNMRQFVKYSRLKQLALQALASTLD
EEELADLRDQFLAIDVDKNGTISLEEMRQALAKDIPWKVKESRVLEILQAMDSNTDGLIDFHEFVAATLHVHQLEEHNSVKWQQISHAAFEKFDVDKDGY
ITAEELRMEQVELSV*
>Eucgr.I02347 Org_Egrandis peptide: Eucgr.I02347.1.p (1 of 1) PF07714//PF13202//PF13499 - Protein
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tyrosine kinase (Pkinase_Tyr) // EF hand (EF-hand_5)  // EF-hand domain pair (EF-hand_7) (PAC:32064182)
MGICASSAARRAGGSAGASTRRNGNRRRERDQDGAGEANRKRKDDRQAKEGGGGGGGGNGKQGGGAVPCGKRADFGYARDFAERYSLGKLLGHGQFGYTY
VAVDKVNGDRVAVKRIDKSKMVLPIAVEDVKREVKILRALTGHENVVQFYDAFEDDSYVYIAMEYCEGGELLDRILAKKDSRYTEKDAAVVVRQMLRVAA
ECHLHGLVHRDMKPENFLFKSSKEDSPLKAIDFGLSDFINPGKRFLDIVGSAYYVAPEVLKRKSGPESDVWSIGVITFILLCGRRPFWDKTEDGIFKEVL
KKKPDFRRRPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGNASDIPIDISVLNNMRQFVKYGRLKQFALRALASTLDGEELADLKDQFAAI
DVDKNGSISLEEMREALAQDLPWKMKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQMEEHDSEKWQLRSQAAFEKFDIDRDGYITPEELRLQTGLKG
SLGPLLEEADIDKDGKISLSEFRKLLRTASMGSQNLPSSSGYRNLRKI*
>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)
MGLCISTTRVSGSSSNAAAAANQKRHEIGRPQAGAAGGTAGANEKNKQKVRGEGGKKKKGSGVIPCGKRTDFGYAKDFDRRYTIGKLLGHGQFGYTYVAT
DKANGDRVAVKRIEKNKMVLPIAVEDVKREVKILQALTGHENVVQFYNAFEDDSYVYIVMELCEGGELLDRILSKKDSRYTEKDAAVVVRQMLKVAAQCH
LHGLVHRDMKPENFLFKSKKDDSSLKATDFGLSDFIKPGKKFPDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKSK
PDFRRRPWPSISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGSASEIPIDISVLHNMRQFVKYNRFKQFALRALASTLDEEELADLKDQFDAIDVD
KNGSISLEEMRQALAKDLPWKLKEPRVLEILQAIDSNTDGLVDFHEFVAATVHVNQLEEHNSEKWLRRSQSAFEKFDLDGDGYITPEELRMHTGLRGSID
PLLEEADIDKDGRISLSEFRRLLRTASMSSKTVSSPSNFRNSRKM*
>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)
MGTCLSTTKVSGANSNNTATTTTNVHHNRKRATKPQSTTAAATATTTTTTTTNQKEQGSQNHHHHANKTQNQRNSQQLKAKEKTGSRRPGGVIPCGKRTD
FGYAKDFDKRYAIGKLLGHGQFGYTYVATDKVNGDRVAVKRIEKSKMVLPIAVEDVKREVKILQALTGHENVVQFYNAFEDENYVYIVMELCEGGELLDR
ILAKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPTISNAAKDFVKKLLVKDPRARLTAAQAL
SHPWVREGGEASEIPIDISVLNNMRQFVKYSRLKQFALRALASTLDDEELADLRDQFAAIDVDKNGSISLEEMRQALAKDLPWKLKDSRVLEILQAIDCN
TDGLVDFTEFVAAALHVHQLEEHDSEKWQHRSRAAFEKFDIDRDGYITPEELRLHTGLKGSIDPLLEEADIDKDGKISLSEFRRLLRTASIGSRNIPSPT
GQRIPRKI*
>Glyma.01G166100 Org_Gmax peptide: Glyma.01G166100.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:30544862)
MGLCFSSTKVSGSSSNNNNNNNASSNRNRKCSAAPAAAAPPEPVTPQKKQPSQAQRRRVPEESRKNPRAKDKAGARRQGTRVPCGKRTDFGYEKDFENRF
SLGKLLGHGQFGYTYVGIDKKNGDRVAVKRLEKSKMVLPIAVEDVKREVKILKELTGHENVVQFFNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYTE
KDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGKRFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRR
PFWDKTEDGIFKEVLRNKPDFRRKPWPTISNAAKDFMKKLLVKDPRARYTAAQALSHPWVREGGEALEIPIDISVLNNMRQFVKYSRLKQFALRALASTL
NEGELSDLKDQFDAIDVDKNGSISLEEMRQALAKDQPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSDKWQQRSQAAFEKFDLDKDG
YITPDELRMHTGLRGSIDPLLEEADIDKDGKISLPEFRRLLRTASMGSRTVMSPSHRHHRKI*
>Glyma.02G048300 Org_Gmax peptide: Glyma.02G048300.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:30506592)
MGACFSATKVSGSNGNGVNVNKKRRGTTKKPKSETAKANPQRHKAASSRHVPCGKRTDFGYKKDFNQRYSLGKLLGHGQFGYTYVGIDKANGDRVAVKRL
EKSKMVLPIAVEDVKREVKILKALTGHENVVQFYNAFEDDSYVFIVMELCEGGELLDRILAKKDGRYTEKDSAVVVRQMLKVAAECHLHGLVHRDMKPEN
FLFKSIKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRKSGPQSDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRKKPDFHRKPWPTISN
AAKDFLKRLLVKDPRARLTAAQGLSHPWVREGGEALEIPIDISVLSNMRQFVKYSRMKQFALRTLASTLNEEELADIKDQFDAIDVDKNGSISLEEMRQA
LAKDLPWKLKESRVLEILQAIDSNTDGLVDFREFVAATLHVHQLEEDSDKWQQLSQAAFEKFDIDKDGYITTEELRMHTCLRGSVDPLLEEADIDKDGKI
SLPEFRRLLRTASMSSKNVSSPSVHRRRRF*
>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)
MGICFSATKVSGSSSNNAAASNRNRKGLAAPAPAPPAQPELEPVTGKQKKQPSQAKRRQVPEDSQKNPRSKDKAGARRQGTHVPCGKRTDFGYEKDFENR
FSLGKLLGHGQFGYTYVGIDKTNGDRVAVKRLEKSKMVLPIAVEDVKREVKILKELTGHENVVQFHNAFDDESYVYIVMELCEGGELLDRILAKKDSRYT
EKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGKRFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGR
RPFWDKTEDGIFKEVLRNKPDFRRKPWPTISNAAKDFVKKLLVKDPRARYTAAQALSHPWVREGGEALEIPIDISVLNNMRQFVKYSRLKQFALRALAST
LNEGELSDLKDQFDAIDVDKNGSISLEEMRQALAKDQPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSDKWQQRSQAAFEKFDLDKD
GFITPDELRMHTGLRGSIDPLLEEADIDKDGKISLPEFRRLLRTASMGSRPIMSPSHRHRKI*
>Glyma.16G128600 Org_Gmax peptide: Glyma.16G128600.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:30560415)
MGTCFSATKVSGSHGNAVTVNKNRKGAAKPKSETATANPLRHKASSRHVPCGKRTDFGYEKDFDQRYSLGKLLGHGQFGYTYVGIDKANGDRVAVKRLEK
SKMVLPIAVEDVKREVKILKALTGHENVVQFYNAFEDGSYVYIVMELCEGGELLDRILAKKDSRYTERDAAVVVRQMLKVAAECHLHGLVHRDMKPENFL
FKSTKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRKSGPQSDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRKKPDFRRKPWPTISNAA
KDFVKKLLVKDPRARLTAAQALSHPWVREGGEALEIPIDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADIKDQFDAIDVDKNGSISLEEMRQALA
KDLPWKLKESRVLEILQAIDNNTDGLVDFREFVAATLHVHQLEEDSDKWQQLSQAAFEKFDLDKDGYITPEELRMHTCLRGSVDPLLEEADIDKDGKISL
PEFRRLLRTASMGSQNVSSPSVHRRQRF*
>Gorai.003G009500 Org_Graimondii peptide: Gorai.003G009500.1 (1 of 3) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:26798333)
MGACLSATKVSGGSSGNTTAHHRKTATNAEKQSQKPNNQQVRCSQPLKNKQKPEKQSGIIPWGKRTDFGYDKDFDQRYTIGKLLGHGQFGYTYVAIDKVN
GDRVAVKKIDKNKMILPIAVEDVKREVKILKALKGHENVVQFYNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAECHLHGL
VHRDMKPENFLFKSTRPDSPLKATDFGLSDFIKPGKRFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGKRPFWDKTEDGIFKEVLKNKPDFR
RKPWPTISDDAKDFLKKMLVKDPRARLTAAQALSHQWVREGGNASDIPVDISILSNLRQFVKYSRLKQFALRALASTLNEEEIADLRDQFDAIDVDKSGS
ISLEEMRQALAKDLPWKLKDSRVLEILQAIDSNTDGLVDFTEFVAAALHVNQMEEHDCDKWQMRLQAAFEKFDVDRDGYITPEELRMHTGLRGSIDPLLE
EADIDKDGKISLSEFRRLLRTASMGSRNVSSPSGNRNTQKL*
>Gorai.007G194500 Org_Graimondii peptide: Gorai.007G194500.1 (1 of 3) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:26781420)
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MGACLSTTKVIGSSSNAAAHHRKHQPSATTVTVNEKKESRKPNNQQGQRQQVRSSQPLKVKGKPSSTRQTGIIPCGKRTDFGYHKDFDQRYTIGKLLGHG
QFGYTYVAIDKANGDRVAVKKIDKNKMVLPMAVEDVKREVKILEALKGHENVVQFYNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQ
MLKVAAECHLHGLVHRDMKPENFLFKSTREDSLLKATDFGLSDFIRPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGKRPFWDKTEDG
IFKEVLKKKPDFRRKPWPTISNGAKDFVKKLLVKDPHARLTAAQALSHRWVREGGNASDIPVDISVLNNLRQFVKYSRLKQFALRALASTLNEEEIADLR
DQFDAIDVDKNGSISLEEMRQALAKDLPWKMKEPRVLEILQAIDSNTDGLVDFKEFVAAALHVNQMEEHDSDKWQMLSQAAFEKFDVDRDGFITPEELRM
HTGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASISSRNVPCSSDQRNSRKL*
>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)
MGICLSTTKVFGTSSNPSPDHHEEKQPVSPTTTTNAKKESHKPTVKHQQQQFKAKPSSRKQGGNVPCGKRTDFGYRKDFEKRYTTGKLLGHGQFGYTYV
AIGNENGNRVAVKKIEKMKMVLPIAVEDVKREVKILEALKGHENVVQFYNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAE
CHLRGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIRPGKRFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGKRPFWDKTEDGIFREVLK
NKPDFRRKPWPTISDSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLSNMRQFVKYSRLKQFALRALASTLNEEEIADLRDQFHAID
VDKNGVISLEEMRQALAKDLPWKLKESRVLEILQAIDINTDGLVDFTEFIAAALHVNQMEEHDSEKWQMRSEAAFQKFDVDRDGFITPDELRMHTGLKGS
IDPLLEEADIDRDGKISLEEFRRLLRTASISVRPNPSHRTTWKL*
>GRMZM2G053868 Org_Zmays peptide: GRMZM2G053868_P01 (1 of 2) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:31049975)
MGACFSSASAAPAGAAVDERRPSKEGDGKKRRRAAGASPDAAAPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRGSGDRVAVKRIDKAKMTRPVA
VEDVKREVKILKALKGHQNIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSNKEDS
PLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWSSISPGAKDFVKRLL
VKNPRARLTAAQALSHPWVREGGEASDIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELSDLKDQFDAIDIDKSGSISIEEMRHALAKDLPWRLK
GPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCQAAFSKFDLDGDGYITPEELRMVQHTGLKGSIEPLLEEADIDKDGKISLSEFRK
LLRTASMSNVPSPRGPPNPQAL*
>GRMZM2G157068 Org_Zmays peptide: GRMZM2G157068_P01 (1 of 2) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30986103)
MGACFSSASAAPAGAAVDERRPSKEGDGKKRRRAAGASPDAAAPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRGSGDRVAVKRIDKAKMTRPVA
VEDVKREVKILKALKGHQNIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSNKEDS
PLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWSSISPGAKDFVKRLL
VKNPRARLTAAQALSHPWVREGGEASDIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELSDLKDQFDAIDIDKSGSISIEEMRHALAKDLPWRLK
GPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCQAAFSKFDLDGDGYITPEELRMVQHTGLKGSIEPLLEEADIDKDGKISLSEFRK
LLRTASMSNVPSPRGPPNPQAL*
>GRMZM2G365035 Org_Zmays peptide: GRMZM2G365035_P01 (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30965679)
MGLCSSSTAARAASDPGAAAAGDAAAAKKGRGIVACGKRTDFGYDKDFEVRYSLGKLLGHGQFGYTFAAVDRASTERVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSKKEDSPLKATDF
GLSDFIKPGRQFRDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKKKPDFRRKPWSNITSSAKDFVQKLLVKDPRAR
LTAAQALSHDWVREGGKASEIPLDISVLHNMRQFVKYSRFKQFALRALASTLNSEEMSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPRVLEI
IEAIDSNTDGLVDFEEFVAATLHVHQLVEHDTEKWKSLSQAAFDKFDVDRDGYITPDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMSA
RNVQTPRGVRKS*
>GSMUA_Achr1G08900_001 Org_Macuminata 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)
MGACFSADAKIRGGTSSAGTRSSRKQQLQPEQKNKAPTTQPQQKDRGSKRRSSGLVPCGRRTDFGYAKDFDSRYSVGKLLGHGQFGYTFVATENATGERV
AVKRIDKNKMVLPIAVEDVKREVKILQALKGHENVVNFHNAFEDDSYVYIVMELCEGGELLDRILAKKDSHYTEKDAAIVVRQMLKVAAECHLHGLVHRD
MKPENFLFKSSKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRRKPW
PTISNSAKEFVKKLLVKDPRVRLTAAQALSHPWVREGGNASEIPLDISVLANMRKFVKYSRLKQFALRAIASTLDEDELADLKDQFQAIDIDKSGSISLD
EMRQALAKDIPWRLKGPRDLDILQAIDSNTDGLVDFTEFVAATLHVHQMEEHDSEKWRSRCKAAFEKFDVDRDGYITPEELRMHTGLKGSIEPLLEEADI
DKDGKISLSEFRKLLRTASMSSNVPSPSGVRNPQKF*
>GSMUA_Achr2G00480_001 Org_Macuminata 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)
MILPVAVEDVKREVKILQALKGHENVVNFHNAYEDDSYVYIVMELCEGGELLDRILAKKDSRYTEKDAAIVVRQMLKVAAECHLHGLVHRDMKPENFLFK
STEENSPLKATDFGLSDFIEPGKKFHAIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFREVLRNKPDFRRKPWPSISNSAKD
FVKKLLVKDPHVRLTAAQALSHPWVREGGNALEIPLDISVLSNMCQFVKYSRVRTLADSKLGIDLFRRSTSLELYRGSSLQVAAQRLQKRFIYCL*
>GSMUA_Achr5G18720_001 Org_Macuminata peptide: GSMUA_Achr5P18720_001 (1 of 1) PF13499//PF14531 - EF-
hand domain pair (EF-hand_7) // Kinase-like (Kinase-like) (PAC:32326160)
MGACLSSATQVSSRNKATAVAAAAAAAEGKHGQPGAKNEQQKQKPRARNCGKLKAVARLSCGRRTNFGYERDFERRYSIGKLLGHGQFGYTFVATDKANG
DRVAVKRIDKNKMILPVAVEDVKREVKILKALKGHENVVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKESRYTEKDAAVVVRQMLKVAAECHLHGLV
HRDMKPENFLFKSTKEDCPLKATDFGLSDFIRPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIYKEVLRTEPDFRR
KPWPNISESAKDFVKKLLVKDPRARLTAAQALSHPWAREGGDALEIPLDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADLKDQFHAIDVDKSGAI
SLEEMRHALAKDLPWKLKEPCVSEIVQAMDSNTDGFIDFEEFVAATLHVHQLVEHDNGKWRSLTKAAFDKFDVDKNGYITPDELRMHTGLKGSIDPLLEE
VDIDKDGKISLDEFRRLLKTASMKPRSVPRQSTTRDRRNTCFFTKQVFVLFFLLFQALIISQSLSHN*
>GSMUA_Achr8G19290_001 Org_Macuminata peptide: GSMUA_Achr8P19290_001 (1 of 4) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:32309843)
MGACISSADPNSDTAAAASTEEQQGRPEANRGQQQQQRVRDGGKEKAAAGGLVPCGRRTNFGYDRDFASKYTIGKLLGHGQFGYTFVATDKAHGDRVAVK
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RIDKNKMILPIAVEDVKREVMILKALKGHENVVHFYNAYEDDSFVYIAMELCEGGELLDRILAKKNSRYTEKDAAVVVRQMLKVAAECHLHGLVHRDMKP
ENFLFKSTKEDSPLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRTSGPESDVWSIGVITYILLCGKRPFWNRTENGIFKEVLKTEPDFQRKPWPSI
SNSAKDFVKKLLVKDPRVRLTAAQALSHSWVREGGDALEIPLDISVLSNMRQFVKYSRFKQFALRALATTLNEEELADLKDQFDAIDVDKSGAISLEEMR
HALAKDLPWKSKESHVLEILQAMDSNTDGLIDFEEFVAAALHMHQLVELDSEKWRSLSQAAFDKFDVDRDGYITPEELRMHTGLKGSIDPLLEEVDIDKD
GKISLDEFRRLLKTASMGSRNVPNRSTGH*
>GSVIVG01018778001 Org_Vvinifera peptide: GSVIVT01018778001 (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:17828604)
MGACLSATKVRSSNSNTTANAAATKNTRPRGSSKTSNKNQQKKPQEGDRNRSNQQHRNPQPQKVKDRANGRRGTGIIPCGKRTDFGYAKDFDARYTIGKL
LGHGQFGYTYVATDKANGDRVAVKRIEKNKMILPIAVEDVKREVKILEALTGHENVVQFHNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAK
VVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYILLCGKRPFWDK
TEDGIFKEVLKNKPDFRRKPWPTISNGAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLSNMREFVKYSHLKQFALRALASTLDDEEL
ADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSDKWRQRSQAAFDKFDVDRDGFITPE
ELKLHTGLRGSIDPLLEEADIDKDGRISLAEFRRLLRTASISSRQVPSSSGFRNPRKI*
>Kaladp0028s0017 Org_Kfedtschenkoi peptide: Kaladp0028s0017.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:35759078)
MGVCFSATKISGSSSNGNRKSRRAAQQQPASTAPGRHKDKPRGDAEGRGRRDVGRMVPCGKRTDFGYLKNFDERYKIGKLLGHGQFGYTYVATDKSNGDR
VAVKRIDKSKMVLPIAVEDVKREVKILQALTGHENVVQFYNAFEDDNYVYIAMELCEGGELLDRILAKKDSRYTEKDAAIIVRQMLKVAAQCHLHGLVHR
DMKPENFLFKSTKEDSPLKATDFGLSDFIRPGRKFHDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKP
WANISNSAKDFVKKLLVKDPRARLTAAQALSHSWVREGGSASEIPVDISVLNNMRQFVKYSRMKQIALRALASTLDEEEIADLRDQFDAIDVDGNGSISL
EEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHNSDKWQQRSQAAFEKFDVDRDGFITPEELKLHTGLKGSIDPLLEEAD
IDKDGKISLPEFRRLLRTASISSRAITSPRRVPSRNK*
>Kalax.0174s0042 Org_Klaxiflora peptide: Kalax.0174s0042.1.p (1 of 6) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:32567177)
MGVCFSATKISGSSSNGNRKSRRAAQQQPASTAPGRHKDKPRGDAEGRGRRDVGRMVPCGKRTDFGYLKNFDERYKIGKLLGHGQFGYTYVATDKSNGDR
VAVKRIDKSKMVLPIAVEDVKREVKILQALTGHENVVQFYNAFEDDNYVYIAMELCEGGELLDRILAKKDSRYTEKDAAIIVRQMLKVAAQCHLHGLVHR
DMKPENFLFKSTKEDSPLKATDFGLSDFIRPGKKFHDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKP
WANISNSAKDFVKKLLVKDPRARLTAAQALSHSWVREGGSASEIPVDISVLNNMRQFVKYSRMKQIALRALASTLDEEEIADLRDQFDAIDVDGNGSISL
EEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHNSDKWQQRSQAAFEKFDVDRDGFITPEELKLHTGLKGSIDPLLEEAD
IDKDGKISLPEFRRLLRTASISSRAITSPRRVPSRNK*
>LOC_Os02g03410 Org_Osativa peptide: LOC_Os02g03410.1 CAMK_CAMK_like.12 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33137776)
MGACFSSHTATAAADGGSGKRQQRKGDHKGKLPDGGGGEKEKEAARVEFGYERDFEGRYQVGRLLGHGQFGYTFAATDRASGDRVAVKRIDKAKMVRPVA
VEDVKREVKILKELKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDS
PLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWNKTEDGIFREVLRNKPDFRKKPWPGISSGAKDFVKKLL
VKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRFKQFALRALASTLKEEELADLKDQFDAIDVDKSGSISIEEMRHALAKDLPWRLK
GPRVLEIIQAIDSNTDGLVDFEEFVAATLHIHQMAELDSERWGLRCQAAFSKFDLDGDGYITPDELRMVQHTGLKGSIEPLLEEADIDKDGRISLSEFRK
LLRTASMSNLPSPRGPPNPQPL*
>LOC_Os07g22710 Org_Osativa peptide: LOC_Os07g22710.1 CAMK_CAMK_like.32 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33114003)
MGLCSSSSARRDAGTPGGGNGAGNKDNAGRKGIVACGKRTDFGYDKDFEARYALGKLLGHGQFGYTFAAVDRRSSERVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSSLKATDF
GLSDFIRPGKHFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPNITPCAKDFVQKLLVKDPRAR
LTAAQALSHEWVREGGQASDIPLDISVLHNMRQFVKYSRFKQFALRALASTLNAEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPRVLEI
VEAIDSNTDGLVDFEEFVAATLHVHQLVEHDTEKWKSLSQAAFDKFDVDGDGYITSDELRMQTGLKGSIDPLLEEADIDRDGKISLDEFRRLLKTASMSS
RNVQTPRSVHRS*
>Lus10028459.g Org_Lusitatissimum peptide: Lus10028459 (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:23166166)
MGSRRVSGTVPFGKRTDFGYDKDFNKRYTIGKLLGHGQFGYTYVATDKGNGDRVAVKRIDKGKMILPIAVEDVKREVKILRQLAGHENVVHFVNAFEDDS
YVFIVMELCEGGELLDRILAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSALKATDFGLSDYIKPGKKFHDIVGSAYYVAP
EVLQRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPTISHSAKDFIRKLLVKDPRARLTAAQALSHPWVREGGDASEIPID
ISVLKNMRQFVKYSRLKQFALRALASTINEEELADLKDQFDAIDIDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFPEFVAAALHV
HQLQEHNSEKWEERSQAAFDKFDIDGDGYITPDELRMHTGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASMGSRTLPSPSGHRNSRRL*
>Manes.01G145800 Org_Mesculenta peptide: Manes.01G145800.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:32358707)
MGVCFSTIKVSGSSSNNNTTASAGHHYHRKERTDTTQSTTTNKQSSDQKNNKDDNNSTNNGTPESRQLQTKPKQQQRQQQQQQQHKVKEKQTSRRQSGV
IPCGKRTDFGYAKDFDRRYMTGKLLGHGQFGYTYVATDKASGDRVAVKRIEKNKMVLPIAVEDVKREVKILRELAGHENVVQFYDAFEDDSYVYIVMELC
EGGELLDRILAKKDSRYTEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKVDSPLKATDFGLSDFIKPGKKFKDIVGSAYYVAPEVLKRRSGP
ESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPSISNSAKDFVKKLLVKDPRVRLTAAQALSHPWVREGGDASEIPIDISVLSNMRQ
FVKYSRLKQFALRALAGTLDDGELADLRDQFDAIDVDRNGSISLEEMRQALAKDLPWKLKDSRVLEILQAIDSNTDGLVDFSEFVAAALHVHQLEEHNSE
KWHMRSQSAFEKFDLDKDGFITPEELRMHTGLKGSIDPLLEEADIDKDGKISLSEFRRLLRTASISSQNLPSPSAHRNSWKI*
>Manes.02G104800 Org_Mesculenta peptide: Manes.02G104800.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:32333786)
MGACFSTIKISGSNSNSTGAAAAGHHYHRKEITNNPQSTTANRQSSNQKNDNNNNETRKSRQLQTQQQQQQHKIKEKQTSRRQSGMIPCGKRTDFGYAKD
FDRRYVIGKLLGHGQFGYTYVATDKANGDRVAVKRIDKNKMVLPIAVEDVKREVKILQELAGHENVVQFYDAFEDDSYVYIVMELCEGGELLDRILAKKD
SRYTEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLLKSSKENSPLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYIL
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LCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPSISNSAKDFVKKLLVKDPRVRLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKYSRLKQFALRA
LASTLDDAELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKMKDSRVLEILQAIDSNTDGLVDFSEFVAAALHVHQLEEHNSEKWHLRSQTAFEKFD
IDKDGYITPEELRMHTGLKGSIDPLLEEADIDKDGKISLSEFRRLLRTASISSRTAPSPSARRNSRMI*
>Mapoly0098s0040 Org_Mpolymorpha peptide: Mapoly0098s0040.1.p (1 of 1) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:33021029)
MGGCLSAPHPGRARKAKAQQVAGQDSAENSANASAPPQQPKKVTPRKSPTKNNTPKKKTTERKRSRITVNHIKDNTSQASIPLGKRTNFGYEREFKTKYK
LGKLLGHGQFGYTYAAVEISTGLKVAVKTIEKKQMLLPISVDDVKREVEILGTLSGHENVVQFHAAFEDDDLVYIVMELCEGGELLDRILSKKDSRYSEK
DAAKIVRQMLKVAARCHLNGVVHRDMKPENFLFKSQKEDSPLKATDFGLSDYIKIGKRFQDVVGSAYYVAPEVLRRKSGPESDVWSIGVITYILLCGRRP
FWAKEEQGIFNEVLKKKPDFKEKPWPSISASAKDFVKKLLVKDPRARLTASQALSHPWAREGGDASDIPLDISVLSNMREFVKYSRLKQMALKALASTLD
GEEIADLRDQFDAIDMDKNGTITLEEIKQALAKDTPWSVKETRVVEILKAMDSNRDGMVDFDEFVAATLHVHQLEESDTDKWQRRSRAAFEKFDFDKDGF
ITAEELKVVLQATGTKGNMETLLEEADTDGDGRISLPEFQRLLRQASLGSRTNGSGSLQHFHRGK*
>Medtr5g022030 Org_Mtruncatula peptide: Medtr5g022030.1 (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:31091524)
MGLCFSSTKVVSGSNSNTTNNDNRKRNQSTTTDTTVTVTTATTAAQKQTAQRRKGGSNETAQKKNHHQHHRLKEKTGSKHVPCGKRTDFGYEKDFDKRFS
LGKLLGHGQFGYTYVGVDKSNGDRVAVKRLEKAKMVLPIAVEDVKREVKILKELTGHENVVQFYNAFDDDSYVYIVMELCEGGELLDRILNKKDSRYTEK
DAAVVVRQMLKVAAQCHLHGLVHRDMKPENFLFKSNKEDSALKATDFGLSDFIKPGKRFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRP
FWDKTEDGIFKEVLRNKPDFRRKPWPTISNAAKDFVKKLLVKDPRARLTAAQALSHPWVREGGEASEIPIDISVLNNMRQFVKYSRLKQFALRALASTLN
EGELSDLKDQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSDKWQQRSQAAFEKFDIDKDGY
ITPEELRMHTGMRGSIDPLLEEADIDKDGKISLPEFRRLLRTASIGSRNVTSPTLRHRRI*
>Migut.H01152 Org_Mguttatus peptide: Migut.H01152.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:28953593)
MGICFSTKKGSAPSTTTTGNVHQQNRRSSATSKPSSFKTTFTASSKKQEGSQNNNLKTRDNHKNQQQQKRSHKIIKNSSKSTSGAIPCGKRTNFGYDKDF
VKKYNIGKLLGHGQFGYTYVAIDKSNGDRVAVKRIEKNKMVLPIAVEDVKREVKILKALAGHENVVHFYNAFEDDSFVYIVMELCEGGELLDRILSKKDS
RYTEKDAAIVVRQMLKVAAECHLHGFVHRDMKPENFLFKSPKEDSHLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLRRKSGAESDVWSIGVITYILL
CGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPGISNAAKDFVNKLLVKDPRARLTAAQALSHPWVREGGEALEIPLDISVLSNMRQFVKYSRFKQFALRAL
ASTIDEEELADLRDQFDAIDVDKNGSISLDEMRQALEKDLPWKMKDSRVVEILQAIDSNTDGLVDFSEFVAATIHVHQLEEHNSEKWQQRSLAAFQKFDV
DRDGFITPHELKMHTGLKGSIDPLLEEADIDKDGRISLHEFRRLLRTASMSSRGGVST*
>Migut.L00702 Org_Mguttatus peptide: Migut.L00702.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:28935439)
MGFKWEGGGVINAHPWYGWNNNNRSRQQQHRHTQQNSKTSSKRPSGGAIPCGKRTDFGYDKDFNSRYTIGKLLGHGQFGYTYVAVDKFNGDRVAVKRIEK
NKMVLPIAVEDVKREVRILKALAGHENVVQFYNAFEDDSYVYIAMELCEGGELLDRILSKKDSRYTEKDAAIVVRQMLKVAAECHLHGLVHRDMKPENFL
FKSPKDDSSLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPGISNAA
KDFVKKILVKDPRARLTAAQALSHPWVREGGEASDIPLDISVLSNMRQFVKYSRFKQFALRALASTLDDEELADIRDQFDAIDVDKNGSISLEEMRQALE
KDIPWKIKDSRVHEILQAIDSNTDGLVDFPEFVAATLHVHQLQEHSSEKWHQRSQAAFEKFDFDKDGFITPDELKMHTCLKGSIEPLLEEADIDKDGKIS
LSEFRRLLRTASLSSRGGVGT*
>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)
MGGCLTTAKVTGSNSNTNNNPATTVTAVVNRKQTTRPQPAQTNHHRPNEAQKKHKHKSKQSSRQKTGVIPCGKRTDFGYDKNFDRRYTIGKLLGHGQFGY
TYVATDRSNGDRVAVKRIDKNKMILPIAVEDVKREVEILQALAGHENVVQFFNACEDDTYVYIVMELCEGGELLDRILEKKDSRYTEKDAAVVVRQMLKV
AAECHLHGLVHRDMKPENFLFKSKALDSPLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVISYILLCGRRPFWDKTEDGIFKE
VLRNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASDIPIDISVLNNMRQFVRYSRLKQFALRALASTLNAEELADLKDQFD
AIDVDKNGSISLEEMRQALAKDIPWKLKDSRVVEILEAIDSNTDGLVDFTEFVAATLHVHQLEEHDSEKWQQLSRAAFEKFDIDRDGYITPDELRMHTGL
KGSIDPLLDEADIDKDGKISLSEFRRLLRTASMSSRKVADPSGQRNSRQV*
>orange1.1g008127m.g Org_Csinensis peptide: orange1.1g008127m (1 of 1) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:18099036)
MGICLSTTKVSGSNSGSNNNNANHHRNANKEEAKRRHNHHARNDTTHKHQHQHQERAKNYQQLKTKQHQKTNSRRQTGVIPCGKRTDFGYDKDFDRRYTI
GKLLGHGQFGYTYVATDKANGDRVAVKKIEKNKMILPIAVEDVKREVKILQALAGHENVVKFYNAFEDDNYVYIAMELCEGGELLDRILAKMISTTLTSA
WFLAIRKDSRYTEKDAAVVVRQMLRVAAECHLHGLVHRDMKPENFLFKSAKEDSSLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLKRKSGPESDVWS
IGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPSISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLNNMRQFVKYSR
LKQFALRALASTLDDEELADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKLKESRVLEILQAIDCNTDGLVDFSEFVAATLHVHQLEEHDSEKWHLRS
QAAFEKFDIDRDGFITPEELRMHTGLKGSIDPLLEEADIDKDGRISLSEFRRLLRTASISSRNVPPSPSGHRNPRKL*
>Oropetium_20150105_14239 Org_Othomaeum peptide: Oropetium_20150105_14239A (1 of 1)
PTHR24349//PTHR24349:SF137 - SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:36005025)
MGVCFSAAAAAARPSKEEKRKRRGAASPDGQGKTVRVEFGYDRDFEARYEVGRLLGHGQFGYTFAATDRDSGDRVAVKRIDKAKMDRPVAVEDVKREVKI
LKALQGHENIVSFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPEVLRNKPDFRKRPWPSISPGAK
DFIKRLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADLKDQFDAIDVDKSGSISIEEMRHIDSN
TDGLVDFREFVAATLHIHQMAELDSERWGLRCQAAFRKLDLDGDGYITPEELRMHTGLKGSIEPLLEEADIDKDGKISLSEFHRLLRTASMSNIPSPRGV
PNPQALSNSGAAIGQEHLG*
>Oropetium_20150105_26612 Org_Othomaeum peptide: Oropetium_20150105_26612A (1 of 1)
PTHR24349//PTHR24349:SF123 - SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:36012113)
MGLCTSSTASADHTDDGAAKAGRKSGAGGRGIVACGKRTDFGYDKDFEARYLLGKLLGHDVKREVKILKALRGHENVVHFYNAFEDENYVYIVMELCEGG
ELLDRILAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGFEKQARFSSETLAKHYAKCKRFCTKVT
SQGSPCKTNCCTGVMEGGKASEIPLDISVLNNMRQFVKYSRFKQFALRALASTLNAEELSDLRDQFDAIDVDKNGTISLEELRQIDSNTDGLVDFEEFVA
ATLHVHQLVEHDTEKWRSLSQAAFDKFDVDGDGYITSDELRMHTGLKGSIDPLLEEADVDKDGKISLYEFRRLLKTASMSARIVQTPRGARINSELIKGV
KH*
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>Pahal.A00155 Org_Phallii peptide: Pahal.A00155.1 (1 of 1) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32529447)
MGACFSSASAAPAGAAERRPSKEDRKRRRGGASPEGAAKAAAAAAAAPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMT
RPVAVEDVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSN
KEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWSSISPGAKDFV
KRLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLP
WRLKGPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCQAAFSKFDLDGDGYITPEELRMHTGLKGSIEPLLEEADIDKDGRISLSEF
RKLLRTASMSNVPSPRGPPPNPQAL*
>Pahal.B01532 Org_Phallii peptide: Pahal.B01532.1 (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32489711)
MGLCSSCTAAADTTRRPGAGAGAAAGKREKEKGRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTFAAVDRASGDRVAVKRIDKNKMVLPVAVEDV
KREVKILKALQGHENVVHFYNAFEDDNFVYIVMELCEGGELLDRILAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKA
TDFGLSDFIRPGKQFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPNITPAAKDFVQKLLVKDP
RARLTAAQALSHDWVREGGKASEIPLDISVLHNMRQFVKYSRFKQFALRALASTLNSEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPRV
LEIIEAIDSNTDGLVDFEEFVAATLHVHQLVEHDTQKWKSLSQAAFDKFDVDGDGYITSDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTAS
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)
MGACFSSASAAPAGAAERRPSKEGEKRRRGGASPEGAAKAAAPVRAEFGYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMTRPVAV
EDVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVIVRQMLKVAAECHLRGLVHRDMKPENFLLKSNKEDSP
LKATDFGLSDFIKPGRKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEAIIYLARLSFSDFCTRCQNTTVTNPPLVV
NLKSGDNLWPQAKNAWTLVLRNKPDFRKRPWSSISPGAKDFVKRLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRFKQFALRA
LASTLNEEELADLKDQFDAIDIDKNGSISIEEMRNALAKDLPWRLKGPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCQAAFSKFD
LDGDGYITPEELRMMQHTGLKGSIEPLLEEADIDKDGRISLSEFRKLLRTASMSNVPSPRGPPPNPQAL*
>Pavir.Ab00120 Org_Pvirgatum peptide: Pavir.Ab00120.1.p (1 of 3) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30234536)
MGACFSSASAAPAGAAERRPSKEDKKGRRGGASPEGAAKAAAAAPVRVEFGYERDFEARFEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMTRPV
AVEDVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVTAECHLRGLVHRDMKPENFLFKSNKED
SPLKATDFGLSDFIKPGRKFHDIVGSAYYVAPEVLKRRSGLESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWSSISPGAKDFVKRL
LVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADLKDQFDAIDIDKNGSISIEEMRNALAKDLPWRL
KGPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCQAAFSKFDLDGDGYITPEELRMMQHTGLKGSIEPLLEEADINKDGRISLSEFR
KLLRTASMSNVPSPRGPPPNPQAL*
>Pavir.Ba02369 Org_Pvirgatum peptide: Pavir.Ba02369.1.p (1 of 3) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30291111)
MGLCSSSTAAADTPRRPGAAAGKRERDKGRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTFAAVDRASGDRVAVKRIDKNKMVLPVAVEDVKREV
KILKALQGHENVVHFYNAFEDDNFVYIVMELCEGGELLDRILAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFG
LSDFIRPGKQFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPNITPAAKDFVQKLLVKDPRARL
TAAQALSHDWVREGGKASEIPLDISVLHNMRQFVKYSRFKQFALRALASTLNSEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPRVLEII
EAIDSNTDGLVDFEEFVAATLHVHQLVEHDTEKWKSLSQAAFDKFDVDGDGYITSDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMSAR
TVQTPRGVRMS*
>PGSC0003DMG400003564 Org_Stuberosum peptide: PGSC0003DMP400006361 Calcium-dependent protein kinase
CPK4 (PAC:37426490)
MGNICFSSSKVSGSNSNTPSTTNTATVNGHRNRRSSAKPVSATTNTSRKQEGSHYNRQKGKDNGGVKQQTKNVKHNTRRQSGVIPCGKRTDFGYDKDFDK
KFTIGKLLGHGQFGYTYVATDKSNGNRVAVKRIEKKKMVVPIAVEDVKREVKILKALAGHENVVDFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRY
TEKDAAIVVGQMLKVAAQCHLHGLVHRDMKPENFLFKSPKEDSPLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITFILLCG
RRPFWDKTEDGIFKEVLRNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLSNMRQFVKYSRLKQFALRALAS
TLDEEELADVRDQFSAIDVDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFPEFVAATLHVHQLEEHNLLKWQQRSQTAFEKFDVDR
DGFITPEELRMHTGLKGSIDPLLEEADIDKDGKISLSEFRRLLRTASISSRMVTSPTVRGSRKI*
>PGSC0003DMG400022562 Org_Stuberosum peptide: PGSC0003DMP400039123 Calcium-dependent protein kinase
(PAC:37463999)
MGSCFSSSKVSGSNSNTPSTNNTATNTNTTVNVHPNRRETSKAPSTTVVNSRNQEGSNYNRGKGNINQKNQQKQPRNSQQNVKPSSRRQGGVIPCGKRTD
FGYDKDFEKRYTIGKLLGHGQFGYTYVATDKSSGDRVAVKRIEKNKMVLPIAVEDVKREVKILKALGGHENVVQFYNSFEDDNYVYIVMELCEGGELLDR
ILSKKDSRYTEKDAAIVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRRSGPESDVWSIG
VITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWSNISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLSNMRQFVRYSHLK
QFALRALASTLDEEEIADLRDQFSAIDVDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFPEFVAATLHVHQLEEHNSAKWQQRSQA
AFEKFDVDRDGFITPEELKMHTGLRGSIDPLLEEADIDKDGKISISEFRRLLRTASMSSPTVRDSRGM*
>Phvul.002G108700 Org_Pvulgaris peptide: Phvul.002G108700.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:37176995)
MGICFSATKVSGSNSNNAGASNRNRKWSAPMTAQVTLQPLTAQKQQSSHKQQSSHKQQSSHGQRRRVPEDSRKNPRAKEKTSGRRQGGNLPCGKRTDFGY
EKDFDKKFSLGKLLGHGQFGYTYVGIDKANGDRVAVKRLEKNKMVLPIAVEDVKREVKILKELTGHENVVQFYNAFEDDSYVYIVMELCEGGELLDRILA
KKDSRYTEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTREDSPLKATDFGLSDFIKPGKRFPDIVGSAYYVAPEVLKRKSGPESDVWSIGVIT
YILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARYTAAQALSHPWVKEGGEALEIPIDISVLNNMRQFVRYSRLKQFA
LRALASTLNEEELSDLKDQFDAIDVDKNGSISLEEMRLALAQDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSFKWQQRSQAAFE
KFDLDKDGYITPDELRMHTGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASIGSRNVLSPNQLRRKM*
>Phvul.003G261700 Org_Pvulgaris peptide: Phvul.003G261700.1.p (1 of 2) PTHR24349:SF87 - CALCIUM-
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DEPENDENT PROTEIN KINASE 16-RELATED (PAC:37145240)
MGICYSATKVSVFNGSPVTVKKNRKRAAAPEKRTPTANTERHKASSRHVPCGKRTDFGYEKHFDTRYTLGKLLGHGQFGYTYVGIDKANGDRVAVKRLEK
SKMVQPIAVEDVKREVKILKALTGHENVVQFYDAFEDDSYVYIVMELCEGGELLDRILAKKESRYTEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFL
LKSTKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRKSGPQSDVWSIGVITYILLSGRRPFWDKTEDGIFKEVLRKKPDFHRKPWTTISNAA
IDFVKKLLVKDPRARLTAAQALSHPWVREGGEASEIPIDISVLSNMRQFVKYSRLKQFALRALASTLNEEELADLKDQFDAIDVDKNGSISLEEMRQALA
KDLPWKLKEPRVLEILQAIDSNTDGLVDFSEFVAATLHVHQLEDDSDKWQLRSQAAFEKFDIDKDGYISPEELKMHTGLRGSIDPLLEEADIDKDGKISL
SEFRRLLRTASMSSQKVSSPTVYKRRI*
>Potri.005G113600 Org_Ptrichocarpa peptide: Potri.005G113600.1 (1 of 2) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:27031190)
MGACFSTIKVSGSNSNNNVIHSRKEPTKPQTKTTKATTATRKKQEVVHHHQNNKNVNNEAEKKLKVKEKQSSKAIPCGKRTDFGYDKDFDMRYTIGKLLG
HGQFGYTYVAIDKANGDRVAVKRIEKNKMVLPIAVEDVKREVKILRELTGHENVVQFYNALEDDSYVYIVMELCEGGELLDRILSKKDSRYTEKDAAVVV
RQMLKVAAECHLHGLVHRDMKPENFLFKSTKGDSPLKATDFGLSDFIKPGRKFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTE
DGIFKEVLKNKPDFRRKPWPTISTSAKDFVNKLLVKDPRARLTAAQALSHPWVREGGVASEIPIDISVLSNMRQFVKYSRLKQFALRALASTIDEEELAD
LKDQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEIVQAIDSNTDGLVDFTEFVAAALHVHQLQEHNSEKWQLRSQAAFEKFDIDRDGYITPEEL
RMHTGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASMSSRNVPSPSGHRKSHKI*
>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)
MGACFSTINISGSNSNNNTKANHNRKEPTKPQTRTTKAATRKKQEVVHHHHQINKNVNNEAEKKLKVKEKQSSKAIPCGKRTDFGYDKDFDIRYTIGKLL
GHGQFGYTYVATDKGNGDRVAVKRIDKNKMVLPIAVEDVKREVRILQELTGHENVVQFHNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYTEKDAAVV
VRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGRKFKDIVGSAYYVAPEVLKRNSGPESDVWSIGVITYILLCGRRPFWDKT
EDGIFKEVLRNKPDFRRKPWPTISTSAKDFVQKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLSNMRQFVKYSRLKQFALRALASTIDEEELA
DLKDQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESLVLEIVQAIDSNTDGLVDFTEFVAAALHVHQLEEHNSEKWQLRSQAAFEKFDIDRDGYITPEE
LRMHSGLRGSVDPLLEEADIDKDGRISLSEFRRLLRTASMSSQNVPDPSGHRNSKKL*
>Pp3c15_5120 Org_Ppatens peptide: Pp3c15_5120V3.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN
KINASE 16-RELATED (PAC:32926634)
MGGCCSKSSVVEQRPQAPHRTEANGKEKEAAYQNKGRDLPVKVGGDPPEKKERDSPEHKGRDLVENTQGSPPEKKARETPDKQVGATKRPIPERKQSRIS
AANLKDNQSHSQPLGKRTNFGYERDFKEKYSLGKLLGHGQFGYTYVATEKATGNKVAAKCIEKKQMKLPISVEDVKREVKILRTLSGHENVVQFFAAFED
DDLVYIVMELCEGGELLDRILAKKDTRYSEKDAAKIVRQMLNVAARCHLNGVVHRDMKPENFLFKSSKDDSPLKATDFGLSDYIKPGKRFRDVVGSAYYV
APEVLNRKSGPESDVWSIGVITYILLCGRRPFWDKTEAGIFNEVLKKKPDFREKPWPSITASAQDFVKKLLRKDPHMRLTAAQALSHPWVKEGGDASDMP
LDISVLSNMREFVKYSRLKQLALRALASTLESDEIRDLRDQFDAMDVDRNGTITLEEIKHALQKDRPWAVKESRVLEILQAMDSNADGMIDFDEFVAATL
HVHQLEQANSAKWQQRSKAAFSKFDVDGDGFITAEELKIATGLKGSVGTLLEEADSDKDGRISLSEFQKLLHQASFGSRTNTDHNRQRT*
>Pp3c9_4620 Org_Ppatens peptide: Pp3c9_4620V3.1.p (1 of 4) PTHR24349:SF87 - CALCIUM-DEPENDENT PROTEIN
KINASE 16-RELATED (PAC:32913651)
MGNCCKKSSVAEEVTRKYKAPEQWITKNEPSAQTHQQKPQNGATHTKPRSRKPPPGVVHSRNRSKKVEKLAESKQPEPWKSPPESTADRKKKPRVRAAIN
GKDNKEMAPLGKRTNFGYGRDFKSKYTLGKLLGHGQFGYTYVAIEKSTGSRVAVKTIEKKQMTLPISVEDVKREVKILRTLSGHENVVQFYASFEDDDLV
YIVMELCEGGELLDRILAKKDSRYSEKDAAKIVRQMLNVAARCHLNGVVHRDMKPENFLFKSTSEDSPLKATDFGLSDYIRPGNRFHDVVGSAYYVAPEV
LKKKSGPESDVWSIGVITYILLCGRRPFWDKTEKGIFDEVLKKNPDYGEKPWPTISSSAKDFVKKLLVKDPAARLTAAQALSHPWAKEGGDALDIPLDIS
VLSNMREFVKYSRLKQLALRALASTLDSSDIADLQDQFNAIDIDRNGKITLEEMREALQKDRPWSIQESRIVEILQAMDSNSDGLVDFDEFVAATLHVHQ
LEETDSEKWQSRSQAAFSQFDFDGDGYITADELKIATGLNGSMDSILVEADIDGDGKISLSEFQKLLRQASLGSRTNEHHTLVTHNHRKC*
>Prupe.7G168400 Org_Ppersica peptide: Prupe.7G168400.1.p (1 of 1) PTHR24349:SF87 - CALCIUM-DEPENDENT
PROTEIN KINASE 16-RELATED (PAC:32104836)
MGGCFSTVKVSGSNSNNTTAPTANHNRKQSTASSQSTTPPVKQEQRRTNRPNEMPRKQLANKPKGKPNSRRQTGVIPCGKRTDFGYDKNFDKRYTIGKLL
GHGQFGYTYVATDKANGDRVAVKRIDKNKMILPIAVEDVKREVKILKELAGHENVVQFYNAFEDDSYVFIVMELCEGGELLDRILEKKDSRYTEKDAAVV
VRQMLKVAAECHLHGLVHRDMKPENFLFKSKALDSPLKATDFGLSDFIKPGKKFQDIVGSAYYVAPEVLRRKSGPESDVWSIGVITYILLCGRRPFWDKT
EDGIFKEVLRNKPDFRRKPWPTISTSAKDFVKKILVKDPRARLTAAQALSHPWVREGGNASEIPIDISVLNNMRQFVRYSRLKQFALRALASTLNAEELS
DLKDQFDAIDVDKNGSISLEEMRQALAKDVPWKLKDSRVLEILEAIDSNTDGLVDFTEFVAATLHVHQLEEHDSEKWQQRSRAAFEKFDIDKDGFITPEE
LKMHTGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASISSKTVTSPPGQRNARKV*
>SapurV1A.0130s0480 Org_Spurpurea peptide: SapurV1A.0130s0480.1.p calcium-dependent kinase
(PAC:31426758)
MGVCFSTIKVSGSNSNNNVNHNRKEATKQQTKTTKATAPTRKKQEVVDHQQNNKNVNNEEEKKLKVKEKQGSKAIPCGKRTDFGYDKDFGMRYTIGKLLG
HGQFGYTYVATDKANGDRVAVKRIEKNKMILPIAVEDVKREVKILRELTGHENVVQFYNALEDDSYVYIVMELCEGGELLDRILSKKDSRYTEKDAAVVV
RQMLKVAAQCHLHGLVHRDMKPENFLFKSTKEDTPLKATDFGLSDFIKPGRKFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTE
DGIFKEVLKNKPDFRRKPWPTISTSARDFVNKLLVKDPRARLTAAQALSHPWVREGGSASEIPIDISVLSNMRQFVKYSRLKQFALRALASTINEEELAD
LKDQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFNEFVAAALHVHQLEEHNSEKWQVRSQAAFEKFDIDRDGYITPEEL
RMHTGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASMSSRNVPGPSGQRKSQKI*
>SapurV1A.0515s0090 Org_Spurpurea peptide: SapurV1A.0515s0090.1.p calcium-dependent kinase
(PAC:31451114)
MGACFSTIKVSGSNSNNTNHNRKESTKPQTSTATTKKQEVLHSHHQINKNVNNEAEKKLRVREKQSSKAIPCGKRTDFGYDKDFDIRYTIGKLLGHGQFG
YTYVATDKANGDRVAVKRIEKNKMVLPIAVEDVKREVKILQELTGHENVVQFHNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYTEKDAAVVVRQMLK
VAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGRKFRDMVGSAYYVAPEVLKRNSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFK
EVLRNKPDFRRKPWPTISTSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPIDISVLSNMRQFVKYSRLKQFALRALASTIDEEELADLKDQF
DAIDVDKNGAISLEEMRQALAKDLPWKLKESLVLEIVQAIDSNTDGLVDFTEFVAAALHVHQLEEHNSEKWQLRSQAAFEKFDIDRDGYITPEELRMHSG
LRGSIDPLLEEADIDKDGRISLSEFRRLLRNASMSSQNVPSPSGQQNSKKL*
>Seita.1G102100 Org_Sitalica peptide: Seita.1G102100.1.p (1 of 1) PTHR24349//PTHR24349:SF137 -
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SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32695536)
MGACFSSASAAPAGAAERRPSKEDKKRRRGGASPEGATKAAAAAAAPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMTR
PVAVEDVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSNK
EDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWSSISPGAKDFVK
RLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLPW
RLKGPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDNERWGIRCQAAFSKFDLDGDGYITPEELRMMQHTGLKGSIEPLLEEADIDKDGRISLSE
FRKLLRTASMSNVPSPRGPPNPQAL*
>Seita.2G111700 Org_Sitalica peptide: Seita.2G111700.1.p (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32718390)
MGLCFSSTAAADSPPRPAAAGGAAGKRERSRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTYAAVDRASGDRVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDF
GLSDFIRPGKQFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPNITPAAKDFVQKLLVKDPRAR
LTAAQALSHDWVREGGKASEIPLDISVLHNMRQFVKYSRFKQFALRALASTLNSEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPRVLEI
IEAIDSNTDGLVDFEEFVAATLHVHQLVEHDTEKWKLLSQAAFDKFDVDGDGYITSDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMSA
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)
MGACFSSASAAPAGAAERRPSKEDKKRRRGGASPEGATKAAAAAAAAPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRQSGDRVAVKRIDKAKMT
RPVAVEDVKREVKILKALKGHENIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSN
KEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWSSISPGAKDFV
KRLLVKNPRARLTAAQALSHPWVREGGEASEIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLP
WRLKGPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCQAAFSKFDLDGDGYITPEELRMMQHTGLKGSIEPLLEEADIDKDGRISLS
EFRKLLRTASMSNVPSPRGPPNPQAL*
>Sevir.2G117500 Org_Sviridis peptide: Sevir.2G117500.1.p (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32636163)
MGLCFSSTAAADSPPRPAAAGGAAGKRERSRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTYAAVDRASGDRVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVIVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDF
GLSDFIRPGKQFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPNITPAAKDFVQKLLVKDPRAR
LTAAQALSHDWVREGGKASEIPLDISVLHNMRQFVKYSRFKQFALRALASTLNSEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPRVLEI
IEAIDSNTDGLVDFEEFVAATLHVHQLVEHDTEKWKLLSQAAFDKFDVDGDGYITSDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMSA
RIVQTPRGIRMS*
>Sobic.002G114800 Org_Sbicolor peptide: Sobic.002G114800.1.p  (PAC:37951044)
MGLCSSCTAARAASDPGAAAAGDAAAAAAKKGRGIVACGKRTDFGYDKDFEARYSLGKLLGHGQFGYTFAAVDRASSERVAVKRIDKNKMVLPVAVEDVK
REVKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKAT
DFGLSDFIKPGRQFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPNITSSAKDFVQKLLVKDPR
VRLTAAQALSHDWVREGGKASEIPLDISVLHNMRQFVKYSRFKQFALRALASTLNSEELSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPRVL
EIIEAIDSNTDGLVDFEEFVAATLHMHQLVEHDTEKWKSLSQAAFDKFDVDRDGYITSDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTASM
SARNVQTPRGVRVS*
>Sobic.004G025000 Org_Sbicolor peptide: Sobic.004G025000.1.p  (PAC:37929853)
MGACFSSSASAAPAGAADDRRPSKDDDGKRRRRAAGASPEAAAAAVPVRVEFGYERDFEARYEVGRLLGHGQFGYTFAATDRASGDRVAVKRIDKAKMTR
PVAVEDVKREVKILKALKGHQNIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSNK
EDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFRKRPWSSISLGAKDFVK
RLLVKNPRARLTAAQALSHPWVREGGEASDIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELADLKDQFDAIDIDKSGSISIEEMRHALAKDLPW
RLKGPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCQAAFSKFDLDGDGYITPEELRMVQHTGLKGSIEPLLEEADIDKDGKISLSE
FRKLLRTASMSNVPSPRGVPNPQAL*
>Solyc02g083850.2 Org_Slycopersicum peptide: Solyc02g083850.2.1 (1 of 1) PTHR24349:SF87 - CALCIUM-
DEPENDENT PROTEIN KINASE 16-RELATED (PAC:36156830)
MGNICFSSSKVSGSNSNTPSTTTTNTAAVNGHRNRRSSANPVSATTNTSRKQEGSHYNRQKGKDNGGVKQQTRNSQKNVKHNTRKQSGIIPCGKRTDFGY
DKDFDNKFTIGKLLGHGQFGYTYVATDKSNGNRVAVKRIEKKKMVVPIAVEDVKREVKILKALAGHENVVDFYNAFEDDNYVYIVMELCEGGELLDRILA
KKDSRYTEKDAAIVVGQMLKVAAQCHLHGLVHRDMKPENFLFKSSKEDSSLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVIT
FILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLSNMRQFVKYSRLKQFA
LRALASTLDEEELADVRDQFSAIDVDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFPEFVAATLHVHQLEEHNLLKWQQRSQTAFE
KFDVDRDGFITPEELRMHTGLKGSIDPLLEEADIDKDGKISLSEFRRLLRTASISSRMVNSPTVRGSRKI*
>Solyc03g033540.2 Org_Slycopersicum peptide: Solyc03g033540.2.1 (1 of 1) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:36136238)
MGSCFSSSKVSGSNSNTPSTNNTTTNTNTAVNAHQNRRETSKAPSTTVVNPRNQEGCRDKGNINQKNQQKQPRNSQQNVKPSSRRQGGVIPCGKRTDFGY
HKDFEKRYTIGKLLGHGQFGYTYVATDKSSGDRVAVKRIEKNKMVLPIAVEDVKREVKILKALGGHENVVQFYNSFEDDNYVYIVMELCEGGELLDRILS
KKDSRYTEKDAAIVVRQMLKVAAECHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIRPGKKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVIT
YILLCGRRPFWDKTEDGIFKEVLRNKPDFRRKPWSNISNSAKDFVKKILVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLSNMRQFVKYSRLKQFA
LRALASTLDEEEIADLRDQFSAIDVDKNGVISLEEMRQALAKDLPWKMKESRVLEILQAIDSNTDGLVDFPEFVAATLHVHQLEEHNSTKWQQRSQAAFE
KFDVDKDGFITPEELKMHTGLRGSIDPLLEEADIDKDGKISISEFRRLLRTASMSSPTVRDSRGM*
>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)
MGSCCTKTSAAQEEQNEHKFAHQNYDQNGAQKHQEQLQHVAHNHKHTPQHHHHHRHAREQERSVVEDLQQPAQAAKKPPAAAVAAVPQSDRRKTTRRRIV
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GSNIRDNTSVPLGKKTNFGYQRDFKAKYTLGKLLGHGQFGYTYVAIQKATGMRVAVKTIEKKQMTLPISVEDVKREVKILDTLSGHENVVQFIASFEDNN
LVYIVMELCEGGELLDRILAKKESRYSEKDAARIVRQMLNVAAQCHLNGVVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGKRFHDVVGSAYYVAP
EVLKRKSGPESDAWSIGVITYILLCGRRPFWEKTEAGIFNEVLKKKPDFREKPWPTISASAKDFVKKLLVKDAFARLTAAQALSHPWVREGGDASDIPLD
ISVLSNMREFVKYSHLKQIALRALASTLDSDEISDLRDQFDAMDMDRNGTITLEEMRIALQKDQPWVLKESRVLEILQAMDTNRDGLVDFDEFVAATLHV
HQLKETDAKKWQMRLQAAFDKFDFDGDGYITAIELKIAMGLKGSMEAILCEADLDGDGRISLPEFQNLVRQASLGSRNNDDNDVRMQQHRRHHREAPLPC
ENQMMMVH*
>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)
MGSCCTKSLAEEQEERNGKQEQKFSHQNHYQHGVQTHQEQQHVVHNHYHAREQGAHYHHYAKEQEHVVELQQQQPGGQEGGKKEPPPPAVHRHSEGKKTK
VSSSSIKDNNSVPLGKKTNFGYARDFKAKYTLGKLLGHGQFGYTYVAVEKATGMRVAVKTIEKKQMALPISVEDVRREVKILETLSGHENVVQFIASFED
DDLVYIVMELCEGGELLDRILAKKDSRYSEKDAARIVRQMLNVAARCHLNGVVHRDMKPENFLFKSPKEDSPLKATDFGLSDYIRPGKRFHDVVGSAYYV
APEVLKRKSGPESDVWSIGVITYILLCGKRPFWDKTEAGIFNEVLKKKPDFRDKPWPTVSASAKDFVKKLLVKDAFARLTAAQALSHPWAREGGDASDIP
LDISVLSNMREFVKYSRLKQIALRALASTLDADEISDLRDQFDAMDMDRNGTITLDEMRIALQKDRPWIVKESRVLEILQAMDSNRDGLVDFNEFVAATL
HVHQLEETDSEKWQMRLQAAFDKFDFDGDGYITANELKIATGLKGSMEAILDEADMDGDGRISLPEFKNLLRQASLGSRNNNDHDVHTQHQRRRVQEAHE
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)
MGCCVSKNPPVHQTQREAGAGGQKQEIVHGPGGHRQQLPPDHGIVNHQLHHDVGEQIHNNRGDGEMKKKAVAAASAAAVKPIRKSSRITAASCDIQNNAP
LHPTAPLQGKRINFGYGRDFDEKYSLGKLLGHGQFGYTYVGTEKATSNEVAVKCIEKKKMKLPVEVEDVKREVRILKTLSGHKNVVQFYAAFEDDFQVYI
VMELCEGGELLDRILAKKNHRYTEKDAAKVVREMLNVVARCHLNGVVHRDIKPENFLFKSQDEDAPLKAVDFGLSDFIRPGKHFHDVVGSAYYVAPEVLK
RRSGPESDVWSIGVIAYILLCGVRPFWDKTEAGIFNEVQKKKPNFTQKPWPRISDSAKEFVKKLLEKDPHLRLTAAQALSHEWVREGGVASDMPLDIAVL
SNMREFVKYSRLKQLALRALASTLDKSEILNLQDQFDAIDVDQNGTITLEEMKNALSADKPWSVREPRISEILQAMDANMDGMIDFDEFVVATMHMHQLE
ENNSKKWQSRSSAAFAKLDMDGDGYVTADELKVAMGLKSSVSILLDEADTDRDGRISLPEFQKLLHQASLGSRTNHNHPHHRH*
>Spipo16G0021400 Org_Spolyrhiza peptide: Spipo16G0021400 Calcium dependent protein kinase 16
(PAC:31516197)
MGACFSTATKAASAAGDPQGPQQAHKPREAQRSTSQSQQQNRKQGQNYQREKGQEKRASGAIPCGKRTNFGYARDFESKYTTGKLLGHGQFGYTFVATQK
ATGDRVAVKRIDKSKMLHSVAVEDVKREVKILQALTGHENVVQFHNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAECHLH
GLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGRKFHDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRKKPD
FRRKPWPNISSSAKDFVTKLLVKDPRARLTAAQALSHPWVREDGDASEIPLDISILNNIREFVKYSRLKQIALRALASTLNPEEMANLRDQFDAIDVDKN
GAISLEEMRHALAKDLPWKLKEPRVMEILQAMDSNTDGLVDFDEFVAATLHVHQLEEHDSEKWQSRSQAAFEKFDVDGDGFITPEELRVHTGLKSSIEPL
LEEADIDKDGKISLPEFRRLLRSVSSRNVPAPSAARNSRKM*
>Spipo17G0030600 Org_Spolyrhiza peptide: Spipo17G0030600 Calcium-dependent protein kinase
(PAC:31514565)
MGACLSNATKVTGCSSSATGSGATDPPRQHKDRPPREGKSPSTQQDHHENQRQRERDQGRRTTGIIPCGKRTSFGYGRDFLSRYTIGKLLGRGQFGHTFV
ATDKANGDKVAVKRIDKNKMILPIAVEDVKREVKILQALTGHENVVQFHNAFEDDSYVYIVMELCEGGELLDRILAKKDSRYTEKDAAKVVRQMLKVAAK
CHLHGLVHRDMKPENFLFKSTKEDSPLKATDFGLSDFIKPGQRFRDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCGKRPFWDRTEDGIFKEVLK
NKPDFRRKPWPSISPSAKDFVKKLLVKDPRARLTAAQALSHPWVREDGDASEIPLDISVLGSMREFVKYSRMKQLALRALASTLDPEELADLRDQFNAID
VDKNGSISLEEMRHALSKDIIWRLREPRVLEILQAIDSNTDGLVDFDEFVAATLHVHQLEKQDSRKWLSRSQAAFEKFDVDRDGFITPEELRMHTGMKGS
IDPLLEEADIDKDGKISLSEFRRLLRNASMGSHNVL*
>Spipo1G0063900 Org_Spolyrhiza peptide: Spipo1G0063900 Calcium dependent protein kinase 18
(PAC:31521583)
MGACFSDPTKVGGSSSSSTGSAVKNLAGKHQHKAQRTQKKSSNGKDQQRKQQEQNPRQNQQNHREKGEVKRTNGVVPYGKRTNFGYPRDFESKYEIGKLL
GHGHFGYTFVAIDKANGNHVAVKRINKQKMVHHTAVEDVKREVKILRALTGHENVVQFYNAFEDDSFVYIVMELCEGGELLDRILAKKDSCYAEKDAAIV
VRQMLRVAAECHLRGLVHRDMKPENFLFKSALENSPLKATDFGLSNFIVPGRKFYDIVGSAYYVAPEVLKQRSGPESDVWSIGVITYILLCGRRPFWDKT
EEGIFKEVLKKKPDFRRKPWPSISNSAKDFVGKLLVKDPRARLTAAQALSHPWVREGGDASEIPLDISVLNNMRRFVKYSCFKQFALRALASTIDQEELA
DLHDQFDAIDVDKNGSISLEEMRHALAKDVPWRTKEPRVLEILRAIDSNTDGRVDFEEFVAATLHVHQLVEHDSEKWLLRSQSAFEKFDLDGDGFITPEE
LRTHIGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASMNS*
>Thecc1EG000206 Org_Tcacao peptide: Thecc1EG000206t1 Calcium dependent protein kinase 16 (71%U)
(PAC:27435494)
MGACLSTTKVSGSSSNAGVNHRKEQQSTTTTTNEKKESQKPSGQQGQQQQQVRNSQPLKVKGKPSARRQSGIIPCGKRTDFGYHKDFDKRYTIGKLLGH
GQFGYTYVATDKANGDRVAVKKIEKNKMVLPIAVEDVKREVKILEALKGHENVVQFYNAFEDDSYVYIVMDFALAISLVLALQLYTFISILLSLDSIICL
LSDARLCEGGELLDRILANCQYFLSVDVSNSVTTSSTLCLPSSVRKDSRYSEKDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTRADSPLKATDF
GLSDFIRPGKRFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGKRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPQAR
LTAAQALSHPWVREGGNASEIPVDISVLNNLRQFVKYSRLKQFALRALAGTLNEEEIADLRDQFDAIDVDKNGSISLEEMRQALAKDLPWKLKESRVLEI
LQAIDSNTDGLVDFTEFVAAALHVNQMEEHDSDKWQQRSQAAFEKFDVDRDGFITPEELRMHTGLRGSIDPLLEEADIDKDGKISLSEFRRLLRTASMGS
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)
MGVCFSAIRVTGASSSSRRSSQTNRKGCKKDKAYKAPIPKEENDKPSTKRRTGAIPCGKRTDFGYAKDFHDQYSIGKLLGHGQFGYTYVAIHKSNGDRVA
VKRLDKSKMVLPIAVEDVKREVQILKALSGHENVVQFYNAFEDEDYVYIVMELCEGGELLDRILSKKDSRYSEKDAAVVVRQMLKVAGECHLHGLVHRDM
KPENFLFKSAKLDSPLKATDFGLSDFIKPGKRFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDRTEDGIFKEVLRNKPDFRRKPWS
TISDSAKDFVKKLLVKDPRARLTAAQALSHAWVREGGNATDIPVDISVLNNLRQFVRYSRLKQFALRALASTLDEAEISDLRDQFDAIDVDKNGVISLEE
MRQALAKDLPWKLKDSRVAEILQAIDSNTDGLVDFTEFVAAALHVHQLEEHDSEKWQLRSRAAFEKFDIDKDGYITPEELRMHTGLRGSIDPLLDEADID
RDGKISLHEFRRLLRTASISSQRVPSPACHRNPR*
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>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)
MGLCFSSAKVSGRHNRSPRNPNPHPPPLPLTVAKHRPPQTPCSFMTVSIQKDHRTQPRRPAKKTPPQTQTRQTPTHGRAREKVSNNNHNGGRRHGEAIPY
GKRIDFGYAKDFDHRYSIGKLLGHGQFGYTYVATDKKTGDRVAVKKIDKAKMTIPIAVEDVKREVKILQALTGHENVVRFYNAFEDKNSVYIVMELCEGG
ELLDRILAKKDSRYSERDAAVVVRQMLKVAAECHLRGLVHRDMKPENFLFKSTEEASPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESD
VWSIGVISYILLCGRRPFWDKTEDGIFKEVLKNKPDFRRKPWPTISNSAKDFVKKLLVKDPRARLTAAQALSHPWVREGGDATEIPIDISVLNNMRQFVK
FSRLKQFALRALATTLDEEELADLRDQFDAIDVDKNGAISLEEMRQALAKDHPWKLKDARVAEILQAIDSNTDGFVDFEEFVAAALHVNQLEEHDSEKWQ
QRSRAAFEKFDIDGDGYITAEELRMHTGLKGSIEPLLEEADIDNDGKISLHEFRRLLRTASIKSRNVRNPPGYLISRKV*
>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)
MGLCFSSPKATRHGTSRRKPNPTPEMPKPQPQGKARKKVSNKNKKKTNNNKIQWRHGGETPYGKGVDFGYAKDFDNHYTIGKLLGHGQFGFTYVATDNVN
EDRVAVKRIDKAKMTVPIEVEDVKREVKILQALGGHENVVAFHNVFEDKNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQYANFLFKSTGEDS
SLKATDFGLSDFIKPGMKFQDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTQDGIFNEVMRKKPDFKTIPWPTISNSAKDFVKKLL
VKEPLARLTAAQALSHPWVREGGEASEIPIDISVLNNMRQFVKFSRLKQIALRALATTIDEDELDDLRDQFDAIDIDKNGSISLEEMRQALAKDVPWKLK
DARVAEILQAIDSNTDGLVDFTEFVVATLHVNQLEEHDCEKWQQRSRAAFDKFDIDRDGYITPEELRLQTGLKGSIEPLLEEAEVDKDGRISIHEFRRLL
RSASLKSIKVKSPPGYQLS*
>Tp57577_TGAC_v2_gene18198 Org_Tpratense peptide: Tp57577_TGAC_v2_mRNA18832 (1 of 1) PTHR24349:SF87 -
CALCIUM-DEPENDENT PROTEIN KINASE 16-RELATED (PAC:35968253)
MGICFSSTKVVSGSNSNTTNNENRKRNSTSTTKTENAPVTTTSATASTTRKRQVPSSNQRRKGSEEAQKKTHQSRHKDKVSSRVPCGKRTDFGYEKDFDK
RFSLGKLLGHGQFGYTYVGVDKSNGDRVAVKRLEKAKMVLPIAVEDVKREVKILKELTGHENVVQFYNAFEDDSYVYIVMELCEGGELLDRILGKKDSRY
TEKDAAVVVRQMLKVAAQCHLHGLVHRDMKPENFLFKSNKDDSALKATDFGLSDFIKPGKRFQDIVGSAYYVAPEVLKRKSGPESDVWSIGVITYILLCG
RRPFWDKTEDGIFKEVLRNKPDFRRKPWPTISNAAKDFVRKLLVKDPRARLTAAQALSHPWVREGGEASEIPVDISVLNNMRQFVKYSRLKQFALRALAS
TLNEGEFSDLKDQFDAIDVDKNGAISLEEMRQALAKDLPWKLKESRVLEILQAIDSNTDGLVDFTEFVAATLHVHQLEEHDSEKWQQRSQAAFDKFDLDK
DGFITPEELRMHTGMRGSIDPLLEEADIDKDGKISLPEFRRLLRTASIGSRNVSSPTHRNRRM*
>Zm00008a008476 Org_ZmaysPH207 peptide: Zm00008a008476_P01 (1 of 1) PTHR24349//PTHR24349:SF123 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:37205832)
MGLCSSSTAARAASDPGAAAAGDAAAAKKGRGIVACGKRTDFGYDKDFEVRYSLGKLLGHGQFGYTFAAVDRASTERVAVKRIDKNKMVLPVAVEDVKRE
VKILKALQGHENVVHFYNAFEDDNYVYIVMELCEGGELLDRILAKKDSRYSEKDAAVVVRQMLKVAAECHLHGLVHRDMKPENFLFKSKKEDSPLKATDF
GLSDFIKPELLPTFLSAAFCQVLFGRMGWFLAEQWEHSVVLKKKPDFRRKPWSNITSSAKDFVQKLLVKDPRARLTAAQALSHDWVREGGKASEIPLDIS
VLHNMRQFVKYSRFKQFALRALASTLNSEEMSDLRDQFNAIDVDKNGTISLEELKQALAKDVPWRLKGPRVLEIIEAIDSNTDGLVDFEEFVAATLHVHQ
LVEHDTEKWKSLSQAAFDKFDVDRDGYITPDELRMHTGMKGSIDPLLEEADIDKDGKISLDEFRRLLKTASMSARNVQTPRGVRKS*
>Zm00008a020829 Org_ZmaysPH207 peptide: Zm00008a020829_P01 (1 of 1) PTHR24349//PTHR24349:SF137 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:37208826)
MEVARSLVCRTGKMTRPVAVEDVKREVKILKALKGHQNIVHFYNAFEDDSYVYIVMELCEGGELLDRILAKKNSRYSEKDAAVVVRQMLKVAAECHLRGL
VHRDMKPENFLFKSNKEDSPLKATDFGLSDFIKPGKKFHDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWDKTEDGIFKEVLRNKPDFR
KRPWSSISPGAKDFVKRLLVKNPRARLTAAQALSHPWVREGGEASDIPVDISVLSNMRQFVKYSRFKQFALRALASTLNEEELSDLKDQFDAIDIDKSGS
ISIEEMRHALAKDLPWRLKGPRVLEIIQAIDSNTDGLVDFKEFVAATLHIHQMAELDSERWGIRCQAAFSKFDLDGDGYITPEELRMHTGLKGSIEPLLE
EADIDKDGKISLSEFRKLLRTASMSNVPSPRGPPNPQAL*
>Zosma34g00020 Org_Zmarina peptide: Zosma34g00020.1 Calcium dependent protein kinase 16 (PAC:33182282)
MGNCIVFRQTKSVVTQAATTSHRPNTPARQHRHEQRKHQDGDKMVASGMKMDFGYDKNFGERYVLGKLLGHGQFGYTFVGTDKINGDRVAVKRIDKNKMM
GVKDVKREVNILRELTGHENVVQFHNAYEDDTYVYIVMELCEGGELLERILSKKNSRYSEIDAAEIVRQMLKVAAQCHLHGLVHRDMKPENFLLESKEED
SRLKATDFGLSDYIKPEKKFSDIVGSAYYVAPEVLKRRSGPESDVWSIGVITYILLCGRRPFWGRTEDGIFNSVLKNKPDFKSKPWPHISDSAKDFVKKL
LVKSPSVRLTASQALSHPWVRENGDASEIPLDISVLSNLRKFMTYNGLKQFALGALASTLNKEELADIRDQFDVIDVDKNGTISLDEMSQALAKYRPWKL
KERHVREILQAIDTNTDGLVDFSEFVTATLRVHQMEVHDSDKWKLLSQTAFDQFDKDKDGFITPEELKMHAGLLGSINSSLEEADTDKDGKLSLAEFRKL
LKPANIHHQPSPSSKRNRHQ*
>Zosma72g00360 Org_Zmarina peptide: Zosma72g00360.1 Calcium-dependent protein kinase (PAC:33169652)
MGACATKVSGASSRRSNNTASKTKPNGGDLEEKKTEGTSGEKVEVPPTQQKKQKGRAVTVPCGKQTNFGYDRDFTRRYSIGKLLGHGQFGYTFVATDKEN
DDRVAVKRISKNKMTLPIAVEDVKREVQILRELTGHENVVQFHNAFEDDSFVYIVMELCEGGELLDRILSKKESRYTENDAAVVVRQMLKVAAECHLHGL
VHRDMKPENFLFISKNENSMLKATDFGLSDYIKPGKNFRDIVGSAYYVAPEVLKRKSGPQSDVWSIGVITYILLCGRRPFWNKTEDGIFKEVLKNKPDFN
RKPWHSISESAKDFVNKLLVKNPDARLTASQALSHPWVREGGDALEIPLDISVLSNLRDFVKYSRLKQFALRVMARTLDDDNEELGNIRDQFNAIDTDGN
GIISPEEMKQALEKNRPWKLKEPKVKEIVQAIDSNTDGYVDFPEFVAATLHIHQMEERDSDKWKALSKTAFDKFDIDKNGFITHDELKMHAGLRGSIDLI
LEEADIDKDGKISLSEFRKLFRTASIQTR*
>Zosma8g01530 Org_Zmarina peptide: Zosma8g01530.1 Calcium-dependent protein kinase 28 (PAC:33183934)
MGNCFRSHIRIINRSTSSKNATATATADDSKSPKPNAAVLKTNQTPRNNDKRLHEKKSTNSVPYGLKTDFGYFKDFDKNYAIGKLLGHGQFGYTFIATNK
STHESVAVKRIEKKKMVLPIAVEDVRREVKILKQLTGHENVVQFHNAFEDDAYVYIVMELCEGGELLDRILSKKDSRYTEKDAAVVVRQMLKVAAECHLH
GLVHRDMKPENFLFQSKREDSVLKATDFGLSDFIKPGKKFPDIVGSAYYVAPEVLRRRSGPESDAWSIGVITYILLCGKRPFWDKTENGIFKEVLKNKPD
FKRNPWPTISDSAKDFVNKLLVKNPRARFTAAQALSHPWVREGGNASEIPLDISVLSNLRDFVKYSRMKQLALRALASTVDDDELADLRDQFDAIDVDKS
GTISFEELKLALAKDLPWRVKEARVVEILEAIDSNTDGLVDFREFVTATLHVHQMEHDSETWNSRCKAAFQKLDVDGNGFLTPEELRLHTGIKGSIDMLL
DEADTDKDGKISLIEFLTVLKTASTPRQRRCAVSDHRNSSHK*
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## 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. moellendorffi, A. trichopoda, O. sativa, A. thaliana, V. vinifera, R. comunis, 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)
MGNCCATPGIKRKERKPNPFAQDGFKGTGPPKVIMKEHAPGMSVQQGVDINEKYVLGKELGRGEFGITYLCTGKESQEDLACKSISKSKLRTAVDIDDVR
REVQIMHHLPRHPNVVALKDVFEDGNAVHLVMELCEGGELFDRIIARGHYSERAAAGITRTIVEVVQVCHKHGVMHRDLKPENFLFANKKENSPLKAIDF
GLSVFFRPGERFSEIVGSPYYMAPEVLKRNYGPEIDVWSAGVILYILLSGVPPFWAESEQGVAQAILRGQIEFKRDPWPKISENAKSLVQNMLMPDPKQR
YTAQQVLDHPWLQNAKKASNVPLGDVVRNRLKQFSAMNKLKRKALQMITELLSGDEVESYKDMFKVMDQKNEGSITYDELKVGLAKIGSQLAESEAKLLM
EAADVNNKGTLDYQEFVAMMIHIQRMDNDEYLRKAFNRLDKDESGFIEKEELREALYDDRGASETEMIDDILQEVDLDKDGKISYEEFASMMRTGTDWRK
ASRHYSRGRYNSLSIRLLRDGSLQSGNYEKR*
>105846 Org_Smoellendorffii peptide: 105846 (1 of 1) PTHR24349:SF126 - CALCIUM-DEPENDENT PROTEIN KINASE
32 (PAC:15417957)
MGNCCATPPREAGDQDSHKPRGKKKRFKGNPYAKDSENGQRKLTVLEAEQRTGSSIKERYNLGRELGRGEFGVTYLCMEQESQELLACKSISKSKLKTAV
DIEDVRREVAIMRHLPPHPNIVALKGAYEDERAVHIVMELCAGGELFDRIIARGHYTERAAAGVIRTIVEVVQACHRQGVMHRDLKPENFLFANRKENSA
LKAIDFGLSVFFRPGERFNEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAESEQGVAQAILRGVLDFRREPWPAVSESAKSLVRRMLE
PDPRLRLSASQVLEHPWLHRAGKHAPNVPLDAVRTRLKQFAALNKLRKKALEIIAEELSQEENAGMREIFEAMDSSGRGGITLDELKIGLAKSPTIVTNE
YAEVELKSVMDAADEDNDGVLNYGEFVTVIVYLQQRFDSDDHLRKAFDRLDKDANGFLDKEDLAAALAEEPGGGDGGEVVADILAEVDADKDGLVSYEEF
ARVMRTGTDWRKASRRYSKGRFNSLSNKLIKDGSLTATA*
>118877 Org_Smoellendorffii peptide: 118877 (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN KINASE
3 (PAC:15411727)
MRNTKSAIAGSSTPLRGSAAFKAGNVLGRPFSDLRQEFALARELGAGQFGVTRLCSRRSTGERLACKSIAKRKLLDRSDAEDVRREVQIMHHLCGHAHIV
ALREVFEDKGSVHLIMELCEGGELFDRIVQRGHYSERAAATLCRTMVLVLQTCHSLGVMHRDLKPENFLFASADEDSPLKATDFGLSVFFKPGETFKDLV
GSAFYVAPEVLRRNYGPEADIWSAGVILYILLSGVPPFWAETEQGIFDEVLRGHLDLSSDPWPSISDGAKDLLRKMLKQDPKERMTPLEVLNHPWLKEDG
EAPDVPLDNAVLSRMKQFSAMNKLKKLALKVIAESLSEEEIMGLKEMFKSIDTDNSGTITYDELKAGLANLGSALAEHEVQQLMRAADVDGNGSIDYTEF
ITATMHLNKTEKEDHLYSAFQFFDKDNSGYITVEELEQALGDLNMQDLTEIIKEVDTDNDGKIDYDEFVAMMRGANPPRTAAVAAKAAEKSSS*
>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)
MYVLGRELGRGQFGVTHLCTDRASGKTYACKTIAKRKLISKADVEDVKREVQIMHHLRGNENIVELRGSYEDKHSVHLVMELCEGGELFDRIIARGHYSE
RAAAALCRTIVRVVYICHSLGVMHRDLKPENFLLADKSESAPLKATDFGLSVFFKHGDKFTDLVGSAYYVAPEVLRRNYGPEADVWSAGVILYILLSGVP
PFWAESEQGIFDAVLRGQVDFVSDPWPSISSSAKDLVKKMLTQDVKKRVTAAEVLSHPWVREDGDAPDAPLDNAVLSRMKQFTAMNKLKKLALKVIAASL
SEEEITGLKEMFSSMDTDGSGTITFDELKAGLERLGSNLRDAEIRQIMNAADVDGNGTIDYLEFITATMQMNKMQKEDHLYSAFQFFDNDNSGYALSFLK
LFMDDWLLRDSYITMEELEEALVKYGMGDHETMKEILKEVDTDNDGKINYDEFVAMMTKGAAPSSEQQNNRRKGQELPVGAPRHRK*
>165073 Org_Smoellendorffii peptide: 165073 (1 of 2) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE
20 (PAC:15410490)
MGDSRPTAAAAVVSPRHGGLTSSVLGRRTENVKDLYVLGRKLGQGQFGTTYVCTEKSSGKHYACKSIPKRKLISLEDVEDVRREIHIMHHLSGHPNVVEI
KGAYEDSSCVHLVMDLCAGGELFDRIIQRGHYSESKAAQLTRTIVGVVVACHSLGVMHRDLKPENFLLANADEDSPLRATDFGLSVFFQPGEVFKDVVGS
PYYVAPEVLRKQYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLQGDIDFESDPWPKISESAKDLIRKMLTRNPRKRLKAQEVLTHPWIMEGGVA
PDAPIDSAVLSRLKHFSAMNKIKKIALRVIAERCTEDEIAGLKEMFKMMDADNSGAITFDELKAGLQRVGSNLKESEIHALMDAADLDKNGTIDYTEFIT
ATLHLNKIEREENLFAAFSYFDRDSSGYITIDELQSACKEHYMGDDLLEDMLREIDQDNDGRIDYNEFVTMMRNGNGGVGRGQMRNSLSLRDVIMVG*
>231127 Org_Smoellendorffii peptide: 231127 (1 of 1) PTHR24349//PTHR24349:SF135 - SERINE/THREONINE-
PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:15414521)
MPQQHIACHRPQRSAQEQQQNTKALPASPPRAASPAAPSPSPSPSPAKPSTAATAKNIVIPSSQPKTDGSNVLGLPLKDVRSAYALGKELGRGQFGITYA
CTDKITGEKLACKTISKRSLRNRTDMEDVQREMQIMQRLAGQHANIVELKAVYEDKQSVHLVMELCAGGELFDRIVSRGHYTEKAAAAVFRTIVRIVQHC
HATGVIHRDLKPENFLLASPAEDAPLKATDFGLSVFYKTGQIFTETVGSAYYVAPEVLKKRYGPEADIWSAGVILYILLCGLPPFWAETEKGIFDSVLRG
ELDFSDDPWPKISSSAKELIRRMLNQNPSERLAIPEILDHPWVRPDGEASDQPLDQSVLARMKGFTAMNKMKKIALKIIAESLSEKEIKGLKELFKKMDV
DKSGTITFEELKSGLAKQGYDMAESEVRAIMESADVDGNGTIDYLEFISATMHMNKMDRENNLLAAFKQFDTDNSGFISVEELEQALYRYGMVDEGMIKD
IIKEVDVNKARREDRLQRVCYDDAASGIEC*
>27777.t000008 Org_Rcommunis peptide: 27777.m000274 calcium-dependent protein kinase, putative
(PAC:16799163)
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LCTEISTGKLYACKSISKRKLVTRNDKEDMKREIQIMQHLSGQPNIVEFKGAYEDKQSVHLVMELCAGGELFDRIIAKGHYSEKEAASICRSIVNVVHAC
HFMGVMHRDLKPENFLLSSKDQNALLKATDFGLSVFIEEGKTYRDIVGSAYYVAPEVLRRRYGKEMDIWSAGVMLYILLSGVPPFWAESEKGIFDAILQG
DIDFESPPWPTISSSAKDLVRRMLTQDPKKRITSTQVLEHPWLKEGGDASDKPIDSAVLSRMKQFRAMNKLKKMALKVIAENLSSDEIQGLKSMFANIDT
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DNSGTITYDELKAGLARLGSKLTETEVKQLMDAADVDGNGTIDYLEFITATMHRHRLEREEHLYKAFQYFDKDNSGFITRDELETAMKDYEMGDDATIKE
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>28308.t000002 Org_Rcommunis peptide: 28308.m000065 calcium-dependent protein kinase, putative
(PAC:16800511)
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EVAIMKHLPKNSSIVSLKEACEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAAVTRTIVEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAFDFG
LSIFFKPGERFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGIIDFKRDPWPNISESAKSLVKQMLEPDPKLRL
TAKQVLEHPWLQNAKKAPNVPLGDVVKSRLKQFSMMNRFKRKALRVIAEFLSTEEIEDIKDMFRKMDTDNDGIVSIEELKSGLQNFNSQLAESEVQMLIE
AVDANGKGTLDYGEFVAVSLHLQRMANDEHLHKAFSYFDKDSNGYIEPDDLRDALMEDGADDCTDMANDIFQEVDTDKDGKISYDEFVAMMKTGTDWRKA
SRHYSRGRFNSLSMKLMKDGSLNLG
>29333.t000041 Org_Rcommunis peptide: 29333.m001078 calcium-dependent protein kinase, putative
(PAC:16802692)
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PLPPKPKDETVQSEVNGIIRNQRGEIKSTRQVSVKEEKKPAVPPRPRKPHNVKRLYSAGLLAESVLRTKTGHLKEYYNLGRKLGHGQFGTTFLCVEKGTG
KEYACKSIAKRKLSTIDDVEDVRREIQIMHHLSGNPNVISIKGAYEDAVAVHVVMELCAGGELFDRIIKRGHYTERKAAQLTRTIVGVVEACHSLGVMHR
DLKPENFLFVNNQEDSPLKAIDFGLSVFFKPGEIFTDVVGSPYYVAPEVLKKRYGPEADVWSAGVMVYILLSGVPPFWAETEQEIFEEVLHGQLDFTSDP
WPHISESAKDLVRRMLVRDPRKRITAHEVLCHPWVRDDGVAPDKPLDPAVLSRMKQFSAMNKLKKMALRVIAENLSEEEIAGLTEMFKMIDTDNSGQITF
EELKVGLRRFGANLNESEIYDLMQAADIDNSGTIDYGEFIAATLHLNKVEREDHLFAAFSYFDKDGSGYITLDELQQACIEFGMEDVHLEEMIREVDQDN
DGRIDYKEFVAMMQKGNSEMGKNGLQGTSFSIGFREALQVC
>29333.t000051 Org_Rcommunis peptide: 29333.m001088 calcium-dependent protein kinase, putative
(PAC:16802702)
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AEDPKPKKSNHFKRVSSAGLQMDSVLGRKTGNLKEIYSLGRKLGQGQFGTTFLCIEKATGRDFACKSIAKRKLTTQEDVEDVRREIQIMHHLEGHPNVIK
IIDAYEDAVAVHVVMELCAGGELFDRIIQRGHYTERKAAELARLIVGVVQACHSLGVMHRDLKPENFLFVDHEEEAALKTIDFGLSVFFRPGETFSDVVG
SPYYVAPEVLKKHYGPECDVWSAGVIIYILLSGVPPFWDETEQGIFEQVLKGELDFISEPWPNISESAKDLVRKMLVRDPKKRLTAHEVLCHPWVQVDGL
APDRPLDSAVLSRLKQFSAMNKLKRIAIRVIAETLSEEEIAGLKEMFKMIDTDGSGQISLDELKTGLERVGAILKDSEIDSLMQAADIDNSGTIDYGEFI
AAMLHLNKIDKEDHLFAAFSYFDKDGSGYITQDELQQACDQFGLGDIHIEDIIREVDQDNDGRIDYSEFVAMMQDSGWSERRSK
>29728.t000018 Org_Rcommunis peptide: 29728.m000812 calcium-dependent protein kinase, putative
(PAC:16806882)
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SMFVHLVMELCAGGELFDRIVAKGQYSEKEAAKLIKTIVGVVEACHSLGVMHRDLKPENFLFDTPGDDAKLKATDFGLSVFYKPGQYFSDVVGSPYYVAP
EVLLKRYGPEVDVWSAGVILYILLSGVPPFWAETESGIFRHILQGKIDFESEPWPKISDSAKDLIKKMLERDPRQRISAHEVLCHPWIVDDTVAPDKPLD
SAVLSRLKKFSAMHKLKKMALRVIAERLSEEEIGGLKELFKMLDTDSSGTITFEELKEGLLRVGSELMECEIKALMEAADIDNSGTIDYGEFLAATLHLN
KMEREENLLAAFSYFDKDGSGYITVDELQQACKDFGLDDVHLDEMIKEIDEDNDGRIDYAEFTSMMRKGDEDIGRSRTMRSHLNFNLADALGVKDLN
>29761.t000015 Org_Rcommunis peptide: 29761.m000421 calcium-dependent protein kinase, putative
(PAC:16808108)
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REVQIMKHLPKHPNIVSLKDTYEDDNAVHLVMELCEGGELFDRIVSRGHYTERAAAAVTKTIVEVVQMCHKHGVMHRDLKPENFLFANKKESAALKAIDF
GLSVFFKPGERFNEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVVDFKRDPWPKVSDNAKDLVKKMLDPDPKRR
LTAQQVLDHPWLQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSVEEVAGIKEGFRLMDTSNKGKINLDELRIGLQKLGHQITDTDVQMLM
EAGDVDRDGHLDYGEFVTISVHLRKMGNDEHLRKAFEYFDKNQSGHIEIEELRNALADELDENSEEIISAIIHDVDTDKDGRISYDEFATMMKAGTDWRK
ASRQYSRERFNNLSLKLMKDGSLQMNEGR
>29842.t000094 Org_Rcommunis peptide: 29842.m003597 calcium-dependent protein kinase, putative
(PAC:16810728)
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ERDAARICKDIVNVVHACHFMGVIHRDLKPENFLLASKDEGATLKATDFGLSVFIEEGKTYRDKVGSAYYVAPEVLSRSYGKEIDVWSAGVILYILLSGV
PPFWAETENGIFDAILQGDIDFESKPWPSISDSAKDLIRRMLTQDPKKRITSAQVLDHPWIKDGGAASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAES
LSEEEIKGLKVMFRNMDTDKSGTITYEELKTGLARLGSRLSETEVKQLMEAADVDGNGTIDYIEFISATMHRYRLERDEHLYKAFQHFDKDSSGYITRDE
LESAMKEYGMGDEATIKEIISEVDTDNDGRINYEEFCAMMRSGIQQAEKLF
>29852.t000019 Org_Rcommunis peptide: 29852.m002000 calcium-dependent protein kinase, putative
(PAC:16811562)
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SVLQTKTGNFKEFYSLGKKLGQGQFGTTFLCVEKATGKEYACKSIAKRKLLTDEDVEDVRREIQIMHHLAGHPNVISIKGAYEDAIAVHVVMELCAGGEL
FDRIIQRGHYSERQAAELTRTIVGVVEACHSLGVMHRDLKPENFLFVNQKEDSLLKTIDFGLSIFFKPGEKFNDVVGSPYYVAPEVLRKRYGPEADVWSA
GVIVYILLSGVPPFWAETEQGIFEHVLHGDLDFSSDPWPSISEGAKDLVKRMLLRDPRRRLTAHEVLCHPWVQEDGVAPDKPMDSAVLSRMKQFSAMNKL
KKMALRVIAESLSEEEIAGLKEMFKMIDTDNSGTISFDELKAGLKRVGANLKESEIYDLMQAADVDNSGTIDYGEFIAATLHLNKIEREDHLFAAFSYFD
KDGSGYITPDELQQACEEFGLEDFRLEEMIREVDQDNDGLIDYNEFVAMMQKGNVGGGPGRKALENSFSIGFREALKL
>29896.t000003 Org_Rcommunis peptide: 29896.m000119 calcium-dependent protein kinase, putative
(PAC:16812395)
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VEDVRREVEIMRHLPKHPNIVSYKEAYEDKEVIYLVMELCEGGELFDRIVAKGHYTERAAAMVTKTILEIVKVCHKHGVIHRDLKPENFLFADVHENSQL
KAIDFGLSIFFQPGQRFSEIVGSPYYMAPEVLRRNYGPEVDVWSAGVILYILLCGVPPFWAETEEGIAHAIVGGKIDFTRDPWPRVSEEAKDLVQNMLDQ
NPYSRLTVQEVLEHPWIHNASDVPNVNLGENVRARIKQFSLMNKFKKRVLRVVADNLTDEQVDGIKQMFHMMDTDNTGDLTFEELKSGLHKIGHPVPDPD
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>30100.t000014 Org_Rcommunis peptide: 30100.m000791 calcium-dependent protein kinase, putative
(PAC:16817768)
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GRKLGQGQFGTTYLCVENSTGTEYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDQLYVHIVMELCSGGELFDRIIQRGHYSERKAA
ELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFTDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWA
ETQQGIFDAVLKGYIDFESDPWPLISDSAKDLIHKMLCGRPSDRLTAHEVLCHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALRVIAESLSEEE
IAGLREMFQTMDTDNSGAITFDELKAGLRRYGSTMKDTEIRDLMDAADVDNSGTIDYGEFIAATVHLNKLEREEHLVAAFQYFDKDGSGYITVDELQQAC
AEHNMTDVLLEDIIREVDQDNDGRIDYSEFVAMMQKGNAGIGRRTMRNSLNMSMRDAPGAQ
>30142.t000025 Org_Rcommunis peptide: 30142.m000651 calcium-dependent protein kinase, putative
(PAC:16819478)
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KATGEQFACKTIAKRKLVNKEDVEDVKREVQIMHHLTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGHYTERAAASLLRTIVQIVHTCHSMG
VIHRDLKPENFLLLNKDENSPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLKRRYGPEADIWSVGVMLYILLSGVPPFWAESEHGIFNAILRGHVDF
TSDPWPQISPQAKDLVRKMLNSDPKQRLTAIQVLSHPWIKEDGEAPDTPLDNAVLSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGIDTDNSG
TITLEELKQGLAKQGTKLSEYEVKQLMEAADADGNGTIDYDEFITATMHLNRMDREEHLYTAFQHFDKDNSGYITTEELEQALREYGMHDGRDIKEIISE
VDSDHDGRINYDEFVAMMRKGNPEANPKKRRDTVFV
>30147.t000328 Org_Rcommunis peptide: 30147.m014057 calcium-dependent protein kinase, putative
(PAC:16820071)
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RKLRTAVDIEDVRREVAIMSNLPDHPNIVKLKATYEDNENVHLVMELCEGGELFDRIVARGHYSERAAANVARTIAEVVRMCHENGVMHRDLKPENFLFA
NKKENSVLKAIDFGLSVFFKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGQIDFKREPWPQISDSAKS
LVRQMLEADPKKRLTAQQVLDHSWLQNAKKAPNVPLGDIVRTRLKQFSLMNRFKKKALRVIAEHLLVEEVEVIKDMFALMDTDNDGKVTYNELRAGLRKV
GSQLAEPEIKMLMEAADVDGNGVLDYGEFVAVTIHLQKMENDEHIRRAFMFFDKDGSGYIELEELREALADEYGETDNDVLHDILREVDTDKDGCISYEE
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>30169.t000219 Org_Rcommunis peptide: 30169.m006442 calcium-dependent protein kinase, putative
(PAC:16821242)
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TAVDIEDVRREVEIMKHLPHHPNIVSLRATYEDDNAVHIVMELCEGGELFDRIVARGHYTERAAAAVMRTIVEVVQMCHKHGVMHRDLKPENFLFGNKKE
TAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPKVSDNAKDLVKK
MLNPDPKLRLTAQQVLGHPWLQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVVAEHLSVEEVAGIKEAFDMMDTTRRGKINLEELRIGLQKIGQQI
PDADLQILMEAADVDGDGSLNYGEFVAVSVHLKKMGNDEHIHKAFAFFDQNQSGYIEIEELREALNDEVDTCSEDVINAIMHDVDTDKDGRISYEEFATM
MKAGTDWRKASRQYSRERFNSLSLKLMRDGSLQVAS
>30170.t000694 Org_Rcommunis peptide: 30170.m014282 calcium-dependent protein kinase, putative
(PAC:16822115)
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KTTGLKYACKSISRRKLVNDKDVEDVRREILILQHLTGQPNIVEFKGAYEDRQNLHLVMELCSGGELFDRIIAKGTYTEREAATITRQIVNVVHACHFMG
VIHRDLKPENFLLVSKAEDSPLKATDFGLSVFIEEGVVYKDIVGSAYYVAPEVLNRSYGKEVDVWSAGIILYILLSGVPPFWGENEKGIFEAIIKGQLDL
QSSPWPKISASAKDLIRKMLARDPKKRITAAEALEHPWLKVGGEASEKPIDSAVLRRLKQFRAMNKLKKLALKVIAENLSEEEIKGLKQMFNNMDTDKSG
TITYEELKDGLKRLGSRLTEAEIMQLMDAADVDKSGTIDYVEFITATMHRHKLDKEEHMFQAFQYFDKDNSGYITRDELRQAMSQYGMGDDATIDEILED
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>30190.t000579 Org_Rcommunis peptide: 30190.m011343 calcium-dependent protein kinase, putative
(PAC:16823697)
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DLKPENFLFLSTDENSPLKATDFGLSVFFKPGDTFKDLVGSAYYVAPEVLRRNYGPAIDIWSAGVILYILLSGVPPFWGETEQAIFDTVLRGHIDFSSDP
WPSISSSAKDLVKKMLTADAKDRISAAEVLNHPWMRVDGDASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIMGLKEMFKSMDTDNNGTITY
EELKAGLPKLGTKLSESEVKQLMEAADVDGNGTIDYIEFITATMHMNRMEREDHLYKAFEYFDKDKSGYITMEELEHALKEYNMGDARTIKEIIAEVDTD
HDGRINYEEFVAMMRKGNPELVTNRRRK
>96034 Org_Smoellendorffii peptide: 96034 (1 of 1) PF00069//PF13499 - Protein kinase domain (Pkinase)
// EF-hand domain pair (EF-hand_7) (PAC:15404581)
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STFEDKSTVYLVMELCQGGELFDRIVSKGHYTEKAASAVCRTIVKVVHTCHSHGVIHRDLKPENFLLANKREDAPVKATDFGLSVFFRSGQVFREIVGSA
YYVAPEVLKKSYGPEADVWSAGVILYVLLAGVPPFWAETEQGIFEAVLRGHLDLNGSPWPTISASAKDLVRKMLKQNPRERLSAADVLQHPWIKEDGDAP
DKLIDGEVLSRMKNFSAMNKLKKVALKIISESLSEEEIIKLKDMFKQMDTDNSGTITFEELKAGLANQGSNMIDAEIRQLMEAADVDGNGTIDYLEFIQA
SMHLNKMDRGDHLHAAFQNIDTDGSGYITMEELEAALVKHGLGVEDAKDIIKEVDTDNDGRINYDEFCAMMLKRNTPPAGAGHRRSINDLPVGIKK*
>99178 Org_Smoellendorffii peptide: 99178 (1 of 2) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN KINASE 20
(PAC:15414412)
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EDAGSVHLVMELCAGGELFDRIIQRGHYSERKAAELIRVIVGVVQACHSLGVMHRDLKPENFLLLSKHEDSLMKATDFGLSVFFKPGEVFTDVVGSPYYV
APEVLRKKYGPEADVWSAGVILYILLSGVPPFWAETEKGIFEQVLKGEIDFESHPWPVISQDAKDLIRKMLCPVPANRLKAHEVLGHPWARADGVAPDKP
LDSAVLSRMKQFSAMNKIKKIALRVIAESLSEEEIAGLKEMFKMMDTDNSGSITFDELKAGLERVGSNLVESEIRDLMAAADVDNSGTIDYKEFITATLH
LNKIEREEHLLAAFAYFDKDNSGYITKDELQQVCAENHMGDEVIEEMMREADQDNDGRIDYSEFVTMMRKGAGGIGRKTMRNSLSITFRDLLTV*
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PROTEIN KINASE 6 (PAC:30636881)
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YLCTELATGVDYACKSISKRKLISKEDVEDVRREIQIMHHLAGHGNIVTIKGAYEDSLYVHIVMELCAGGELFDRIIQRGHYSERKAAELTKIIVGVVEA
CHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSIFFKPGQIFTDVVGSPYYVAPEVLLKRYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLK
GYIDFDSDPWPVISDSAKDLIRRMLCSKPAERFTAHEVLRHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALKVIAESLSEEEIAGLREMFQAMD
TDNSGAITFDELKAGLRKYGSTLKDTEIHDLMEAADVDNSGTIDYSEFIAATIHLNKLEREEHLVAAFQYFDKDGSGYITIDELQQACVEHSMTDVFLED
IIKEVDQNNDGKIDYGEFVEMMQKGNAGVGRRTMRNSLNISMRDA*
>Brara.A01217 Org_BrapaFPsc peptide: Brara.A01217.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
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LLETETILGKPFEQIKRLYTLGHEIGRGQFGITYTCKENSTGNTYACKSILKRKLTRKQDRDDVKKEIQIMQHLSGQQNIVEIRGAYEDRQSIHLVMELC
GGGELFDRIIAQGHYSERAAAGVIRSVLNVVQICHFMGVMHRDLKPENFLLSSKDEDAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRSYGKEI
DIWSAGIILYILLCGVPPFWAETEKGIFEEIIKGEIDFESQPWPSISESAKDLVRKLLTMDPRKRISAAQALEHPWIRGGEAPDNPIDSAVLSRMKQFRA
MNKLKKLALKVIAESLSEEEIKGLKTMFANMDTDQSGTITYEELKTGLARLGSKLSEAEVKQLMEAADVDGNGTIDYIEFISATMHRYRLDRDEHLFKAF
QYFDKDNSGFITMDELESAMKEYGMGDETSIKEVIAEVDTDNDGRINYEEFCAMMRSGTTQPQQGKTSSIPLTD*
>Brara.A01377 Org_BrapaFPsc peptide: Brara.A01377.1.p (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:30640163)
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NFLFLSKDESSPLKATDFGLSVFFKPGDKFKDLVGSAYYVAPEVLKRNYGPEADIWSAGVILYILLSGVPPFWGENETGIFDAILEGKLDFSADPWPDVS
NGAKDLVKKMLTYDPKDRLTASEVLNHPWIKEDGEASDKPLDNAVLSRMKQFRAMNKLKKMALKVIAENLSEEEIIGLKEMFKALDTDKNGIVTLEELRT
GLPKLGSKISEAEIKQLMEAADMDGDGSIDYLEFISATMHMNRIEREDHLYTAFQYFDKDNSGYITMEELEQAMKKYNMGDDKSIKEIIAEVDTDRDGKI
NYEEFVAMMKKGHPELVTNRRRVNM*
>Brara.B00448 Org_BrapaFPsc peptide: Brara.B00448.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30609053)
MGNCCSQGRDSADNADGYTQDKGITASTAEPSVPQSKHAPPSPPPATKQGPIGPVLGRPMEDVKSSYSLGKELGRGQFGVTHLCTQKATGQQFACKTIAK
RKLVNKEDIEDVRREVQIMHHMTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIIHTCHSMGVIHRDLKPENFLLL
SKDENAPLKATDFGLSVFYKPGDVFKDIVGSAYYIAPEVLKRKYGPEADIWSIGVMLYILLCGVPPFWAESENGIFNAILKGHVDFSSDPWPSLSPQAKD
LVKKMLNSDPKQRLTAAQVLNHPWIKEDGEAPDVPLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDSSGTITLEELRQGLAKQ
GTRLSEYEVQQLMEAADADGNGTIDYGEFIAATMHINRLDREEHLYSAFQHFDKDNSGYITMEELEQALREFGMNDGRDIKEIISEVDGDNDGRINYDEF
VTMMRKGNPDPIPKKRRELSFK*
>Brara.B00817 Org_BrapaFPsc peptide: Brara.B00817.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30607754)
MGNCCGRDTGNNNGEPTYENGVSAEASVKASRHPPASPPPATKQGPIGPVLGRPMEDVKSSYSLGKELGRGQFGVTHLCTQKATGLQFACKTIAKRKLAN
KEDIEDVRREVQIMHHLTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIIHTCHSMGVIHRDLKPENFLLLNKDEN
SPLKATDFGLSVFYKPGEEFKDIVGSAYYIAPEVLRRKYGPEADIWSIGVMLYILLSGVPPFWAESENGIFNAILSGQIDFSTDPWPAISHQAKDLVRKM
LNSDPKQRLTAAQVLNHPWIKEDGEAPDVPLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDDSGTITLEELRQGLAKQGTRLS
EYEVQQLMEAADADGNGTIDYGEFIAATMHINRLDREEHLYSAFQHFDKDNSGYITMEELEQALREFGMNDGRDIKEIISEVDGDNDGRINYEEFVAMMR
KGNPDPNPKKRREMSFK*
>Brara.B00823 Org_BrapaFPsc peptide: Brara.B00823.1.p (1 of 3) PTHR24349:SF116 - CALCIUM-DEPENDENT
PROTEIN KINASE 7 (PAC:30610970)
MGNCCASPGSDTKSKASRPKTKSNPFYSEAYTTTNSSGTGFKLSVLKDPTGHDISLMYDLGREVGRGEFGITYLCTDIKTGEKYACKSISKKKLRTAVDI
EDVRREVEIMKHMPKHPNIVTLKDAFEDDDAVHIVMELCEGGELFDRIVARGHYTERAAAAVMKTILEVVQICHKNGVMHRDLKPENFLFANKKENSPLK
AIDFGLSVFFKPGEGFNEIVGSPYYMAPEVLRRHYGPEVDIWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPRVSDTAKDLVRRMLEPD
PKKRLSAAEVLEHPWIQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSVEEVAGIKEAFEMMDSKKTGKINLEELKHGLHKLGQQQIPDTD
LQILMEAADVDGDGTLNYGEFVAVSVHLKKMANDEHLHKAFSFFDKNQSNYIEIEELREALNDEVDTSSEEVIAAIMQDVDTDKDGRISYEEFAAMMKAG
TDWRKASRQYSRERFNSLSLKLMRDGSLQLEGET*
>Brara.B02654 Org_BrapaFPsc peptide: Brara.B02654.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:30608873)
MGCLSSKHRQEETAAKPSTPITPAQTHVVPEHRKPQTPPTHHQISAPPATVRDPDTILGKPFEDIRKFYSLGKELGRGQFGITYRCREISTGNTYACKSI
LKRKLISKQDKEDVKREIQIMQYLSGQANIVEIKGAYEDRQSVHLVMELCAGGELFDRIIAQGHYSERAAAGIIRSIVNVVQICHFMGVVHRDLKPENFL
LSSKEENAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRSYGKEIDIWSAGVILYILLSGVPPFWAENEKGIFDEVVKGEIDFESQPWPSISESA
KDLVRKMLTKDPRRRITAAQVLEHPWIKGGEAPDKPIDSAVLSRMKQFRAMNKLKKLALKVIAESLSEEEIKGLKTMFANMDTDKSGTITYEELKTGLTR
LGSKLSETEVKQLMEAADVDGNGTIDYFEFISATMHRYKLDRDEHVYKAFQHFDKDNSGHITRDELESAMKEYGMGDEASIKEVISEVDTDNDGRINFEE
FCAMMRSGTTQPQGKLLPFH*
>Brara.B03710 Org_BrapaFPsc peptide: Brara.B03710.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30607565)
MASESRTRWVLPYRTKNLKDDYLLGRVLGQGQFGTTFLCSHNETGQKLACKSIPKRTLLCQEDCDQVLREIQIMHHLSEYPNVVRIQSTYEDETSVHLVM
ELCEGGELFDRIAEKGHYSERDAAKVIKTIVSVVEACHSLGVMHRDLKPENFLFSSSDEDASLKSTDFGVSVFCEPDTTFSELVGSAYYVAPEVLLKHYG
RECDVWSAGVILYVLLCGFAPFDAGTDNGIFREILQGKLDFETDPWPSISESAKDLTMKMLESDPKKRLTAHQVLCHPWIVDDTVAPDKPLDFAVVSRLK
RFSAMNKLKKMALRVVAERLSEEEIGGLKELFKMIDRDNSGTITFKELKDCIRRVGSELVESEIQELLQAADVDGSGTIDYGEFLAATIHLNKLEREENL
VAAFSFFDKDSSGCITLEELQQAWKQFGIKDSNLDKMIKDIDQDNDGQINYGEFVAMMRKGNGNVGISRRTMRNTLNFENFLPE*
>Brara.B03711 Org_BrapaFPsc peptide: Brara.B03711.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30607630)
MVLPHSLVKQDSHTMASESRTRWVLPYKTKNLQDDYLLGRVLGQGQYGTTFLCTHNETGQKLACKSIPKRKLLRQEHFDRVLREIQIMHHLSENPNVVRI
QSTYEDATSVHLVMELCEGGELFERIAKKGHHSEREAAKLTKTIVAVIEACHSLGVMHRDLKPENFLFSSCDEDASIKSIDFGLSVFCKPGSTFSKLVGS
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AYYVAPEVLRRHYDRECDVWSAGVILYMLLCGFPPFNAGTERGIFRKILQGKLDFETDPWPSISESAKDLIKKMLESDPKRRLTAHQVLCHPWIVDDTVA
PDKPLGFAVVSRLKRFSAMNKLKKMALRVVAERLSEEEIGGLKELFKMIDTDNSGTITFEELKDSVRCVGSELVESEIQELLQAADVDESGTIDYGEFLA
ATIHLNKLEREENLVAAFSFFDKDASGCITVDELQQAWKQFGIKDSNLDKMIKDIDQDSDGRIDYGEFVAMMRKGNGGSDGISRGTMRNIQLWNFLDRTF
CFCFKSSYVFNKN*
>Brara.B03712 Org_BrapaFPsc peptide: Brara.B03712.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30608180)
MASESRTRWVLPYKTKNLRDDYVLGRFLGQGQYGTTSLCTHKETGQKLACKTIPKRKLLCQEDYDDVLREIQIMHHLSEYPNVVRIQETYEDDTSVHLVM
ELCEGGELFDRITQKGHYSERDAAKVIKTIVSVVEACHSLGVVHRDLKPENFLFSSTDEDSSLKSTDFGLSVFFKPGATFTDLVGSAYYVAPEVLNRHYG
RECDVWSAGVILYILLCGFPPFNAGTKYGIFRKIRQGKVEFETSPWPSISESAKDLIGKMLESNPQKRLTAHQVLCHPWIVDDTVAPDKPLDFAVVSRLK
RFSAMNKLKKTALRVVAERLSEEEIGGLKELFKMIDTDNSGTITFEELKDSVRRVGSELVESEIKELLEAADVDESGTIDYGEFLAATIHLNKLEREENL
VNAFSFFDKDSSGCITMDELQQAWKQFGIKDSHLDEMIKDIDHDNDGQINYGEFVAMMRKGNDNVGISRRTMRNTLNFENPLPDESNELS*
>Brara.C00182 Org_BrapaFPsc peptide: Brara.C00182.1.p (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:30618202)
MGNTCVGPSRNGFLHSVSAAMWRPRDAADDSVSQTNVDTASEAVSGELRSPSSDQVLNKPPEQLTMPKPGGTNIEIKAKDNVEIQPESKLEEKEETKPET
KEETPADAKPPKKPKHMKRVTSAGLRTESVLQRKTENFKEFYSLGRKLGQGQFGTTFLCVEKSTGKEFACKSIAKRKLLTDEDVEDVRREIQIMHHLSGH
QNVISIKGAYEDVMAVHLVMECCAGGELFDRIIQRGHYTERKAAELTKTIVGVVEACHSLGVMHRDLKPENFLFVSKDEDSLLKTIDFGLSIFFKPDDVF
TDVVGSPYYVAPEVLRKQYGPEADVWSAGVIVYILLSGVPPFWAESEQGIFEQVLHGDLDFSSDPWPSISESAKDLVRKMLVRDPKKRLTAHQVLCHPWV
QVDGVAPDKPLDSAVLSRMKQFSAMNKFKKMALRVIAESLSEEEIAGLKEMFNMIDADKSGQITFEELKAGLKRVGANLKESEILDLMQAADVDNSGTID
YKEFIAATLHLNKIEREDHLFAAFTYFDKDGSGYITPDELQQACEEFGVEDVRIEEMMRDVDQDNDGRIDYNEFVAMMQKGSMTGGGGPVKMGGLEKSFS
NIALKL*
>Brara.C00506 Org_BrapaFPsc peptide: Brara.C00506.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30618726)
MGNCCSGRDSEDGHTQDKGLTDSNTAGPTAEPPVAQSKHAPPSPPPATKQGPIGPVLGRPMEDVKASYSLGKELGRGQFGVTHLCTQKATGQQFACKTIA
KRKLVNKEDIEDVRREVQIMHHMTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIIHTCHSMGVIHRDLKPENFLL
LSKDESSPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLKRKYGPEADIWSIGVMLYILLCGVPPFWAESENGIFNAILKSHVDFSSDPWPSISPQAK
DLVKKMLNSDPKQRLTAAQVLNHPWIKEDGEAPDVPLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDSSGTITLEELRQGLAK
QGTRLSEYEVQQLMEAADADGNGTIDYGEFIAATMHINRLDREEHLYSAFQHFDKDNSGYITMEELEQALREFGMSDGRDIKEIISEVDGDNDGRINYDE
FVAMMRKGNPDQIPKKRRELSFK*
>Brara.C01607 Org_BrapaFPsc peptide: Brara.C01607.1.p (1 of 3) PTHR24349:SF160 - CALCIUM-DEPENDENT
PROTEIN KINASE 24 (PAC:30616615)
MGSCVSSPLKGSPFGKRPVRRRNNSHSKTSSSNPKFVSSTNLSRRLLFQPPSRVLPEPIGDGILLKYELGKELGRGEFGVTHECIEITTRKRFACKRISK
EKLRTEIDVEDVRREVEIMSCLPKHPNIVTFKEAFEDEDAVYLVMEICEGGELFDRIVARGHYTERAAASVTKTILEVVKVCHEHGVIHRDLKPENFLFS
NGTETAQLKAIDFGLSINFKHGQRFNEIVGSPYYMAPEVLRRDYGPEIDVWSAGVILYILLCGVPPFWAETEEGIAHAIVRGHIDFERDPWPKVSKEAKQ
LVKSMLDANPYSRLTVQEVLEHPWIQNAERAPNVNLGDNVRTNIQQFVLMNRFKKKVLRIVADNLPNEEIAAIVQMFETMDTDKNGHLTFEELRDGLKNL
GQVCPDGDVKMLMDAADTDGNGMLSCEEFVTLSIHLKRIGCDEHLQEAFKYFDKNGNGFIELDELKEALFDDKLGQGSDQWIKDIFFDVDLNKDGRISFD
EFKAMMKSGTDWKMASRQYSRALLNALSMKMFKEDFGDSAPKSQSMEFPIARKRAKILDSPKNKSMELGLSKTYKPSGLRY*
>Brara.C01607 Org_BrapaFPsc peptide: Brara.C01607.2.p (1 of 3) PTHR24349:SF160 - CALCIUM-DEPENDENT
PROTEIN KINASE 24 (PAC:30616616)
MGSCVSSPLKGSPFGKRPPPSRVLPEPIGDGILLKYELGKELGRGEFGVTHECIEITTRKRFACKRISKEKLRTEIDVEDVRREVEIMSCLPKHPNIVTF
KEAFEDEDAVYLVMEICEGGELFDRIVARGHYTERAAASVTKTILEVVKVCHEHGVIHRDLKPENFLFSNGTETAQLKAIDFGLSINFKHGQRFNEIVGS
PYYMAPEVLRRDYGPEIDVWSAGVILYILLCGVPPFWAETEEGIAHAIVRGHIDFERDPWPKVSKEAKQLVKSMLDANPYSRLTVQEVLEHPWIQNAERA
PNVNLGDNVRTNIQQFVLMNRFKKKVLRIVADNLPNEEIAAIVQMFETMDTDKNGHLTFEELRDGLKNLGQVCPDGDVKMLMDAADTDGNGMLSCEEFVT
LSIHLKRIGCDEHLQEAFKYFDKNGNGFIELDELKEALFDDKLGQGSDQWIKDIFFDVDLNKDGRISFDEFKAMMKSGTDWKMASRQYSRALLNALSMKM
FKEDFGDSAPKSQSMEFPIARKRAKILDSPKNKSMELGLSKTYKPSGLRY*
>Brara.C01984 Org_BrapaFPsc peptide: Brara.C01984.1.p (1 of 1) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:30618339)
MGNTCTGPKLNPNGFLQSVSAAVWRNQKPDESLESNKDDSSKKKSVHGGDNAPSAVDPTPSTPPPPVKMANEEAPKCINNDENPKPKKEAHMKRMASAGL
QIDSVLGRKTENLKEIYSVGRKLGQGQFGTTFLCVDKKTNKELACKTIAKRKLTTPEDIEDVRREIQIMHHLSGHPNVIQIVGAYEDAVGVHVVMEICAG
GELFDRIIQRGHYTERKAAELARTIVGVIEACHSLGVMHRDLKPENFLFVSGDEEAALKTIDFGLSVFFKPGETFSDVVGSPYYVAPEVLKKHYSHECDV
WSAGVIIYILLSGVPPFWDETEQGIFEQVLKGDLDFVSEPWPSVSESAKDLVRRMLIRDPKKRMTAHEVLCHPWARVDGVALDKPLDSAVLSRLKQFSAM
NKLKKIAIKVIAESLSEEEIAGLKEMFKMIDTDNSGHITLEELKKGLDRVGANLKDSEILGLMQAADIDNSGTIDYGEFIAAMVHLNKIQKEDHLFTAFS
YFDKDGSGYITREELQQGCKQFGLADVHLDDIISEVDKDNDGRIDYSEFVEMMQDTGFGKMGLRVS*
>Brara.C02607 Org_BrapaFPsc peptide: Brara.C02607.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30617300)
MEKPSSRRPSSSVLPYETPRLRDHYLLGKKLGQGQFGTTYLCTEKSSSANYACKSIPKRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVH
IVMEVCEGGELFDRIVSKGHFSEREAAKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPNDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK
CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLS
RLKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMERE
ENLVVAFSYFDKDGSGYITIDELQQACTEFGLCDTPLDDMIKEIDLDNDGRIDFSEFTAMMKKGDGVGRSRTMMKNLNFNIADAFGVEETSSAETDDKPN
*
>Brara.C03333 Org_BrapaFPsc peptide: Brara.C03333.1.p (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:30617367)
MGNVCVGPTISGNSFVQAVSAAIWRPRIGAEQQASSHGKGEASKEAASSHGKGEASKEAASSHGKAEVSKEASSSEPLPDQVQNKPPEQVTMSNPRTIPE
AETKSKPEEVKQEVVVQVETTKPETKSETKPETKPDPNKPKHMRRVSSAGLRTESVLQRKTENFKEFYSLGRKLGQGQFGTTFLCVEKGTGKEYACKSIS
KRKLLTDEDVEDVRREIQIMHHLAGHPNVISIKGAYEDVVAVHLVMELCSGGELFDRIIQRGHYTERKAAELARTIVGVLETCHSLGVMHRDLKPENFLF
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VSKEEDSLLKTIDFGLSMFFKPDEIFTDVVGSPYYVAPEVLRKRYGSESDVWSAGVIVYILLSGVPPFWAETEQGIFEQVLHGDLDFSSDPWPSISEGAK
DLVQKMLVRDPKRRLTAHQVLCHPWVQIDGVAPDKPLDSAVLSRMKQFSAMNKFKKMALRVIAESLSEEEIAGLKEMFKMIDADNSGQITFEELKVGLKR
VGANLKESEILDLMQAADVDNSGTIDYKEFIAATLHLNKIEREDHLFAAFSYFDKDDSGFITHDELQQACEEFGVEDARIEEMIRDVDQDKDGRIDYNEF
VAMMQKGSIMGGGPMKMGLEKSISISLKH*
>Brara.C03790 Org_BrapaFPsc peptide: Brara.C03790.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:30617675)
MGNCFAKNHGLMKPQQNGQTRSVEVDQTHQDPPSYTPQPRSQTPEKPSSETNQPPPWRMAAPAPSPKAAKSSSTSILENAYEDVKLFYTLGKELGRGQFG
VTYLCTENSTGKKYACKSISKKKLVTKADKDDMRREIQIMQHLSGQPNIVEFKGAYEDEKAVNLVMELCAGGELFDRIIAKGHYSERAAASVCRQIVNVV
KICHFMGVLHRDLKPENFLLSSKDDKALIKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRRYGKEVDIWSAGIILYILLSGVPPFWAETEKGIFDAI
LEGHIDFESQPWPSISNSAKDLVRKMLTADPKRRISAADVLGHPWLREGGEASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAENINTEEIQGLKAMFAN
IDTDNSGTITYEELKEGLAKLGSKLTEAEVKQLMDAADVDGNGSIDYIEFITATMHRHRLESDENLYKAFQHFDKDGSGYITIDELEVALKEYGMGDDAT
IKEVLSDVDSDNDGRINYEEFCAMMRSGNPQQQQQQQPPRLF*
>Brara.C04385 Org_BrapaFPsc peptide: Brara.C04385.1.p (1 of 3) PTHR24349//PTHR24349:SF145 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30616576)
MGNCCRSPASVAREDVKSNYSGNDHRRKDAAGGKKPAPIRVLGDVPKENIEDRYLLDRELGRGEFGVTYLCIVRSTRDLLACKSISKRKLRTDVDVEDVK
REVAIMQHLPESSSIVTLKEACEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAGVTKTIMEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGEKFSTIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGIIDFKREPWPNISETAKSLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFKRKALRVIAEFLSTQEVEDIKEMFNKMDTDKDGIVTIEELKAGLRDFGTQLAESEVQMLI
EAVDTKGKGTLDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPQELCEALKEDGGDDCVDVANDIFQEVDTDKDGRISYEEFAAMMKTGTDWRK
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)
MGNCCRSPAAVAREDVKSNYSGRDHHRKDASGGKKLAPIRVLSEVPKENIEERYLLDRELGRGEFGVTYLCIERSTRDLLACKSISKRKLRTAVDIEDVK
REVAIMKHLPKSSSIVTLKEACEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAGVTKTIVEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGEKFSEIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGIIDFKREPWPNISETAKNLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFKRKALRVIAEFLSTQEVEDIKEMFNKMDTDKDGIVTIEELKAGLRDFGTQLAESEVQMLI
EAVDTKGKGTLDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPQELCEALKEDGGDDCVDVANDIFQEVDTDKDGRISYEEFAAMMKTGTDWRK
ASRHYSRGRFNSLSIKLMKDGSLNLGNE*
>Brara.D00630 Org_BrapaFPsc peptide: Brara.D00630.2.p (1 of 3) PTHR24349//PTHR24349:SF145 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30621871)
MGNCCRSPAAVAREDVKSNYSGRDHHRKDASGGKKLAPIRVLSEVPKENIEERYLLDRELGRGEFGVTYLCIERSTRDLLACKSISKRKLRTAVDIEDVK
REVAIMKHLPKSSSIVTLKEACEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAGVTKTIVEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGEKFSEIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGIIDFKREPWPNISETAKNLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFKRKALRVIAEFLSTQEVEDIKEMFNKMDTDKDGIVTIEELKAGLRDFGTQLAESEVQMLI
EAVDTKGKGTLDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPQELCEALKEDGGDDCVDVANDIFQEVDTDKDGRISYEEFAAMMKTGTDWRK
ASRHYSRGRFNSLSIKLMKDGSLNLGNE*
>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)
MGSCVSSPLKGSPFRKRPVRRRKSSKSKTSTNPRVDSSTNLSRRLIFQPPSRVLPEPIGDGIFVKYELGKELGRGEFGVTHECIEITTRERFACKRISKE
KLRTEIDVEDVRREVEIMRSLPKHPNIVSFKEAFEDKEAVYLVMEICEGGELFDRIVSRGHYTERAAASVAKTILEVVKVCHEHGVIHRDLKPENFLFSN
ETETAQLKAIDFGLSIFFKPGQRFNEIVGSPYYMAPEVLRRNYGPEVDVWSAGVILYILLCGVPPFWAETEEGIAHAIVRGNIDFERDPWPKVSAEAKEL
VKDMLDANPYSRLTVQEVLEHPWIQNAERAPNVNLGDNVRTKIQQFLLMNRFKKKVLRIVADNLPNKEIEEIVQMFRTMDTDKNGRLTFEELRDGLKKFG
TVCPDGDVKMLMDAADTDGNGMLSCEEFVTLAIHLKRMGCDEHLQQAFKYFDKNGNGSIELDELKEALFDDDKLGQGNDQWIKDIFFDVDLNKDGRISFD
EFKAMMKSGTDWKMASRQYSRALLNALSIKMFKEDGGNNGPKFHSMEFPVARKKANILDPKNKSMELVHSRTYKPSGLRN*
>Brara.D02174 Org_BrapaFPsc peptide: Brara.D02174.1.p (1 of 2) PTHR24349:SF128 - CALCIUM-DEPENDENT
PROTEIN KINASE 25 (PAC:30621670)
MGNVCIHMVNNCVDTKSNTWVRPTDLIMDHPVKPQLPDKPPQQMLMHKDDDKPKLETSGEDPKLLEESDSHQEQQEGSTSEERKKRAARIACGNSKRKPH
NVKRLMSAGLQAESVLKTKTGHLKEYYNLGSKLGHGQFGTTFVCTEKGTGEEYACKSIPKRKLENEEDVEDVRREIEIMKHLLGQPNVISIKGAYEDAVA
VHMVMELCRGGELFDRIVERGHYSERKAAHLAKVILGVVQTCHSLGVMHRDLKPENFLFVDDQEDSPLKAIDFGLSMFVKPGENFSDVVGSPYYIAPEIL
NKDYGPEADIWSAGVMIYVLLSGSAPFWGETEEEIFNEVLEGELDLSSDPWPQVSESAKDLIRKMLERDPKKRLTAQQVLGHPWIRDEGNAPDTPLDATV
LNRLKKFSETDKLKKIALQVTVERLSEEKIRSLRETFKIIDSEKSGKVTYKELKSILERFDTNLDNSDISGLMQMPMNEHLEDTVDYEEFIAAIVRLKEL
QDEEANDRLDSSTKV*
>Brara.D02546 Org_BrapaFPsc peptide: Brara.D02546.1.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT
PROTEIN KINASE 14 (PAC:30623178)
MGNCCGTGGTLIGNDKNKKGFKIANPFSIDYGRRHDGDKLVVLKEPTGRDIKLRYNLGRELGRGEFGVTYLCTDNETGESFACKSILKKKLRTAVDIDDV
RREAEIMRVMPEHPNIVTLKETYEDDKAVHLVMELCGGGELFDRIVARGHYTERAAASVIKTIMEVVQMCHKHGVMHRDLKPENFLFANKKETAPLKAID
FGLSIFFKPGEKFNEIVGSPYYMAPEVLKQSYGPEIDIWSAGVILYILLCGVPPFWAETDHGVAKAILKSVIDFRRDPLPKVSSNAKDLIKRMLHPDPKL
RLTAQQVLDHPWIQDGKNASNVSLGESVRARLKQFTVMNKLKKRALRVIAEHLSVEEASGIIERFQVMDTSNRGKITIQELRLGLRKLGIVVPQDDIQIL
MDAGDVDKDGYIDINEFVAISVHIRKMGNDEHLKKAFKFFDLDKSGYIEIDELRDALADEFDTTSEEVVEAIIYDVDTNKDGRISYEEFATMMKTGTDWR
KASRQYSRDRFKNLSRKLMQDGSLQSHGDTK*
>Brara.E00252 Org_BrapaFPsc peptide: Brara.E00252.1.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT
PROTEIN KINASE 14 (PAC:30626664)
MGNCCGTAGSLIVNEKLKKGLKLANPFSIDYGHRHDGEKLVVLKEPTGREIKLRYKLGRELGRGEFGVTYLCTDNETGDVFACKSILKKKLRTAVDIDDV
RREAEIMRIMPEHPNIVTLKETYEDDKAVHLVMELCEGGELFDRIVARGHYTERAAASVVKTIMEVVQMCHKHGVMHRDLKPENFLFANKKETASLKAID
FGLSVFFKPGERFNEIVGSPYYMAPEVLKQSYGPEIDIWSAGVILYILLCGVPPFWAETDHGVAKAILRSVIDFRRDPWPKVSANAKDLIKKMLHPDPKR
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RLTAQQVLEHPWLQDGKNAPNVSLGETVRARLKQFTVMNKLKKRALRVIAEHLSVEEASGIKERFQVMDTSNRGKITIEELRIGLRKLGIVVPQDDIQIL
MDAGDVDKDGYLDVNEFVAISVHIRKMGSDEHLKTAFSFFDQNKSGYIEIEELREALANEFDTTSEEVVEAIILDVDTNKDGRISYEEFATMMKTGTDWR
KASKQFSRDRFKNLSIKLKEEGSLNSNNCDAE*
>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)
MGSCVSSPLKGSPFGKRPARRRNNSSSTKTSSNPKTDTSSTSTLSRRLIFQPPSRVLPEPIGDGIFLKYELGKELGRGEFGVTHECIEISTRERFACKRI
SKEKLRTEIDVEDVRREVEIMRSLPKHANIVSFKEAFEDKDAVYLVMEICEGGELFDRIVSRGHYTERAAASVAKTILEVVKVCHEHGVIHRDLKPENFL
FSNETETAQLKAIDFGLSIFFKPAQRFNEIVGSPYYMAPEVLRRNYGPEIDVWSAGVILYILLCGVPPFWAETEEGIAHAIVRGNIDFERDPWPKVSREA
KELVKNMLDANPYSRLTVQEVLEHPWIQNAERAPNVNLGDGVRTKIQQFLLMNRFKKKVLRVVADNLPNEEIESIIQMFQTMDTDKNGHLTFEELRDGLK
KIGQVCPDGDVKMLMDAADTDGNGTLSCEEFVTLAIHLKRMGCDEHLQQAFKYFDKNGNGSIELDELKEALFDDDKLGHGGDQWIKDIFFDVDLNKDGRI
SFDEFRAMMKSGTDWKMASRQYSRALLNALSIKMFKEDVGDNGPKSYSMEFPLARKKAKLLDAPKNKSMELVHSKTYRPSGLRN*
>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)
MGCFWSKNQPPSDGELQNILGKPLGDIKNYYSFGKELGKGNLGTTYMCEEILTGRSYACKSIPKGKLKSQEDKEAVKKEIEIMFRLSCQHNIVSIKSVYE
DRECIHVVMELCGGGELSSRIEAHSYYSEKDSAGILKSIVNALQTCHSMSVIHRDVKPENFLFSSEVENTVLKAIGFGSSVYIKQETELKRKVESKYYLA
PEVLQGKSYGKEIDIWSAGVILYLLLCGKHPFETESKIRRGSLDLESKPWPCVSESAKDLVKKMLTKDPKSRISASDVLEHSWIKMQAPYKPIDNVLVLC
MKRFGAMNKLKKLALNADVDGNGRIDLCEYISATTETNVLVTDENLHKAFQFFDKDGSGYITKDNLMKHVVGNEANAKDIISEVDTDNDGRIDYEEFCAM
MRDGKLQPQGKRVRIN*
>Brara.E01819 Org_BrapaFPsc peptide: Brara.E01819.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30623678)
MEKANPRRPSNTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVH
LVMEVCEGGELFDRIVAKGHFSEREAVKLIKTILAVVEACHSLGVMHRDLKPENFLFDSPKEDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK
CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEEAAPDKPLDPAVLS
RLKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMERE
ENLVAAFSYFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMKKGDGVGRSRTMMKNLNFNIADAFGVDEQSAQKSDD*
>Brara.E02997 Org_BrapaFPsc peptide: Brara.E02997.1.p (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:30626505)
MGNVCVGPNLSGNGFLQTVSAALWKPRIGAEQASSSHGNAQQVPKEAAAEVSKEAVPDQVQNKPPEQVTMPNPSSIPEAETKPKPEPEEAKQEVVVQVET
STKTETKPEPKPEPTKPETKPETNPETKPDPNKPKHMRRVSSAGLRTESVLQRKTENFKEFYSLGRKLGQGQFGTTFLCLEKGTGNEYACKSISKRKLLT
DEDVEDVRREIQIMHHLAGHPNVISIKGAYEDVVAVHLVMELCSGGELFDRIIQRGHYTERKAAELARTIVGVLETCHSLGVMHRDLKPENFLFVSREED
SLLKTIDFGLSMFFKPDEVFTDVVGSPYYVAPEVLRKRYGPESDVWSAGVIVYILLSGVPPFWAETEQGIFEQVLHGDLDFSSDPWPSISDGAKDLVQKM
LVRDPKRRLTAHQVLCHPWVQIDGVAPDKPLDSAVLSRMKQFSAMNKFKKMALRVIAESLSEEEIAGLKEMFKMIDADNSGQITFEELKAGLKRVGANLK
ESEILDLMQAADVDNSGTIDYKEFIAATLHLNKIEKEDHLFAAFSYFDKDGSGFITPDELQHACEEFGVEDARIEEMMRDVDQDKDGRIDYNEFVAMMQK
GSIMGGPMKMGLEKSISISLKH*
>Brara.F01336 Org_BrapaFPsc peptide: Brara.F01336.1.p (1 of 3) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:30630361)
MGNCNVCVKPPNSEDSTQKPKTPNRDRKPNPYAAGAIVRSPGTTLKDAVIPTSHRTKISDKYILGRELGRGEFGITHLCTDRETREALACKSISKRKLRT
AVDVEDVRREVAIMSTLPDHPNVVKLRATYEDGENVHLVMELCEGGELFDRIVARGHYTERAAAGVARTIAEVVMMCHSNGVVHRDLKPENFLFANKKEN
SALKAIDFGLSVFFKPGDKFTEIVGSPYYMAPEVLKRDYGPEVDVWSAGVIIYILLCGVPPFWAETEQGVALAILRGVIDFKRDPWPQVSESAKSLVRQM
LDPDPAKRLTAQQVLAHPWIQHAKKAPNVPLGDIVRSRLKQFSMMNRFKKKVLRVIAEHLSVQEVEVIKDMFSLMDEDNDGRITYPELKAGLQKVGSQLG
EPEIKMLMEVADVDGNGFLDYGEFVAVIIHLQKIENDELFKLAFMFFDKDGSTYIELDELREALTDELGEPDVSVLNDIMREVDADKDGRINYDEFVTMM
KAGTDWRKASRQYSRERFKSLSLNLMKDGSLHLHDALTGQSVPV*
>Brara.F02560 Org_BrapaFPsc peptide: Brara.F02560.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:30631163)
MGNSCRGSFKDKVYEGNNSRPEENSRTTTNDHSPTAEQDFPKEDSNNNPVPVKEPFIRRNMDNQAYYVLGHKTPNIRDLYTLSRKLGQGQFGTTYLCTEV
ATGVDYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDPLYVHIVMEVCAGGELFDRIIQRGHYSERKAAELTKIVVGVVEACHSLGV
MHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFKDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGDVDFE
SDPWPVISDSAKDLISKMLCSRPSERLTAHEVLRHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALKVIAESLSEEEIAGLRAMFEAMDTDNSGA
ITFDELKAGLRRYGSTLKDTEIRDLMEAADVDNSGTIDYSEFIAATIHLNKLDREEHLVSAFQYFDKDGSGYITIDELQQSCVEHGMTDVFLEDVIKEVD
QDNDGRIDYGEFVAMMQKGNAGVGRRTMKNSLNISMRDV*
>Brara.F02597 Org_BrapaFPsc peptide: Brara.F02597.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30631379)
MHHLSEYPNVVRIQDTYEDSNSVHLVMELCEGGELFDRIVKKGHYSEREAAKLMKTIVGVVETCHSLGVLHRDLKPENFLFASCDEDASLKSTDFGLSVF
CKPGATFSELVGSAYYVAPEVLHKHYSRECDVWSAGVILYILLCGFPPFWAESEIGIFRKILQGKLNFETNPWPSISESAKDLIKKMLEGNPKKRLTAHQ
VLCHPWIVDDTVAPDKPLDCAVVSRLKKFSAMNKLKKMALRVIAERLSEEEIGGLKEMFKMIDTDDSGTITFEELKDSMKRVGSELMESEIQELLHAADV
DESGTIDYGEFLAATIHLNKLEREENLVAAFSFFDKDASGYITIDELQQAWKEFGINDSHLDEMIKDIDQDNDGQIDYGEFVAMMRKGNGNGGIGRRTMR
NTLSFENPLPDESING*
>Brara.F03923 Org_BrapaFPsc peptide: Brara.F03923.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:30629157)
MKHSGGNQACFVLGQKTPSIRDLYSLGHKLGQGQFGTTYMCREISTGREYACKSITKRKLISKEDVEDVRREIQIMHHLAGYKNIVTIKGAYEDPLYVHI
VMELCSGGELFDRIIQRGHYSERKAAELIKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFEDVVGSPYYVAPEVLLKH
YGPEADVWTAGVILYILVSGVPPFWAETQQGIFDAVLKGHIDFDSDPWPLISDSAKDLIRGMLCSRPSERLTAHQVLRHPWICENGVAPDRALDPAVLSR
LKQFSAMNKLKQMALRVIAESLSEEEIAGLKEMFKAMDTDNSGAITFDELKAGLRRYGSTLKDTEIRDLMEAADIDKSGTIDYGEFIAATIHLNKLDREE
HLLSAFSYFDKDGSGYITIDELQQACAEQGMSDVFLEDVIKEVDQDNDGRIDYGEFVAMMQKGIAGRTMRQSINMSLRKNA*
>Brara.G01743 Org_BrapaFPsc peptide: Brara.G01743.1.p (1 of 2) PTHR24349:SF126 - CALCIUM-DEPENDENT
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PROTEIN KINASE 32 (PAC:30633874)
MGNCCGTAGSFPQNDDSNKPKKGKKKQNPFSIDYGLHHNGGGGGGLKLTVLSDPTGREIEQKYTLGRELGRGEFGVTYLCTDKETGGVLACKSILKKKLR
TAVDIEDVRREAEIMRHMPEHPNLVTLKETYEDEYAVHLVMELCEGGELFDRIVARGHYTERAAAAVTKTIIEVVQVCHKHGVMHRDLKPENFLFANKKE
TAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYGPEVDIWSAGVILYILLCGVPPFWAETEQGVAQAIIRSQLDFRRDPWPKVSEHAKDLIRK
MLDPDQKRRLTAQQVLDHPWLQNANTAPNVSLGETVRARLKQFTVMNKLKKRALRVIAEHLSDEEASGIREGFQIMDTSQRGKINIDELKIGLQKLGHNI
PQDDIQILMDAGDTDKDGYLDCDEFIAISVHLRKMGNDEHLKKAFAFFDQDNNGYIEIEELREALSDEVGTSEEVVDAIIRDVDTDKDGRISYEEFVTMM
KTGTDWRKASRQYSRERFTSISLKLMQDASLHANGDTR*
>Brara.G03159 Org_BrapaFPsc peptide: Brara.G03159.1.p (1 of 3) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:30635005)
MGNCIACVNFDPEADSKQTKNQTKKRHVRKPNAYHDPDGLRSHGPIRVLPDVPMSHRTQISDKYILGRELGRGEFGITYLCTDRETREALACKSISKRKL
RTAVDVEDVRREVTIMSTIPDHPNVVKLKATYEDNENVHLVMELCEGGELFDRIVARGHYTERAAATVARTIAEVVKMCHMNGVMHRDLKPENFLFANKK
ENSALKAIDFGLSVLFKPGERFTEIVGSPYYMAPEVLKRDYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVLDFKRDPWSQISESAKSLVK
QMLNPDPTKRLTAQQVLDHPWIQNAKKAPNVPLGDIVRSRLKQFSMMNRLKKKALRVIAEHLSIQEVEVIRDMFTLMDDDNDGKITYPELRAGLKKVGSQ
LGEPEIKMLMEVADVNGNGCLDYGEFVAVIIHLQKMENDEHFRQAFMFFDKDGSGYIESDELRRALTDELGEPDNSVVIDIMREVDTDKDGRINYDEFVV
MMKAGTDWRKASRQYSRERFKSLSINLMKDGSLHLHDALTGQSVAV*
>Brara.G03397 Org_BrapaFPsc peptide: Brara.G03397.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:30635009)
MFRKLNKATRNKRNQNTRTKHFFNRMGFCFSKSQTQEIPISSSSDSTPPHRYQPLPKPTNPQTQTSTFPTTPKPKPAPPPSSSGSQIGPILNRPMIDLSA
LYDLHKELGRGQFGITYRCTDKSNGREYACKSISKRKLIRQKDIEDVRREVMILQHLTGQPNIVEFRGAYEDKDNLHVVMELCSGGELFDRIIKKGSYSE
KEAANIFRQIVNVVHVCHFMGVVHRDLKPENFLLVSADDDSPIKATDFGLSVFIEEGKVYKDVVGSAYYVAPEVLHRNYGKEIDVWSAGVMLYILLCGVP
PFWGETEKTIFEAVLEGNLDLESSPWPTISESAKDLIRKMLARDPKKRITAAEALAHPWLTDSEVSDKPIDSAVLIRMKQFRAMNKLKKLALKVIAENLS
EEEIKGLKQMFKNIDTDGSGTITFDELRTGLHRLGSKLTESEIKQLMEAADVDKSGTIDYIEFITATMHRHRLEKEEHLLEAFKYFDKDRSGYITRDELK
HSMTQYGMGDDATIDEVINDVDTDNDGRINYEEFVAMMTKGTTDHSDAKLIR*
>Brara.I00608 Org_BrapaFPsc peptide: Brara.I00608.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30643355)
MANKSRTRWVLPYTTKNVEDDYFLGQILGQGQFGTTFLCTHKKTAQKLACKSIPKRKLLCQEDYDDVLREIQIMHHLSEFPNVVRIEGAYEDTSSVHIVM
ELCEGGELFDRIVKRGHYSEREAAKLIKTIVGVVEACHSLGVMHRDLKPENFLFASCDEDASLKSTDFGLSVFCKPGATFSELVGSAYYVAPEVLHKHYS
RECDVWSAGVILYILLCGFPPFWDESEFGIFRKILQGKIDFETSPWPSISESAKDLIVKMLEKDPKKRLTAHQVLCHPWIVDDKVAPDKPLDCAVLSRLK
NFSAMNKLKKMAFRVIAERLSEEEIGGLKELFRMIDTDNSGTITFEELKDTVKRVGADLMESEIQELLRSADVDENGSIDYGEFLAATIHLNKLEREENL
VAAFSFFDKDGSGYITVDELQHALKEFGINDSHLDEMIKDIDQDNDGQIDYGEFVAMMRKGNGSGGISRRTMRNTLNFANWKVASS*
>Brara.I01019 Org_BrapaFPsc peptide: Brara.I01019.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:30646539)
MGNSCRGSFKDKTYEGNNNLPEENSITITHVSSVHSPTTEQDFPKEDNNNNNNKSPVLVLPVKEPFMRRNMDNQAYYVLGHKTPNIRDLYTLSRKLGQGQ
FGTTYLCTEVATGVDYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDPLYVHIVMEVCAGGELFDRIIQRGHYTERKAAELTKIVVG
VVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFKDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFD
AVLKGDIDFESDPWPVISDSAKDLIRKMLCSNPSERLTAHEVMRHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALKVIAESLSEEEIAGLRAMF
EAMDTDNSGAITFDELKAGLRRYGSTLKDTEIQDLMEAADVDNSGTIDYSEFIAATIHLNKLDREEHLVSAFQYFDKDGSGYITIDELQQSCVEHGMTDV
FLEDVIKEVDQDNDGRIDYGEFVAMMQKGNAGIGRRTMRNSLNISMRDA*
>Brara.I02207 Org_BrapaFPsc peptide: Brara.I02207.1.p (1 of 3) PTHR24349:SF23 - MAP KINASE-ACTIVATED
PROTEIN KINASE 5 (PAC:30643178)
MGCCGSKSLPASDLVTEREPAGTILGKPLVEFKKLYKLGEELGKGGFATTYMCQEISTGRSFACKSIPKRNLTSQEAVKTEIEIMENLSGVSNIVQFHAS
YEDKNFVHIVMELCRGGELFDRIHALVKSHRYYTEKDAAGIFKSIVNAVQICHSMNVIHRDVKPENFLFSSDDEESSKLKAIDFGCSVYIKEGVELKEKV
GSLYYIAPEVLREESYGKEIDIWSAGVILYILLSGSPPFGNDDEIKKGIIDFDSQPWPCISVGAKDLIKRMLNKNQKERISAENVLEHPWILSEAPDKPI
DGVIAEGLSEEEIRSLKTMFESMDTDKSGSITYEELKTGLNRLGSKLPEAEVKQLMEAADVDGNGTIDYIEFITATMQRHRLERDEHLHKAFLHFDKDNS
GYITKDELEIAMKEHGMGDEACAKEIISEIDKNYDGKIDYEEFCAMMRSVNLQGQLIHH*
>Brara.I03514 Org_BrapaFPsc peptide: Brara.I03514.1.p (1 of 3) PTHR24349//PTHR24349:SF145 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:30643998)
MGNCCRSPAAVAREDVKSNYSGHDHPRKDSTNGKKSAPIRVLTDVPKENIEDRYLLDRELGRGEFGVTYLCIERATRDLLACKSISKRKLRTAVDIEDVK
REVAIMRHLPKSSSIVTLKEACEDDSAVHLVMELCEGGELFDRIVARGHYTERAAAGVTKTIVEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGEKFSEIVGSPYYMAPEVLKRSYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGIIDFKREPWPNISETAKSLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFKRKALRVIAEFLSSQEVEDIKEMFNKMDTDKDGIVTIEELKAGLRDFGTQLAESEVQMLI
EAVDTKGKGALDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPEELCEALKEDGGDDCVDVANDIFQEVDTDKDGRISYEEFAAMMKTGTDWRK
ASRHYSRGRFNSLSIKLMKDGSLNLGNE*
>Brara.I03972 Org_BrapaFPsc peptide: Brara.I03972.1.p (1 of 2) PTHR24349:SF126 - CALCIUM-DEPENDENT
PROTEIN KINASE 32 (PAC:30646230)
MGNCCGSAGSLANNDNNKPTKGRKKQNPFSIDYGLHHGNNNGGVKVKPLKLIVLTDPTGREISQKYKLGRELGRGEFGVTYLCTDKETEEVFACKSILKK
KLRTAVDIEDVRREVEIMRHMPEHPNVVTLKETYEDEIAVHLVMELCEGGELFDRIVARGHYTERAAAVVTKTIMEVVQVCHKHGVMHRDLKPENFLFAN
KKETAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYGPEVDIWSAGVILYILLCGVPPFWAETEQGVALAIIRSQLNFRRDPWPKVSENAKDL
IRKMLDPDQKRRLTAQQVLDHPWLQNAKTAPNVSLGETVRARLKQFTVMNKLKKRALRVIAEHLSDEEASGIREGFQIMDTNQRGKINIDELKIGLQKLG
HAVPQDDLQILMDAGDIDKDGYLDCDEFIAISVHLRKMGNGEHLKKAFAFFDQDNNGYIEIEELREALSDEVGTSEEVVEAIIRDVDTDKDGRISYEEFA
TMMKTGTDWRKASRQYSRERFNSISQKLMQDASLHVNSEAI*
>Brara.I04763 Org_BrapaFPsc peptide: Brara.I04763.1.p (1 of 3) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:30641261)
MGNCNVCVRPPPNPEESKPTPKPKKTNQNRKLNPFTSDFIRSPVRTRAAKDAVIPTSHQTKITDKYILGRELGRGEFGITYLCTDRESREALACKSISKR
KLRTAVDVEDVRREVSIMSTLPDHPNVVKLRATYEDGENVHLVMELCEGGELFDRIVARGHYTERAAAGVARTIAEVVMMCHVNGVVHRDLKPENFLFAN
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KKENSALKAIDFGLSVFFKPGEKFKEIVGSPYYMAPEVLKRDYGPEVDVWSAGVIIYILLCGVPPFWAETEQGVALAILRGVIDFKRDPWPQISESAKSL
VRQMLNPDPTKRLTAQQVLAHPWVQNAKKAPNVPLGDIVRSRLKQFSMMNRFKKKVLRVIAEHLSIQEVEVIKDMFSLMDEDNDGRITYLELKAGLQKVG
SQLGEPEIKMLMEVADVDGNGFLDYGEFVAVIIHLQKIENDELFKLAFMFFDKDGSTYIELDELREALTDELGEPDVSVLNDIMREVDSDKDGRINYDEF
VTMMKAGTDWRKASRQYSRERFKSLSINLMKDGSLHLHDALTGQSVPV*
>Brara.J01554 Org_BrapaFPsc peptide: Brara.J01554.1.p (1 of 8) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:30611977)
MSDSQTMASESRTSWVLPYKTKNLKDDYVLDRVLGQGQFGTTFLCTHSETGQKLACKSIPKRKLLCQEDCDDVLREIQIMHHLSEYPNVVRIQSTYEDAN
DVHLVMELCEGGELFDRIEKKGHYSEREAAKLIKTIVAVVEACHSLGVMHRDLKPENFLFSSDDEDASLKSTDFGLSVFCKPGATFTQLVGSAYYVAPEV
LHRHYGRECDVWSAGVILYIMLCGFAPFDAGTQYGIFRKILQGKLDFETSPWPSISESAKDLIKKMLESNPKKRLTAHQVLCHPWIVDDTVAPDKPLDFA
VVSRLKRFSAMNKLKKMALRIVAERLSEEEIGGLKELFKMIDTDNSGTITFEELKDSIRRVGSELVESEIQELLQAADVDESGTIDYGEFLAATIHLNKL
EREENLVDAFSFFDKDASGCITIDELQQAWNQFGIKDSHLDEMIKDIDQDNDGQIDYGEFVAMMRKGNGNVGISRRTMRNTLSFENPPPQESNE*
>Brara.J01642 Org_BrapaFPsc peptide: Brara.J01642.1.p (1 of 3) PTHR24349:SF116 - CALCIUM-DEPENDENT
PROTEIN KINASE 7 (PAC:30611728)
MGNCCATPGSDSKSKDAKPKTRNNPFYSEAYTTTNRSGAGFKLSVLKDPTGHDITLMYDLGREVGRGEFGITYLCTDINTGEKYACKSISKKKLRTAVDI
EDVRREVEIMKHMPKHPNIVSLKDAFEDDDAVHIVMELCEGGELFDRIVARGHYTERAAAAVMKTILEVVQVCHKNGVMHRDLKPENFLFANKKETSPLK
AIDFGLSVFFRPGEGFNEIVGSPYYMAPEVLRRNYGPEVDIWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPRVSDTAKDLVRKMLEPD
PKKRLSAAEVLEHSWIQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSVEEVAGIKEAFEMMDSNKTGKINLEQLKHGLHKLGQQQMADAD
LQILMEAADVDGDGTLNYGEFVAVSVHLKKMANDEHLHKAFSFFDQNQSNYIEIEELRQALNDEEDTSSEEVIAAIMQDVDTDKDGRISYEEFVAMMKAG
TDWRKASRQYSRERFNSLSLKLMRDGSLQLEGET*
>Brara.J01648 Org_BrapaFPsc peptide: Brara.J01648.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30611859)
MGNCCAHGREEPTQEKGLGDGAEASVKASRHSPASPPPATKQGPIGPVLGRPMEDVKSSYSLGKELGRGQFGVTYLCTQKATGLQFACKTIAKRKLVNKE
DIEDVRREVQIMHHLTGQPNIVELKGAYEDKHNVHLVMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIIHTCHSMGVIHRDLKPENFLLLNKEENSP
LKATDFGLSVFYKPGEEFKDIVGSAYYIAPEVLKRKYGPEADIWSIGVMLYILLCGVPPFWAESENGIFNAILSGQIDFASDPWPAISHQAKDLVRKMLN
SDPKQRLTAAQVLNHPWIKEDGEAPDVPLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDDSGTITLEELRQGLAKQGTRLSEY
EVQQLMEAADADGNGTIDYGEFIAATMHINRLDREEHLFSAFQHFDKDNSGYITMEELEQALREFGMSDGRDIKEIISEVDGDNDGRINYEEFVAMMRKG
NPDPNPKKRRELSFDTT*
>Brara.J02143 Org_BrapaFPsc peptide: Brara.J02143.1.p (1 of 3) PTHR24349:SF116 - CALCIUM-DEPENDENT
PROTEIN KINASE 7 (PAC:30612058)
MGNCCGSPSSATIESGHGKPKNKNNPFHSNEANGSGAGFKLSVLKDPTGHDISSQYDLGREVGRGEFGVTYLCTDIQTGDKYACKSISKKKLRTAVDIGD
VRREVEIMRHMPKHPNIVSLKDSFEDDDAVHIVMELCEGGELFDRIVARGHYTERAAAAVMKTIVEVVQICHKQGVMHRDLKPENFLFANKKESSALKAI
DFGLSVFFKPGEQFNEIVGSPYYMAPEVLRRNYGPEIDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPRVSESAKDLVRKMLEPDPK
KRLSAAEVLEHTWILNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSVEEAAGIKEAFEMMDVNKRGKINLEELKYGLQKAGQQIADADLQI
LMEATDVDGDGTLNYGEFVAVSVHLKKMANDEHLHKAFNFFDQNQSGYIETEELREALNDELDETSSEEVIAAIMQDVDTDKDGRISYEEFAAMMKAGTD
WRKASRQYSRERFNSLSLKLMRDGSLQLAGEA*
>Brara.J02172 Org_BrapaFPsc peptide: Brara.J02172.1.p (1 of 5) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:30612624)
MGNCCSNGRDSGDNGDTRGITASNAGPTAEASVPQSKHAPPSPPPATKQGPIGPVLGRPMEDVKSSYSLGKELGRGQFGVTHLCTQKATGQQFACKTIAK
RKLVNKEDIEDVRREVQIMHHLTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIVHTCHSMGVIHRDLKPENFLLL
SKDEKAPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLKRKYGPEADIWSIGVMLYILLCGVPPFWAESENGIFNAILKSHVDFSSDPWPSISPQAKD
LVKKMLNSDPKQRLTAAQVLNHPWIKEDGEAPDVPLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDNSGTITLEELRQGLAKQ
GTRLSEYEVQQLMEAADADGNGTIDYGEFIAATMHINRLDREEHLYSAFQHFDKDNSGYITMEELEQALREFGMNDGRDIKEIISEVDGDNDGRINYDEF
VAMMRKGNPDPIPKKRRDLSFK*
>Brara.J02705 Org_BrapaFPsc peptide: Brara.J02705.1.p (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:30611720)
MGNTCVGPSRNGFLQSVSAAMWRPRDGDDSVSQSNGDTTSEAAVSGELRSPSSPDHQVLNKPPEHLTMPKPVETKAKSDVLETQPESPKPETKADASPAK
PKKPKHMKRVTSAGLRTESVLQRKTENFKEFYSLGRKLGQGQFGTTFLCVEKATGKEFACKSIAKRKLLSDEDVEDVRREIQIMHHLSGHPNVISIKGAY
EDVVAVHLVMECCAGGELFDRIIQRGHYTERKAAELTRTIVGVVEACHSLGVMHRDLKPENFLFVSKHEDSLLKTIDFGLSMFFKPDDVFTDVVGSPYYV
APEVLRKQYGPEADVWSAGVIVYILLSGVPPFWAESEQGIFEQVLHGDLDFSSDPWPSISESAKDLVRKMLVRDPKKRLTAHQVLCHPWVQVDGVAPDKP
LDSAVLSRMKQFSAMNKFKKMALRVIAESLSEEEIAGLKEMFNMIDADQSGQITFEELKAGLKRVGANLKESEILDLMQAADVDNSGTIDYKEFIAATLH
LNKIEREDHLFAAFTYFDKDGSGYITPDELQQACEEFGVEDVRIEEMMRDVDQDNDGRIDYNEFVAMMQKGSITGGPVKMGLEKSFSIALKL*
>Brara.K00298 Org_BrapaFPsc peptide: Brara.K00298.1.p (1 of 5) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:30646929)
MGNSCRGSFKDKLFQTNNSSNKLEDNSKTSTNVTSNRSSSTNTEEFSPKKDNNSKNSPLVIPSKEPIMRRNMDNQAYYILGHKTPNIRDLYTLSRKLGQG
QFGTTYLCTELTTSVDYACKSISKRKLISKEDVEDVRREIQIMHHLAGHGNIVTIKGAYEDFLYVHIVMELCAGGELFDRIIQRGHYSERKAAELTKIIV
GVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSDFFKPGQIFTDVVGSPYYVAPEVLLKRYGPEADVWTAGVILYILLSGVPPFWAETQQGIF
DDVLKGYIDFDSDPWPVISNSAKDLIRRMLSSKPAERLTAHEVLPMYIHIKAYIYLFAGHPWICKNGVAPDRPLDPAVLSRLKQFSAMNKLKKMALKVIA
ESLSEEEIAGLREMFQAMDTDNSGAITFDELKAGLRKYGSTLKDTEIHDLMEAADVDNSGTIDYSEFIAATIHLNKLEREEHLVAAFQYFDKDRSGYITI
DELQQTCVEHSMTDVFLEDIIKEVDQNNDGQIDYGEFVEMMQKGNAGVGRRTMRNSLNINMRDA*
>Brara.K00706 Org_BrapaFPsc peptide: Brara.K00706.1.p (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:30614569)
MGHRHSKSKSSGPPPSSSSSSSSTNVVHHVQPSGERRGSSGSGPTPVGSSSTGGSRSAASAQQNGRILGRPMENVRGTYDFGKELGRGQFGVTYLVTHKE
TKKLFACKSIPTRRLVHRDDIEDVRREVQIMHHLSGHRNIVDLKGAYEDRHSVNLIMELCEGGELFDRIIAKGHYTERAAADLCRQMVMVVHSCHSMGVM
HRDLKPENFLFLSKDENSPLKATDFGLSVFFKPGDKFKDLVGSAYYVAPEVLKRNYGPEADIWSAGVILFILISGVPPFWGENETGIFDAILKGELDFSA
DPWPTVSAGAKDLVKKMLKYDPKDRLTASEVLNHPWIKEDGEASDKPLDNAVLSRMKQFRAMNKLKKMALNVIAENLSEEEIIGLKEMFKALDTDKNGIV
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TLEELRTGLPKLGNKISEAEIKQLMEAADMDGDGSIDYLEFISATMHMNRIEREDHLYTAFQYFDKDNSGYITMEELEQAMKKYNMGDDKSIKEIIAEVD
TDRDGKINYEEFVAMMKKGNPELVTNRRRVNM*
>Brara.K01255 Org_BrapaFPsc peptide: Brara.K01255.1.p (1 of 5) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:30614939)
MACLCINFKKKPKKPIPVSNGQENTEFESGESTKKQPLRQRQTAPRANIQIVVQPHKLPLPVPISHPQEQQKLMHQPEPISGKPFEDVKETYSLGRELGQ
ISSGKNFACKSILKRKLIRTQDREDVRREIQIMQYLSGQPNIVEIKGAYEDRQSVHLVMELCEGGELFDKISKRGHYSEKAAAEIIRCVVKVVEICHFMG
VIHRDLKPENFLLSGKDEASAMLKATDFGVSVFIEEGKVYKDIVGSAYYVAPEVLKRNYGKEIDIWSAGVILYILLCGTPPFWAETDKGIFEEILRGEID
FEFKPWPSISESAKDLVMNMLKSDPKSRYTASQVLEHPWIREGGEASDKPIDSAILSRMKQLQAMNKLKKLALKFIAQSSKFDR*
>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)
MGDCFSKPKFPESPPRRTLPVSNGSSPVPSLPKKEQPTRPANRPSTHQQTRKPATPSNPSANRQPLPLTSALKSHVSAENTILGKPMVDVSSLYALDREL
GRGQFGVTYLCTERTTGLQYACKSVSKRKLMSKSDVEDIKREVLILQHLTGQPNIVEFKGAYEDKQSVHMVMELCSGGELFDRIIAKGSYSERAAASVCR
AIVNVVYVCHFMGVMHRDLKPENFLLTSKDENAALKATDFGLSVFIEEGKVHREIVGSAYYVAPEVLRRNYGKEIDVWSAGVILYILLSGVPPFWAETEK
GIFDAILQGDIDFASDPWPSISNSAKDLIRKMLTQDPKNRITASQVLEHPWMKADAASDKPISSAVLTRMKQFRAMNKLKKLALKVIAENLSEEEIKGLK
QMFKNMDTDGSGTITYEELRAGLNRLGSRLSEAEVKQLMDAADVDRSGSIDYIEFITATMHRHRLEREENLYKAFQYFDTDNSGFITRDELEIAMKDYGM
GDDATIKEVIQEVDTDNDGRINYQEFVAMMRK*
>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)
MGNCCVKVGNSSSSSTSSRRRKHRNKEKRPNPFAEDLGLDPCGTPRLRVLKEEAAVGCCNITDKYILGRELGRGEFGVTYLCTDKETREALACKSISKRK
LRTAVDVEDVRREVAIMSSLPEHPNVVRLKAAYEDSEAVHLVMELCEGGELFDRIVARGHYSERAAANVTRTIVEMCHKNGVMHRDLKPENFLYANKKEN
APLKAIDFGLSVFFRPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRVVIDFKRDPWPKVSDSAKSLVRQM
LESDPRRRLSAQQVLEHPWLTNAKKAPNIPLGDIVRSRLKQFSVMNRFKKKALGVIAEHLSVEEVEIIRDMFKLMDTDNNGKVTFEELKAGLKKVGSQLA
ESEMKLLMEAADVDGNGALDYGEFVAVTIHLQRMENDEHFRRAFMFFDKDGSGFIEIDELREALMDESGQTDTEVLNNIMREVDTDKDNRISYEEFVSMM
KTGTDWRKASRHYSRERFKNLSVNLMKDGSLKMTDDFGV*
>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)
MGNTCVGPSLTKNGFFQTVSAAASGPYRLWRARTPEEMLPPDNTENTDDHHQPNSKTETPPIPNKPPETVRIQENESNPTEPTKPKKPNSAVMKRISSAG
LQIDSVLQRKTEILKEHYSLGRKLGQGQFGTTFLCIEKATGKEYACKSIAKRKLTTEEDVEDVRREIQIMHHLAGHPNVISIKGAYEDAVAVHVVMELCA
GGELFDRIIQRGHYSERKAADLARIIVSVVEACHSLGVMHRDLKPENFLFVDTNEESPLKTIDFGLSIFFKPGETFTDVVGSPYYVAPEVLRKHYGPEAD
VWSAGVIIYILLSGVPPFWAETEQGIFEQVLHGELDFSSEPWPGISESAKDLIKRMLMRNPKKRLTAHEVLCHPWVQDDGVAPDKPLDSAVLTRLKQFSA
MNKLKKMALRVIAESLSEEEIAGLKEMFKMIDTDGSGSITFEELKAGLKRVGANLTESEIHALMEAADIDNNGSIDYGEFIAATLHLNKAEREDHLFAAF
SYFDKDGSGYITQDELQQACEEFGIEDVRLEEMIREVDQDNDGSIDYNEFVAMMQKGNPVFGKKGLQNNFSIGFRGALKLG*
>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)
MGNCCRSPAAAAREDVKSNYSVHDQSKKEGNSNKKLTVLSGSIKGGVDEKYVVDRELGRGEFGVTYLCIDRSTQELLACKSISKRKLRTTVDIEDVRREV
AIMNHLPIHSNIVSLKETCEDENAVHLVMELCEGGELFDRIVARGHYTERAAAGVTKTIMEVVQVCHKHGVIHRDLKPENFLFANKKENSPLKAIDFGLS
IFFKPGETFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGLIDFKRDPWPSISENAKSLVRQMLEPDPKLRLTA
KQVLEHPWLQNAKKAPNVPLGDIVKTRLKQFSMLNRFKRRALRVIAEHLSIEEVEDIKEMFKMMDTDNDGTVTYEELKAGIQKLGSQLSEADVQLLMEAV
DADGNGTLDYGEFIAVSLHLQRMANDEHLRKAFSYFDKDGNGFIEPEELREALVEDGITDSVDVANDIFLEVDTDKDGRISYEEFLAMMKTGTDWRKASR
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)
MGMCLSHQETPPEYPTKPGNHTPHHPSPGNHTPRHGNHTPNHPSPGNHTPHRRSPNHTPPLSPARFFNLRPRVGTVLGRPLADVWASYSKGKELGRGQFG
ITHLCTDLSTGRQLACKTIAKRKLTHKDDIEDMRREVQIMHHLAGHESIVELVDSFEDRHSVNLVMGLCSGGELFDRIIKRGHYSEREAAGLVRAMARVV
HTCHSMGVVHRDLKPENFLFLSEEEDSPLVVTDFGLSVFYKPGDVFKDVVGSAYYVAPEVLKRNYGPEIDIWSIGVILYILLCGTPPFWAESDEGIFDEI
MRGLIDFRSEPWPSISAGAKDLVRKMLNPDPKQRLTAFQVLNHRWTKEDGEASDTPLDNAVLNRLKQFRAMNKFKKIALRVIAKGLSEEEIMGLKEMFKG
MDRDKSGTITFEELRRGLAAQGSKLTETEVKQLMEAADVDGNGTIDYDEFVTATMRLNKIHKEDHLYTAFQYFDRDNSGYITKEELEQALREHGLYDGRD
IRDIIAEVDADNDGRINYDEFAAMMNKENAEPKAKKRQDIFAYDPK*
>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)
MKKGLAASIMASPVLRQQNGNLRDLYLIGRKLGQGQFGTTYLCTEKATGKEYACKSIAKRKLICMEDIEDVRREIEIMHHLSGHPNVVTIKGAYEDSVFV
HLVMELCAGGELFDRIIQKGHYSERQAAHLIKVIVGVVEACHSLGVMHRDLKPENFLFLSEDEDAPLKATDFGLSVFYQPGETFTDVVGSPYYVAPEVLR
KHYGPESDVWSAGVILYILLSGVPPFWAETEQGIFRQILQGPLDFESEPWPGISESAKDLIRKMLNRNPKKRVTAHEVLCHPWIVDDSVAPDRPLDSAVL
SRLKQFTAMNKLKKMALKVIAESMSEEEIGGLKELFKMIDTDGSGTITFEELKEGLKRVGSELMESEIKALMDAADLDHSGTIDYGEFLAATMHLNKMER
EENLASAFSYFDKDGSGYITIDELQQACREFGLSDFHLDDMIQEIDQDNDGRIDYSEFAAMMRRGNGGVGRKTMRNSLNISMRDALKISDQ*
>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)
MGNSCRGSFRNTVIQGYKEPTDRSGRTNGSVDGRSNSDYSPHSLNSQVIAEEFAKDNSKRGNPGSNNIFDLSTKDNIMRRGGENQTYYVLGHKTENIRDL
YTLGRKLGQGQFGTTYLCTEIATGKEYASKSISKRKLISKEDVEDVRREIQIMHHLSGHKNVVTIKGAYEDSLFVHIVMELCSGGELFDRIIQRGHYSER
KAAELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDSSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLCKHYGPEADVWTAGVILYILLSGVPP
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FWAETQQGIFDAVLKGVIDFETDPWPVISDSAKDLIKKMLCWRPSERLTAHEVLCHPWICENGVAPDRPLDPAVLSRLKQFSAMNKLKKMALRVIAESLS
EEEIAGLREMFTAMDTDNSGAITFDELKAGLKRYGSNLKESEIRDLMDAADVDNSGTIDYGEFVAATVHLNKLEREEHLVAAFSYFDKDGSGYITVDELQ
HACSEHNISDVPIEDIIREVDQDNDGRIDYNEFVAMMLKGNGGLGRRTMRNSLNVSMRDAPGAH*
>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)
MGNCCSNPGEPNQKTQKKQKKPNPFSVDYPGSYNSSNSGSKPPVLKDPTGRDIASRYDLGRELGRGEFGITYLCTDRDTGEVLACKSISKKKLRTAVDIE
DVRREVAIMGHLPKHPNIVSLKDTYEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAVVTRTIVEVVQLCHKHGVMHRDLKPENFLFANKKETSPLKA
IDFGLSVFFKPGEHFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPKVSDNAKNLVKRMLEPDP
KLRLTAQEVLDHPWLQNAKKAPNVSLGETVRARLKQFSVMNKLKKRALRVIAEFLSVEEAAGIKDTFQMMDINNNGKITFEELKVGLQKIGQQAQDADVQ
MLMEAADADGDGTLNYAEFVAVSIHLRKIGNDDHLRKAFLYFDQNQSGYIEIEELRDSLADDLADNCEEVINAIIHDVDTDKDGRISYDEFATMMKAGTD
WRKASRQYSRERFTSLSLKLLQDGSLQLTN*
>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)
MGNCNGVPTDEEQHEAAAALPHNSKTGIHVSPPAPPPPKPVSHLQTHSLSASPSPPPQHIAGIGRILGRPMEDGRSTYIFGKELGRGQFGVTYMCTHRET
KEVLACKSIATRKLITKDDIEDVRREVQIMHHLTGHRNIVELKGAYEDRNSVNLVMELCAGGELFDRIIAKGHYSERAAATLCREIVTVVHTCHSMGVMH
RDLKPENFLFLNKDEASPLKATDFGLSVFFKPGEVFRDLVGSAYYVAPEVLRRHYGVEADIWSAGVILYILLSGVPPFWAENEHGIFDAILRGHIDFSSD
PWPSISSGAKELVKKMLKADPTDRLSAIQILNHPWIREDGVASDQPIDVTVLTRMKQFRAMNKLKKVALKVIAENLSEEEIMGLKEMFRSMDTDNSGTIT
FEELKAGLPKLGTRISESEVRQLMEAADVDGNGTIDYIEFITATMHLNRMEKEDHLYTAFEYFDKDKSGYITMEELEQALKKYNMGDEKTINEIIAEVDT
DRDGRINYDEFVTMMRKGNQDMAANRRRSVTVGAPKYK*
>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)
MGMCFSQAGRKGPKPDANAKEPPSGPKPDPPIATSKPTPTPPPSKPPPIGPVLGRPMEDVRATYIMGKELGRGQFGITHLCTHKATGQPFACKTIAKRKL
VNKEDIEDVRREVQIMYHLTGQPNIVELKGAFEDKQSVHLVMELCAGGELFDRIIAKGHYTERAAAALMRTIVQIVHTCHSMGVVHRDLKPENFLLLSKD
EDAPLKATDFGLSVFFKQGEVFRDIVGSAYYIAPEVLKRKYGPEVDIWSIGVMLYILLSGVPPFWAESEHGIFNAILRGQIDFTSDPWPSISVGAKDLVK
KMLNSDPKHRLTAFQVLSHPWIKDGEAPDIPLDNAVLSRLKQFRAMNKFKKVALKVIAGCLSEEEIMGLKEMFKNMDTDNSGTITLEELKQGLSKQGTKL
SEYEVKQLMEAADADGDGTIDYDEFITATMHMNRMDREEHLYTAFQYFDKDNSGYITPEELEQALLEYGMHDGRDIKDILSEVDADNDGRINYDEFVAMM
RKGNPEANPKKRRDKFV*
>GSVIVG01000238001 Org_Vvinifera peptide: GSVIVT01000238001 (1 of 1) PTHR24349:SF166 - CALCIUM-
DEPENDENT PROTEIN KINASE 11-RELATED (PAC:17816817)
MHRDLKPENFLFDTTAEDAALKATDFGLSVFYKPGETFSDVVGSPYYVAPEVLCKHYGPEADVWSAGVILYILLSGVPPFWAETETGIFRQILQGKLDFE
SEPWPCISETAKELLRKMLDRNPKKRLTAHEVLSHPWVVDDRMAPDKPLDSAVLSRLKQFSAMNKLKKMALRVIAEGLSEEEIGGLRELFKMIDTDNSGT
ITFDELKDGLKRVGSELMESEIRDLMNAADIDNSGTIDYGEFLAATVHLNKLEREENLVSAFSFFDKDKSGYITIDELQQACKEFGLSEAHLDDMIKEID
QDNDGQIDYGEFAAMMRKGNGGIGRRTMRNNLNLGDVLGIPDMRLTN*
>GSVIVG01001931001 Org_Vvinifera peptide: GSVIVT01001931001 (1 of 1) PTHR24349:SF161 - CALCIUM-
DEPENDENT PROTEIN KINASE 1-RELATED (PAC:17817910)
MHRDLKPENFLLVNEEEDSLLKTIDFGLSVFFKPGEKFTDVVGSPYYVAPEVLRKRYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLHGDLDFS
SDPWPSISESAKDLVRRMLVRDPRRRLTAHEVLCHPWVQVDGVAPDKPLDSAVLSRLKQFSAMNKLKKMALIVIAENLSEEEIAGLKEMFKMIDTDNSGQ
ITFEELKAGLKRVGANLKESEIYDLMHAADVDNNGTIDYGEFIAATLHLNKVEREDHLFAAFSYFDKDGSGYITPDELQQACEEFGLEDVRLEEMIREVD
QDNDGRIDYNEFVAMMQKGNPGIGKKGLQTSFSMGFREALKH*
>GSVIVG01008077001 Org_Vvinifera peptide: GSVIVT01008077001 (1 of 2) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:17820750)
MELCEGGELFDRIVARGHYSERAAAGVARTIAEVVRMCHENGVIHRDLKPENFLFANKRESSPLKAIDFGLSVFFRPGERFSEIVGSPYYMAPEVLKRNY
GPEVDIWSAGVILYILLCGVPPFWAETEQGVALAILRGVIDFKREPWPQISDNAKSLVRQMLEQDPRKRLTAQQVLEHSWLQNAKKAPNVPLGDIVRTRL
KQFSCMNRFKKKAMRVIAEHLSVEEVEVIRDMFTLMDTDNDGKVTYEELKAGLRKVGSQLGEPEIKLLMEVADVDGNGVLDYGEFVAVTIHLQRMENDEH
FQRAFMFFDKDGNGFIDLIELQEALADESGETDADVVNEIMREVDTDKDGRINYDEFVAMMKTGTDWRKASRQYSRERFKSLSLNLMKDGSLHLEDRITG
QSIAV*
>GSVIVG01008749001 Org_Vvinifera peptide: GSVIVT01008749001 (1 of 4) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:17821297)
MGFCFSRPRDIPISSSSSSDGDFTNHHYQPIPISSSKESLDIPPPLSMSVPKPPTSSQIGTVLGRPLCEITSIYDIGKELGRGQFGITYLCTEKSTGLKY
ACKSISKRKLKSGKDIEDVKREILILEHLTGQPNIVEFKGAYEDKQNLHLVMELCSGGELFDRITAKGSYSEREAADICRQIVTVVHVCHFMGVMHRDLK
PENFLMVSREENSPLKATDFGLSVFIEDNEVYKDVVGSAYYVAPEVLRRSYGKEIDVWSAGVILYILLSGVPPFWGENEKSIFDAVLQGYVDFDSAPWPS
ISSSAKDLIKKMLMKDPKRRITASDALNHPWLREDGEASDKPIDSAVLVRMKQFRAMNKLKKLALKVIAENLSEEDIKGLKQMFNNMDTDRSGTITFEEL
KTGLSRLGSKLSELEIKQLMDAVDVDQNGTLDYTEFITATMQRHRLEKEENLFKAFQFFDKDGSGFITREELKQAMTQYGMGDEATIDEVIDDVDTDKDG
RINYEEFVAMMKKGPQDTELKQR*
>GSVIVG01010743001 Org_Vvinifera peptide: GSVIVT01010743001 (1 of 3) PTHR24349:SF126 - CALCIUM-
DEPENDENT PROTEIN KINASE 32 (PAC:17822813)
MHSYSMNGAHTLIMTSLRTNNPMGGCISMPAKAGQKKKAKAKKIIPESGDDVFRKSVTIRPISVLKEPSGKDIYKTYRLGKELGRGEFGVTHQCFDLETG
EIFACKTISKSKLTTEIDIQDVRREVEIMKHLPKHPNIVRLKEAYEDKDNVHLVMELCEGGELFDRIVARGHYTERAAADVTRSIVEILQICHQHGVMHR
DLKPENFLFADASEASPLKAIDFGLSIFFKPGQRFNEIVGSPYYMAPEVLRRHYGPEVDVWSAGVILYILLCGVPPFWAETEEGIAQAIVKSVVDFERDP
WPHVSEDAKDLVRSMLDPNPYNRLTVEEVLAHPWIKNATSIPNVSLGENVRTRIKQFSLMNKFKKRVLRVVADNLPNEQRDGIRQIFHMMDTDKNGNLSF
EELKDGLHKIGHPVADPDVKMLIEAADMDGTGTLNCDEFVTISVHLRKISSDENLSEAFRAFDKNDSGYIEFEELREALREDNLGPNNEQVIQDIIFDVD
LDKDGRISYDEFKAMMKTGMDWKMSSRQYSRAMLNALSMRIFKDKSMPLQNKSMQLENRSMLLKNRSMRLQNQVFV*
>GSVIVG01011167001 Org_Vvinifera peptide: GSVIVT01011167001 (1 of 3) PTHR24349//PTHR24349:SF145 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:17823124)
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MVDRELGRGEFGYCELEGGLCHKHGVIHRDLKPENFLFANKKENSPLKAIDFGLSIFFKPGERFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILL
CGVPPFWAESEQGVAQAILRGLIDFKRDPWPNISESAKSLVRQMLEPDPKLRLTAKQVLEHSWLQNAKKAPNVPLGDVVKARLKQFSMMNRFKRKALRVI
ADHLSTEEVEDIKESFKKMDTDNDGIVSIEELKSGLRKFGSQLAEAEVQMLIETVDTNGKGTLDYGEFVAVSLHLQRMANDEHLRKAFSYFDRDGNGYIE
RDELRDALMEDGADDCTDVANDIFQEVDTDKDGKISYDEFAAMMKTGTDWRKASRHYSRGRFNSLSIKLMKDGSLNLGNE*
>GSVIVG01012730001 Org_Vvinifera peptide: GSVIVT01012730001 (1 of 4) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:17824232)
MGCFSSKERVTERDIKGGRSERGAPTQTYHQPPPQPPLKPSHPNTRAIQKPDTILGRPFDDIKHYYTLGKELGRGQFGVTYLCTQNSTGNTYACKSILKR
KLVTKNDKEDIKREIQIMQHLTGQPNIVEFKGAYEDRHSVHLVMELCAGGELFDRIISQGHYSERAAAAICRAIVNVVHICHFMGVMHRDLKPENFLLSS
KDEAAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRNYGKEIDIWSAGVILYILLSGVPPFWAETEKGIFDAILQGEIDFESQPWPAISNGAKDL
VRKMLTQDRNKRITSAQVLEHPWIREDGEASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAENLSEEEIKGLKAMFTNMDTDKSGTITYEELKSGLARLG
SRLSETEVQQLMEAADVDGNGTIDYIEFITATMHRHRLERDEHLYKAFNYFDKDNSGFITRDELENAMKEYGMGDEDSIKEIINEVDTDKDGRINYKEFC
TMMRSGTQPPVKLF*
>GSVIVG01019446001 Org_Vvinifera peptide: GSVIVT01019446001 (1 of 1) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:17829068)
MHHLTGHRNIVELKGAYEDRHSVNLVMELCAGGELFDRIIAKGHYSERAAAALCRQIVTVVHNCHTMGVMHRDLKPENFLFLSTAEDSPLKATDFGLSVF
FKPGDVFKDLVGSAYYVAPEVLRRSYGAEADIWSAGVILFILLSGVPPFWGENEQSIFDTILRGHIDFSSDPWPSISNSAKDLVKKMLRADPKERLTAID
VLNHPWMKEDGASDKPIDIAVLTRVKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGTITYEELKNGLPKLGTKLSESEVRQLMEAADVD
GNGTIDYIEFISATMHMNRMEREDHLYRAFEYFDKDKSGYITMEELEHALKRYNMGDEKTIKEIIAEVDTDHDGRINYEEFAAMMRKGNPDLITNRRRK*
>GSVIVG01022524001 Org_Vvinifera peptide: GSVIVT01022524001 (1 of 1) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:17831346)
MGNTCVGPNLAANGFLQSVSAAVWRTRPPEDMLPPPNADGSSSGDNAGSDGAKGSDPPMPKAEKSDGNSGKQKKQTHMKRLSSAGLQIDSVLQRNTENLK
EIYSLGRKLGQGQFGTTYLCVEKANGKEFACKSIAKRKLTTREDVEDVRREIQIMHHLAGHPNVISIVGAFEDAVAVHVVMELCVGGELFDRIIQRGHYT
ERKAADLARVIVGVVEACHSLGVMHRDLKPENFLFINQDEDSPLKTIDFGLSMFFRPGEIFTEVVGSPYYVAPEVLRKHYGPECDVWSAGVIIYILLSGV
PPFWDETEQGIFEQVLKGDLDFVSEPWPSISDSAKDLVRKMLVRDPKKRLTAHEVLCHPWVQVNGVAPDKPLDSAVLTRLKQFSAMNKLKKIAIRVIAES
LSEEEIAGLKEMFKMIDVDNSGNITLEELKTGLERVGADLKDSEIIRLMQAADIDNSGTIDYGEFVAAMLHLNKIEKEDHLYAAFSYFDKDGSGYITQDE
LQQACEQFGLEAIHLEDVIREVDQDNDGRIDYSEFVAMMQDRDFGKKGYKIT*
>GSVIVG01022606001 Org_Vvinifera peptide: GSVIVT01022606001 (1 of 1) PTHR24349:SF128 - CALCIUM-
DEPENDENT PROTEIN KINASE 25 (PAC:17831388)
MGNNCVGSMVPEHGLFESISNSIWWTRASDKEQKSPPPVQNKPPEEVELINPPEVMKITKEETKPTPTPKRPLLMKRLPSAGLEVDLVLKDKTDHLKEHY
NLGRKLGHGQFGTTFLCVEKETGKEYACKSIAKRKLLTRDDIEDVRREIQIMHHLAGHSNIISIKGAYEDAVAVHLVMELCTGGELFDRIAKRGHYTERK
AAQLARTIIGVVEACHSLGVMHRDLKPENFLFVNEQEESLLKTIDFGLSVFFKPGEIFTDVVGSPYYVAPEVLRKCYGPEADVWSVGVIIYILLSGVPPF
WAESEQEIFQEVLHGDLNFSSDPWPHISESAKDLIRRILVRDPKKRLTAHEVLCHPWIQVDGVAPDKTLDSAVISRLKQFSAMNKLKKMALRVIAENLSE
EEIAGLKEMFKIIDTDNSGQITFEELKAGLKRFGANLNEAEIYDLMQAADVDNSGTIDYGEFIAATFHLNKIEREDHLFAAFSYFDKDGSGYITPDELQK
ACEEFGMEDVHLEEMIQEVDQDNDGRIDYNEFVAMMQQGNNNDFGKKGLQNGISFGFRQPLPVY*
>GSVIVG01023866001 Org_Vvinifera peptide: GSVIVT01023866001 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:17832178)
MGNTCRGSFRGKYFQGYGQPEEQSTSKRNSDRSNSDYSPSSLNSQQLTANIRDLYSLGRKLGQGQFEDVRREIQIMHHLAGHKNILFDRIIQRGHYSERK
AAELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLCKHYGPEADVWTAGVILYILLSGVPPF
WAETQQGIFDAVLKGFIDFESEPWPLISDSAKDLIRKMLCSRPADRLTAHEVLCHPWICENGVAPDRSLDPAVLSRLKQFSAMNKLKKMALRVIAESLSE
EEIAGLREMFKAMDTDSSGAITFDELKAGLRRYGSTLKESEIRDLMDAADVDNSGTIDYGEFIAATVHLNKLEREEHLVAAFQYFDKDGSGYITVDELQQ
ACAEHNMTDVFLEDIIKEVDQDNDGRIDYSEFVAMMQKGNAGIGRRTMRNSLNMSMRDAPGAF*
>GSVIVG01025249001 Org_Vvinifera peptide: GSVIVT01025249001 (1 of 3) PTHR24349:SF126 - CALCIUM-
DEPENDENT PROTEIN KINASE 32 (PAC:17833278)
MGNCCASPGSEKENPYLIDYNVLHGSVSRNRGPVLKDPTGRDISLKYELGREMGRGEFGVTYMCTEKSTNEKYACKSIAKKKLRTAVDIEDVRREVQIMK
RLPMHPNIVSLKDTFEDENAVHIVMELCEGGELFDRIVSRGHYTERAAAGVMRTIVEVVQICHKHGVMHRDLKPENFLFANKKEAAPLKIIDFGLSVDFK
HGERFSEIVGSPYYMAPEVLKHNYGPEIDIWSAGVILYILLCGIPPFWAETEQGVAQAIIRAVVDFKRDPWPKVSDKAKELVKKMLDPDPKKRLTAQEVL
DHPWLQDAKSVPNVSLGESVKARLKQFSMMNKLKKKALQVMAEHLSMEEVAGIKEAFKTMDINNRGQINLDELRSGLQKLGQPIPDSDLQILMEAADLDG
DGTLNYAEFVAVSIHIKKITNEEHLHKAFAFFDQNQSGYIEIEELQNALADELSTNSEEVINAIMHDVDTDKDGRISYEEFAAMMKAGTDWRKASRQYSR
ERFNTLSLKLTRDGKDGQ*
>GSVIVG01033306001 Org_Vvinifera peptide: GSVIVT01033306001 (1 of 3) PTHR24349:SF126 - CALCIUM-
DEPENDENT PROTEIN KINASE 32 (PAC:17839046)
MELCEGGELFDRIVARGHYTERAAAAVTKTIVEVVQMCHKHGVMHRDLKPENFLFANKKETAPLKAIDFGLSVFFKPGERFTEIVGSPYYMAPEVLKRNY
GPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVLDFKRDPWPKVSENAKDLVKKMLDPDPKRRLSAQEVLDHPWLQNAKKAPNVSLGETVRARL
KQFSMMNKLKKRALRVIAEHLSVEEVAGIKEGFQLMDTGNKGKINMDELRVGLQKLGHQIPEQDLQILMEAGDVDGDGHLDYGEFVAISVHLRKMGNDDH
LLKAFEFFDQNNSGYIEIEELRDALAGELESNSEEVINAIIHDVDTDKDGRISYDEFAAMMKAGTDWRKASRQYSRERFNNLSLKLIRDGSLEVRP*
>GSVIVG01034489001 Org_Vvinifera peptide: GSVIVT01034489001 (1 of 1) PTHR24349//PTHR24349:SF117 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:17839939)
MHRDLKPENFLFESTDEDAKLKATDFGLSVFYKPGEVFFEVVGSPYYVAPEVLRKHYGHEVDVWSAGVILYILLSGVPPFWAENDTGIFKEILKGKLDFK
SDPWPSISESAKDLIKKMLEMDPKKRISAHEVLCHPWIVDDRVAPDKPLDSAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGT
ITFEELKEGLRKVGSELMESEIKTLMDAADIDNSGTIDYGEFLAATLHLNKMEREENLIAAFSFFDKDGSGYITIDELQQACREFGLGDAHLDEMIREID
QDNDGRIDYGEFTAMMRKGDGGIGSRTMRNNLNFNLADAFGINDTT*
>GSVIVG01037295001 Org_Vvinifera peptide: GSVIVT01037295001 (1 of 1) PTHR24349:SF131 - CALCIUM-
DEPENDENT PROTEIN KINASE 17-RELATED (PAC:17841971)
MGNCCSQGNTNDGPANDKGETIPEPTTNPETAAPESSAAQNKPAARKELGRGQFGVTHLCTSKATGEQFACKTIAKRKLVNKEDIEDVRREVQIMHHLTG
QPNIVELKGAYEDKQSVHLVMELCAGGELFDRIISKGHYTERGAASLLRTIVQIVHTCHSMGVVHRDLKPENFLLLNKDENAPLKATDFGLSVFFKQGEV
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FRDIVGSAYYIAPEVLKRRYGPEVDIWSVGVMLYILLCGVPPFWAESEHGIFNAILRGHIDFTSDPWPTISSGAKDLVRKMLTSDPKQRITAFQVLNHPW
IKEDGEAPDTPLDNAVFERFKQFRAMNKFKKVALRVIAGCLSEEEIMGLKQMFKGMDTDNSGTITLEELKQGLSKQGTKLSEYEVKQLMEAADADGNGTI
DYDEFITATMHLNRMDKEDHLYTAFQYFDKDNSGYITTEELEQALHEFGMHDGRDIKEILNEVDGDNDGRINYDEFVTMMRKGNPEPNPKKRRDVFV*
>GSVIVG01037652001 Org_Vvinifera peptide: GSVIVT01037652001 (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:17842193)
MGVMHRDLKPENFLLSSKGENALLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRRYGKEIDIWSAGVILYILLSGVPPFWAETEKGIFDAILQGHI
DFETSPWPSISSSAKDLVRKMLTQDPQKRITSAQVLEHPWIKEDGEASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAENLSEEEIQGLKAMFTNMDTDK
SGTITYEELKSGLARLGSKLTEAEVQQLMEAADVDGNGTIDYIEFITATVNRHKLERDEHLFKAFQYFDKDSSGFITRDELKAAMKEHGMGDDDTIAEII
SEVDTDNDDKINYGEFCSMMRGGTQQGLKVF*
>LOC_Os01g43410 Org_Osativa peptide: LOC_Os01g43410.1 CAMK_CAMK_like.9 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33123266)
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KLAHRDDIEDVRREVQIMHHLTGHRNIVELRGAYEDRHSVNLIMELCEGGELFDRIIARGHYSERAAAALCREIVAVVHSCHSMGVFHRDLKPENFLFLS
KSEDSPLKATDFGLSVFFKPGEHFKDLVGSAYYVAPEVLKRNYGAEADIWSAGVILYILLSGVPPFWAESEDGIFDAVLRGHIDFSSEPWPSISNGAKDL
VKKMLRQDPKERLTSAEILNHPWIREDGEAPDKPLDITVISRMKQFRAMNKLKKVALKVVAENLSDEEITGLKEMFRSLDTDNSGTITLEELRSGLPKLG
TKISESEIRQLMEAADVDGNGTIDYAEFISATMHMNRLEKEDHILKAFEYFDKDHSGYITVDELEEALKKYDMGDDKTIKEIIAEVDTDHDGRINYQEFV
AMMRNNNPEIAPNRRRMF*
>LOC_Os01g59360 Org_Osativa peptide: LOC_Os01g59360.1 CAMK_CAMK_like.10 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33119807)
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PLKATDFGLSVFFKQGEVFKDIVGSAYYIAPEVLKRSYGPEADIWSVGVILYILLCGVPPFWAESEHGIFNSILRGQVDFTSDPWPRISASAKDLVRKML
NSDPKKRISAYEVLNHPWIKEDGEAPDTPLDNAVMNRLKQFRAMNQFKKAALRVIAGCLSEEEIRGLKEMFKSMDSDNSGTITVDELRKGLSKQGTKLTE
AEVQQLMEAADADGNGTIDYDEFITATMHMNRMDREEHLYTAFQYFDKDNSGCISKEELEQALREKGLLDGRDIKDIISEVDADNDGRIDYSEFAAMMRK
GNPEANPKKRRDVVI*
>LOC_Os01g61590 Org_Osativa peptide: LOC_Os01g61590.1 CAMK_CAMK_like.1 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33126149)
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ELLACKSISKRKLRTAVDVEDVRREVAIMRHLPKSASIVSLREACEDEGAVHLVMELCEGGELFDRIVARGHYTERAAANVTRTIVEVVQLCHRHGVIHR
DLKPENFLFANKKENSPLKAIDFGLSIFFKPGEKFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAETEQGVAQAILRGNIDFKREP
WPNVSENAKDLVRRMLEPDPKLRLTAKQVLEHPWLQNAKKAPNVPLGDIVKSRLKQFSRMNRFKRRALRVIADHLSAEEVEDIKEMFKAMDTDNDGIVSY
EELKSGIAKFGSHLAESEVQMLIEAVDTNGKDALDYGEFLAVSLHLQRMANDEHLRRAFLFFDKDGNGYIEPEELREALVDDGAGDSMEVVNDILQEVDT
DKDGKISYDEFVAMMKTGTDWRKASRHYSRGRFNSLSMKLIKDGSVKLVNE*
>LOC_Os02g46090 Org_Osativa peptide: LOC_Os02g46090.1 CAMK_CAMK_like.15 - CAMK includes
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GQFGTTYLCTDLATGVDYACKSIAKRKLITKEDVEDVRREIQIMHHLAGHRNVVAIKGAYEDPQYVHIVMELCAGGELFDRIIERGQFSERKAAELTRII
VGVIEACHSLGVIHRDLKPENFLLANKDDDLSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLRKCYGPEADVWTAGVILYILLSGVPPFWAETQQGI
FDAVLKGVIDFDSDPWPVISDSAKDLIRRMLNPRPKERLTAHEVLCHPWICDHGVAPDRPLDPAVLSRIKQFSAMNKLKKMALRVIAESLSEEEIAGLKE
MFKAMDTDNSGAITYDELKEGMRKYGSTLKDTEIRDLMEAADVDNSGTIDYIEFIAATLHLNKLEREEHLVAAFSYFDKDGSGYITVDELQQACKEHNMP
DAFLDDVIKEADQDNDGRIDYGEFVAMMTKGNMGVGRRTMRNSLNISMR*
>LOC_Os02g58520 Org_Osativa peptide: LOC_Os02g58520.1 CAMK_CAMK_like.16 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33136325)
MGNYYSCGASSTSSPTSPSLVDYYYCYHRYPSSCSSTSTATSSGGRMPIRSHQQRLSSPTAVLGHETPALREVYTVGRKLGQGQFGTTYLCTQVSTGAEY
ACKSIAKRKLLSPEDVEDVRREIQIMHHLAGHGSVVTIQGAYEDNLYVHIVMELCEGGELFDRIVERGYFSERKAAEITRVIVGVVEACHSLGVMHRDLK
PENFLLKESSSSSSLKAIDFGLSVFFKPGQVFSDVVGSPYYVAPEVLCKHYGPEADVWTAGVIVYILLSGVPPFWAETQQGIFDAVLRGSLDFDSDPWPT
ISDSAKDLIRRMLRSPPRERLTAHQVLCHPWVCDDGVAPDRPLAPAVLSRLKQFSAMNRLKKMALRVIARNLSEEELAGLKEMFKAMDTDASGAITFDEL
KEGLRRYGSNLREAEIRDLMDAADVDKSGTIDYDEFIAATVHLNKLEREEHLLAAFAYFDRDGSGYITVDELEHACRDHNMADVGIDDIIREVDQDNDGR
IDYGEFVAMMKKGAIDIIGNGRLTIGRPTTATSDDPSPTISSSSR*
>LOC_Os03g03660 Org_Osativa peptide: LOC_Os03g03660.1 CAMK_CAMK_like.17 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33128275)
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TGCEYACKTIPKRKLITKEDVEDVRREIQIMHHLSGHKNVVAIKDVYEDGQAVHIVMELCAGGELFDRIQEKGHYSERKAAELIRIIVSIVAMCHSLGVM
HRDLKPENFLLLDKDDDLSIKAIDFGLSVFFKPGQVFTELVGSPYYVAPEVLHKRYGPESDVWSAGVILYVLLSGVPPFWAETQQGIFDAVLKGHIDFQS
DPWPKISDSAKDLIRKMLSHCPSERLKAHEVLRHPWICENGVATDQALDPSVISRLKQFSAMNKLKKLALRVIAERLSEEEIAGLREMFKAVDTKNRGVI
TFGELREGLRRFGAEFKDTEIGDIMEAAHNDNNVTIHYEEFIAATLPLNKIEREEHLLAAFTYFDKDGSGYITVDKLQRACGEHNMEDSLLEEIISEVDQ
NNDGQIDYAEFVAMMQGSNVGLGWQTMESSLNVHSLCWLFFQRPVLRNESRHVCVTLISMLAFL*
>LOC_Os03g03660 Org_Osativa peptide: LOC_Os03g03660.2 CAMK_CAMK_like.17 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33128278)
MGNQCQNGTLGSDYHNRFPREHAVGYVQGDSYLDLKKFDDTWPEVNNFKPTAASILRRGLDPTSINVLGRKTADLREHYIIGRKLGQGQFGTTYLCTEIN
TGCEYACKTIPKRKLITKEDVEDVRREIQIMHHLSGHKNVVAIKDVYEDGQAVHIVMELCAGGELFDRIQEKGHYSERKAAELIRIIVSIVAMCHSLGVM
HRDLKPENFLLLDKDDDLSIKAIDFGLSVFFKPGQVFTELVGSPYYVAPEVLHKRYGPESDVWSAGVILYVLLSGVPPFWAETQQGIFDAVLKGHIDFQS
DPWPKISDSAKDLIRKMLSHCPSERLKAHEVLRHPWICENGVATDQALDPSVISRLKQFSAMNKLKKLALRVIAERLSEEEIAGLREMFKAVDTKNRGVI
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>LOC_Os03g03660 Org_Osativa peptide: LOC_Os03g03660.3 CAMK_CAMK_like.17 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33128276)
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HRDLKPENFLLLDKDDDLSIKAIDFGLSVFFKPGQVFTELVGSPYYVAPEVLHKRYGPESDVWSAGVILYVLLSGVPPFWAETQQGIFDAVLKGHIDFQS
DPWPKISDSAKDLIRKMLSHCPSERLKAHEVLRHPWICENGVATDQALDPSVISRLKQFSAMNKLKKLALRVIAERLSEEEIAGLREMFKAVDTKNRGVI
TFGELREGLRRFGAEFKDTEIGDIMEAAHNDNNVTIHYEEFIAATLPLNKIEREEHLLAAFTYFDKDGSGYITVDKLQRACGEHNMEDSLLEEIISEVDQ
NNDGQIDYAEFVAMMQGSNVGLGWQTMESSLNVALRDAPQVH*
>LOC_Os03g03660 Org_Osativa peptide: LOC_Os03g03660.4 CAMK_CAMK_like.17 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33128277)
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HRDLKPENFLLLDKDDDLSIKAIDFGLSVFFKPGQVFTELVGSPYYVAPEVLHKRYGPESDVWSAGVILYVLLSGVPPFWAETQQGIFDAVLKGHIDFQS
DPWPKISDSAKDLIRKMLSHCPSERLKAHEVLRHPWICENGVATDQALDPSVISRLKQFSAMNKLKKLALRVIAERLSEEEIAGLREMFKAVDTKNRGVI
TFGELREGLRRFGAEFKDTEIGDIMEAAHNDNNVTIHYEEFIAATLPLNKIEREEHLLAAFTYFDKDGSGYITVDKLQRACGEHNMEDSLLEEIISEVDQ
NNDGQIDYAEFVAMMQGSNVGLGWQTMESSLNVALRDAPQVH*
>LOC_Os03g48270 Org_Osativa peptide: LOC_Os03g48270.1 CAMK_CAMK_like.21 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33127982)
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AAAAAARTVAEVVRACHAHGVMHRDLKPENFLYAGKAEDAQLKAIDFGLSVFFRPGERFREIVGSPYYMAPEVLRRDYGPEVDIWSAGVILYILLCGVPP
FWAETEQGVARAILRGAADFDREPWPRISRAAKSLVRQMLDVDPRRRPTAQQVLDHPWLHHAARAPNVPLGDVVRARLKQFSLMNRLKKKAMRVIAEHLS
VEEVEVIKDMFALMDTDNNGRVTLQELKDGLTKVGSKLAEPEMELLMEAADVDGNGYLDYGEFVAVTIHLQRLSNDNHLRTAFLFFDKDGSGYIDRAELA
DALADDSGHADDAVLDHILREVDTDKDGRISYEEFVAMMKSGTDWRKASRQYSRERFKTLSNSLIKDGSITMAR*
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YEDAVAVHLVMELCAGGELFDRIVQKGHYTERKAAELARVIVGVVEVCHSMGVMHRDLKPENFLFADQTEEAALKTIDFGLSIFFRPGQVFTDVVGSPYY
VAPEVLKKKYGQEADVWSAGVIIYILLCGVPPFWAENEQGIFEEVLHGRLDFQSEPWPSISEGAKDLVRRMLVRDPKKRLTAHEVLRHPWVQVGGLAPDK
PLDSAVLSRMKQFSAMNKLKKMALRVIAENLSEDEIAGLKEMFKMIDTDNSGQITFEELKVGLKKVGANLQESEIYALMQAADVDNSGTIDYGEFIAATL
HMNKIEREDHLFAAFQYFDKDGSGYITADELQLACEEFGLGDVQLEEMIREVDEDNDGRIDYNEFVAMMQKPTMGLPAKKSGGLQNSFSIGFREALRMS*
>LOC_Os03g57510 Org_Osativa peptide: LOC_Os03g57510.1 CAMK_CAMK_like.23 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33131565)
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KRDVNTARLKDLYTIGKKLGQGQFGTTYLCVEKATGREFACKSIAKRKLLTQEDVEDVRREIQIMHHLAGHANVVSIVGAYEDAVAVQLVMELCAGGELF
DRIIQRGHYSEKAAAQLARVIVGVIEACHSLGVMHRDLKPENFLFIHQKEDSPLKAIDFGLSIFFKPGETFTDVVGSPYYVAPEVLMKHYGREVDVWSAG
VIIYILLSGVPPFWDESEQGIFEQVLKGDLDFSSEPWPNISESAKDLVRKMLIRDPKKRLTAHEALCHPWVCVDGVAPDKPLDSAVLSRLKQFSAMNKLK
KMALRVIAESLSEEEIAGLKEMFKMLDTDNSGHITLEELKTGLQRVGANLMDSEIDALMEAADIDNSGTIDYGEFIAATLHINKVEKEDKLFAAFSYFDK
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>LOC_Os03g59390 Org_Osativa peptide: LOC_Os03g59390.1 CAMK_CAMK_like.24 - CAMK includes
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RTPVDVEDVRREVEIMRHMPSHPNIVSLRAAYEDEDNVHLVMELCEGGELFDRIVARGHYTERAAAAVTRTIVEVVQMCHRHGVMHRDLKPENFLYANKK
DSSPLKAIDFGLSVFFRPGERFTEIVGSPYYMAPEVLKRHYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVVDFKREPWPRVSEPAKDLVK
RMLDPNPMTRLTAEQVLEHPWLHDSKKMPDIPLGDAVRARLQQFAAMNKLKKKALKVIAEHLSAEEAADIKDMFDKMDVSKNGQLTFEDFKAGIRKLGNQ
MPDSDLKILMDAADIDKNGILDYQEFVAVSIHVRKIGNDEHIQKAFSYFDQNKSGYIEIEELREALVDEIDGNDEDIINSIIRDVDTDKDGKISYDEFAV
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>LOC_Os04g47300 Org_Osativa peptide: LOC_Os04g47300.1 CAMK_CAMK_like.26 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33109983)
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QFGTTYLCTERATGNRYACKSVSKRKLVRRTDVDDVRREITILQHLSGQPNIAEFRGAYEDNDHVHLVMEFCSGGELFDRITAKGSYSERQAAAVCRDIL
TVVHVCHFMGVIHRDLKPENFLLASADDDAPLKAIDFGLSVFIEEGKVYKDIVGSAYYVAPEVLQRNYGKEADIWSAGVILYILLCGTPPFWAETEKGIF
DAILVNQVDFSTSPWPSISESAKDLIRQMLHRDPQKRITASQALEHRWLKEGGASDRPIDSAVLSRMKQFKAMNKLKQLALKVIAENLSPEEIKGLKQMF
NNMDTDRSGTITVEELKVGLTKLGSRISEAEVQKLMEAVDVDKSGSIDYSEFLTAMINKHKLEKEEDLLRAFQHFDKDNSGYITRDELEQAMAEYGMGDE
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>LOC_Os04g49510 Org_Osativa peptide: LOC_Os04g49510.1 CAMK_CAMK_like.27 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33112648)
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EACHSLGVMHRDLKPENFLLANKDDDLSLKAIDFGLSVFFKPGQTFTDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAV
LKGFIDFDSDPWPVISESAKDLITKMLNPRPKERLTAHEVLCHPWIRDHGVAPDRPLDPAVLSRIKQFSAMNKLKKMALRVIAESLSEEEIAGLKEMFQT
MDADNSGAITYDELKEGLRKYGSTLKDTEIRDLMDAADIDNSGTIDYIEFIAATLHLNKLEREEHLVAAFSYFDKDGSGYITVDELQQACKEHNMPDAFL
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>LOC_Os04g49510 Org_Osativa peptide: LOC_Os04g49510.2 CAMK_CAMK_like.27 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33112649)
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TTYLCTELSTGVDYACKSISKRKLITKEDIEDVRREIQIMHHLSGHKNVVAIKGAYEDQLYVHIVMELCAGGELFDRIIQRGHYSERKAAELTRIIVGVV
EACHSLGVMHRDLKPENFLLANKDDDLSLKAIDFGLSVFFKPGQTFTDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAV
LKGFIDFDSDPWPVISESAKDLITKMLNPRPKERLTAHEVLCHPWIRDHGVAPDRPLDPAVLSRIKQFSAMNKLKKMALRVIAESLSEEEIAGLKEMFQT
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>LOC_Os05g39090 Org_Osativa peptide: LOC_Os05g39090.1 CAMK_CAMK_like.29 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33159975)
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ENFLFANKKENSPLKAIDFGLSIFFKPGEKFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAETEQGVAQAILRGNIDFKREPWPNV
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SGIAKFGSHLAESEVQMLIEAVDTNGRGALDYGEFLAVSLHLQRMANGEHLRRAFLFFDKDGNGYIEPEELQEALVEDGATDIMEVVKDILQEVDTDKDG
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>LOC_Os05g41270 Org_Osativa peptide: LOC_Os05g41270.1 CAMK_CAMK_like.4 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33156904)
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LSKDEHAPLKATDFGLSVFFKEGEVFRDIVGSAYYIAPEVLKRSYGPEADIWSIGVMLYILLCGVPPFWAESEHGIFNSILRGHVDFSSEPWSRISHGAK
DLVRRMLHSDPKQRISAYDVLNHPWIKEDGEAPDTPLDNAVLGRLKQFRAMNQFKKAALRVIAGCLSEEEIRGLKEMFKSMDSDNSGTITVDELRKGLAK
KGTKLTEAEVQQLMEAADADGNGTIDYEEFITATMHMNRMDREEHLYTAFQYFDKDNSGYITIEELEQALREKGLMDGREIKDIISEVDADNDGRINYTE
FVAMMRKGDPEANPKKRRDVVL*
>LOC_Os05g50810 Org_Osativa peptide: LOC_Os05g50810.1 CAMK_CAMK_like.5 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33157415)
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DRIIARGHYSERAAAALCREIVSVVHSCHSMGVMHRDLKPENFLFLNKREDSPLKATDFGLSVFFKPGEQFRDLVGSAYYVAPEVLKRLYGAEADIWSAG
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>LOC_Os05g50810 Org_Osativa peptide: LOC_Os05g50810.2 CAMK_CAMK_like.5 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33157416)
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DRIIARGHYSERAAAALCREIVSVVHSCHSMGVMHRDLKPENFLFLNKREDSPLKATDFGLSVFFKPGEQFRDLVGSAYYVAPEVLKRLYGAEADIWSAG
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>LOC_Os07g06740 Org_Osativa peptide: LOC_Os07g06740.1 CAMK_CAMK_like.31 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33117996)
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HYSEKAAAQLARVIIGVVEACHSLGVMHRDLKPENFLFVNHKEDSPLKTIDFGLSIFFKPGENYSDVVGSPYYVAPEVLMKHYGREVDVWSAGVIIYILL
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AENLSEDEIAGLREMFKMLDTDNSGQITLEELKTGLRRVGANLKDSEITTLMEAADIDNSGSIDYGEFIAATMHLNKVEREDNLFAAFSYFDKDSSGYIT
QDELQKACEEFGIGDAHLEDIIKDIDQDNDGRIDYNEFVTMMQKGNNPLGKKGQGQLSFGLREALKLG*
>LOC_Os07g06740 Org_Osativa peptide: LOC_Os07g06740.2 CAMK_CAMK_like.31 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33117995)
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HYSEKAAAQLARVIIGVVEACHSLGVMHRDLKPENFLFVNHKEDSPLKTIDFGLSIFFKPGENYSDVVGSPYYVAPEVLMKHYGREVDVWSAGVIIYILL
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AENLSEDEIAGLREMFKMLDTDNSGQITLEELKTGLRRVGANLKDSEITTLMEAADIDNSGSIDYGEFIAATMHLNKVEREDNLFAAFSYFDKDSSGYIT
QDELQKACEEFGIGDAHLEDIIKDIDQDNDGRIDYNEFVTMMQKGNNPLGKKGQGQLSFGLREALKLG*
>LOC_Os07g33110 Org_Osativa peptide: LOC_Os07g33110.1 CAMK_CAMK_like.33 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33116748)
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ISEVDTDNDGRINYEEFCAMMRGGGMQQPMRLK*
>LOC_Os07g33110 Org_Osativa peptide: LOC_Os07g33110.2 CAMK_CAMK_like.33 - CAMK includes calcium/calmodulin depedent protein kinases, expressed (PAC:33116745)

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ISEVDTDNDGRINYEEFCAMMRGGGMQQPMRLK*
>LOC_Os07g33110 Org_Osativa peptide: LOC_Os07g33110.3 CAMK_CAMK_like.33 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33116747)
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ISEVDTDNDGRINYEEFCAMMRGGGMQQPMRLK*
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calcium/calmodulin depedent protein kinases, expressed (PAC:33116746)
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ISEVDTDNDGRINYEEFCAMMRGGGMQQPMRLK*
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calcium/calmodulin depedent protein kinases, expressed (PAC:33116046)
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>LOC_Os08g42750 Org_Osativa peptide: LOC_Os08g42750.1 CAMK_CAMK_like.37 - CAMK includes
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AANIFRTIVDVVQLCHSNGVIHRDLKPENFLFANKSEDSPLKVIDFGLSVFFKPGDRFTEVVGSAYYMAPEVLRRSYGPEVDVWSAGVILYILLCGVPPF
WGDNDEKIAQAILRGAIDFNREPLPRVSANAKDLVRRMLDPNPSTRLTAKQVLEHPWLKNADTAPNVSLGDAVRARLQQFSAMNKFKKKALGVVARNLPG
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>LOC_Os12g07230 Org_Osativa peptide: LOC_Os12g07230.1 CAMK_CAMK_like.45 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33152950)
MQPDPQPHGRGREKAAGAGPRLPPPVTAPSVGRPASVLPHKTANVRDHYRIGKKLGQGQFGTTYLCVGKPDGGEYACKSIPKRKLLCREDYEDVWREIQI
MHHLSEHPNVVRIRGAYEDALFVHIVMELCAGGELFDRIVAKGHYTERAAALLIRTIVGVVEGCHSLGVMHRDLKPENFLFASTAEDAPLKATDFGLSVF
YKPGDKFSDVVGSPYYVAPEVLQKIYGPEADVWSAGVILYILLCGVPPFWAETESGIFRQILRGKLDLESDPWPSISDSAKDLVRNMLIRDPTKRFTAHE
VLCHPWIVDDAVAPDKPIDSAVLSRLKHFSAMNKLKKMALRVIAESLSEEEIGGLKELFKMIDTDNSGTITYDELKNGLKRVGSDLMEPEIQALMDAADI
DNSGTIDYGEFLAATLHMNKLEREENLVSAFTFFDKDGSGFITIDELSQACEQFGLSDVHLEDMIKDVDQNNDGQIDYSEFAAMMRKGNAGGANAGGVTS
TGGTGRRTMRNSLRVNLGDILKPNEN*
>LOC_Os12g12860 Org_Osativa peptide: LOC_Os12g12860.1 CAMK_CAMK_like.46 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33151749)
MGNCCVSRPSGADKRRRCGSSTAPHTRGGRRVIGAANMRCLSTVSSVSDAARAVMSNEPATVLGNSGSSGNGGVMAAEEMLRRYEIGEELGRGEFGVTRR
CRDAVTGERLACKSISKRKLRSSVDVEDVRREVAIMRSLPAHANVVRLREAFEDADAVHLVMEVCEGGELFDRIVARGHYTERAAAAVMRTIMDVVQHCH
KNGVMHRDLKPENFLYANASENSPLKVIDFGLSVCFKPGARFNEIVGSPYYMAPEVLKRNYGQEIDIWSAGVILYILLCGVPPFWAETDEGIAQAIIRSH
IDFQREPWPKVSDNAKDLVRRMLDPNPYTRLTAQQVLEHPWIQNASAAPNIPLGEAVRSRLKQFTVMNKFKKKALLVVAEYLPTEELDAIRELFNMLDTK
KKGHLTLEELRKGLQVIGHNIHDTDVDMLMEAADIDGNGILDCKEFVTVSIHLKKIRSDEHLPKVFSFFDKNGSGYIEIEELKEALSPRGDQKSIDDIFL
DVDIDKDGKISYEEFELMMSAGMDWRNASRQYSRAVYNTLSRKIFKEVSLKLDHSGPLVAAGK*
>LOC_Os12g30150 Org_Osativa peptide: LOC_Os12g30150.1 CAMK_CAMK_like.47 - CAMK includes
calcium/calmodulin depedent protein kinases, expressed (PAC:33154342)
MGNVCIGPRRNFAKNGLLGILRPRHAAPSSPSQPTTTSRSIPVVLPSAPSSKPPPPTQTAPPVPVVISEPPPPQPQPEPQPAAPSQPPPPQEQPSPPPPA
SSNTTQQPPPPQQRQQSRAKKPAHIKRISSAGLQVESVLRRKTENLKDKYSLGRKLGQGQFGTTYLCVDKANGGEYACKSIAKRKLLTDEDVEDVRREIQ
IMHHLAGHPNIISIRGAYEDAVAVHVVMELCAGGELFDRIVRKGHYTERQAAGLARVIVAVVESCHSLGVMHRDLKPENFLFVGNEEDAPLKTIDFGLSM
FFRPGEVFTDVVGSPYYVAPEVLKKSYGQEADVWSAGVIIYILLCGVPPFWAETEQGIFEQVLHGTLDFESDPWPNVSDGAKDLLRKVLVRDPKKRLTAH
EVLCHPWLQMSGSAPDKPLDSAVLSRLRQFSAMNKLKKMALRVIAENLSEEEIAGLKEMFKMMDTDNSGQINYEELKAGLERVGANMKESEIYQLMQAAD
IDNSGTIDYGEFIAATLHLNKVEREDHLYAAFQYFDKDGSGYITSDELQQACDEFGIEDVRLEDMIGEVDQDNDGRIDYNEFVAMMQKTTTGFGKKGGHN
FSGFRDALKSHS*
>Mapoly0004s0215 Org_Mpolymorpha peptide: Mapoly0004s0215.1.p (1 of 3) PTHR24349:SF81 - CALCIUM-
DEPENDENT PROTEIN KINASE 20 (PAC:33015907)
MTKSGSIRYKVPNSILQRETENPKDLFIIGRRLGAGQFGTTYSCTEKATGKEYACKVIPKRKLLLKEDAEDVRREIQIMHLLSGHPNIVDIKGAYEDTGN
VYMVMELCAGGELFDRITQRGHYSEAQASAAIRAILEAIEICHELGVFHRDLKPENFLLADKDEDAPLKVIDFGLSTYFKIDEVFTDIVGSPYYIAPEVL
LRNYGPEADVWSAGVILYILLSGIPPFWAENEDAIFKLILTSDVVFMSETWKSISLPAKDLIQKMLIRNPLKRPTAREALMHPWIQEDGVAPDVPMDPIV
QCRLKKFSAMNKLKKMAIRVIAENLSEEEIAGLKEIFKMVDTDNSSTITFEELKIALRRFGSVLKDSEIHDLLDAADVDQNGIIDYGEFIAATISLNKVS
QQENLHIAFQYFDRDNSGYITKDELQQACVEHHLKDVQVDDMIKELDKDNDGRIDYNEFSAMFTRVNSGLSRRASRNSLRSTFGTC*
>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)
MGNTCLGSSVGKNGFFQGVTHPNSYTPWGRQNSFTSQGNSGTSPANRRSSEPNSAIRSKDLNENSSSNLVSHQESSFDTPIYPFATQHRPPVANHIPPGG
AAAQPGKGPQSAANHRPSHTTVTVADPVNPGDPMARRAQPVSVVPGQSLTHSVLQRTTEPLKELFTLGRKLGQGQFGTTYLCIEKSTGREYACKSIAKRK
LISQEDVEDVRREIQIMHHLSGHPNIVMIKGAYEDSSSVHLVMELCAGGELFDRIIQRGHYSEAKAAALTRTIVGVVQACHSLGVMHRDLKPENFLLANR
HEDAPLKATDFGLSVFFKPEEVFTDVVGSPYYVAPEVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLRGDIDFMSDPWPTISESAKDLI
RKMLHPNPAKRLKAHQVLSHPWIQEEGVAPDRPIDPAVQSRLKQFSAMNKLKKMALRVIAESLSEEEIAGLKEMFKMMDTDNSGTITFEELKAGLKRVGS
DLMESEIHELMEAADVDRDGAIDYGEFIAATINLNKIEREENLFAAFSYFDKDKSGYITVDELQQACVDHNLGDVRIDEMIREVDQDNDGRIDYNEFVTM
MRKGNGGIGRHTMRNSLRASLSDVLMEEVQQRMVNTHVDPRAAGHRDNVNGGRK*
>Mapoly0017s0021 Org_Mpolymorpha peptide: Mapoly0017s0021.1.p (1 of 2) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:33005537)
MGNCCACGPSKPHPKSQKSNVYSGDGYPSKVLVFKDVKQGENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRKLRTAVDVEDVRREVAVMH
HLPSHPNIVTLRGVYQDDAAVHLVMELCEGGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFANKENNSPLKAIDFGLSCFFT
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVLDFSRDPWPKVSDNAKSLVRHMLEADPKSRYTAQQVL
QHPWLQNAKKAPNAALGDAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLLMDAADVDG
NGTLDYGEFVAASIHLQRMDNEEHLQKAFAHFDRNGSGYIDMDELRDALGDDLGPNDTDVIQDIMHEVDTDKDGQISYEEFASMMRTGTDWRKASRHYSR
ELFNSLSTRLFRDGSFQAGNYSSREKR*
>Mapoly0017s0021 Org_Mpolymorpha peptide: Mapoly0017s0021.2.p (1 of 2) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:33005538)
MGNCCACGPSKPHPKSQKSNVYSGDGYPSKVLVFKDVKQGENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRKLRTAVDVEDVRREVAVMH
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HLPSHPNIVTLRGVYQDDAAVHLVMELCEGGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFANKENNSPLKAIDFGLSCFFT
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVLDFSRDPWPKVSDNAKSLVRHMLEADPKSRYTAQQVL
QHPWLQNAKKAPNAALGDAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLLMDAADVDG
NGTLDYGEFVAASIHLQRMDNEEHLQKAFAHFDRNGSGYIDMDELRDALGDDLGPNDTDVIQDIMHEVDTDKDGQISYEEFASMMRTGTDWRKASRHYSR
ELFNSLSTRLFRDGSFQAGNYSSREKR*
>Mapoly0017s0021 Org_Mpolymorpha peptide: Mapoly0017s0021.3.p (1 of 2) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:33005539)
MGNCCACGPSKPHPKSQKSNVYSGDGYPSKVLVFKDVKQGENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRKLRTAVDVEDVRREVAVMH
HLPSHPNIVTLRGVYQDDAAVHLVMELCEGGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFANKENNSPLKAIDFGLSCFFT
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVLDFSRDPWPKVSDNAKSLVRHMLEADPKSRYTAQQVL
QHPWLQNAKKAPNAALGDAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLLMDAADVDG
NGTLDYGEFVAASIHLQRMDNEEHLQKAFAHFDRNGSGYIDMDELRDALGDDLGPNDTDVIQDIMHEVDTDKDGQISYEEFASMMRTGTDWRKASRHYSR
ELFNSLSTRLFRDGSFQAGNYSSREKR*
>Mapoly0089s0009 Org_Mpolymorpha peptide: Mapoly0089s0009.1.p (1 of 1) PTHR24349:SF95 - CALCIUM-
DEPENDENT PROTEIN KINASE 3 (PAC:33014564)
MGNCVGGHSDRKNGLNPNEPAPTNVQRGTGAPQGTHGGAGTAGVSAHGSTPAPMGGISAKQKPTLTGNVLGRPLEDVRSIYTLGRELGRGQFGVTHLCTH
KVTGELLACKSIAKRKLTNKDDVEDVRREVQIMHHLEGQKNIVELKGAYEDKHNVHLVMELCAGGELFDRIIQRGHYSERAAAALCRTIVQVVQTCHSLG
VMHRDLKPENFLLANKKEDAPLKATDFGLSVFFKPGEVFTDIVGSAYYVAPEVLRRNYGPEADVWSAGVILYILLCGVPPFWAETEQGIFDAVMHGHIDF
TSDPWPSISQKAKDLVKKMLKQNPKERLTAHEVLSHPWISVDGEAPDKPLDNAVLSRLKQFTAMNKLKKLALKVIAESLSEEEIMGLKEMFKSMDTDNSG
TITFEELKDGLQKQGSNLAESEVRQLMAAADVDGNGTIDYLEFITATMHLNKIEKEDHLYAAFQHFDQDSSGFITMEELEQALIKHGMGDPDTLKEIIRE
VDTDHDGRINYDEFVAMMRKGTPGHQEGHRRSISNMAPVGAPRQHHHK*
>Mapoly0214s0015 Org_Mpolymorpha peptide: Mapoly0214s0015.1.p (1 of 3) PTHR24349:SF81 - CALCIUM-
DEPENDENT PROTEIN KINASE 20 (PAC:33016405)
MAPTRPPAMKMVTGNPIADSVLQRKTEDVNEVYTLGHKLGQGQFGVTYFCQEKATGQTYACKSIAKRKLVLQDDVEDVRREIQIMHHLSGHPNVVTIKDA
YEDETHVHLVMELCAGGELFDRIVKKGNYSEAAAASLTRTIVGVIAACHSLNVMHRDLKPENFLMANKTEESPLKTTDFGLSVFFKPGETFTNLVGSPYY
IAPEVLNKLYGPEADVWSAGVILYILLSGVPPFWGETDQVIFRKIQRGRVDYNSYPWPSISASAKDLVRRMLDMNPKTRITALEVLNHPWVAVDGVAPTE
PFDPAVQTRLKQFSAMNKLKKMALRVIAESLSAEEIAGLKEMFKAMDADNSGNITFDELKGGLKRVGSKLSESEIHDLMEAADVDQDGTIDYGEFIAATV
SLSKVEKEENLFAAFSYFDKDKSGYITVDELQQACIDHNLGEVRIEEMLKEIDQNNDGRIDYNEFVKMMRMGRLNI*
>MapolyY_A0006 Org_Mpolymorpha peptide: MapolyY_A0006.1.p (1 of 2) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:33010283)
MGNCCACGPSKPHTKSQKSNVYSGDGYPSKVLVFKDVKQGENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRKLRTAVDVEDVRREVAVMH
HLPSHPNIVTLRGVYQDDAAVHLVMELCEGGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFASKDANSPLKAIDFGLSCFFT
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVLDFSRDPWPKVSDNAKSLVRHMLEADPKCRYTAQQVL
GHPWLQHAKKAPNTALGDAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLLMEAADVDG
NGTLDYGEFVAASIHLQRMDNEEHLQKAFAHFDRNGSGYIDMDELREALGDDLGPNDTDVIQDIMHEVDTDKDGQISYEEFASMMRTGTDWRKASRHYSR
ELFNSLSTRLFRDGSLQAGNYSSREKR*
>MapolyY_A0006 Org_Mpolymorpha peptide: MapolyY_A0006.2.p (1 of 2) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:33010284)
MGNCCACGPSKPHTKSQKSNVYSGDGYPSKVLVFKDVKQGENLHDKYTLGRELGRGEFGITYLCRDKETQEQLACKSISKRKLRTAVDVEDVRREVAVMH
HLPSHPNIVTLRGVYQDDAAVHLVMELCEGGELFDRIIARGHYSEREAAAVTRTIVEVVQVCHKHRVMHRDLKPENFLFASKDANSPLKAIDFGLSCFFT
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVLDFSRDPWPKVSDNAKSLVRHMLEADPKCRYTAQQVL
GHPWLQHAKKAPNTALGDAVRARLKQFSAMNKLKKKALRIIAEHLSGEEIEGLRDMFQMMDTDNSGAITFEELKAGLQKIGSQLAESEVRLLMEAADVDG
NGTLDYGEFVAASIHLQRMDNEEHLQKAFAHFDRNGSGYIDMDELREALGDDLGPNDTDVIQDIMHEVDTDKDGQISYEEFASMMRTGTDWRKASRHYSR
ELFNSLSTRLFRDGSLQAGNYSSREKR*
>Medtr0028s0170 Org_Mtruncatula peptide: Medtr0028s0170.1 (1 of 3) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:31092213)
MGNCCSQGGDTPADNPAVADKGETNTNQDNEPSTNPITTPPPTSKPPQSTAPPSSKPSKPAAVGPVLQRPMEDVRATYSIGKELGRGQFGVTHLCTHKVT
KEQFACKTIAKRKLVNKEDIEDVRREVQIMHHLTGQANIVELKGAYEDKQSVHLVMELCAGGELFDRIIAKGHYTERAAASLMRTIVQIIHTLHSMGVIH
RDLKPENFLLLNKDENAPLKATDFGLSVFFKEGEMFKDIVGSAYYIAPEVLKRRYGPEVDIWSIGVMLYILLSGVPPFWAESEHGIFNAILRGHIDFTSD
PWPSISPAAKDLVRKMLNSDPKQRLTAFEVLNHPWIKEDGEAPDKPIDNAVLNRLKQFRAMNQFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDNSGTIT
VEELKQGLAKQGTKLSEQEVKQLMDAADADGNGTIDYDEFITATMHMNRMNREEHLYTAFQYFDKDNSGFITTEELDQALREYNMHDGRDIKEILQEVDG
DNDGRINYDEFAAMMRKGNPEAHTKKRRDSFVSH*
>Medtr1g026190 Org_Mtruncatula peptide: Medtr1g026190.1 (1 of 7) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:31099703)
MGHCFTKPHDNRVPISYDYGTNSQPPQRNQPRQPRYPHHIAAKSDPTSYSSASSSNANASDHHQPILGRPYIDMKTLYSIGKELGRGQFGVTYLCTENAT
GRNYACKSISRRKLTRKKEIEDVKREIMILQDLSGQPNIVEFKGAYEDRESVHLVMELCLGGELFDRITARITAKGSYSEREAASIFKQIMNVVHACHFM
GVMHRDLKPENFLLASKDHKAPLKATDFGLSVFIEEGKVYKELVGSAYYVAPEVLKRSYGKEIDIWSAGIILYILLSGVPPFWAETEKGIFQAILEGKLD
LESAPWPSISVAAKDLIRKMLSYDPKKRITASDALEHPWMKEGGEASDKPLDNAVLIRMKQFRAMNKMKKLALKVIAENLSDEEIKGLKQMFNNIDTDRS
GTITYEELKSGLSKLGSKLSESEIKQLMDAADVDKNGTIDYHEFITATINRHKLEREENLFKAFQYFDKDNSGYVTREELRQALAEYQMGDEATIDEVID
DVDTDNDGRINYQEFATMMRKGTLDNDDKEKPR*
>Medtr1g041150 Org_Mtruncatula peptide: Medtr1g041150.1 (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:31095901)
MGNTCVGPSISKNGIIQSFSAAIWRSQPPDAEGSVSNRGSVNEGRTDNEPESPLPVQNKPPEQITMPKPEIKQEAKSEPESEKEKKKHRRPSVKRSSSAG
LRVDSVLQRETGNFKEFYSLGKKLGQGQFGTTFLCIEKATGYQYACKSIAKRKLVTDEDVEDVRREIQIMHHLAGHPNVISIKGAYEDAMAVHVVMELCA
GGELFDRIIQRGHYTERKAAELIRTIVGVVEACHSLGVMHRDLKPENFLFVNQQEDSLLKTIDFGLSVFFMPGDTFIDVVGSPYYVAPEVLKKRYGPEAD
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VWSAGVILYILLSGVPPFWAESEQGIFEQVLRGDLDFVSDPWPAISESAKDLVRKMLVRDPKRRMTAHQVLCHPWIQVDGVAPDKPLDSAVLSRLKQFSA
MNKLKKMALIVIAESLSEEELAGLKEMFKMIDTDNSGQITFEELKVGLKKVGANLKESEIYDLMQAADVDNSGTIDYGEFIAATLHINKIEREDHLFAAF
SYFDKDGSGYITQEELQQACDEFGIKDVRLEEIIKEIDEDNDGRIDYNEFAAMMQKGNLPMVGKKGLENNFSIRFKEALKL*
>Medtr1g041150 Org_Mtruncatula peptide: Medtr1g041150.2 (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:31095900)
MGNTCVGPSISKNGIIQSFSAAIWRSQPPDAEGSVSNRGSVNEGRTDNEPESPLPVQNKPPEQITMPKPEIKQEAKSEPESEKEKKKHRRPSVKRSSSAG
LRVDSVLQRETGNFKEFYSLGKKLGQGQFGTTFLCIEKATGYQYACKSIAKRKLVTDEDVEDVRREIQIMHHLAGHPNVISIKGAYEDAMAVHVVMELCA
GGELFDRIIQRGHYTERKAAELIRTIVGVVEACHSLGVMHRDLKPENFLFVNQQEDSLLKTIDFGLSVFFMPGDTFIDVVGSPYYVAPEVLKKRYGPEAD
VWSAGVILYILLSGVPPFWAESEQGIFEQVLRGDLDFVSDPWPAISESAKDLVRKMLVRDPKRRMTAHQVLCHPWIQVDGVAPDKPLDSAVLSRLKQFSA
MNKLKKMALIVIAESLSEEELAGLKEMFKMIDTDNSGQITFEELKVGLKKVGANLKESEIYDLMQAADVDNSGTIDYGEFIAATLHINKIEREDHLFAAF
SYFDKDGSGYITQEELQQACDEFGIKDVRLEEIIKEIDEDNDGRIDYNEFAAMMQKGNLPMVGKKGLENNFSIRFKEALKL*
>Medtr1g052530 Org_Mtruncatula peptide: Medtr1g052530.1 (1 of 1) PTHR24349:SF126 - CALCIUM-DEPENDENT
PROTEIN KINASE 32 (PAC:31094145)
MGNCCTNPITKLRRKEKPKKDHGPTTKNKTNKIKNTLVVLKKPTGREILQQYELGRELGRGEFGITYLCKDRETGEELACKSISKDKLRTAIDIEDVRRE
VEIMRHLPKHPNIVTLKDTYEDDDNVHLVMELCEGGELFDRIVAKGHYTERAAATVVKTIVQVVQMCHEHGVMHRDLKPENFLFANKKETSPLKAIDFGL
SITFKPGDKFNEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGIPPFWAETEQGIAQAIIRSVIDFKKEPWPKVSDNAKDLIKKMLDPDPKRRLT
AQEVLDHPWLQNAKTAPNVSLGETVRARLMQFSVMNKLKKTALRIIADHLSVEEVAGIKEGFQVMDTENKGKINLDELRVGLLKLGHQIPEGDVQILMEA
GDVDKDGFLDYGEFVAISIHLRKISHDEHLQRAFQFFDKNESGFIELEELRNALADEVDTNSEEVINAIMHDVDTDKDGKISYEEFATMMKAGTDWRKAS
RQYSRERFTSLSIKLMKEGSLELNNEGR*
>Medtr1g052530 Org_Mtruncatula peptide: Medtr1g052530.2 (1 of 1) PTHR24349:SF126 - CALCIUM-DEPENDENT
PROTEIN KINASE 32 (PAC:31094146)
MGNCCTNPITKLRRKEKPKKDHGPTTKNKTNKIKNTLVVLKKPTGREILQQYELGRELGRGEFGITYLCKDRETGEELACKSISKDKLRTAIDIEDVRRE
VEIMRHLPKHPNIVTLKDTYEDDDNVHLVMELCEGGELFDRIVAKGHYTERAAATVVKTIVQVVQMCHEHGVMHRDLKPENFLFANKKETSPLKAIDFGL
SITFKPGDKFNEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGIPPFWAETEQGIAQAIIRSVIDFKKEPWPKVSDNAKDLIKKMLDPDPKRRLT
AQEVLDHPWLQNAKTAPNVSLGETVRARLMQFSVMNKLKKTALRIIADHLSVEEVAGIKEGFQVMDTENKGKINLDELRVGLLKLGHQIPEGDVQILMEA
VSIFPLSGIFFFYLFHN*
>Medtr1g054865 Org_Mtruncatula peptide: Medtr1g054865.1 (1 of 1) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:31098861)
MGNNCVGPNLGNNGGFLQSVSAAVWKTRPPEARLPPPNAEDKNKTPTTPENAVTGSSKPESCAGGKVSEHVSVQSTPPEQVKIAAAEIKPLEHEKPVKAA
ASSAVAGGGGGVAAATAGAGGAGEGDADKPKKPTHVKRLSSIGLQVESVLGRKTENIKDFYSLGRKLGQGQFGTTFLCMAKGTNKEFACKSIAKRKLTTQ
EDVEDVRREIRIMHHLAGHPNVIQIVGAYEDAVAVHVVMELCAGGELFDRIIQRGHYSERKASELTRLILGVVQACHSLGVMHRDLKPENFLFVSHDEES
ALKTIDFGLSVFFRPGETFTDVVGSPYYVAPEVLRKNYGQECDVWSAGVIIYILLSGVPPFWDETEQGIFEQVLKGELDFISDPWPSISESAKDLVRRML
IRDPKKRMTAHEVLCHPWVQVGGVAPDKPLDSAVLSRLKQFSAMNKLKKIAIRVIAENLSEEEIAGLKEMFKMIDTDNSGQISLEELKNGLERVGSVLKD
SEINWLMQAADVDNSGTIDYGEFIAAMLHLNKVQKEDHLFAAFNYFDKDGSGYITKDELQQACNQFGLQEDHLDDIIREADRDNDGRIDYSEFVAMMQDT
DFGKKGL*
>Medtr1g055255 Org_Mtruncatula peptide: Medtr1g055255.1 (1 of 4) PTHR24349:SF161 - CALCIUM-DEPENDENT
PROTEIN KINASE 1-RELATED (PAC:31096757)
MGNNCVGTRTFFSKDESSSRATFPSPSCWSRSKKDSAHKTSPTKPKESVQNNPPPVMKIEKEDEKPPPQQHHHQKPRQKPQTNEAVVATPAKPKRPHNVK
RLASAGLKADSVLQRKTVSLKEFYTLGPKLGQGQFGTTFLCVEKSTGKEYACKSIMKRKLLTEEDVEDVRREIQIMHHLAGSSNVISIKEASEDAVAVHV
VMELCAGGELFDRIVERGHYTERKAAKLARTIVGVIQSCHSLGVMHRDLKPENFLFVNQQEESPLKAIDFGLSCFFKPGDIFNDVVGSPYYVAPEVLRKR
YGPEADVWSAGVILYILLCGVPPFWGESEQDIFEAILNSDLDFSSDPWPSISESAKDLVKKMLVRDPSKRLTAFDVLRHPWILIDGAAPDKPLDSAVLSR
MKQFTAMNKLKKMALRVIAENLSEEEIAGLKEMFKMIDTDNSGHITFEELKVGLKRFGANLKESEIYDLMKAADVDNSGTIDYGEFIAATLHLNKVDRED
HLHAAFSYFDKDGSGYITKDELQKACEEFGFRDVPLEEMIREVDQNNDGRIDYNEFVAMMHRGNAEMGKRGRKGSSSFSIGFREALPVC*
>Medtr1g096490 Org_Mtruncatula peptide: Medtr1g096490.1 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:31095859)
MQKHNLGSSKSSSKCTAVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTHKSTGKLYACKSIPKRKLLCKEDYDDVWREIQIMHHLSEHPNVVQIQGTYED
SVFVHLVMELCAGGELFDKIIQKGHYSEKEAAKLMKTIVGVVETCHSLGVMHRDLKPENFLFDTPGEDAEMKATDFGLSVFYKPGQTFHDVVGSPYYIAP
ELLCKIYGPQVDVWSAGVILYILLSGVPPFWAETESGIFRQILHGDLDFESEPWPTISESAKDLVKKMLERDPKQRISAHEVLCHPWILDDTVAPDQPLD
SAVLTRLKHFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITYEELKDGLKQVGSNLMESEIKSLMESADIDNNGTIDYGEFLAATLHLN
KMEREENLVAAFAYFDKDGSGYITIDELQQACKDFGLGEVHLDDMIKEIDQDNDGRIDYGEFVAMMKKGDDDQVGRSRTKKGNINFNIADAFGVKEESS*
>Medtr3g051770 Org_Mtruncatula peptide: Medtr3g051770.1 (1 of 7) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:31058617)
MGCLLSKDKDSEPEHNNGGYRYGEHNHRNNHEQVNTSRTAPTSSYQPQIPTKPSSISAPSPKPLIKQDSNTILGKGLEDVKQFYTLGKELGRGQFGVTFL
CTENSTGLLYACKSISKRKLVSKSDREDIKREIQIMQHLSGQPNIVEFKGAYEDRNSVHVVMELCAGGELFDRIIAKGHYSEKAAASICRQIVNVVNICH
FMGVMHRDLKPENFLLASKDENALLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRRCGKEIDIWSAGVILYILLSGVPPFWAETEKGIFDAILEGH
IDFESEPWPKISDSAKDLVRKMLIQEPKKRITAAQVLEHPWIKDGNASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAENMSEEEIRGLKAMFTNMDTDN
SGTITYEELKAGLQRLGSKLSEAEVKQLMEAADVDGNGTIDCIEFITATMHRHKLERDDHLYKAFQYFDKDSSGFITRDELETAMKEYGMGDDATIKEII
SEVDTIISEVDTDHDGRINYEEFCAMMRSGNQQQVKLF*
>Medtr3g098070 Org_Mtruncatula peptide: Medtr3g098070.1 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:31057225)
MSKSNTTNTTPPKPTWVLPYVTENLREVYTLGRKLGQGQFGITYHCIHNSTGRTYACKSISKKKLLCKEDYDDVWREIQIMHHLSENPNVVRIHGTYEDS
FSVHLVMELCEGGELFDRIVQKGHYSERQAAKLIRTIVEVVEACHSLGVMHRDLKPENFLFDSVDEDALLKTIDFGLSVFYKPGEIFSDVVGSPYYVAPE
VLHKHYGPEADVWSAGVILYILLSGVPPFWAETDQGIFRQIFQGKLDFRSEPWPGISDSAKDLIRKMLDRNPKTRFTAHQVLCHPWIVDDNIAPDKPLDS
AVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFRMLDADNSGTITLEELKEGLKRVGSELMESEIKDLMDAADIDNNGTLDYGEFIAATVHLNK
LEREENLLSAFSYFDKDCSGYITIDEIQAACKEFGLDDVHIDEMVKEIDQDNDGQIDYGEFAAMMRKGNGGIGRRTMTSTLNFRDALGIIGNGSN*
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>Medtr3g098090 Org_Mtruncatula peptide: Medtr3g098090.1 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:31060081)
MSKSNIPDKTTPTTPKTTWVLPRVTKNLHEVYTLGRKLGQGQFGITYHCTHNSTGRTYACKSISKKKLLCKEDYDDAWREIQIMHHLSEHPNVVRIRETY
EDSFFVHLVMELCEGGELFDRIVQKGHYSERQAAKLIKTIVEVVEACHSLGVMHRDLKPENFLFDSVDEDAVLKTIDFGLSVFYKPGEIFSDISGSPYYV
APEVLHKKYGSEADVWSAGVILYILLSGRLPFCADTENGIFRQICRGRLNFQSEPWPEISYSAKDLIRKMLDRNPRTRFTAHQVLCHPWIVDDNIAPDKP
LDSAVLSRLKQFSAMNKLKKMALHVIAKRLNEEEIGGLKELFRMLDADNSGTITLDELKEGLQRVGSELMESEIKDLMDAADIDNNGTLDYGEFIAATVH
LNKLEREENLLSAFSYFDKDGSGYITIDEIQAACKEFGLDDVHIDEMVKEIDQDNDGQIDYGEFAAMMRKGNGGIGRRTMSSTLDSRDALEIIGNGSN*
>Medtr4g066660 Org_Mtruncatula peptide: Medtr4g066660.1 (1 of 2) PTHR24349:SF160 - CALCIUM-DEPENDENT
PROTEIN KINASE 24 (PAC:31111529)
MGSCVSTQGKHGGRKKSKDHHINTKHKINDQNHEPNTPTTRRSSVTGRRSSVTSRQLNVVTNPSPGNIFDKYELGKELGRGEFGVTHRCVELKTGEAFAC
KKIAKTKLRTEIDIQDVRREVQIMRHLPEHPNIVAFREAYEDRDAVYLVMELCEGGELFDRIVAKGHYTERAAANVAKTILEVCKVCHEHGVIHRDLKPE
NFLFADGSEAASLKAIDFGLSTFYVNGDRFNEIVGSPYYMAPEVLRRNYGPEIDIWSTGVILYILLCGVPPFWAETEEAIAQAIIRGNVDFTRDPWPKVS
EEAKYLVKRMLDPNPFSRITVQEVLDHSWIQNREHGKNVSLGDQVRSRIKQFSLMNRFKKKVLRVVADNLPDEQIDGFRKMFDMMDKDKNGHLTFEELKD
GFAEIGNVIPDPDLQMLMDAADFDGNGTLNCEEFITMSVHMRRLGNDEHLTEAFNFFDKNKSGYVEFDELKDALSDNGSTDDQVIRDILNDVDLDKDGRV
SFEEFKAMMKTGGDWKMASRQYSKAFLNALSFRMFKDKSTGVATN*
>Medtr4g107490 Org_Mtruncatula peptide: Medtr4g107490.1 (1 of 2) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:31106321)
MGNCNTCINKDAIESTGKAKTSSTTESNSNHGRRRKTKPKPKSNPYTEQSLTPGATIRVLKESNPRNRINDKYILGRELGRGEFGITYLCTDKETKQELA
CKSISKRKLRTAVDVEDVRREVAIMSTLPEHPNVVKLKATYEDDENVHLVMELCEGGELFDRIVARGHYSERAAAHVARTIAEVVRMCHVNGVMHRDLKP
ENFLFANKKENSVLKAIDFGLSVFFKPGERFSEIVGSPYYMAPEVLKRNYGPEVDIWSAGVILYILLCGVPPFWAETEQGVALAILRGVIDFKREPWPQI
SDSAKSLVRQMLEPDPKKRLTAEQVLEHPWLQNAKKASNVPLGDIVRTRLKQFSLMNRFKKRALRVIAEHLSLEEVEIIKDMFTLMDTDKDGRITYEELK
AGLRKVGSQLAEPEIKLLMDVADVDGNGVLDYGEFVAVTIHLQRMENDEHFRKAFKFFDKDESGYIELSELEAALVDDLGETDTNVLNEIMREVDTDKDG
RISYEEFVAMMKTGTDWRKASRQYSRERFKSLSINLMKDGSLQLHDEISGQAVVV*
>Medtr4g132040 Org_Mtruncatula peptide: Medtr4g132040.1 (1 of 7) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:31115236)
MGCYTSKPEVDKFAPHRGYAAITADDDTTYRYVTVSAYSNQIQITTTPPKLDSLASPVTAPPNPKPSPTAQNVKTVQKTQKTILEKPYEDIKKLYTFGKE
LSRGKFGITYFCTENSTGQNYACRSILKRKLVSKADKEDIKREIQILQHFSGQPNIVKFKGAYEDSLSIHLVLEHCAYGELFDTINAHPHGYSERVVASL
CRCIVNVVHTCHCMGVMHRDLNPENFLFSTKDKALTLKAVDFRFSVFIEEGKIYNDMVGSGCYVAPEVLLRSYGKEIDIWSAGIILYILLSGGPPFSPGT
DKGLLNAVLEGELDLLSEPWPSISDSAKDLVKKMLTPDPKKRITSKQVLEHTWMRDGGEASDKPIDISVLSRMKQFRAINTFTKLGLKVMAENLAEEVKG
LKETFENMDTDSSGTITYEELKTGLAQIGSELSEAEENQLMKAADVDGKGSIDYLEFISATMHRYRLERDENIHKAFQYFDKDSSGHITREELETALTKH
GISDEAKIKEIVTEVYTDNDGKINYDEFCAMMRSGMPHQGPLF*
>Medtr4g132070 Org_Mtruncatula peptide: Medtr4g132070.1 (1 of 7) PTHR24349:SF89 - CALCIUM-DEPENDENT
PROTEIN KINASE 29 (PAC:31108323)
MGCHGSKEKKHAKDEFTARQRSSPARPTAPPSRPAGVDSNFRYINVPPQVQQSSTPSSNPKPSAITTQKPVQQKVDTTILGKPYEDIKKFYTLGKELGRG
QFGITYFCTENSTGLNYACKSILKRKLVSKADREDIKREIQILQHLSGQPNIVEFKGAFEDRFSVHLVMELCAGGELFDRIIAQGHYSERAAASICRDVV
KVVHICHFMGVLHRDLKPENFLLSSKDDGAALKATDFGLSVFIEEGKVYRDMVGSAYYVAPEVLRRNYGKEIDIWSAGIILYILLSGVPPFWAETEKGIF
NAILEGELDFVSEPWPSISDSAKDLVRKMLTPDPKKRITSTEVLEHPWMREGGEASDKPIDSAVLSRMKQFRAMNKFKKLALKVMAENLSEEEIKGLKAM
FANMDTDSSGTITYEELKTGLARIGSRLSEAEVKQLMEAADVDGNGSIDYLEFISATMHRHRLERDEHLYKAFQYFDKDNSGHITREELETAMTKHGMGD
EATIKEIISEVDTDNDGRINYEEFCAMMRSGMPHQGPLF*
>Medtr5g009830 Org_Mtruncatula peptide: Medtr5g009830.1 (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:31086214)
MGNRISSKHKPSSDSQTRSKSEPSHSTPTSFHPPNRTPKQSTHTPTPSSSPLGRVLGKPMEDVRSTYTFGRELGRGQFGVTYLVTHKLTKEQFACKSIAT
RKLIRRDDLDDIRREVQIMHHLTGHRNIVELKGAYEDRHSVNLIMELCAGGELFDRIISKGHYSERAAAELCRQIVTVVHNCHTMGVMHRDLKPENFLFL
SKHENSPLKATDFGLSVFFKPEDVFKDLVGSAYYVAPEVLRRSYGPEADIWSAGIILYILLSGVPPFWAENEQGIFDAILRGHLDFASDPWPKISSIAKD
LIKKMLRADPKERISAVEVLDHSWMKEDGASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGTITFEELKAGLPKLG
TKISESEVRQLMEAADVDGNGTIDYIEFITATMHLNRMEREDHLYKAFEYFDNDKSGYITKEELESALTKYNMGDEKTIKEIIDEVDSDNDGRINYEEFV
AMMRKGNPDLITNKRRK*
>Medtr5g009830 Org_Mtruncatula peptide: Medtr5g009830.2 (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:31086213)
MGNRISSKHKPSSDSQTRSKSEPSHSTPTSFHPPNRTPKQSTHTPTPSSSPLGRVLGKPMEDVRSTYTFGRELGRGQFGVTYLVTHKLTKEQFACKSIAT
RKLIRRDDLDDIRREVQIMHHLTGHRNIVELKGAYEDRHSVNLIMELCAGGELFDRIISKGHYSERAAAELCRQIVTVVHNCHTMGVMHRDLKPENFLFL
SKHENSPLKATDFGLSVFFKPEDVFKDLVGSAYYVAPEVLRRSYGPEADIWSAGIILYILLSGVPPFWAENEQGIFDAILRGHLDFASDPWPKISSIAKD
LIKKMLRADPKERISAVEVLDHSWMKEDGASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGTITFEELKAGLPKLG
TKISESEVRQLMEAADVDGNGTIDYIEFITATMHLNRMEREDHLYKAFEYFDNDKSGYITKEELESALTKYNMGDEKTIKEIIDEVDSDNDGRINYEEFV
AMMRKGNPDLITNKRRK*
>Medtr5g009830 Org_Mtruncatula peptide: Medtr5g009830.3 (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:31086215)
MGNRISSKHKPSSDSQTRSKSEPSHSTPTSFHPPNRTPKQSTHTPTPSSSPLGRVLGKPMEDVRSTYTFGRELGRGQFGVTYLVTHKLTKEQFACKSIAT
RKLIRRDDLDDIRREVQIMHHLTGHRNIVELKGAYEDRHSVNLIMELCAGGELFDRIISKGHYSERAAAELCRQIVTVVHNCHTMGVMHRDLKPENFLFL
SKHENSPLKATDFGLSVFFKPEDVFKDLVGSAYYVAPEVLRRSYGPEADIWSAGIILYILLSGVPPFWAENEQGIFDAILRGHLDFASDPWPKISSIAKD
LIKKMLRADPKERISAVEVLDHSWMKEDGASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGTITFEELKAGLPKLG
TKISESEVRQLMEAVRFLLHHYLSVTVYYNLYF*
>Medtr5g089320 Org_Mtruncatula peptide: Medtr5g089320.1 (1 of 3) PTHR24349:SF131 - CALCIUM-DEPENDENT
PROTEIN KINASE 17-RELATED (PAC:31086627)
MGNCCSGGTEDPEDKGENNQQNNDANGDSSATTPPPWSKPSPQPSKPSKPSAIGPVLGRPMEDVKATYSMGKELGRGQFGVTHLCTHKTTGKQYACKTIA
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KRKLANKEDIEDVRREVQIMHHLTGQPNIVELIGAFEDKQSVHLVMELCAGGELFDRIIAKGHYTERAAASLLRTIVQIVHTCHSMGVIHRDLKPENFLL
LSKDENSPLKATDFGLSVFYKQGDQFKDIVGSAYYIAPDVLKRKYGPEVDIWSVGVMLYILLCGVPPFWAESENGIFNAILRGHVDFSSDPWPSISPSAK
DLVRKMLNSDPKQRITAYEVLNHPWIKEDGEAPDTPLDNAVLNRLKQFRAMNQFKKVALKVIASCLSEEEIMGLKQMFKGMDTDNSGTITIEELKQGLAK
QGTRLSETEVKQLMEAADADGNGIIDYDEFITATMHMNRLNREEHVYTAFQFFDKDNSGYITIEELEQALHEYNMHDGRDIKEIISEVDADNDGRINYDE
FVAMMGKGNPEANTKKRRDSTLY*
>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)
MGGCLSKKESKPDHRHVGVSGIHNHNHNHNHNHNHNHNHKNHEPYVNQSKTPSQQPYQSPNKHAPRSPKPIVQRPNTNAILGKQFEDVKQIYTLGKELGR
GQFGVTYLCTENSTGLKYACKSISKRKLVSKSDKEDIKREIQIMQHMSGQPNIVEFKGAYEDKNSVHVVMELCAGGELFDRIIAKGKYSERAAASICRQI
VNVVHICHFMGVMHRDLKPENFLLSSKDDKATIKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRKYGKETDIWSAGVILYILLCGVPPFWAETEKGI
FDAILQGHIDFESRPWPSISNSAKDLVSRMLMQDPKKRITASQVLDHPWLKEGGNASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAENLSSEEIQGLKA
MFTNMDTDKSGTITYEELRAGLQRLGSKLTEAEVRQLMEAADVDGNGTIDYIEFITATMHRHRLERDEHLYKAFQYFDKDNSGFITRDELETAMKEYGMG
DEETIREIISEVDTDNDGRINYEEFCTMMRSGVQQQGKLF*
>Medtr5g099240 Org_Mtruncatula peptide: Medtr5g099240.1 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:31089325)
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KLGQGQFGTTFLAIDNSTSIEYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDALYVHIVMELCSGGELFDRIIQRGHYTERKAAEL
TRIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAET
QQGIFDAVLKGHIDFDSEPWPLISDSGKDLIRKMLCSRPSDRLTAHEVLCHPWICENGVAPDRSLDPAVLSRLKQFSAMNKLKKMALRVIAESLSEEEIA
GLREMFQTMDTDNSGAITFDELKAGLRRYGSTLKDIEIRDLMEAADVDNSGTIDYGEFIAATVHLNKLEREEHLVAAFQYFDKDGSGYITVDELQQACTE
HNMTDVFLEDIIKEVDQDNDGRIDYGEFVAMMQKGNVGIGRRTMRNSLNLSMRDAPSAH*
>Medtr5g099240 Org_Mtruncatula peptide: Medtr5g099240.2 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:31089328)
MRRGPDNQTYYVLGHKTPNIRDLYTLGRKLGQGQFGTTFLAIDNSTSIEYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDALYVHI
VMELCSGGELFDRIIQRGHYTERKAAELTRIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLLKH
YGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFDSEPWPLISDSGKDLIRKMLCSRPSDRLTAHEVLCHPWICENGVAPDRSLDPAVLSR
LKQFSAMNKLKKMALRVIAESLSEEEIAGLREMFQTMDTDNSGAITFDELKAGLRRYGSTLKDIEIRDLMEAADVDNSGTIDYGEFIAATVHLNKLEREE
HLVAAFQYFDKDGSGYITVDELQQACTEHNMTDVFLEDIIKEVDQDNDGRIDYGEFVAMMQKGNVGIGRRTMRNSLNLSMRDAPSAH*
>Medtr5g099240 Org_Mtruncatula peptide: Medtr5g099240.3 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:31089327)
MRRGPDNQTYYVLGHKTPNIRDLYTLGRKLGQGQFGTTFLAIDNSTSIEYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDALYVHI
VMELCSGGELFDRIIQRGHYTERKAAELTRIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLLKH
YGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFDSEPWPLISDSGKDLIRKMLCSRPSDRLTAHEVLCHPWICENGVAPDRSLDPAVLSR
LKQFSAMNKLKKMALRVIAESLSEEEIAGLREMFQTMDTDNSGAITFDELKAGLRRYGSTLKDIEIRDLMEAADVDNSGTIDYGEFIAATVHLNKLEREE
HLVAAFQYFDKDGSGYITVDELQQACTEHNMTDVFLEDIIKEVDQDNDGRIDYGEFVAMMQKGNVGIGRRTMRNSLNLSMRDAPSAH*
>Medtr5g099240 Org_Mtruncatula peptide: Medtr5g099240.4 (1 of 1) PTHR24349:SF83 - CALCIUM-DEPENDENT
PROTEIN KINASE 6 (PAC:31089326)
MRRGPDNQTYYVLGHKTPNIRDLYTLGRKLGQGQFGTTFLAIDNSTSIEYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDALYVHI
VMELCSGGELFDRIIQRGHYTERKAAELTRIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLLKH
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LKQFSAMNKLKKMALRVIAESLSEEEIAGLREMFQTMDTDNSGAITFDELKAGLRRYGSTLKDIEIRDLMEAADVDNSGTIDYGEFIAATVHLNKLEREE
HLVAAFQYFDKDGSGYITVDELQQACTEHNMTDVFLEDIIKEVDQDNDGRIDYGEFVAMMQKGNVGIGRRTMRNSLNLSMRDAPSAH*
>Medtr7g068710 Org_Mtruncatula peptide: Medtr7g068710.1 (1 of 1) PTHR24349//PTHR24349:SF145 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:31078445)
MGNCCRSPAAVAREDVKSSFSNHDHPKRTETTANKKSPPVTVLAATKTSDNMEDRYLIDRELGRGEFGVTYLCIDRDTRELLACKSISKRKLRTAVDVDD
VRREVAIMRHLPKSSSIVTLREACEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAAVARTIVEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAI
DFGLSIFFKPGEKFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGLIDFKREPWPSISESAKSLVKQMLEPDPK
LRLTAKQVLEHPWLQNAKKAPNVPLGDVVKSRLKQFSMMNRFKRKALRVIADFLSNEEVEDIKEMFKKMDTDNDGIVSIEELKVGFRNHQSQLAESEVQM
FIEAVDNNGKGTLDYGEFVAISLHLKRMANDEHLHKAFSYFDKDGNGYIEPEELRNALMEDGTDDCTDVANDIFQEVDTDKDGKISYDEFVAMMKTGTDW
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>Medtr7g091890 Org_Mtruncatula peptide: Medtr7g091890.1 (1 of 1) PTHR24349:SF93 - CALCIUM-DEPENDENT
PROTEIN KINASE 14 (PAC:31078915)
MGNCCATPAVAGEEITNKKNKKGKKENPFATDYAYNNNTTSKLTVLKDPTGNEIETRYELGRELGRGEFGVTYLCTDKETREELACKSISKKKLRTAIDI
EDVRREVEIMRHMPKHNNIVTLKDTYEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAAVTKTIVEVVQMCHKHGVMHRDLKPENFLFANKKETAALK
AIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYGPEVDIWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVVDFKRDPWPKVSDNAKDLVKKMLNPD
PKRRLTAQEVLDHPWLINAKKAPNVSLGETVRARLKQFSVMNKLKKRALRVIAEHLSVEEAAGLKEGFNLMDTTNRGKINIDELRTGLHKLGHQVPDSDL
QILMEAGDIDRDGYLDYGEYVAISVHLRKMGNDEHLHKAFDFFDQNQTGYIEIEELRNALSDEIETNSEEVISAIMHDVDTDKDGKISYEEFANMMKAGT
DWRKASRQYSRERFNSLSLKLMKDGSLQLNNDR*
>Medtr7g091890 Org_Mtruncatula peptide: Medtr7g091890.2 (1 of 1) PTHR24349:SF93 - CALCIUM-DEPENDENT
PROTEIN KINASE 14 (PAC:31078916)
MGNCCATPAVAGEEITNKKNKKGKKENPFATDYAYNNNTTSKLTVLKDPTGNEIETRYELGRELGRGEFGVTYLCTDKETREELACKSISKKKLRTAIDI
EDVRREVEIMRHMPKHNNIVTLKDTYEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAAVTKTIVEVVQMCHKHGVMHRDLKPENFLFANKKETAALK
AIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYGPEVDIWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVVDFKRDPWPKVSDNAKDLVKKMLNPD
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>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)
MGNNCVGPRRTYEHESFQTSFWWPWSLSWSYPINQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNTASDRQTSISQEDAEPVTQLKEKATPTKT
MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGKFGTTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVRREIEIMHHLVGIPNVISIK
GAYEDPVVVYIVMELCEGGELFDRIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA
YYVAPEVIEECYGPEADVWSAGVIIYILLCGTPPFYGELDREIFDEVLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP
DRPLDSATLSRLKQFSAMNKLKKMALRVIAKNLSEEEISGLKESFKTIDTDNTGQITFEKLKVGLKKFGANLSESEIFDLMQAADIDNNGMIDYGEFIAA
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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)
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MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGKFGTTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVRREIEIMHHLVGIPNVISIK
GAYEDPVVVYIVMELCEGGELFDRIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA
YYVAPEVIEECYGPEADVWSAGVIIYILLCGTPPFYGELDREIFDEVLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP
DRPLDSATLSRLKQFSAMNKLKKMALRVIAKNLSEEEISGLKESFKTIDTDNTGQITFEKLKVGLKKFGANLSESEIFDLMQAADIDNNGMIDYGEFIAA
TLHLNKVDKEDHLVAAFSYFDKDGNGYITQDELQQVCKEFGMKDVHFEEMIREADQNNVSTYYNVMCFHFRTTE*
>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)
MGNNCVGPRRTYEHESFQTSFWWPWSLSWSYPINQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNTASDRQTSISQEDAEPVTQLKEKATPTKT
MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGKFGTTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVRREIEIMHHLVGIPNVISIK
GAYEDPVVVYIVMELCEGGELFDRIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA
YYVAPEVIEECYGPEADVWSAGVIIYILLCGTPPFYGELDREIFDEVLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP
DRPLDSATLSRLKQFSAMNKLKKMALRVSTFSIT*
>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)
MGNNCVGPRRTYEHESFQTSFWWPWSLSWSYPINQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNTASDRQTSISQEDAEPVTQLKEKATPTKT
MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGKFGTTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVRREIEIMHHLVGIPNVISIK
GAYEDPVVVYIVMELCEGGELFDRIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA
YYVAPEVIEECYGPEADVWSAGVIIYILLCGTPPFYGELDREIFDEVLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP
DRPLDSATLSRLKQFSAMNKLKKMALRVIAKNLSEEEISGLKESFKTIDTDNTGQITFEKLKVGLKKFGANLSESEIFDLMQAVSIKSKIIVNSLNVTQQ
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)
MGNNCVGPRRTYEHESFQTSFWWPWSLSWSYPINQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNTASDRQTSISQEDAEPVTQLKEKATPTKT
MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGKFGTTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVRREIEIMHHLVGIPNVISIK
GAYEDPVVVYIVMELCEGGELFDRIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA
YYVAPEVIEECYGPEADVWSAGVIIYILLCGTPPFYGELDREIFDEVLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP
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)
MGNNCVGPRRTYEHESFQTSFWWPWSLSWSYPINQTQISVSQNTNSSQTYQQNPPHVHKIENKDMKTLQSNTASDRQTSISQEDAEPVTQLKEKATPTKT
MMSKNINIRRVTPKSAGLRAESVLLTNNGPFREFYKLGDELGKGKFGTTSLCLEKSTRKTYACKAIPKVKLFRENDIEDVRREIEIMHHLVGIPNVISIK
GAYEDPVVVYIVMELCEGGELFDRIVERRHYTERKAAKLARTIVNVVEACHSRGVMHRDLKPENFLFVDGDEDSTLMAIDFGLSIFFKPGEKFSDFVGSA
YYVAPEVIEECYGPEADVWSAGVIIYILLCGTPPFYGELDREIFDEVLHGEVDFCSDPWPSISESAKDLVKKMLDRDPKTRIKAHEVLSHPWIQVDGVAP
DRPLDSATLSRLKQFSAMNKLKKMALRVSTFSIT*
>Medtr8g095440 Org_Mtruncatula peptide: Medtr8g095440.1 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:31073956)
MAKENPTPTIALKPVTWVLPYRTEKVTEIYRMGRKLGQGQFGTTYLCTHKSTNKKFACKSIPKRKLFCKEDYEDVWREIQIMHHLSEHPHVVRIEGTYED
STAVHIVMELCEGGELFDRIVKKGHYSERQAAGLIKTIVEVVESCHSLGVMHRDLKPENFLFDTVDEDAKLKATDFGLSVFYKPGESFSDVVGSPYYVAP
EVLRKLYGPESDVWSAGVILYILLSGVPPFWAETEPGIFRQILLGKLDFQSEPWPSISDSAKDLIRKMLDQNPRTRLTAHEVLRHPWIVDDNIAPDKPID
SAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDSSGTITFDELKDGLKRVGSELMESEIQDLMDAADVDKSGTIDYGEFIAATVHLN
KLEREENLLSAFAYFDKDASGYITIDEISQACKDFGLDDIHIDEMIKEIDQDNDGQIDYSEFAAMMRKGNGGIGRRTMRNTLNLRDALGLVGNGSNQVID
GYL*
>Medtr8g095440 Org_Mtruncatula peptide: Medtr8g095440.2 (1 of 6) PTHR24349:SF166 - CALCIUM-DEPENDENT
PROTEIN KINASE 11-RELATED (PAC:31073957)
MAKENPTPTIALKPVTWVLPYRTEKVTEIYRMGRKLGQGQFGTTYLCTHKSTNKKFACKSIPKRKLFCKEDYEDVWREIQIMHHLSEHPHVVRIEGTYED
STAVHIVMELCEGGELFDRIVKKGHYSERQAAGLIKTIVEVVESCHSLGVMHRDLKPENFLFDTVDEDAKLKATDFGLSVFYKPGESFSDVVGSPYYVAP
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EVLRKLYGPESDVWSAGVILYILLSGVPPFWAETEPGIFRQILLGKLDFQSEPWPSISDSAKDLIRKMLDQNPRTRLTAHEVLRHPWIVDDNIAPDKPID
SAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDSSGTITFDELKDGLKRVGSELMESEIQDLMDAVSVFLWEDNSFFFMQALNLTQS
SLP*
>Medtr8g099095 Org_Mtruncatula peptide: Medtr8g099095.1 (1 of 2) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:31073428)
MGGNCSTGAGAGINTTTTTPHSDPPPKNAPTILPQNFTPSPPQPPLPTTTLGRILNRPMEDVRSIFIFGRELGRGQFGVTYLVTHKVTKEQFACKSIATR
KLVNRDDIDDVRREVQIMHHLTGHRNIVELKGAYEDKHSVNLVMELCAGGELFDRIILKGHYSERAAANLCRQIVTVVHNCHTMGVMHRDLKPENFLFLG
KEENSPLKATDFGLSVFFKPGDVFKDLVGSAYYVAPEVLRKSYGPETDIWSAGIILYILLSGVPPFWAENEQGIFDAILRGQIDFASDPWPSISSSAKDL
VKKMLRNDAKERISAVEVLNHPWMRVDGDASDKPLDIAVLSRMKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGTITFEELKAGLPKLG
SKMSESEVRQLMEAADVDGNGTIDYIEFITATMHMNRMEREDHLYKAFEYFDQDKSGYITKEELESALKKYNMGDENTIKEIIAEVDTDNDARINYDEFV
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)
MADFEVLVGFQEHVPLPALLQNATDDLEKLYSLGKKLGEGQFGTTYLCTERATGLQFACKCIPKRKLISSEEIEDVGREVEVMYHLSGHPNIVTLKGAYE
DATNVYLVMELCEGGELFDRIIERGTYTEAEAARLTRTIVSVVEACHKSGVVHRDLKPENFLFKTKEDDSVLKAADFGSARFFEPGDVFTDIVGSPYYVA
PEVLDRHYGPEADIWSAGVMLYILLSGAPPFWAETVQGIFEKVMEGEPPTFTADPWPNISEVAKDLIRKMLDPNPEKRLKAHEVLNHPWIREDGVAPKKP
IASLVQFRMKQFAAMNKLKKLAIRIIAETLSEEEIANLKEIFTEMDSDNDGAISFEELKAGLLRVGTSLKDAELFDLMDAADVDHDGMIDCGEFLAATLS
LNHIELEENLMAAFQYLDKSGSGYITTDELLAVCFEFHMEDVRLEDLLHDVSIGADGSIDYKMFVTMMRKCNGGMGHQNLRCTLGITDVLTLEEQY*
>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)
MADFEVLVGFQEHVPLPALLQNATDDLEKLYSLGKKLGEGQFGTTYLCTERATGLQFACKCIPKRKLISSEEIEDVGREVEVMYHLSGHPNIVTLKGAYE
DATNVYLVMELCEGGELFDRIIERGTYTEAEAARLTRTIVSVVEACHKSGVVHRDLKPENFLFKTKEDDSVLKAADFGSARFFEPGDVFTDIVGSPYYVA
PEVLDRHYGPEADIWSAGVMLYILLSGAPPFWAETVQGIFEKVMEGEPPTFTADPWPNISEVAKDLIRKMLDPNPEKRLKAHEVLNHPWIREDGVAPKKP
IASLVQFRMKQFAAMNKLKKLAIRIIAETLSEEEIANLKEIFTEMDSDNDGAISFEELKAGLLRVGTSLKDAELFDLMDAADVDHDGMIDCGEFLAATLS
LNHIELEENLMAAFQYLDKSGSGYITTDELLAVCFEFHMEDVRLEDLLHDVSIGADGSIDYKMFVTMMRKCNGGMGHQNLRCTLGITDVLTLEEQY*
>Pp3c11_4640 Org_Ppatens peptide: Pp3c11_4640V3.1.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32959137)
MGNCCVGSTTKKPKQRPNPFAQDGYQTNLQILKNQPKSRILDKYNLGRELGRGEFGITYLCTDKETGEVFACKSISKKKLRTAVDVEDVRREVAIMKHLL
EHPNIVTLKGAYEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVMHRDLKPENFLFANKNENSPLKAIDFGLSVFFKPGE
RFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKRDPWPKVSDSAKSLVRHMLEPDPKARYSAQQVLDHP
WLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEIFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVDGNGTL
DYGEFVAATVHLQRLDDDEHLRRAFDFFDVDRSGYIETEELREAVGEPLNGSPSETDVVQAILLEVDIDKDGRISYEEFATMMRRGTDWRKASRQYSRDR
FNSLSMRLLRDGSLNPDKIVAVR*
>Pp3c11_4640 Org_Ppatens peptide: Pp3c11_4640V3.2.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32959139)
MKHLLEHPNIVTLKGAYEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVMHRDLKPENFLFANKNENSPLKAIDFGLSVF
FKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKRDPWPKVSDSAKSLVRHMLEPDPKARYSAQQ
VLDHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEIFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVD
GNGTLDYGEFVAATVHLQRLDDDEHLRRAFDFFDVDRSGYIETEELREAVGEPLNGSPSETDVVQAILLEVDIDKDGRISYEEFATMMRRGTDWRKASRQ
YSRDRFNSLSMRLLRDGSLNPDKIVAVR*
>Pp3c11_4640 Org_Ppatens peptide: Pp3c11_4640V3.3.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32959138)
MKHLLEHPNIVTLKGAYEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVMHRDLKPENFLFANKNENSPLKAIDFGLSVF
FKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKRDPWPKVSDSAKSLVRHMLEPDPKARYSAQQ
VLDHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEIFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVD
GNGTLDYGEFVAATVHLQRLDDDEHLRRAFDFFDVDRSGYIETEELREAVGEPLNGSPSETDVVQAILLEVDIDKDGRISYEEFATMMRRGTDWRKASRQ
YSRDRFNSLSMRLLRDGSLNPDKIVAVRFCAGFFGLFFRCLLKDHCH*
>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.1.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956551)
MGNCCVGSSTKKSRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
HLPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVEGN
GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQYS
RDRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.2.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956552)
MGNCCVGSSTKKSRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
HLPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVEGN
GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQYS
RDRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.3.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956553)
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MGNCCVGSSTKKSRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
HLPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVEGN
GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQYS
RDRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.4.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956554)
MGNCCVGSSTKKSRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
HLPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVEGN
GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQYS
RDRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.5.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956558)
MKHLPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVF
FKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQ
VLDHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVE
GNGTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQ
YSRDRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.6.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956555)
MGNCCVGSSTKKSRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
HLPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVEGN
GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQYS
RDRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.7.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956556)
MGNCCVGSSTKKSRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
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PROTEIN KINASE 10-RELATED (PAC:32956559)
MKHLPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVF
FKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQ
VLDHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVE
GNGTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQ
YSRDRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5760 Org_Ppatens peptide: Pp3c11_5760V3.9.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32956557)
MGNCCVGSSTKKSRKERRQNPFAPQDGYQTNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMK
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PGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVEGN
GTLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQYS
RDRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5820 Org_Ppatens peptide: Pp3c11_5820V3.1.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32957965)
MGNCCVGSSSNKSRRARRANLFAHDRYYGNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMKH
LPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVFFKP
GERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQVLD
HPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVEGNG
TLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQYSR
DRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c11_5820 Org_Ppatens peptide: Pp3c11_5820V3.2.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32957966)
MGNCCVGSSSNKSRRARRANLFAHDRYYGNNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEVFACKSISKKKLRTAVDVEDVRREVAIMKH
LPHHPHIVTLEGAYEDDVAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVIHRDLKPENFLFANTNENAPLKAIDFGLSVFFKP
GERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQVLD
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HPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDKTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVEGNG
TLDYGEFVAATVHLQRLDDDEHLRRAFDVFDVDGSGYIETEELREAVGEAMTELSSEPDVVQAILSEVDLDKDGRISYEEFAVMMRRGTDWRKASRQYSR
DRFNSLSMRLLRDGSLNPPSYSMSSMR*
>Pp3c12_190 Org_Ppatens peptide: Pp3c12_190V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32975193)
MGNTCVGAAGYFQGFTSAIALGGRSSRSNSERSPTASKIDDSDRKVEVDTPATQQNPPRQNHIPSVDTADQQQFKEVIEAMKKGREIKSVSGQSLTHSVL
QRKTENLRDLYILGKKLGQGQFGTTYLCIEKATNKEYACKSIAKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDR
IIQRGQYSEAKAAVLTRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEVFRDVVGSPYYVAPEVLRKNYGPEADVWSAGVI
LYILLSGVPPFWAETEQGIFEQVLKSELDFASDPWPKISDSAKDLIRKMLNPQASKRLKAHQVLCHPWICEDGVAPDRPIDSAVQSRLKHFSAMNKLKKI
AIRVIAESLSEEEIAGLKEMFKMMDTDNSGSISYDELKAGLKKVGSILKEEDIRQLMDAADVDGNGTIDYGEFLAATLHLNKIERDENMLAAFSYLDKDN
SGYLTIDELQHALAQFNMGDISVDELLHEVDQNNDGQIDYAEFVTMMRKGNPGAAGRSSFRNSQSLSLNDVLMMG*
>Pp3c12_190 Org_Ppatens peptide: Pp3c12_190V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32975194)
MGNTCVGAAGYFQGFTSAIALGGRSSRSNSERSPTASKIDDSDRKVEVDTPATQQNPPRQNHIPSVDTADQQQFKEVIEAMKKGREIKSVSGQSLTHSVL
QRKTENLRDLYILGKKLGQGQFGTTYLCIEKATNKEYACKSIAKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDR
IIQRGQYSEAKAAVLTRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEVFRDVVGSPYYVAPEVLRKNYGPEADVWSAGVI
LYILLSGVPPFWAETEQGIFEQVLKSELDFASDPWPKISDSAKDLIRKMLNPQASKRLKAHQVLCHPWICEDGVAPDRPIDSAVQSRLKHFSAMNKLKKI
AIRVIAESLSEEEIAGLKEMFKMMDTDNSGSISYDELKAGLKKVGSILKEEDIRQLMDAADVDGNGTIDYGEFLAATLHLNKIERDENMLAAFSYLDKDN
SGYLTIDELQHALAQFNMGDISVDELLHEVDQNNDGQIDYAEFVTMMRKGNPGAAGRSSFRNSQSLSLNDVLMMG*
>Pp3c12_21850 Org_Ppatens peptide: Pp3c12_21850V3.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:32973633)
MGNISGRPRKNRGHGTKGMNLGRPTDPRQKNESERPMYEGSTQRSSAVASSYGGGTQHKQDGSTRPATTGSTHAEGGHAARPSSGATPSERPPGPMSAPM
PRPRPTSYSANGVLGKPLVDIRQTYSLGRELGRGQFGVTYLCTHKTTGEILACKSIAKRKLTTKEDVEDVKREVQIMHHLSGTPNIVDLKGVYEDRHSVH
LVMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHTLGVFHRDLKPENFLLSSEAEDAQLKATDFGLSTFFKPGEVFHDIVGSAYYVAPEVLRR
NYGPEADVWSAGVIVYILLCGVPPFWAETEQGIFDAVLRGHIDFVSDPWPKISSGAKDLVRKMLNMNVKERLTAYQVLNHPWMEEGGDASDTPLDNAVLT
RLKNFSTANKMKKLALKVIAKNLSEEEIVGLRELFKSMDTDNSGMVTFEELKDGLLRQGSKLRESDIRELMEAADVDGNGKIDFNEFISATMHMNKLEME
DHLFAAFSHFDTDGSGYITIDELQEAMEKNGMGDPQTIQEIINEVDTDRDGRIDYDEFVAMMRKGNPITEDGGKHRHR*
>Pp3c12_21850 Org_Ppatens peptide: Pp3c12_21850V3.2.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:32973634)
MGNISGRPRKNRGHGTKGMNLGRPTDPRQKNESERPMYEGSTQRSSAVASSYGGGTQHKQDGSTRPATTGSTHAEGGHAARPSSGATPSERPPGPMSAPM
PRPRPTSYSANGVLGKPLVDIRQTYSLGRELGRGQFGVTYLCTHKTTGEILACKSIAKRKLTTKEDVEDVKREVQIMHHLSGTPNIVDLKGVYEDRHSVH
LVMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHTLGVFHRDLKPENFLLSSEAEDAQLKATDFGLSTFFKPGEVFHDIVGSAYYVAPEVLRR
NYGPEADVWSAGVIVYILLCGVPPFWAETEQGIFDAVLRGHIDFVSDPWPKISSGAKDLVRKMLNMNVKERLTAYQVLNHPWMEEGGDASDTPLDNAVLT
RLKNFSTANKMKKLALKVIAKNLSEEEIVGLRELFKSMDTDNSGMVTFEELKDGLLRQGSKLRESDIRELMEAADVDGNGKIDFNEFISATMHMNKLEME
DHLFAAFSHFDTDGSGYITIDELQEAMEKNGMGDPQTIQEIINEVDTDRDGRIDYDEFVAMMRKGNPITEDGGKHRHR*
>Pp3c12_21880 Org_Ppatens peptide: Pp3c12_21880V3.1.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
PROTEIN KINASE 5 (PAC:32974473)
MGNSSGRPRDSRKGSGGGSQGGSSQGSYPRNEGSYPRGSGHGGSTQPRGCNQGGSTQPRGSNQGGSTQPRGGSHGNAGGYRQAPKYTPPVPKPKPVAPGF
LGKPLSDILNSYTLGKELGRGEFGVTYTCTHKDTNEVYACKTIAKRKLTHKDDIEDVKREVQIMHHLSGTLNIVTLKAVFEDKHNIHLVMELCAGGELFD
RIVAKKCYSERAASDLCRVIVNVVHRCHSLGVFHRDLKPENFLFTSMAEDAPLKATDFGLSTFFKPGERFQDLVGTAYYIAPEVLRKDYGPEADVWSAGV
ILYILLCGVPPFWAETEKGIFDAIMRGTLDFTSDPWPRISDDAKVLVKGMLNPDVNARLTAQQVLDHPWMKEDGASNAPLDNAVLTRLKNFSAANKMKKL
ALKVIAQNLSEEEIAGLRQLFKSIDVDNSGTVTLLELKEGLIKQGSKFSESDIAKLMESADLDGNGKIDFNEFISATMHMNKLEKEDHLFAAFHHFDRDN
SGYITVFELQQALEENGVGDYDTIQEIIDEVDTDNDGRIDYDEFVAMMRKGNPGAEEGEKHNHRHRY*
>Pp3c12_21880 Org_Ppatens peptide: Pp3c12_21880V3.2.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
PROTEIN KINASE 5 (PAC:32974474)
MGNSSGRPRDSRKGSGGGSQGGSSQGSYPRNEGSYPRGSGHGGSTQPRGCNQGGSTQPRGSNQGGSTQPRGGSHGNAGGYRQAPKYTPPVPKPKPVAPGF
LGKPLSDILNSYTLGKELGRGEFGVTYTCTHKDTNEVYACKTIAKRKLTHKDDIEDVKREVQIMHHLSGTLNIVTLKAVFEDKHNIHLVMELCAGGELFD
RIVAKKCYSERAASDLCRVIVNVVHRCHSLGVFHRDLKPENFLFTSMAEDAPLKATDFGLSTFFKPGERFQDLVGTAYYIAPEVLRKDYGPEADVWSAGV
ILYILLCGVPPFWAETEKGIFDAIMRGTLDFTSDPWPRISDDAKVLVKGMLNPDVNARLTAQQVLDHPWMKEDGASNAPLDNAVLTRLKNFSAANKMKKL
ALKVIAQNLSEEEIAGLRQLFKSIDVDNSGTVTLLELKEGLIKQGSKFSESDIAKLMESADLDGNGKIDFNEFISATMHMNKLEKEDHLFAAFHHFDRDN
SGYITVFELQQALEENGVGDYDTIQEIIDEVDTDNDGRIDYDEFVAMMRKGNPGAEEGEKHNHRHRY*
>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32905868)
MGNTCIGAAGYFQGFSAAIALGGRSFTSNSEISPSAKADGDRHKAGGDSTATQQKAPRQNYIPSVEATDQQEFRDVIEAMRKGREIEPVPGQSLTHSVLQ
RKTENLRDLYTLGKKLGQGQFGTTYLCIEKATSKEYACKSIAKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDRI
IQRGHYSEAKAAILIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEIFRDVVGSPYYVAPEVLRKNYGPEADVWSAGVIL
YILLCGVPPFWAETEQGIFEQVLKSELDFATDPWPKISDSAKDLIRKMLNPEASKRMKAHHVLCHPWICEDGVAPDRPIDSAVQSRLKHFSAMNKLKKIA
IRVIAESLSEEEIAGLKEMFKMMDADNSGSISYEELKEGLKKVGSILKEEDMRQLMDAADVDGNGTIDYGEFLAATLHLNKIERDENMLAAFSYLDKDKS
GYLTVDEVQHALAEFRMGDLSVDELLREVDQNNDGRIDYAEFVAMMRKGNTGGAGRSSLRNSQSLSLNDVLMVG*
>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32905869)
MGNTCIGAAGYFQGFSAAIALGGRSFTSNSEISPSAKADGDRHKAGGDSTATQQKAPRQNYIPSVEATDQQEFRDVIEAMRKGREIEPVPGQSLTHSVLQ
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IQRGHYSEAKAAILIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEIFRDVVGSPYYVAPEVLRKNYGPEADVWSAGVIL
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IRVIAESLSEEEIAGLKEMFKMMDADNSGSISYEELKEGLKKVGSILKEEDMRQLMDAADVDGNGTIDYGEFLAATLHLNKIERDENMLAAFSYLDKDKS
GYLTVDEVQHALAEFRMGDLSVDELLREVDQNNDGRIDYAEFVAMMRKGNTGGAGRSSLRNSQSLSLNDVLMVG*
>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32905870)
MGNTCIGAAGYFQGFSAAIALGGRSFTSNSEISPSAKADGDRHKAGGDSTATQQKAPRQNYIPSVEATDQQEFRDVIEAMRKGREIEPVPGQSLTHSVLQ
RKTENLRDLYTLGKKLGQGQFGTTYLCIEKATSKEYACKSIAKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDRI
IQRGHYSEAKAAILIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEIFRDVVGSPYYVAPEVLRKNYGPEADVWSAGVIL
YILLCGVPPFWAETEQGIFEQVLKSELDFATDPWPKISDSAKDLIRKMLNPEASKRMKAHHVLCHPWICEDGVAPDRPIDSAVQSRLKHFSAMNKLKKIA
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GYLTVDEVQHALAEFRMGDLSVDELLREVDQNNDGRIDYAEFVAMMRKGNTGGAGRSSLRNSQSLSLNDVLMVG*
>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.4.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32905871)
MGNTCIGAAGYFQGFSAAIALGGRSFTSNSEISPSAKADGDRHKAGGDSTATQQKAPRQNYIPSVEATDQQEFRDVIEAMRKGREIEPVPGQSLTHSVLQ
RKTENLRDLYTLGKKLGQGQFGTTYLCIEKATSKEYACKSIAKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDRI
IQRGHYSEAKAAILIRTIVGVVETCHSLGVMHRDLKPENFLFSSTKEDAALKTTDFGLSVFFKPGEIFRDVVGSPYYVAPEVLRKNYGPEADVWSAGVIL
YILLCGVPPFWAETEQGIFEQVLKSELDFATDPWPKISDSAKDLIRKMLNPEASKRMKAHHVLCHPWICEDGVAPDRPIDSAVQSRLKHFSAMNKLKKIA
IRVIAESLSEEEIAGLKEMFKMMDADNSGSISYEELKEGLKKVGSILKEEDMRQLMDAADVDGNGTIDYGEFLAATLHLNKIERDENMLAAFSYLDKDKS
GYLTVDEVQHALAEFRMGDLSVDELLREVDQNNDGRIDYAEFVAMMRKGNTGGAGRSSLRNSQSLSLNDVLMVG*
>Pp3c17_2480 Org_Ppatens peptide: Pp3c17_2480V3.5.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32905872)
MGNTCIGAAGYFQGFSAAIALGGRSFTSNSEISPSAKADGDRHKAGGDSTATQQKAPRQNYIPSVEATDQQEFRDVIEAMRKGREIEPVPGQSLTHSVLQ
RKTENLRDLYTLGKKLGQGQFGTTYLCIEKATSKEYACKSIAKRKLISKEDVEDVRRELQIMHHLSGHPNIVMIKGAYEDPASVHLVMELCAGGELFDRI
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>Pp3c20_12010 Org_Ppatens peptide: Pp3c20_12010V3.1.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32946771)
MAKSPPPNSIQMSAVLDHRGSNVIPHDLISSLDRESNLVNLKVGYNKAELELSPGSSCPSPDNTPRVAVEKKPEVKYTTQNSKQVEGVIQAIKASDNKDQ
KKGKLTVCVLQHVTEDVRDVYTLGKKLGAGNFGITYLCTEKSTGDDYACKTISKKKLKSKDDVADVRKELQIMHHLSGHPNIVAIKGAFEDEASVHFVME
LCAGGELFTRITEKGHYSEAAAASAMRTIVSVIETCHILGVIHRDLKPENFLLLNKREDSPLKATDFGLSTFFKPGEVCKDVVGSAFYVAPEVLRRKYGP
ESDIWSAGVILYILLSGVPPFWADTEDGIFAEVLKAKVDFDTDPWPKISKDAKDLIRKILNPDVKARLTASEVLAHPWVREKGVASTKPMDSSVQNRLKR
FAAMNKMKKLAVRVIAQSMSEEEIAGLRNIFKIMDVDGSGTITFEELKQGLQKVGSNMREADVRDLMDAADVDKNGTIDYGEFLAATINMNKVEREENML
AAFRYLDKDNSGYITGEELQNACAEFNMGEMNLEDLMRDVDLDNDGRIDYQEFVAMMRKGTGTAPPQRGARMEPSFGFSAALQL*
>Pp3c20_12010 Org_Ppatens peptide: Pp3c20_12010V3.2.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32946772)
MNPQQSLCSSLFIRGLSLSQGSSCPSPDNTPRVAVEKKPEVKYTTQNSKQVEGVIQAIKASDNKDQKKGKLTVCVLQHVTEDVRDVYTLGKKLGAGNFGI
TYLCTEKSTGDDYACKTISKKKLKSKDDVADVRKELQIMHHLSGHPNIVAIKGAFEDEASVHFVMELCAGGELFTRITEKGHYSEAAAASAMRTIVSVIE
TCHILGVIHRDLKPENFLLLNKREDSPLKATDFGLSTFFKPGEVCKDVVGSAFYVAPEVLRRKYGPESDIWSAGVILYILLSGVPPFWADTEDGIFAEVL
KAKVDFDTDPWPKISKDAKDLIRKILNPDVKARLTASEVLAHPWVREKGVASTKPMDSSVQNRLKRFAAMNKMKKLAVRVIAQSMSEEEIAGLRNIFKIM
DVDGSGTITFEELKQGLQKVGSNMREADVRDLMDAADVDKNGTIDYGEFLAATINMNKVEREENMLAAFRYLDKDNSGYITGEELQNACAEFNMGEMNLE
DLMRDVDLDNDGRIDYQEFVAMMRKGTGTAPPQRGARMEPSFGFSAALQL*
>Pp3c20_4100 Org_Ppatens peptide: Pp3c20_4100V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32945505)
MGNTCVGAASKAGFFEFPQEGGSPSPSVTPKGTQPEEPAAKPNNPSPEERRKSGAGVEQEARAELKPQLSLTIQAPAVIRIAPTVYPSAANRRQENCVVP
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DQMAVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDQSEGAALKTTDFGLSVFFKPGEVFTDVVGSPYYVA
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DPAVQSRLKQFSAMNKLKKVAIRVIAELLSEEEIAGLREMFKMIDTDHSGTITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHL
NKIEREENLFAAFSWLDKDNSGYLTVDELQQACSKYNMGETSIEDLIREVDQDNDGRIDYNEFVTMMRKGNGAVGRTTLRNSLSLSDALMNPQ*
>Pp3c20_4100 Org_Ppatens peptide: Pp3c20_4100V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32945506)
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DQMAVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDQSEGAALKTTDFGLSVFFKPGEVFTDVVGSPYYVA
PEVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLKGELDFVSEPWPSISDSAKDLIRRMLDPNAKRRLKAHQVLSHPWIGEEGVAPDRPM
DPAVQSRLKQFSAMNKLKKVAIRVIAELLSEEEIAGLREMFKMIDTDHSGTITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHL
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>Pp3c20_4170 Org_Ppatens peptide: Pp3c20_4170V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32948019)
MGNTCVGAASKAGFFEFPQERGSPSPSVTPKGTQPEEPAAKPNNPSPEERRKSGAGVEQEARAELKPQLSLTIQAPAVIRIAPTVYPSAANRRQENCVVP
AMRRAGLNLIPGLSFTHSVLQRQTENLKDLYRLGRKLGQGQFGTTYLCVEKATGREYACKSIAKRKLISQEDVDDVRRELHIMHHLSGHPNIVTIKGAYE
DQMAVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDQSEGAALKTTDFGLSVFFKPGEVFTDVVGSPYYVA
PEVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLKGELDFVSEPWPSISDSAKDLIRRMLDPNAKRRLKAHQVLSHPWIGEEGVAPDRPM
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>Pp3c20_4170 Org_Ppatens peptide: Pp3c20_4170V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32948021)
MRRAGLNLIPGLSFTHSVLQRQTENLKDLYRLGRKLGQGQFGTTYLCVEKATGREYACKSIAKRKLISQEDVDDVRRELHIMHHLSGHPNIVTIKGAYED
QMAVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDQSEGAALKTTDFGLSVFFKPGEVFTDVVGSPYYVAP
EVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLKGELDFVSEPWPSISDSAKDLIRRMLDPNAKRRLKAHQVLSHPWIGEEGVAPDRPMD
PAVQSRLKQFSAMNKLKKVAIRVIAELLSEEEIAGLREMFKMIDTDHSGTITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLN
KIEREENLFAAFSWLDKDNSGYLTVDELQQACSKYNMGETSIEDLIREVDQDNDGRIDYNEFVMMMRKGNGAVGRTTLRNSLSLSDALMNPQ*
>Pp3c20_4170 Org_Ppatens peptide: Pp3c20_4170V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32948020)
MGNTCVGAASKAGFFEFPQERGSPSPSVTPKGTQPEEPAAKPNNPSPEERRKSGAGVEQEARAELKPQLSLTIQAPAVIRIAPTVYPSAANRRQENCVVP
AMRRAGLNLIPGLSFTHSVLQRQTENLKDLYRLGRKLGQGQFGTTYLCVEKATGREYACKSIAKRKLISQEDVDDVRRELHIMHHLSGHPNIVTIKGAYE
DQMAVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDQSEGAALKTTDFGLSVFFKPGEVFTDVVGSPYYVA
PEVLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLKGELDFVSEPWPSISDSAKDLIRRMLDPNAKRRLKAHQVLSHPWIGEEGVAPDRPM
DPAVQSRLKQFSAMNKLKKVAIRVIAELLSEEEIAGLREMFKMIDTDHSGTITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHL
NKIEREENLFAAFSWLDKDNSGYLTVDELQQACSKYNMGETSIEDLIREVDQDNDGRIDYNEFVMMMRKGNGAVGRTTLRNSLSLSDALMNPQ*
>Pp3c23_18880 Org_Ppatens peptide: Pp3c23_18880V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32950805)
MRRGVNLVPGQSFTHSVLQRNTENLKDLYTLGRKLGQGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHHLSGHPNIVTIKGAYEDQ
VSVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVVGSPYYVAPE
VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLAGELDFVSEPWPSISESAKDLIRRMLDPVAKRRLKAHQVLSHPWIREAGVAPDRPMDP
AVQSRLKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKMIDTDHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK
IEREENLFAAFSWLDKDHSGYLTVDELQHACSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKGNGTVGRATLRNSLSLSDALMHTN*
>Pp3c23_18880 Org_Ppatens peptide: Pp3c23_18880V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32950806)
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VSVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVVGSPYYVAPE
VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLAGELDFVSEPWPSISESAKDLIRRMLDPVAKRRLKAHQVLSHPWIREAGVAPDRPMDP
AVQSRLKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKMIDTDHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK
IEREENLFAAFSWLDKDHSGYLTVDELQHACSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKGNGTVGRATLRNSLSLSDALMHTN*
>Pp3c23_18880 Org_Ppatens peptide: Pp3c23_18880V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32950804)
MRRGVNLVPGQSFTHSVLQRNTENLKDLYTLGRKLGQGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHHLSGHPNIVTIKGAYEDQ
VSVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVVGSPYYVAPE
VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLAGELDFVSEPWPSISESAKDLIRRMLDPVAKRRLKAHQVLSHPWIREAGVAPDRPMDP
AVQSRLKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKMIDTDHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK
IEREENLFAAFSWLDKDHSGYLTVDELQHACSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKGNGTVGRATLRNSLRMGNGKATAAVDGSERGGA
SAAMSVQRCGGVDSIRENAARNSKGVGGEGGRVCWLSGRGGLETMPRLGTVGVHEVKNGGLERAAEQGVG*
>Pp3c23_18930 Org_Ppatens peptide: Pp3c23_18930V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32950555)
MRRGVNLVPGQSFTHSVLQRNTENLKDLYTLGRKLGQGQFGTTYLCVEKTTGKEYACKSIAKRKLISQEDVDDVRRELHIMHHLSGHPNIVTIKGAYEDQ
VSVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVVGSPYYVAPE
VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLAGELDFVSEPWPSISESAKDLIRRMLDPVAKRRLKAHQVLSHPWIREAGVAPDRPMDP
AVQSRLKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKMIDTDHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK
IEREENLFAAFSWLDKDHSGYLTVDELQHACSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKGNGTVGRATLRNSLSLSDALMHTN*
>Pp3c23_18930 Org_Ppatens peptide: Pp3c23_18930V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32950556)
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VSVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVVGSPYYVAPE
VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLAGELDFVSEPWPSISESAKDLIRRMLDPVAKRRLKAHQVLSHPWIREAGVAPDRPMDP
AVQSRLKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKMIDTDHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK
IEREENLFAAFSWLDKDHSGYLTVDELQHACSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKGNGTVGRATLRNSLSLSDALMHTN*
>Pp3c23_18930 Org_Ppatens peptide: Pp3c23_18930V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32950557)
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VSVHLVMELCAGGELFDRIIQRGHYSEAQAAELCRVIVGVVETCHSLGVMHRDLKPENFLLSDPSENAALKTTDFGLSVFFKPGEVFTDVVGSPYYVAPE
VLRKHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLAGELDFVSEPWPSISESAKDLIRRMLDPVAKRRLKAHQVLSHPWIREAGVAPDRPMDP
AVQSRLKQFSAMNKLKKVAIRVIAEFLSEEEIAGLREMFKMIDTDHSGSITFEELKSGLERVGSNLVESEIRQLMDAADVDQNGTIDYGEFLAATLHLNK
IEREENLFAAFSWLDKDHSGYLTVDELQHACSEYNIGDTSIEELIREVDQDNDGRIDYNEFVTMMRKGNGTVGRATLRNSLSLSDALMHTN*
>Pp3c3_37890 Org_Ppatens peptide: Pp3c3_37890V3.1.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
PROTEIN KINASE 5 (PAC:32944916)
MGNTSSRGSRKSTRQVNQGVGSQDTREKNDSVNPKTRQGGSVGANNYGGKPSSGAQAGERSTSAPAALPRPKPASRSVSGVLGKPLSDIRQSYILGRELG
RGQFGVTYLCTDKMTNEAYACKSIAKRKLTSKEDIEDVKREVQIMHHLSGTPNIVVLKDVFEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAADMCRV
IVNVVHRCHSLGVFHRDLKPENFLLASKAEDAPLKATDFGLSTFFKPGDVFQDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEQG
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EMFKSIDTDNSGTVTFEELKEGLLKQGSKLNESDIRKLMEAADVDGNGKIDFNEFISATMHMNKTEKEDHLWAAFMHFDTDNSGYITIDELQEAMEKNGM
GDPETIQEIISEVDTDNDGRIDYDEFVAMMRKGNPGAENGGTVNKPRHR*
>Pp3c3_37890 Org_Ppatens peptide: Pp3c3_37890V3.2.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
PROTEIN KINASE 5 (PAC:32944917)
MGNTSSRGSRKSTRQVNQGVGSQDTREKNDSVNPKTRQGGSVGANNYGGKPSSGAQAGERSTSAPAALPRPKPASRSVSGVLGKPLSDIRQSYILGRELG
RGQFGVTYLCTDKMTNEAYACKSIAKRKLTSKEDIEDVKREVQIMHHLSGTPNIVVLKDVFEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAADMCRV
IVNVVHRCHSLGVFHRDLKPENFLLASKAEDAPLKATDFGLSTFFKPGDVFQDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEQG
IFDAVLKGHIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQQVLNHPWMKEDGDAPDVPLDNAVLTRLKNFSAANKMKKLALKVIAESLSEEEIVGLR
EMFKSIDTDNSGTVTFEELKEGLLKQGSKLNESDIRKLMEAADVDGNGKIDFNEFISATMHMNKTEKEDHLWAAFMHFDTDNSGYITIDELQEAMEKNGM
GDPETIQEIISEVDTDNDGRIDYDEFVAMMRKGNPGAENGGTVNKPRHR*
>Pp3c3_37890 Org_Ppatens peptide: Pp3c3_37890V3.4.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
PROTEIN KINASE 5 (PAC:32944918)
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IVNVVHRCHSLGVFHRDLKPENFLLASKAEDAPLKATDFGLSTFFKPGDVFQDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEQG
IFDAVLKGHIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQQVLNHPWMKEDGDAPDVPLDNAVLTRLKNFSAANKMKKLALKVIAESLSEEEIVGLR
EMFKSIDTDNSGTVTFEELKEGLLKQGSKLNESDIRKLMEAADVDGNGKIDFNEFISATMHMNKTEKEDHLWAAFMHFDTDNSGYITIDELQEAMEKNGM
GDPETIQEIISEVDTDNDGRIDYDEFVAMMRKGNPGAENGGTVNKPRHR*
>Pp3c3_37890 Org_Ppatens peptide: Pp3c3_37890V3.5.p (1 of 2) PTHR24349:SF23 - MAP KINASE-ACTIVATED
PROTEIN KINASE 5 (PAC:32944919)
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RGQFGVTYLCTDKMTNEAYACKSIAKRKLTSKEDIEDVKREVQIMHHLSGTPNIVVLKDVFEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAADMCRV
IVNVVHRCHSLGVFHRDLKPENFLLASKAEDAPLKATDFGLSTFFKPGDVFQDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEQG
IFDAVLKGHIDFENDPWPKISNGAKDLVRKMLNPNVKIRLTAQQVLNHPWMKEDGDAPDVPLDNAVLTRLKNFSAANKMKKLALKVIAESLSEEEIVGLR
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GDPETIQEIISEVDTDNDGRIDYDEFVAMMRKGNPGAENGGTVNKPRHR*
>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.1.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919729)
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HLVMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPENFLFASKDEDAPLQATDFGLSTFFKLGEVFRDIVGSAYYVAPEVLK
RNYGPEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEPWPRISSGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVL
DRLKNFSAANKMKKLALKVIANSLSEEEIVGLRELFKSMDTDNSGMVTFEELKQGLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEK
EDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKIDYDEFVAMMRKGNPDTEDGVMVVPPRHR*
>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.2.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919722)
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SSHNASTHSNQGGSTRPASTGSSHGESGHSARPSSGTAPAERPRVPMAAPRPRSVSNVGVLGKPLVDIRQTYSLGKELGRGQFGVTYLCTHKETGEKLAC
KSIAKRKLIAKEDIEDVKREVQIMHHLSGTPNIVDLKGVYEDRHSVHLVMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPE
NFLFASKDEDAPLQATDFGLSTFFKLGEVFRDIVGSAYYVAPEVLKRNYGPEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEPWPRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLKNFSAANKMKKLALKVIANSLSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEDGVMVVPPRHR*
>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.3.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919723)
MGNVSGRQSKNRGQQGGMSQEGSADTRFKSESERPRAEGSNQRSSATSSSRGASTHPNQGGSARPASTGSAHTGSAHNASTHHNQGGSTRPASTGSTHTG
SSHNASTHSNQGGSTRPASTGSSHGESGHSARPSSGTAPAERPRVPMAAPRPRSVSNVGVLGKPLVDIRQTYSLGKELGRGQFGVTYLCTHKETGEKLAC
KSIAKRKLIAKEDIEDVKREVQIMHHLSGTPNIVDLKGVYEDRHSVHLVMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPE
NFLFASKDEDAPLQATDFGLSTFFKLGEVFRDIVGSAYYVAPEVLKRNYGPEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEPWPRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLKNFSAANKMKKLALKVIANSLSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEDGVMVVPPRHR*
>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.4.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919724)
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SSHNASTHSNQGGSTRPASTGSSHGESGHSARPSSGTAPAERPRVPMAAPRPRSVSNVGVLGKPLVDIRQTYSLGKELGRGQFGVTYLCTHKETGEKLAC
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NFLFASKDEDAPLQATDFGLSTFFKLGEVFRDIVGSAYYVAPEVLKRNYGPEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEPWPRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLKNFSAANKMKKLALKVIANSLSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEDGVMVVPPRHR*
>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.5.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919725)
MGNVSGRQSKNRGQQGGMSQEGSADTRFKSESERPRAEGSNQRSSATSSSRGASTHPNQGGSARPASTGSAHTGSAHNASTHHNQGGSTRPASTGSTHTG
SSHNASTHSNQGGSTRPASTGSSHGESGHSARPSSGTAPAERPRVPMAAPRPRSVSNVGVLGKPLVDIRQTYSLGKELGRGQFGVTYLCTHKETGEKLAC
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GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEDGVMVVPPRHR*
>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.6.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919726)
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SSHNASTHSNQGGSTRPASTGSSHGESGHSARPSSGTAPAERPRVPMAAPRPRSVSNVGVLGKPLVDIRQTYSLGKELGRGQFGVTYLCTHKETGEKLAC
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NFLFASKDEDAPLQATDFGLSTFFKLGEVFRDIVGSAYYVAPEVLKRNYGPEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEPWPRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLKNFSAANKMKKLALKVIANSLSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEDGVMVVPPRHR*
>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.7.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919727)
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SSHNASTHSNQGGSTRPASTGSSHGESGHSARPSSGTAPAERPRVPMAAPRPRSVSNVGVLGKPLVDIRQTYSLGKELGRGQFGVTYLCTHKETGEKLAC
KSIAKRKLIAKEDIEDVKREVQIMHHLSGTPNIVDLKGVYEDRHSVHLVMELCAGGELFDRIIAKGHYSERAAADLCRVIVNVVHRCHSLGVFHRDLKPE
NFLFASKDEDAPLQATDFGLSTFFKLGEVFRDIVGSAYYVAPEVLKRNYGPEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEPWPRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLKNFSAANKMKKLALKVIANSLSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
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DYDEFVAMMRKGNPDTEDGVMVVPPRHR*
>Pp3c4_7390 Org_Ppatens peptide: Pp3c4_7390V3.8.p (1 of 5) PTHR24349//PTHR24349:SF135 -
SERINE/THREONINE-PROTEIN KINASE // SUBFAMILY NOT NAMED (PAC:32919728)
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NFLFASKDEDAPLQATDFGLSTFFKLGEVFRDIVGSAYYVAPEVLKRNYGPEADVWSAGVIVYILLCGVPPFWAESEQGIFDAVLKGHIDFESEPWPRIS
SGAVDLVRNMLNPNVKERLTAYQVLNHPWMQEGGDASDEPLDNAVLDRLKNFSAANKMKKLALKVIANSLSEEEIVGLRELFKSMDTDNSGMVTFEELKQ
GLIRQGTGLKEADIRKLMEAADVDGNGKIDFHEFISATMHMNKTEKEDHLWAAFKHFDTDNSGYITHEELQEALENSGMGDPQAIQEIIREVDTDNDGKI
DYDEFVAMMRKGNPDTEDGVMVVPPRHR*
>Pp3c6_50 Org_Ppatens peptide: Pp3c6_50V3.1.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32978421)
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ETMVYLVMELCEGGELFDRIIERGTYTEAKAADLTRTIVGVVEACHNSGVVHRDLKPENFLFQTKHEDSMLKAADFGSSRFFEPGDVFTEIVGSPFYVAP
EVLDRHYGPEADIWSAGVILYILLSGVPPFWAETVQGIFEEVMKGEPPSFAADPWPNISEGAKDLIRQMLNPDPRKRLTAAEVLKHPWIREDGVASNKPI
ASLVQFRLKQFSAMNKLKKLAIRIIAEKLSEEEIACLKEIFSEMDRDKDGAISFEELKEGLLKAGTTLKDPEIFDLMDAADIDQDGIIDYGEFLAATLSL
NHIELEENLFAAFQYFDKDGSGHITMDEVLAVCREFNMEDVLIEDLLHEVDVDHDGTIDYKMFVTMMRKGNGGVGHQTLRCTLGITDVLAHDMT*
>Pp3c6_50 Org_Ppatens peptide: Pp3c6_50V3.2.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32978422)
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ETMVYLVMELCEGGELFDRIIERGTYTEAKAADLTRTIVGVVEACHNSGVVHRDLKPENFLFQTKHEDSMLKAADFGSSRFFEPGDVFTEIVGSPFYVAP
EVLDRHYGPEADIWSAGVILYILLSGVPPFWAETVQGIFEEVMKGEPPSFAADPWPNISEGAKDLIRQMLNPDPRKRLTAAEVLKHPWIREDGVASNKPI
ASLVQFRLKQFSAMNKLKKLAIRIIAEKLSEEEIACLKEIFSEMDRDKDGAISFEELKEGLLKAGTTLKDPEIFDLMDAADIDQDGIIDYGEFLAATLSL
NHIELEENLFAAFQYFDKDGSGHITMDEVLAVCREFNMEDVLIEDLLHEVDVDHDGTIDYKMFVTMMRKGNGGVGHQTLRCTLGITDVLAHDMT*
>Pp3c6_50 Org_Ppatens peptide: Pp3c6_50V3.3.p (1 of 9) PTHR24349:SF81 - CALCIUM-DEPENDENT PROTEIN
KINASE 20 (PAC:32978423)
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ETMVYLVMELCEGGELFDRIIERGTYTEAKAADLTRTIVGVVEACHNSGVVHRDLKPENFLFQTKHEDSMLKAADFGSSRFFEPGDVFTEIVGSPFYVAP
EVLDRHYGPEADIWSAGVILYILLSGVPPFWAETVQGIFEEVMKGEPPSFAADPWPNISEGAKDLIRQMLNPDPRKRLTAAEVLKHPWIREDGVASNKPI
ASLVQFRLKQFSAMNKLKKLAIRIIAEKLSEEEIACLKEIFSEMDRDKDGAISFEELKEGLLKAGTTLKDPEIFDLMDAADIDQDGIIDYGEFLAATLSL
NHIELEENLFAAFQYFDKDGSGHITMDEVLAVCREFNMEDVLIEDLLHEVDVDHDGTIDYKMFVTMMRKGNGGVGHQTLRCTLGITDVLAHDMT*
>Pp3c7_22440 Org_Ppatens peptide: Pp3c7_22440V3.1.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925272)
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KFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGVLDFKRDPWPKVSDSAKSLVRRMLEPDPKARYNAQQVLDHP
WLQNAKKNPNVPLDTVRSRLKQFSAMNKLKKRALQVIAESLGGEEMNGLKEMFEKLDSDNAGVITFEKLKMGLIEIGSQLTEHEVRMLMGAADVDGNGAL
DYGEFVAAAVHLQRLGDDEYLRKAFDVFDVDGSGYIETEELRVAVGEPLNGSPSESDVVQGILLEVDVDKDGRISYEEFSAMMRRGTDWRKASRQYSRDR
FNSLSMRLVREGSLNPDKSVAVR*
>Pp3c7_22440 Org_Ppatens peptide: Pp3c7_22440V3.2.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925273)
MGNCCAGSATKKPKQRPNPFAQDGYQANSQILKNQPKAKILDKYILGRELGRGEFGITYLCTDKETGETLACKSISKKKLRTAVDVEDVRREVAIMKHLP
EHPNIVTLNGAFEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHIQGVIHRDLKPENFLFANKNENSVLKAIDFGLSVFFKPGE
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WLQNAKKNPNVPLDTVRSRLKQFSAMNKLKKRALQVIAESLGGEEMNGLKEMFEKLDSDNAGVITFEKLKMGLIEIGSQLTEHEVRMLMGAADVDGNGAL
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FNSLSMRLVREGSLNPDKSVAVR*
>Pp3c7_22440 Org_Ppatens peptide: Pp3c7_22440V3.3.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925274)
MGNCCAGSATKKPKQRPNPFAQDGYQANSQILKNQPKAKILDKYILGRELGRGEFGITYLCTDKETGETLACKSISKKKLRTAVDVEDVRREVAIMKHLP
EHPNIVTLNGAFEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHIQGVIHRDLKPENFLFANKNENSVLKAIDFGLSVFFKPGE
KFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGVLDFKRDPWPKVSDSAKSLVRRMLEPDPKARYNAQQVLDHP
WLQNAKKNPNVPLDTVRSRLKQFSAMNKLKKRALQVIAESLGGEEMNGLKEMFEKLDSDNAGVITFEKLKMGLIEIGSQLTEHEVRMLMGAADVDGNGAL
DYGEFVAAAVHLQRLGDDEYLRKAFDVFDVDGSGYIETEELRVAVGEPLNGSPSESDVVQGILLEVDVDKDGRISYEEFSAMMRRGTDWRKASRQYSRDR
FNSLSMRLVREGSLNPDKSVAVR*
>Pp3c7_22440 Org_Ppatens peptide: Pp3c7_22440V3.4.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925275)
MGNCCAGSATKKPKQRPNPFAQDGYQANSQILKNQPKAKILDKYILGRELGRGEFGITYLCTDKETGETLACKSISKKKLRTAVDVEDVRREVAIMKHLP
EHPNIVTLNGAFEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHIQGVIHRDLKPENFLFANKNENSVLKAIDFGLSVFFKPGE
KFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGVLDFKRDPWPKVSDSAKSLVRRMLEPDPKARYNAQQVLDHP
WLQNAKKNPNVPLDTVRSRLKQFSAMNKLKKRALQVIAESLGGEEMNGLKEMFEKLDSDNAGVITFEKLKMGLIEIGSQLTEHEVRMLMGAADVDGNGAL
DYGEFVAAAVHLQRLGDDEYLRKAFDVFDVDGSGYIETEELRVAVGEPLNGSPSESDVVQGILLEVDVDKDGRISYEEFSAMMRRGTDWRKASRQYSRDR
FNSLSMRLVREGSLNPDKSVAVR*
>Pp3c7_22710 Org_Ppatens peptide: Pp3c7_22710V3.1.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925774)
MGNCCVGSSTKKSRQERRTNPFAPQDGFQSTNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQDVFACKSISKKKLRTAVDVEDVRREFAIMK
HLPEHPHVVTLKGAYEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIMEVVQACHRQGVMHRDLKPENFLFANKDENSPLKAIDFGLSVFFK
PGEKFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKRDPWPKVSESAKSVVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDTVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDNTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVDGN
RTLDYGEFVAATVHLQRLDDDDHLRRAFDVFDVNESGFIEVEELREAVGESLMGSSSESDVVQAILSEVDLDKDGRISYEEFAMMMRRGTDWRKASRQYS
RDRFNSLSTRLLRDGSLNPSSYSTR*
>Pp3c7_22710 Org_Ppatens peptide: Pp3c7_22710V3.2.p (1 of 4) PTHR24349:SF167 - CALCIUM-DEPENDENT
PROTEIN KINASE 10-RELATED (PAC:32925775)
MGNCCVGSSTKKSRQERRTNPFAPQDGFQSTNQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQDVFACKSISKKKLRTAVDVEDVRREFAIMK
HLPEHPHVVTLKGAYEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIMEVVQACHRQGVMHRDLKPENFLFANKDENSPLKAIDFGLSVFFK
PGEKFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKRDPWPKVSESAKSVVRHMLEPDPKARYNAQQVL
DHPWLQNAKKNPNVPLDTVRSRLKQFSAMNKLKKRALQVIAEHLGGEEIDGLKEMFEKLDSDNTGTITFEKLKMGLIEIGSQLTEHEVRMLMEAADVDGN
RTLDYGEFVAATVHLQRLDDDDHLRRAFDVFDVNESGFIEVEELREAVGESLMGSSSESDVVQAILSEVDLDKDGRISYEEFAMMMRRGTDWRKASRQYS
RDRFNSLSTRLLRDGSLNPSSYSTR*
>Pp3c7_25180 Org_Ppatens peptide: Pp3c7_25180V3.1.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32925156)
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LPEHPHVVTLKGAYEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVMHRDLKPENFLFANKNENSPLKAIDFGLSVFFKP
GEKFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGLLDFKRDPWPKVSDSAKSLVRHMLEPDPKARYNAQQVLD
HPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAERLGGEEIDGLKEILEKLDIDNMGVITFEKLKMGLIEIGSQLTEHEVRLLMEAADVDGNG
TLDYGEFVAAAVHLQRLDDDEHLRKAFDVFDVNESGFIEVEELREAVGESLTGSPSESDVVQGILSEVDLDKDGRISYEEFATMMRRGTDWRKASRQYSR
DRFNSLSMRLLRDGSLNPPSYSMR*
>Pp3c7_25180 Org_Ppatens peptide: Pp3c7_25180V3.2.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32925157)
MGNCCVGSSTKKSRKERRPNPFAQGDYHTNLQILKNQPKARILDKYVLGRELGRGEFGITYLCTDKETQEIFACKSISKKKLRTAVDVEDVRREVAIMKH
LPEHPHVVTLKGAYEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVMHRDLKPENFLFANKNENSPLKAIDFGLSVFFKP
GEKFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGLLDFKRDPWPKVSDSAKSLVRHMLEPDPKARYNAQQVLD
HPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAERLGGEEIDGLKEILEKLDIDNMGVITFEKLKMGLIEIGSQLTEHEVRLLMEAADVDGNG
TLDYGEFVAAAVHLQRLDDDEHLRKAFDVFDVNESGFIEVEELREAVGESLTGSPSESDVVQGILSEVDLDKDGRISYEEFATMMRRGTDWRKASRQYSR
DRFNSLSMRLLRDGSLNPPSYSMR*
>Pp3c7_25180 Org_Ppatens peptide: Pp3c7_25180V3.3.p (1 of 2) PTHR24349:SF93 - CALCIUM-DEPENDENT PROTEIN
KINASE 14 (PAC:32925158)
MKHLPEHPHVVTLKGAYEDDNAVHLVMELCEGGELFDRIIARGHYTERGAAQVTRTIVEVVQACHRQGVMHRDLKPENFLFANKNENSPLKAIDFGLSVF
FKPGEKFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGLLDFKRDPWPKVSDSAKSLVRHMLEPDPKARYNAQQ
VLDHPWLQNAKKNPNVPLDAVRSRLKQFSAMNKLKKRALQVIAERLGGEEIDGLKEILEKLDIDNMGVITFEKLKMGLIEIGSQLTEHEVRLLMEAADVD
GNGTLDYGEFVAAAVHLQRLDDDEHLRKAFDVFDVNESGFIEVEELREAVGESLTGSPSESDVVQGILSEVDLDKDGRISYEEFATMMRRGTDWRKASRQ
YSRDRFNSLSMRLLRDGSLNPPSYSMR*
>Pp3c8_690 Org_Ppatens peptide: Pp3c8_690V3.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN
KINASE 3 (PAC:32965098)
MGNTSARPRDGRKHKASQGNDSVQPKSHQGSSHGDSGHPGGSHRGGSYGGSQSRHVPKMKSSSTGILGKPLRDIKLHYTLGRELGRGQFGVTYLCTDKET
GISYACKTIAKRKLTNKDDIEDVKREVQIMHHLSGTPNIVELKDVFEDKQNVNLVMELCAGGELFDRIIAKGHYSERDAADMCRVIVTVVHRCHSLGVFH
RDLKPENFLLASKDKNAPLKATDFGLSIFFKPGDEFHDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEKEIFDTIMRGHIDFKSD
PWPKISDEAKDLVKKMLNSNVKERLTAQEVLNHPWMQRDGVPDVPLDNAVLTRLRNFSAANKMKKLALKVIADNLSEEEIVGLRELFKSIDTDNSGTVTI
DELKKGLLKQGTRLTEADVRKLMEAADVDGNGKIDFNEFISATMHMNKTQKEDHLHAAFQHFDTDNSGYITIYELQEAMEKQGMGDPETLQEIINEVDTD
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HDGRIDYDEFVAMMRKGNPGTEDGGNLKSPRHRW*
>Pp3c8_690 Org_Ppatens peptide: Pp3c8_690V3.2.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN
KINASE 3 (PAC:32965099)
MGNTSARPRDGRKHKASQGNDSVQPKSHQGSSHGDSGHPGGSHRGGSYGGSQSRHVPKMKSSSTGILGKPLRDIKLHYTLGRELGRGQFGVTYLCTDKET
GISYACKTIAKRKLTNKDDIEDVKREVQIMHHLSGTPNIVELKDVFEDKQNVNLVMELCAGGELFDRIIAKGHYSERDAADMCRVIVTVVHRCHSLGVFH
RDLKPENFLLASKDKNAPLKATDFGLSIFFKPGDEFHDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEKEIFDTIMRGHIDFKSD
PWPKISDEAKDLVKKMLNSNVKERLTAQEVLNHPWMQRDGVPDVPLDNAVLTRLRNFSAANKMKKLALKVIADNLSEEEIVGLRELFKSIDTDNSGTVTI
DELKKGLLKQGTRLTEADVRKLMEAADVDGNGKIDFNEFISATMHMNKTQKEDHLHAAFQHFDTDNSGYITIYELQEAMEKQGMGDPETLQEIINEVDTD
HDGRIDYDEFVAMMRKGNPGTEDGGNLKSPRHRW*
>Pp3c8_690 Org_Ppatens peptide: Pp3c8_690V3.3.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN
KINASE 3 (PAC:32965100)
MGNTSARPRDGRKHKASQGNDSVQPKSHQGSSHGDSGHPGGSHRGGSYGGSQSRHVPKMKSSSTGILGKPLRDIKLHYTLGRELGRGQFGVTYLCTDKET
GISYACKTIAKRKLTNKDDIEDVKREVQIMHHLSGTPNIVELKDVFEDKQNVNLVMELCAGGELFDRIIAKGHYSERDAADMCRVIVTVVHRCHSLGVFH
RDLKPENFLLASKDKNAPLKATDFGLSIFFKPGDEFHDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEKEIFDTIMRGHIDFKSD
PWPKISDEAKDLVKKMLNSNVKERLTAQEVLNHPWMQRDGVPDVPLDNAVLTRLRNFSAANKMKKLALKVIADNLSEEEIVGLRELFKSIDTDNSGTVTI
DELKKGLLKQGTRLTEADVRKLMEAADVDGNGKIDFNEFISATMHMNKTQKEDHLHAAFQHFDTDNSGYITIYELQEAMEKQGMGDPETLQEIINEVDTD
HDGRIDYDEFVAMMRKGNPGTEDGGNLKSPRHRW*
>Pp3c8_690 Org_Ppatens peptide: Pp3c8_690V3.4.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN
KINASE 3 (PAC:32965101)
MGNTSARPRDGRKHKASQGNDSVQPKSHQGSSHGDSGHPGGSHRGGSYGGSQSRHVPKMKSSSTGILGKPLRDIKLHYTLGRELGRGQFGVTYLCTDKET
GISYACKTIAKRKLTNKDDIEDVKREVQIMHHLSGTPNIVELKDVFEDKQNVNLVMELCAGGELFDRIIAKGHYSERDAADMCRVIVTVVHRCHSLGVFH
RDLKPENFLLASKDKNAPLKATDFGLSIFFKPGDEFHDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEKEIFDTIMRGHIDFKSD
PWPKISDEAKDLVKKMLNSNVKERLTAQEVLNHPWMQRDGVPDVPLDNAVLTRLRNFSAANKMKKLALKVIADNLSEEEIVGLRELFKSIDTDNSGTVTI
DELKKGLLKQGTRLTEADVRKLMEAADVDGNGKIDFNEFISATMHMNKTQKEDHLHAAFQHFDTDNSGYITIYELQEAMEKQGMGDPETLQEIINEVDTD
HDGRIDYDEFVAMMRKGNPGTEDGGNLKSPRHRW*
>Pp3c9_21410 Org_Ppatens peptide: Pp3c9_21410V3.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN
KINASE 3 (PAC:32913788)
MGNQCVGAIGGPYKQEKAHHHVGHGRDGGVRGVGHGQGQNQQHYRQQNVQERGVETTTTRTAPPVTMPKPRPVNVAAGTVLGKPLSDVRSVYTLGKELGR
GQFGVTYACTNIKTGEHLACKSIAKRKLISKEDIEDVRREVQIMHHLSGTPNVVELKGVFEDKHHVHIVMELCAGGELFDRIIAKGHYSERAAAALCRTI
VSVVHRCHSLNVFHRDLKPENFLLANKAENSSLKATDFGLSVFFKPGEVFHEIVGSAYYVAPEVLRRNYGPEADVWSAGVIVYILLCGVPPFWAESEQGI
FDAVLKGYIDFKSDPWPKVSAAAKDLVSKMLKQDPKERLTAQEVLKHPWMKEDGDAPDEPLDNAVLTRLKNFSSANKMKKLALQVIAQSLSEDEIMGLKE
MFKAMDTDNSGTITFDELKEGLHRQGSKLVESDVKKLMEAADVDGNGKIDFSEFISATMHMNKVEKEDHLAEAFQHFDTDGSGYITVEELQEAMAKNGMG
DPETINEIIREVDTDNDGRIDYDEFVAMMRKGNEVPQMTTRRHRR*
>Pp3c9_21410 Org_Ppatens peptide: Pp3c9_21410V3.2.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT PROTEIN
KINASE 3 (PAC:32913789)
MGNQCVGAIGGPYKQEKAHHHVGHGRDGGVRGVGHGQGQNQQHYRQQNVQERGVETTTTRTAPPVTMPKPRPVNVAAGTVLGKPLSDVRSVYTLGKELGR
GQFGVTYACTNIKTGEHLACKSIAKRKLISKEDIEDVRREVQIMHHLSGTPNVVELKGVFEDKHHVHIVMELCAGGELFDRIIAKGHYSERAAAALCRTI
VSVVHRCHSLNVFHRDLKPENFLLANKAENSSLKATDFGLSVFFKPGEVFHEIVGSAYYVAPEVLRRNYGPEADVWSAGVIVYILLCGVPPFWAESEQGI
FDAVLKGYIDFKSDPWPKVSAAAKDLVSKMLKQDPKERLTAQEVLKHPWMKEDGDAPDEPLDNAVLTRLKNFSSANKMKKLALQVIAQSLSEDEIMGLKE
MFKAMDTDNSGTITFDELKEGLHRQGSKLVESDVKKLMEAADVDGNGKIDFSEFISATMHMNKVEKEDHLAEAFQHFDTDGSGYITVEELQEAMAKNGMG
DPETINEIIREVDTDNDGRIDYDEFVAMMRKGNEVPQMTTRRHRR*
>Sphfalx0012s0095 Org_Sfallax peptide: Sphfalx0012s0095.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32627609)
MGNCCLGFSPAESRKERKPNPFAQDGESQQASAAVHILKNQPKSRISDKYVMGGELGRGEFGVTYLCTDIENNGGGRGEKYACKSISKRKLRTAIDVEDV
RREVAIMNHLPQHPNIVKLKAAYEDEHAVHLVMELCEGGELFDRIVARGHYTERAAAVVTRTIVEVVQVCHQHGVMHRDLKPENFLFANKKEVSPLKAID
FGLSVFFKPGEKFVEIVGSPYYMAPEVLKRNYGPEIDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGTLDFKRDPWPLVSDAAKSLVHHMLEPDPTA
RFNAQQVLDHPWLQNAKTNPNIPLDAVRSRLKQFSAMNKLKKKALQVIAEILGSEEIQKLQDMFETMDTDKNGAITLEELKNGLVQIGSQLTEGEVQQLM
DAADVDGNGTLDYGEFVAATIHLQRLDNDDHLQKAFTHFDTDRSGYIEVEELRVAIGNDSAAAEASVINGILEEVDTDKDGRISYDEFSAMMRRGTDWRK
ASRQYSRDLFNSLSMRLLRNGTVNPANQSER*
>Sphfalx0019s0046 Org_Sfallax peptide: Sphfalx0019s0046.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32600007)
MGNCCVGASSAAPKPKKEKKSNPFAQDGYQVSGNQILKNQPKVSIADKYMLGRELGRGEFGITYLCVDKESQEVYACKSISKRKLRTAVDVEDVRREVAI
MGHLPKHPNIVTLKGAYEDDQAVHLVMELCEGGELFDRIIARGHYTERAAAVVTRTIVEVVQLCHIKGVMHRDLKPENFLFANSNENSPLKAIDFGLSVF
FKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLSGVPPFWAETEQGVAQAILRGILDFKREPWPKVSETAKSLVRHMLEPDPKARYNAQQ
VLDHPWLQNAKKNSNVPLDAVRSRLKQFAAMNKLKRKALQIIAEHLDGDEIDGLRDMFQMMDTDNMGAITFEKLKAGLIQIGSHLTEAEVRMLMDAADVD
GNGTLDYGEFVAATIHLQRLDNDDHLHKAFAQFDANGSGYIEMDELRAAIGDHLVSDEMSVINAILEEVDTDRDGRISFDEFAAMMRRGTDWRKASRQYS
RDRFNSLSVRLFRDGSVNPPMYSKR*
>Sphfalx0022s0143 Org_Sfallax peptide: Sphfalx0022s0143.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:32616043)
MGNQCGSGSDSPNSDKTYTSPHVATHNSHTSSAPSSAAPAAAHSNHDSNMAHKVPPALILPPMPKPHSNFPTIGHVLGRPLEDVRQTYTLGRELGRGQFG
VTYLCTHNISREVFACKSIAKRKLTTKEDIEDVKREVQIMHHLSGHENIVELKGVYEDRHSVHLVMELCAGGELFDRIIKRGHYSERAAASLCRTIVKVV
QACHSLGVMHRDLKPENFLLADKSENAAVKATDFGLSVFFKPSQVFTDIVGSAYYVAPEVLRRNYGPEADVWSAGVILYILLCGVPPYWAETEQGIFDAV
LLGEVDFRSDPWPDISSGAKDLVKKMLQQDPKLRLTAHQVLNHEWVREDGKAPDKPLDSAVLTRMKQFSAMNKMKKLALKVIAESLSEDEIMGLKEMFKS
MDTDNSGTITFEELKEGLQKQGSKLAESEVQQLMQAADVDGNGTIEFNEFITATMHLNKMEKEDHMYVAFQHFDTDHSGYITMDELEQAMTKHNMGDEDT
IKDIIREVDTDNDGRINYDEFVAMMRKGTPGFDGPKKHRQVNRTQ*
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>Sphfalx0034s0077 Org_Sfallax peptide: Sphfalx0034s0077.1.p (1 of 5) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32628748)
MRRYEEAARVMLGQSMPASVLQRQTENLWDLYSLGRKLGQGQFGTTYLCVEISTQKEFACKSIAKRKLISREDVEDVRRELHIMHHLSGHPNIVTIEGAY
EDASSVHLVMELCAGGELFDRIIQRGHYSEAKAAQLTRTIVGVVEACHSLGVMHRDLKPENFLFSNHTEDAALKTTDFGLSVFFKPGEVFTDVVGSPYYV
APEVLKRHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFDQVMKGDLDFVSDPWPNISESAKDLICKMLNPNPARRLTAHQVLCHPWIREEGVAPDMP
IDSAVQSRLKQFSAMNRLKKIAIRVIAESLSEEEIVGLKEMFKMMDTDGSGSISFEELKEGLRKVGSNLMEEDVRQLMDAADVDHNGTIDYGEFLAATLN
LNKIEREENVFAAFSYLDKDKSGYLTTDELQQACIDLHMGDMCVEDMIREVDQDNDGRIDYNEFVTMMRKGNGGIGRSSLRNSLSWSLSDHLMAG*
>Sphfalx0034s0079 Org_Sfallax peptide: Sphfalx0034s0079.1.p (1 of 5) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32628931)
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ASVLQRQTENLRDLYTLGRKLGQGQFGVTYLCVEKSTGKEFACKSIAKRKLISMEDVEDVRRELHIMHHLSGHPNIVNIKGAYEDVTSVHLVMELCAGGE
LFDRIIQRGHYSEAKAAELTRTIVGVVEACHSLGVMHRDLKPENFLFSNHSEDAALKTTDFGLSVFFKPGEIFTDVVGSPYYVAPEVLRKHYGPEADVWS
AGVILYILLSGVPPFWAETEQGIFEQVLKSELDFVSDPWPKISESAKDLLRKMLNPNVAKRLKSHQVLCHPWIREDGVAPDRPIDPAVQTRLKQFSAMNK
LKKIAIRVIAESLSEEEIAGLKEMFLMMDSDGSGAISFEELKEGLKKVGSNLMEADIRQLMDAADVDHNGTIDYGEFLAATLNLNKIEREENLYAAFSYL
DKDKSGYLTTDELQQACNDFHMGDMCVEDLIREVDQDNDGRIDYNEFVTMMRKGNGGVGRSSLRNNLSWGLSDALMGA*
>Sphfalx0038s0118 Org_Sfallax peptide: Sphfalx0038s0118.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:32603542)
MGNQCGGNSHTSSGKADAAAFSTSHHPQTSSAPASYGNHNNNTHTVPPVPPVTPAIPRPQRSPAIGHVLGRPLEDVRKTYTLGRELGRGQFGVTYLCTHN
ETGEVFACKSIAKRKLITKEDFEDVKREVQIMHHLSGHENIVELKGAYEDKQSVHLVMELCAGGELFDRIIKRGHYSERAAASLCRTIVKVVQICHSLGV
MHRDLKPENFLLANKAENAALKATDFGLSVFFKPSEVFTDIVGSAYYVAPEVLRRNYGPEADVWSAGVILYILLCGVPPFWAETEQGIFDAVLRGELDLK
SDPWPEISSGAKDLIKKMLQQDPKCRLTAHEVLTHDWVKEDGEAPDKPLDSAVLSRLKQFSAMNKLKKMALKVIAESLSEDEIMGLKEMFKSMDTDNSGT
ITFEELKTGLAKQGSKLLESEVRQLMQAADVDGNGTIEFNEFITATMHLNKMEKEDHLYAAFQHFDTDHSGYITIDELEQAMMKNNMGERGTIKDIIREV
DTDHDGRINYDEFVAMMRKGMPGLDSHRKSMRGNGTR*
>Sphfalx0040s0092 Org_Sfallax peptide: Sphfalx0040s0092.1.p (1 of 5) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32624088)
MNNYGSEMRVLPGQSITASVLQRHTENLRDLYILGRKLGQGQFGVTYHCTEKATGLHFACKSIAKRKLISREDVEDVRREIHIMHHLSGHPNIVTIKGAY
EDATSVHLVMELCAGGELFDRIIQRGHYSEAKAAELTRTIVGVVETCHSLGVMHRDLKPENFLLANQREDAPLKTTDFGLSVFFKPGEIFTDVVGSPYYV
APEVLRRHYGPEADVWSAGVILYILLSGVPPFWAETEQGIFEQVLKSELDFVSDPWPKISDDAKDLIQKMLNPHIESRLKAHQVLCHPWIREEGVASDRP
IDPAVQSRLKQFSAMNKLKKIAIRVIAESLSEEEIAGLKEMFKMMDTDGSGAISFEELKEGLKRVGSNLKEADVRELMDAADVDHNGTIDYGEFLAATLN
LNKIEREENLYSAFSYLDKDKSGYLTKDELQAAITDFHMGDISIDDMIREVDQDNDGRIDYNEFVTMMRNGNGGVGRTALRSNLSLGLSDTNAA*
>Sphfalx0048s0038 Org_Sfallax peptide: Sphfalx0048s0038.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32612500)
MGNCCVGSSAASRRNSRKERKTNPFSEHGYQVSGNQILKTQPKVGIADKFTLGSELGRGEFGITYLCVDKDTQEVYACKSISKRKLRTAIDVEDVRREVA
IMGHLPHHGNIVTLKGAYEDDQAVHLVMELCEGGELFDRIIARGHYTERAAAVVTRTIMEVVQLCHIKGVMHRDLKPENFLFANKSENSPLKAIDFGLSI
FFKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKREPWPKVSDIAKALVRHMLEPDPKARYNAQ
QVLDHPWLQHAKRNSNVPLDAVRSKLKQFAAMNKLKKKALQIIAEHLEGDEVEGLRDMFQMMDTDNSGAITFEKLKVGLIQIGSHLTEADVQMLMDAADV
DGNGTLDYGEFVAATIHLQRLDNDDLLHKAFAQFDANSSGYIEMEELRTAIGDHLVSDGMSVINAILEEVDTDRDGCISFDEFAAMMRRGTDWRKASRQY
SRDRFNSLSIKLFRDGSINPPNYSK*
>Sphfalx0049s0049 Org_Sfallax peptide: Sphfalx0049s0049.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32617816)
MGNCCGGSSGANSRKERRPNPFAQDGYHVSGNQILVNQPKASIVDKYTLGAELGRGEFGITYSCVDKDTQEVYACKSISKRKLRTAVDVEDVRREVAIMG
HLPQHPNIVSLKGAYEDDEAVHLVMELCEGGELFDRIIARGHYTERAAAGVTRTIVEVVQLCHIQGVMHRDLKPENFLFANKTEDSLLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEIDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGNLDFRREPWPKVSDSAKSLVRHMLEPDPKERYNAQQVL
DHPWLQNAKKNSNVPLDAVRSRLKQFAAMNKLKKKALQIIAEHLEGDEIEGLRDMFQMMDTDNSGAITFEKLKAGLIQIGSHLTEAEVQLLMDAADVDSN
GSLDYGEFVAATIHLQRLDNDDHLHKAFTHFDANNSGYIEMQELRAAIGDNLVADEMSVINGILEEVDTDRDGRISFEEFAAMMRRGTDWRKASRQYSRD
RFNSLSMKLFRDGSMQPSNYSRR*
>Sphfalx0049s0049 Org_Sfallax peptide: Sphfalx0049s0049.2.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32617817)
MGNCCGGSSGANSRKERRPNPFAQDGYHVSGNQILVNQPKASIVDKYTLGAELGRGEFGITYSCVDKDTQEVYACKSISKRKLRTAVDVEDVRREVAIMG
HLPQHPNIVSLKGAYEDDEAVHLVMELCEGGELFDRIIARGHYTERAAAGVTRTIVEVVQLCHIQGVMHRDLKPENFLFANKTEDSLLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEIDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGNLDFRREPWPKVSDSAKSLVRHMLEPDPKERYNAQQVL
DHPWLQNAKKNSNVPLDAVRSRLKQFAAMNKLKKKALQIIAEHLEGDEIEGLRDMFQMMDTDNSGAITFEKLKAGLIQIGSHLTEAEVQLLMDAADVDSN
GSLDYGEFVAATIHLQRLDNDDHLHKAFTHFDANNSGYIEMQELRAAIGDNLVADEMSVINGILEEVDTDRDGRISFEEFAAMMRRGTDWRKASRQYSRD
RFNSLSMKLFRDGSMQPSNYSRR*
>Sphfalx0049s0049 Org_Sfallax peptide: Sphfalx0049s0049.3.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32617818)
MGNCCGGSSGANSRKERRPNPFAQDGYHVSGNQILVNQPKASIVDKYTLGAELGRGEFGITYSCVDKDTQEVYACKSISKRKLRTAVDVEDVRREVAIMG
HLPQHPNIVSLKGAYEDDEAVHLVMELCEGGELFDRIIARGHYTERAAAGVTRTIVEVVQLCHIQGVMHRDLKPENFLFANKTEDSLLKAIDFGLSVFFK
PGERFSEIVGSPYYMAPEVLKRNYGPEIDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGNLDFRREPWPKVSDSAKSLVRHMLEPDPKERYNAQQVL
DHPWLQNAKKNSNVPLDAVRSRLKQFAAMNKLKKKALQIIAEHLEGDEIEGLRDMFQMMDTDNSGAITFEKLKAGLIQIGSHLTEAEVQLLMDAADVDSN
GSLDYGEFVAATIHLQRLDNDDHLHKAFTHFDANNSGYIEMQELRAAIGDNLVADEMSVINGILEEVDTDRDGRISFEEFAAMMRRGTDWRKASRQYSRD
RFNSLSMKLFRDGSMQPSNYSRR*
>Sphfalx0073s0063 Org_Sfallax peptide: Sphfalx0073s0063.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32615718)
MGNCCTAPGGATAGPKHRKKPKRPNPYAQDGYYQPGSGNLILKNQELRNLRDEYGLGREVGRGEFGITYMCTHKATQAVYACKSISKSKLRTPVDVEDVR
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REVAIMQHMPSHPHIVTLRAAYEDENAVHLVMELCEGGELFDRIIERVHYTERAAAGVTRTIVEVVQACHKEGVMHRDLKPENFLFANKKENSPLKAIDF
GLSVFFKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGVLDFKREPWPEVSDSAKSLVRHMLEPDPKLR
YTAQQVLDHPWLLNARKNPNVPLDAVRSKLKQFSAMNKLKKKALQVIAEHLGGEEIEGLKEMFQMMDTDDRGAITFENLKAGLLRIGSHLTEAEVRLLME
AADLDGNGTLDYGEFVAATIHLQRLDNDEHLHKAFNFFDVDGSGYIEMDELREALGQDMVVNESDVIKDILQEVDIDKDGRISYEEFAAMMRRGTDWRKA
SRQYSRDRFNSLSTRLFRDGSTNPPNFSKQNER*
>Sphfalx0095s0016 Org_Sfallax peptide: Sphfalx0095s0016.1.p (1 of 3) PTHR24349:SF95 - CALCIUM-DEPENDENT
PROTEIN KINASE 3 (PAC:32601305)
MGNQCIGSSRTSNDKIETPFPTPYNPHTSSAPAVHSNHHSSSNTQNAHPPPVASPVPRPRVSPNVGHVLGRPLEDVNQTYTLGRELGRGQFGITYLCTDN
NTGAVFACKSIAKRKLMTKEDFEDVKREVQIMHHLSGHENIVELKGVYEDKHFVNLVMELCAGGELFDRIIQRGHYSERAAASLCRTIVKVVQICHSLGV
MHRDLKPENFLLADKSENSALKATDFGLSVFFKPSEVFTDIVGSAYYVAPEVLRRKYGPEADVWSVGVILYILLCGVPPFWAETEQGIFDAVLQGDIDFR
SDPWPEISPAAKDLVKKMLRHDPKHRLTAHEVLTHHWIKEDGEAPDKPLDSAVLTRLKQFSAMNKMKKLALKVIAESLSEDEIMGLKEMFKCMDTDNSGT
ITFEELKEGLQKQGSKLAESEVRQLMQAADVDGNGTIEFNEFITATMHLNKMEKEEHLYVAFQHFDTDHSGYITIDELEQAMTRNNMGDDATIRDIIKEV
DTDHDGRINYDEFVAMMRKGTPGMDVQRKSMRGNRTR*
>Sphfalx0112s0037 Org_Sfallax peptide: Sphfalx0112s0037.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32630832)
MGNCCVGISAASQSKKDRKPNPFAQDGGGAYPASAAAAQILKNQSKCKITDKYALGKELGRGEFGITYLCTDIESGDKDACKSISKRKLRTAVDVEDVRR
EVAIMHHLPKHPNIVKLKGEYEDEQAVHLVMELCEGGELFDRIIARGHYTERAAAVVTRTIVEVVQVCHQHGVMHRDLKPENFLFANKKESSPLKAIDFG
LSVFFKPGEKFCEIVGSPYYMAPEVLKRNYGPEIDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGILDFKRDPWPVVSDSAKALVRHMLEPDPKARY
NAQQVLDHPWLQNAKKNSTLPLDAVRSRLKQFSAMNKLKKKALQVIAEILGGEEVEKLRDMFDMMDTDRSGAITFEKLKTGLIQIGSQLTEGEVRQLMDV
ADVDGNGTLDYGEFVAATVHLQRFDNDDHLHKAFTHFDADGSGYIEVEELRVAIGDDDPSSDAETSVISSILEEVDTDKDGRISYDEFAAMMRRGTDWRK
ASRQYSRDRFNSLSMTLLRNGSVTPAAVQNTKI*
>Sphfalx0133s0014 Org_Sfallax peptide: Sphfalx0133s0014.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32631140)
MGNCCSGPAPPPTSPNNRKKHRRANPYAQDGYCQPGSGNLILKKQEKTDLRKEYGLGREVGRGEFGITYMCTHKTTQAVYACKSISKSKLRTPVDVEDVR
REVAIMQHMPPHPHIVTLRAAYEDDDAVHLVMELCEGGELFDRIIARGHYTERAAAGVTRTIVEVVQVCHKEGVMHRDLKPENFLFANKKENSPLKAIDF
GLSVFFKPGDRFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAILRGKLDFKREPWPKVSESAKSLVRHMLEPDPKLR
YSAQQVLDHPWMVNSKKNPNVPLDAVRSRLKQFSAMNKLKKKALQVIAEHLGGQEIEGLKDMFQMMDTDKRGVITFDNLKAGLLHIGSQLTEGEVRLLME
AADVDGNGTLDYGEFVAATIHLQRLDNDEHLHKAFNFFDSDGSGYIEVEELREILGDDMAVNGTDVITDILQEVDIDKDGRISFDDFAAMMRRGTDWRKA
SRQYSRDRFNSLSTRLFRDGSTNPPIYSKRNER*
>Sphfalx0159s0028 Org_Sfallax peptide: Sphfalx0159s0028.1.p (1 of 5) PTHR24349:SF81 - CALCIUM-DEPENDENT
PROTEIN KINASE 20 (PAC:32627846)
MISKGNSLKAGNKYDKDKSEQVAGIVYALKEGASKKLKPGENLTSSVLQRPTDNLKSLYILGKKLGQGQFGITYLCTEKATGKEYACKTIAKRKLICQAD
VDDVRREIHIMHHLSGHPNIVTIKGAYEDASAVHLVMELCAGGELFERIVKKGHYSEAKASELARTVVDVVEACHSLGVMHRDLKPENFLLLNQNENSVM
KATDFGLSIFFKPGETFKDVVGSPYYVAPEVLRKHYGIEADIWSAGVIIYILLCGVPPFWADNEQGIFESVSKAEFDLESEPWPNISESAKDLIRKMLNP
SRVRRLKAHEVLSHPWIHEEGVAPDKPMDSAVQSRLKQFSAMNKLKKLAIRVIAESMSEEEIVGLKEMFKTIDTDSSGAISFEELKEGLRKVGSNLTEAD
IRDLMDSADIDQNGTIDYGEFLAATLHMNKINREENLFAAFKFLDKDNSGYITIDELQQACIQYNMGDIPIEDLIRDVDQDNDGRLDYHEFVAMMRKGNE
DASQTTRTDSLFFEAIKPTKPKAKLPMDNLDWMG*
>Sphfalx0202s0012 Org_Sfallax peptide: Sphfalx0202s0012.1.p (1 of 8) PTHR24349:SF167 - CALCIUM-
DEPENDENT PROTEIN KINASE 10-RELATED (PAC:32627879)
MGNCCVGSSSSRSAASRSRKERKPNPFAQDGYQISAVQILKNQSKSRITDKYVLGGELGRGEFGITYLCTDMENGCGEKYACKSISKRKLRTAVDVEDVR
REVAIMHHLPQHPNIVKLKAAYEDDHAVHLVMELCEGGELFDRIIARGHYTERAAAVITRTIVEVVQVCHQHGVMHRDLKPENFLFANKKEASPLKAIDF
GLSVFFKPGEKFYEIVGSPYYMAPEVLKRNYGPEIDVWSAGIILYILLCGVPPFWAETEQGVAQAILRGALDFKRDPWPVVSDSAKSLVRHMLEPDPTAR
FDAQQVLDHPWLQNTKKNSNVPLDAVRSRLKQFSAMNKLKKKALQVIAEILGGEEIEKLRDMFEMIDSDKDGAITFEELKNGLIQIGSQLTEAEVRQLMD
AADVDGNGALNYGEFVAATIHLQRLDNDDHLRKAFAHFDTDGSGFIEMEELRVAIGDDSTSAETSVINGILEEVDTDKDGCISYDEFAAMMRRGTDWRKA
SRQYSRDRFNSLSVRLFRDGSVNPANESKR*
>Thecc1EG001677 Org_Tcacao peptide: Thecc1EG001677t1 Calcium-dependent protein kinase 2 (79%T)
(PAC:27436851)
MSKTSSGTKPSRVLPYTTPSLADHYSLGKTLGQGQFGTTYLCTHKPTGQQYACKSIPKRKLICQEDYEDVWREIQIMHHLSEHPHVVRIRGTYEDQLSVH
LVMELCEGGELFDRIVKKGHYSEREAAKLIKTIVGVVETCHSLGVMHRDLKPENFLFDTVDEDAALKATDFGLSVFYKPGESFCDVVGSPYYVAPEVLRK
HYGPEADVWSAGVILYILLSGVPPFWAETEMGIFRQILQGKIDFDSEPWPAISESAKDLIRKMLDRNPKGRLTAYQVLCHPWIVDDTIAPDKPLDSAVLS
RLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDSSGTITFEELKDGLKRVGSELMESEIKDLMDAADIDNSGTIDYGEFLAATVHLNKLERE
ENLVSAFAFFDKDGSGYITIDELQQACKEFGLSDVHLDEMIKEIDQDNDGQIDYGEFAAMMRTGNGGIGRRTMRRTINLGDALAVMANGSKKIE*
>Thecc1EG001677 Org_Tcacao peptide: Thecc1EG001677t2 Calcium-dependent protein kinase 2 (79%T)
(PAC:27436852)
MSKTSSGTKPSRVLPYTTPSLADHYSLGKTLGQGQFGTTYLCTHKPTGQQYACKSIPKRKLICQEDYEDVWREIQIMHHLSEHPHVVRIRGTYEDQLSVH
LVMELCEGGELFDRIVKKGHYSEREAAKLIKTIVGVVETCHSLGVMHRDLKPENFLFDTVDEDAALKATDFGLSVFYKPGESFCDVVGSPYYVAPEVLRK
HYGPEADVWSAGVILYILLSGVPPFWAETEMGIFRQILQGKIDFDSEPWPAISESAKDLIRKMLDRNPKGRLTAYQVLCHPWIVDDTIAPDKPLDSAVLS
RLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDSSGTITFEELKDGLKRVGSELMESEIKDLMDAADIDNSGTIDYGEFLAATVHLNKLERE
ENLVSAFAFFDKDGSGYITIDELQQACKEFGLSDVHLDEMIKEIDQDNDGQIDYGEFAAMMRTGNGGIGRRTMRRTINLGDALAVMANGSKKIE*
>Thecc1EG007580 Org_Tcacao peptide: Thecc1EG007580t1 Calmodulin-domain protein kinase 5 (84%T)
(PAC:27464444)
MGNTCRGSFKGKLYQGYSQPEDHSSKRNNTSSDRSNSDYSPTSLNAQQLIAQEFSKETTKKDTHLALISPTKKDNIMRRGIDNQAYYVLGHKTPNIRDLY
TLGRKLGQGQFGTTYLCIEISTGIEYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDSLYVHIVMELCSGGELFDRIIQRGHYSERK
AAELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPF
WAETQQGIFDAVLKGHIDFDSDPWPLISDSAKDLIRKMLCSRPSERLTAHEVLCHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALRVIAESLSE
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EEIAGLREMFTTMDTDNSGAITFDELKAGLRRYGSTLKDTEIRDLMDAADVDNSGTIDYGEFIAATVHLNKLEREEHLVAAFQYFDKDGSGYITVDELQQ
ACAEHNMTDVLLEDIIREVDQDNDGRIDYGEFVAMMQKGNAGIGRRTMRNSLNMSMRDAPGA*
>Thecc1EG007580 Org_Tcacao peptide: Thecc1EG007580t2 Calmodulin-domain protein kinase 5 (84%T)
(PAC:27464445)
MGNTCRGSFKGKLYQGYSQPEDHSSKRNNTSSDRSNSDYSPTSLNAQQLIAQEFSKETTKKDTHLALISPTKKDNIMRRGIDNQAYYVLGHKTPNIRDLY
TLGRKLGQGQFGTTYLCIEISTGIEYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDSLYVHIVMELCSGGELFDRIIQRGHYSERK
AAELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQVFTDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPF
WAETQQGIFDAVLKGHIDFDSDPWPLISDSAKDLIRKMLCSRPSERLTAHEVLCHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALRVIAESLSE
EEIAGLREMFTTMDTDNSGAITFDELKAGLRRYGSTLKDTEIRDLMDAADVDNSGTIDYGEFIAATVHLNKLEREEHLVAAFQYFDKDGSGYITVDELQQ
ACAEHNMTDVLLEDIIREVDQDNDGRIDYGEFVAMMQKGNAGIGRRTMRNSLNMSMRDAPGA*
>Thecc1EG013784 Org_Tcacao peptide: Thecc1EG013784t1 Calcium-dependent protein kinase 30 (83%T)
(PAC:27449469)
MGNCNACVRPDDSPESKPNRSEHSQRGKKKTRERKPNPYAEKVPSPAPIRVLKDVIPLSHRTRIGDKYILGRELGRGEFGITYLCTDRETREALACKSIS
KRKLRTAVDIEDVRREVAIMSTLPEHPNIVKLKATYEDNENVHLVMELCEGGELFDRIVARGHYTERAAANVAKTIAEVVRMCHENGVMHRDLKPENFLF
ANKKEHAPLKAIDFGLSVFFKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVIDFKREPWPQVSESAK
SLVRQMLEPDPKKRLTAQQVLEHSWLQNAKKAPNVPLGDIVRTRLKQFSVMNRFKKKALRVIAEHLSVEEVEVIRDMFTLMDTDNDGKVSYEELKAGLRK
VGSQLAEPEIKMLMEVADVDGNGVLDYGEFVAVTIHLQKMENDEHFRRAFMFFDKDGSGYIELDELQEALADESGEADVDVLNDIMREVDTDKDGCISYD
EFVAMMKAGTDWRKASRQYSRERFKSLSLNLMKDGSLQLHDAVTGQAVAV*
>Thecc1EG013784 Org_Tcacao peptide: Thecc1EG013784t2 Calcium-dependent protein kinase 30 (83%T)
(PAC:27449470)
MGNCNACVRPDDSPESKPNRSEHSQRGKKKTRERKPNPYAEKVPSPAPIRVLKDVIPLSHRTRIGDKYILGRELGRGEFGITYLCTDRETREALACKSIS
KRKLRTAVDIEDVRREVAIMSTLPEHPNIVKLKATYEDNENVHLVMELCEGGELFDRIVARGHYTERAAANVAKTIAEVVRMCHENGVMHRDLKPENFLF
ANKKEHAPLKAIDFGLSVFFKPGERFSEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVIDFKREPWPQVSESAK
SLVRQMLEPDPKKRLTAQQVLEHSWLQNAKKAPNVPLGDIVRTRLKQFSVMNRFKKKALRVIAEHLSVEEVEVIRDMFTLMDTDNDGKVSYEELKAGLRK
VGSQLAEPEIKMLMEVVWVNSCLHRI*
>Thecc1EG016367 Org_Tcacao peptide: Thecc1EG016367t1 Calcium-dependent protein kinase 6 (81%P)
(PAC:27449549)
MGNCNGHPSADNQFRPDSDSGGGPHNGINIKAGPSPPRPQQHSTTHHSSSAASNHRLATPTTPPIGRVLGRPMEDVRSNYVFGRELGRGQFGITYLVTHK
ETKQQFACKSIATRKLINRDDIEDVRREVQIMHHLTGHRNIVELKGAYEDRHSVNLIMELCAGGELFDRILAKGHYSEREAANLCRQIVMVVHNCHSMGV
MHRDLKPENFLFLSKDEDSPLKATDFGLSVFFKRGDVFKDLVGSAYYVAPEVLRRRYGPEADIWSAGVILYILLSGVPPFYGETEQSIFDSILRGNIDFS
SDPWPSVSSSAKDLVRKMLLDDPKERLSASEVLNHPWMREDGDASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGT
ITYEELKAGLPKLGTKLSESEVRQLMEAADVDGNGTIDYIEFITATMHMNRMEREEHLYTAFQYFDKDNSGYITMEELEQALRKYNMGDEKTIKEIIAEV
DTDRDGRINYDEFVAMMRKGNPDLVGNRRRK*
>Thecc1EG016367 Org_Tcacao peptide: Thecc1EG016367t2 Calcium-dependent protein kinase 6 (81%P)
(PAC:27449550)
MGNCNGHPSADNQFRPDSDSGGGPHNGINIKAGPSPPRPQQHSTTHHSSSAASNHRLATPTTPPIGRVLGRPMEDVRSNYVFGRELGRGQFGITYLVTHK
ETKQQFACKSIATRKLINRDDIEDVRREVQIMHHLTGHRNIVELKGAYEDRHSVNLIMELCAGGELFDRILAKGHYSEREAANLCRQIVMVVHNCHSMGV
MHRDLKPENFLFLSKDEDSPLKATDFGLSVFFKRGDVFKDLVGSAYYVAPEVLRRRYGPEADIWSAGVILYILLSGVPPFYGETEQSIFDSILRGNIDFS
SDPWPSVSSSAKDLVRKMLLDDPKERLSASEVLNHPWMREDGDASDKPLDIAVLTRMKQFRAMNKLKKVALKVIAENLSEEEIIGLKEMFKSMDTDNSGT
ITYEELKAGLPKLGTKLSESEVRQLMEAADVDGNGTIDYIEFITATMHMNRMEREEHLYTAFQYFTTWDREIVLAF*
>Thecc1EG020113 Org_Tcacao peptide: Thecc1EG020113t1 Calcium-dependent protein kinase 24 (69%T)
(PAC:27455265)
MGSCISTPSRLVGVVSKKSYYNTSKTKRKLHASFDHEAARKSMNLRVTNGKVLKDSSGDNILERYELGKELGRGEFGVTHQCFDLVTGEAYACKKISKAK
LRSEIDVEDVRREVEIMRHLPKHPNIVTFREAFEDKEAVYLVMELCHGGELFDRIVAKGHYTERAAATAIKTILEIVKVCHEHGVIHRDLKPENFLLADE
SETAPIKAIDFGLSIFYEPGQRFSDIVGSPYYMAPEVLRRNYGKEVDIWSIGVILYILLCGVPPFWADTEEGIAHAIIKGDIDFERDPWPKVSEEAKDLV
RSMLDPNPYSRMTVQEVFEHPWIQNLEHAPNVNLGENVRTRIKQFSFMSKFKKKVLRVVAGNLPNEQTDAIVQIFRMMDTDENGHLSFEELRDGLQKIGH
CVADPDVQLLMDAADIDGNGTLSCEEFVTMAVHLKRMSNDEHLSQAFHHFDKNQSGYIEFEELQEALLHDDLGPNNEQVIRDIIHDVDLDKDGRISYEEF
KAMMLTGMDWKMASRQYSRALLNAVSIKILKQSGQLR*
>Thecc1EG021684 Org_Tcacao peptide: Thecc1EG021684t1 Calcium-dependent protein kinase 13 (85%T)
(PAC:27420927)
MGNCCRSPAAVAREDVKSNFSAHDHARKDSVSKQKPPITVLNGVPKENIEEKYLVDRELGRGEFGVTYLCIDRGTRELLACKSISKRKLRTAVDIEDVRR
EVAIMKHLPKNSSIVSLKEACEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAAVTRTIVEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAIDFG
LSIFFKPGERFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGLIDFKRDPWPNISESAKSLVRQMLEPDPKLRL
TAKQVLGSKISSVLCLGELVYVSWEGAGWGLGVQHPWLQNAKKAPNVPLGDVVKSRLKQFSMMNRFKRKALRVIAEFLSIEEVEDIKEMFKKMDTDNDGI
VSIEELKAGFRNFGSHLAESEVQMLIEAVDANGKGTLDYGEFLAVSLHLQRIANDEHLRKAFSYFDKDGNGYIEPDELRDSLMEDGADDCTNVANDIFQE
VDTDKDGRISYDEFTAMMKTGTDWRKASRHYSRGRFNSLSMKLMKDGSLNLGNE*
>Thecc1EG021684 Org_Tcacao peptide: Thecc1EG021684t2 Calcium-dependent protein kinase 13 (85%T)
(PAC:27420928)
MGNCCRSPAAVAREDVKSNFSAHDHARKDSVSKQKPPITVLNGVPKENIEEKYLVDRELGRGEFGVTYLCIDRGTRELLACKSISKRKLRTAVDIEDVRR
EVAIMKHLPKNSSIVSLKEACEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAAVTRTIVEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAIDFG
LSIFFKPGERFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGLIDFKRDPWPNISESAKSLVRQMLEPDPKLRL
TAKQVLEHPWLQNAKKAPNVPLGDVVKSRLKQFSMMNRFKRKALRVIAEFLSIEEVEDIKEMFKKMDTDNDGIVSIEELKAGFRNFGSHLAESEVQMLIE
AVDANGKGTLDYGEFLAVSLHLQRIANDEHLRKAFSYFDKDGNGYIEPDELRDSLMEDGADDCTNVANDIFQEVDTDKDGRISYDEFTAMMKTGTDWRKA
SRHYSRGRFNSLSMKLMKDGSLNLGNE*
>Thecc1EG023099 Org_Tcacao peptide: Thecc1EG023099t1 Calcium dependent protein kinase 1 (68%T)
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(PAC:27421427)
MGNSCITLRKDGLFQTISNSIWWSRPAEVGNEDKKQIGNEAHSESTEAEAVQNQPPEEMKIVKEETGREQQGKSQEETQRQQSKSAPQRLNSKPSQLAGF
NKEETKVEPGKPRKPHNVKRQSCAGLQVDSVLQTKTGHLKEYYNLGRKLGHGQFGTTFLCVEKGSGKECACKSIAKRKLTTQDDVDDVRREIQIMHHMAG
HPNVISIKGAYEDSVAVHVVMELCAGGELFDRIVKRGHYTERKAAELARTIVGVVEACHSMGVMHRDLKPENFLFVNEEEDSPLKAIDFGLSIFFKPGDI
LSDVVGSPYYVAPEVLRKRYGPEADVWSAGVIIYILLSGVPPFWGETEQEIFDEVLHGDLDFTSDPWPSISDSAKDLVRKMLVRDAKKRITAYEVLRHPW
VQVDGVAPDKPLDSIVLSRMKQFSAMNKLKKMALRVIAQRLSEEEIAGLKEIFKMIDTDNSGQITYEELKAGLKKFGANLAESEFHALMQAADVDNSGTI
DYEEFIAATLHLNKIEREDHLFAAFSYFDRDGSGYITQDELQKACQEFGIEDISLDEMIQEVDQDNDGRIDYNEFVAMMQKGNPEFGMKGPQGKGFSIGF
REALPVC*
>Thecc1EG024724 Org_Tcacao peptide: Thecc1EG024724t1 Calcium-dependent protein kinase 19 (81%T)
(PAC:27422680)
MGNCCATPSTGSHEKKNKGKKKQNPFSIDYGQHHQGNGGHKLSVLKDPTGTEIEQSYELGRELGRGEFGITYLCTDKVTGDTFACKSISKKKLRTAVDID
DVRREVEIMKHLPKHPNIVSLKDTYEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAVVTKTIVEVVQMCHKHGVMHRDLKPENFLFANKKETAALKA
IDFGLSVFFKPGERFTEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSFIDFKRDPWPKVSDNAKDLVRKMLNPDP
KQRLTAQEVLDHPWLQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSVEEVAGIKEVFQLMDTGNRGKINIDELRVGLHKLGHTIPDADLQ
ILMEAGDVDRDGYLDYGEFVAISVHLRKMGNDEHLKKAFEFFDRNQSGFIEIEELRDALADEVETNSEEVISAIMHDVDTDKDGRISYDEFAAMMKAGTD
WRKASRQYSRERFNSLSLKLMRDGSLQSNNEPR*
>Thecc1EG030220 Org_Tcacao peptide: Thecc1EG030220t1 Calcium-dependent protein kinase 21 (76%T)
(PAC:27441153)
MGCCGSKHKLSEPDYKDYRSGMPPSRPVQPASQPQPVQTQKMSVPQIQAPQMRQPQPIPAPLKPSPASSRPVQGQETILGKPLEDIKQYYTLGKELGRGQ
FGITYLCTENSTGNTYACKSILKRKLKNKQDREDIKKEVQIMQHLSGQPNIVEFRGAYEDRQSVHLVMELCAGGELFDRITAQGHYSERAAAAICRSVVN
VVHICHFMGVMHRDLKPENFLLSSKDEGAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRSYGKEIDIWSAGIILYILLSGVPPFWAETEKGIFD
AITEGELHFESQPWPSISESAKDLIRKMLTMDPKKRLTSAQVLEHPWMREGGEASDKPIDSAVLSRLKQFRAMNKLKKLALKVIAENLSEEEIKGLKAMF
TNMDTDKSGTITYEELKAGLARLGSKLSEAEVKQLMQAADVDGNGTIDYIEFISATMHRYRLERDEHLYKAFQYFDKDNSGYITKDELETAMKEYGMGDE
ASIREVISEVDTDNDGKINYEEFCTMMRSGTQQTGKPF*
>Thecc1EG030220 Org_Tcacao peptide: Thecc1EG030220t2 Calcium-dependent protein kinase 21 (76%T)
(PAC:27441154)
MGCCGSKHKLSEPDYKDYRSGMPPSRPVQPASQPQPVQTQKMSVPQIQAPQMRQPQPIPAPLKPSPASSRPVQGQETILGKPLEDIKQYYTLGKELGRGQ
FGITYLCTENSTGNTYACKSILKRKLKNKQDREDIKKEVQIMQHLSGQPNIVEFRGAYEDRQSVHLVMELCAGGELFDRITAQGHYSERAAAAICRSVVN
VVHICHFMGVMHRDLKPENFLLSSKDEGAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRSYGKEIDIWSAGIILYILLSGVPPFWAETEKGIFD
AITEGELHFESQPWPSISESAKDLIRKMLTMDPKKRLTSAQVLEHPWMREGGEASDKPIDSAVLSRLKQFRAMNKLKKLALKVIAENLSEEEIKGLKAMF
TNMDTDKSGTITYEELKAGLARLGSKLSEAEVKQLMQAADVDGNGTIDYIEFISATMHRYRLERDEHLYKAFQYFDKDNSTSQRMN*
>Thecc1EG030220 Org_Tcacao peptide: Thecc1EG030220t3 Calcium-dependent protein kinase 21 (76%T)
(PAC:27441155)
MGCCGSKHKLSEPDYKDYRSGMPPSRPVQPASQPQPVQTQKMSVPQIQAPQMRQPQPIPAPLKPSPASSRPVQGQETILGKPLEDIKQYYTLGKELGRGQ
FGITYLCTENSTGNTYACKSILKRKLKNKQDREDIKKEVQIMQHLSGQPNIVEFRGAYEDRQSVHLVMELCAGGELFDRITAQGHYSERAAAAICRSVVN
VVHICHFMGVMHRDLKPENFLLSSKDEGAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRSYGKEIDIWSAGIILYILLSGVPPFWAETEKGIFD
AITEGELHFESQPWPSISESAKDLIRKMLTMDPKKRLTSAQVLEHPWMREGGEASDKPIDSAVLSRLKQFRAMNKLKKLALKVIAENLSEEEIKGLKAMF
TNMDTDKSGTITYEELKAGLARLGSKLSEAEVKQLMQAADVDGNGTIDYIEFISATMHRYRLERDEHLYKAFQYFDKDNSG*
>Thecc1EG030876 Org_Tcacao peptide: Thecc1EG030876t1 Calmodulin-domain protein kinase 9 (74%T)
(PAC:27445147)
MGGCLTKSKEPKPKHNGYRSGATTTVAVHQQRYQEPVRPAPVQPQFHHIPEKPGAQTPWKPVAPAPSPKPAPRVDTILGKPYEDIRMRYTIGKELGKGQF
GVTYLCTENSTGKQYACKTISKRKLVTKNDKEDMKREIQIMQHLSGQPNIVEFKGAYEDKQSVHLVMELCAGGELFDRIIAKGHYSERAAASICRAIVNV
VHACHFMGVMHRDLKPENFLLSSKDENALLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRRYGKEIDVWSAGVMLYILLSGVPPFWAETEKGIFDA
ILEGEIDFESQPWPSISDSAKELVCRMLTQDPKKRITSAQVLEHPWIREGGSASDKPLDSAVLSRMKQFRRMNKLKQLALKVIAENLSTEEIQGLKQMFA
NIDTDNSGTITYDELKNGLARLGSKLTEAEVQQLMEAADVDGNGSIDYIEFITATMHRHRLERDEHLYKAFQHFDKDNSGYITRDELETAMKEYGMGDND
TIKEIISEVDTDNDGKINYEEFRDMMRSGTQQGQLF*
>Thecc1EG030876 Org_Tcacao peptide: Thecc1EG030876t2 Calmodulin-domain protein kinase 9 (74%T)
(PAC:27445148)
MGGCLTKSKEPKPKHNGYRSGATTTVAVHQQRYQEPVRPAPVQPQFHHIPEKPGAQTPWKPVAPAPSPKPAPRVDTILGKPYEDIRMRYTIGKELGKGQF
GVTYLCTENSTGKQYACKTISKRKLVTKNDKEDMKREIQIMQHLSGQPNIVEFKGAYEDKQSVHLVMELCAGGELFDRIIAKGHYSERAAASICRAIVNV
VHACHFMGVMHRDLKPENFLLSSKDENALLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRRYGKEIDVWSAGVMLYILLSGVPPFWAETEKGIFDA
ILEGEIDFESQPWPSISDSAKELVCRMLTQDPKKRITSAQVLEHPWIREGGSASDKPLDSAVLSRMKQFRRMNKLKQLALKVGHCRKSFY*
>Thecc1EG034289 Org_Tcacao peptide: Thecc1EG034289t1 Calcium-dependent protein kinase 29 (68%T)
(PAC:27459424)
MGLCQSQGFCLRKSGTHEIPISSSSDSSPRPYQPLPKAAREEFNPPRQKPASENQNPSSSQIGSILLKPYVDITTFYDLDKELGRGRFGITYLCTEKATG
RKYACKSISRRKLTSDKYIKVVRREILILQHLTGQPNIVEFKGAYEDRHNLHLVMELCSGGELFDRIIAKGTYSERQAASIGRQIVKVVHDCHFMGVMHR
DLKPENFLLVSKDENSPIKATGFGLSVFIEEGKWYRDLVGSAYYVAPEVFNRKYGKEIDVWSAGVILYILLSGVPPFWGETEEKILKAVLEGNLDLKSQP
WPSISDAAKDLLRKMLARDPQRRITASQALEHPWMKEGGDTSDKPVGSAVLSRLKQFRVMNKLKKLALKVIAENLSSEEEVKGLKYMFNNFDTDGSGTIT
LEELRVGLARLGSKLTEAETQQLMDAADVDKNGIVDYIEFITATMHRHWLEREDNIYKAFQFFDKDNSGFITRDELRHAMTEYGMGDEATIDEVIEDVDI
DKDGRINYEEFVAMMRRGTQDGDGKDR*
>Thecc1EG034291 Org_Tcacao peptide: Thecc1EG034291t1 Calcium-dependent protein kinase 29 (71%T)
(PAC:27458029)
MGLCQSLGFCLRKSGTHEIPISSSSESSPRPGEEFIPPWQQPALENQNPSSSQIGSILRKPYVDITTFYDLDKELGRGQFGITYLCTEKATGRKYACKSI
SRGKLKSDKDREDVRREILILQHLTGQPNIVKFKGAYEDRHNLHLVMELCSGGELFDRIIAKGTYSERQAASIGRQIVNVVHVCHFMGVMHRDLKPENFL
LVSKDENSPIKATDFGLSVFIEEDRWYKDLVGSAYYVAPEVLNRKYGKEIDVWSAGVILYILLSGVPPFWGETEQEIFKAVIEGNLDLKSQPWPSISDGA
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KDLLSKMLARDPKKRITAAQALEHPWIKEGGDASDKPMDSAVLSRLRQFRVMNKLKKLALKVIAETLSSEEEVKGLKQMFNNIDTDGSGTITIEELRVGL
ARLGSKLTEAEIQQLMDAADVDRSGSIDYIEFITATMPRHRLEREDNIYKAFQFFDKDNSGFITRDELRQAMTEYGMGDEATIDEVIEDVDTDKDGRINY
EEFVAMMKRGTQDGDR*
>Thecc1EG036367 Org_Tcacao peptide: Thecc1EG036367t1 Calcium-dependent protein kinase 2 (81%P)
(PAC:27458877)
MGWNGMEWLIPWNQTKLLRTIRRSPIQLQAYNKKQKKEEENNSKQEGRKKVKEKEIPSEIFSAMNKKTNSSSSSSTTTKPAGTVLPYQTPRLRDHYLLGK
KLGQGQFGTTYQCTHKATGTLYACKSIPKRKLLCREDYDDVWREIQIMHHLSEHPSVVQIKGTYEDSVFVHLVMELCAGGELFDRIVAKGHYSEREAVKL
IKTIVGVVEACHSLGVMHRDLKPENFLFDSPADDAILKATDFGLSIFYKPGQYFSDVVGSPYYVAPEVLCKYYGPEVDIWSAGVILYILLSGVPPFWAET
ESGIFRQILHGKIDFASEPWPSISDSAKDLIRKMLERDPRQRISAHEVLCHPWIVDDRVAPDKPLDSAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIG
GLKELFKMIDTDNSGTITFQELKDGLKKVGSELMESEIKSLMEAADIDNSGTIDYGEFLAATLHINKMEREENLVAAFSFFDKDGSGYITIDELQNACKE
FGLGDVHLDEMIKEIDQDNDGRIDYGEFTAMMRKGDGIGRSRTMRSNLNFTIADAFGVKDPTSDSN*
>Thecc1EG036367 Org_Tcacao peptide: Thecc1EG036367t2 Calcium-dependent protein kinase 2 (81%P)
(PAC:27458879)
MNKKTNSSSSSSTTTKPAGTVLPYQTPRLRDHYLLGKKLGQGQFGTTYQCTHKATGTLYACKSIPKRKLLCREDYDDVWREIQIMHHLSEHPSVVQIKGT
YEDSVFVHLVMELCAGGELFDRIVAKGHYSEREAVKLIKTIVGVVEACHSLGVMHRDLKPENFLFDSPADDAILKATDFGLSIFYKPGQYFSDVVGSPYY
VAPEVLCKYYGPEVDIWSAGVILYILLSGVPPFWAETESGIFRQILHGKIDFASEPWPSISDSAKDLIRKMLERDPRQRISAHEVLCHPWIVDDRVAPDK
PLDSAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFQELKDGLKKVGSELMESEIKSLMEAVNIPS*
>Thecc1EG036367 Org_Tcacao peptide: Thecc1EG036367t3 Calcium-dependent protein kinase 2 (81%P)
(PAC:27458878)
MNKKTNSSSSSSTTTKPAGTVLPYQTPRLRDHYLLGKKLGQGQFGTTYQCTHKATGTLYACKSIPKRKLLCREDYDDVWREIQIMHHLSEHPSVVQIKGT
YEDSVFVHLVMELCAGGELFDRIVAKGHYSEREAVKLIKTIVGVVEACHSLGVMHRDLKPENFLFDSPADDAILKATDFGLSIFYKPGQYFSDVVGSPYY
VAPEVLCKYYGPEVDIWSAGVILYILLSGVPPFWAETESGIFRQILHGKIDFASEPWPSISDSAKDLIRKMLERDPRQRISAHEVLCHPWIVDDRVAPDK
PLDSAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFQELKDGLKKVGSELMESEIKSLMEAADIDNSGTIDYGEFLAATL
HINKMEREENLVAAFSFFDKDGSGYITIDELQNACKEFGLGDVHLDEMIKEIDQDNDGRIDYGEFT
>Thecc1EG036367 Org_Tcacao peptide: Thecc1EG036367t4 Calcium-dependent protein kinase 2 (81%P)
(PAC:27458880)
MNKKTNSSSSSSTTTKPAGTVLPYQTPRLRDHYLLGKKLGQGQFGTTYQCTHKATGTLYACKSIPKRKLLCREDYDDVWREIQIMHHLSEHPSVVQIKGT
YEDSVFVHLVMELCAGGELFDRIVAKGHYSEREAVKLIKTIVGVVEACHSLGVMHRDLKPENFLFDSPADDAILKATDFGLSIFYKPGQYFSDVVGSPYY
VAPEVLCKYYGPEVDIWSAGVILYILLSGVPPFWAETESGIFRQILHGKIDFASEPWPSISDSAKDLIRKMLERDPRQRISAHEVLCHPWIVDDRVAPDK
PLDSAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFQELKDGLKKVGSELMESEIKSLMEAVNIPS*
>Thecc1EG040717 Org_Tcacao peptide: Thecc1EG040717t1 Calcium-dependent protein kinase 19 (87%T)
(PAC:27430665)
MGNCCATPGSPVQSNKKGKNKNKANPFFGDDYAVTNGSATTFKLRVLKEPTGHDISAQYDLGRELGRGEFGVTYLCTDVSSGDKFACKSISKKKLRTAVD
IEDVRREVQIMKHLPKHPNIVSLKDTYEDDDAVHIVMELCEGGELFDRIVARGHYTERAAAGVMRTIVEVVQMCHKHGVMHRDLKPENFLFANKKETAPL
KAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPKVSDNAKDLVRKMLNP
DPKQRLTAQEVLEHPWLQNAKKAPNVPLGETVKARLKQFSVMNKLKKRALRVIAEHLSLEEVAGIKEAFKMMDTRKQGKINLDELRMGLQKLGQQIPDAD
LQILMEAADVDGDGTLNYGEFVAVSVHLKKMANDEHLHKAFAFFDLNKSGYLEIEDLRDALNDEVDTSSEEVIDAIMHDVDTDKDGRISYEEFVAMMKAG
TDWRKASRQYSRERFNSLSLKLMRDGSLQLAN*
>Thecc1EG040717 Org_Tcacao peptide: Thecc1EG040717t2 Calcium-dependent protein kinase 19 (87%T)
(PAC:27430666)
MELCEGGELFDRIVARGHYTERAAAGVMRTIVEVVQMCHKHGVMHRDLKPENFLFANKKETAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNY
GPEVDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPKVSDNAKDLVRKMLNPDPKQRLTAQEVLEHPWLQNAKKAPNVPLGETVKARL
KQFSVMNKLKKRALRVIAEHLSLEEVAGIKEAFKMMDTRKQGKINLDELRMGLQKLGQQIPDADLQILMEAADVDGDGTLNYGEFVAVSVHLKKMANDEH
LHKAFAFFDLNKSGYLEIEDLRDALNDEVDTSSEEVIDAIMHDVDTDKDGRISYEEFVAMMKAGTDWRKASRQYSRE
>Thecc1EG040893 Org_Tcacao peptide: Thecc1EG040893t1 Calcium-dependent protein kinase 17 (83%T)
(PAC:27426008)
MGNCCSRGNPAGAPNTNEKGDATPDNNGNNPSSSSLQDSSANNPPRHSQPSPSPGASSKPSKPNPIGPVLGRPMEDIKSTYTIGKELGRGQFGVTHLCTN
KATGEQFACKTIAKRKLVNKEDIEDVRREVQIMHHLTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGHYTERAAASLLRTIVQIVHTCHSMG
VIHRDLKPENFLLLNKDENSPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLKRRYGPEADIWSIGVMLYILLSGVPPFWAESEHGIFNAILRGHIDF
TSDPWPSISHQAKDLVRKMLNSDPKQRLTAIQVLSHPWIKEDGEAPDTPLDNAVLTRLKQFKAMNKFKKVALRVIAGCLSEEEIMGLKEMFRGMDTDNSG
TITLEELKQGLAKQGTKLSEYEVKQLMEAADADGNGTIDYDEFITATMHMNRMDREDHLYHAFQHFDKDNSGYITTEELEQVLREYGMHDGRDIKEILSE
VDSDNDGRINYDEFVAMMRKGNPETNPKKRRDVFV*
>Thecc1EG044380 Org_Tcacao peptide: Thecc1EG044380t1 Calcium dependent protein kinase 1 (82%T)
(PAC:27442713)
MGNSCVGPSISKNGFFQSVSAAMWRSRIPDDSVSHTNGETGSEVASKEPESPLPVQNKPPEQVTMPKPETKPENKPETNPEKPSKPKSPHMKRVSSAGLR
TESVLQRKTGNFKEYYSLGRKLGQGQFGTTFLCVEKATGKEYACKSIAKRKLVTDDDVEDVRREIQIMHHLAGHPNVISIKGAYEDAVAVHVLMELCAGG
ELFDRIVQRGHYTERKAAALTRTIVGVVEACHSLGVMHRDLKPENFLFVNQQEDSLLKTIDFGLSIFFKPGEKFTDVVGSPYYVAPEVLRKRYGPEADVW
SAGVILYILLSGVPPFWAESEQGIFEQVLHGDLDFESDPWPSISESAKDLVRRMLVRDPRRRLTAHEVLCHPWIQIDGVAPDKALDSAVLSRMKQFSAMN
KLKKMALRVIAESLSEEEIAGLKEMFKMIDTDNSGQITFEELKAGLKRVGANLKESEIYDLMKAADVDNSGTIDYGEFVAATLHLNKIEREDHLFAAFSY
FDKDGSGYITPDELQQACEEFGIEDVRLEEMIREVDQDNDGRIDYNEFVAMMQKGNLASNVAGAGKKGLQNSFSIGFREALKL*
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Note that the below sequence corresponds to the representative gene model and not the queried gene model.

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>AT1G08650.1 | Symbols:PPCK1,ATPPCK1 | phosphoenolpyruvate carboxylase kinase 1,PHOSPHOENOLPYRUVATE
CARBOXYLASE KINASE 1 |  Chr1:2752206-2753232 FORWARD LENGTH=284
MTCSQTLGNNNTNKYQICEEIGRGRFGTVSRVYAPATGDFFACKTIDKASLSDDLDRACLDNEPKLMALLSYHPNIVQIHDLIDTDSTLSIFMELVHPSV
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SIYDRLVSSGTFFEPQTASFAKQILQALSHCHRYGVVHRDIKPENILVDLRNDTVKICDFGSGIWLGEGETTEGVVGTPYYVAPEVLMGYSYGEKVDLWS
AGVVLYTMLAGTPPFYGETAEEIFEAVLRGNLRFPTKIFRGVSSMAKDFLRKLICKDASRRFSAEQALRHPWIQRAGETEERFI
>AT1G35670.1 | Symbols:ATCDPK2,ATCPK11,CDPK2,CPK11 | calcium-dependent protein kinase 2 |
Chr1:13205456-13208058 FORWARD LENGTH=495
METKPNPRRPSNTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFV
HIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLK
KCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVL
SRLKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMER
EENLVAAFSYFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNFNIADAFGVDGEKSDD
>AT1G50700.1 | Symbols:CPK33 | calcium-dependent protein kinase 33 |  Chr1:18782214-18784385 FORWARD
LENGTH=521
MGNCLAKKYGLVMKPQQNGERSVEIENRRRSTHQDPSKISTGTNQPPPWRNPAKHSGAAAILEKPYEDVKLFYTLSKELGRGQFGVTYLCTEKSTGKRFA
CKSISKKKLVTKGDKEDMRREIQIMQHLSGQPNIVEFKGAYEDEKAVNLVMELCAGGELFDRILAKGHYSERAAASVCRQIVNVVNICHFMGVMHRDLKP
ENFLLSSKDEKALIKATDFGLSVFIEEGRVYKDIVGSAYYVAPEVLKRRYGKEIDIWSAGIILYILLSGVPPFWAETEKGIFDAILEGEIDFESQPWPSI
SNSAKDLVRRMLTQDPKRRISAAEVLKHPWLREGGEASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAENIDTEEIQGLKAMFANIDTDNSGTITYEELK
EGLAKLGSRLTEAEVKQLMDAADVDGNGSIDYIEFITATMHRHRLESNENVYKAFQHFDKDGSGYITTDELEAALKEYGMGDDATIKEILSDVDADNDGR
INYDEFCAMMRSGNPQQPRLF
>AT1G74740.1 | Symbols:ATCPK30,CPK30,CDPK1A | CALCIUM-DEPENDENT PROTEIN KINASE 1A,calcium-dependent
protein kinase 30 |  Chr1:28080199-28082476 REVERSE LENGTH=541
MGNCIACVKFDPDNSKPNQKKKPPRGRQRNPYDDPDGLRTHAPLRVIPMSHQSQISDKYILGRELGRGEFGITYLCTDRETREALACKSISKRKLRTAVD
VEDVRREVTIMSTLPEHPNVVKLKATYEDNENVHLVMELCEGGELFDRIVARGHYTERAAATVARTIAEVVRMCHVNGVMHRDLKPENFLFANKKENSAL
KAIDFGLSVLFKPGERFTEIVGSPYYMAPEVLKRNYGPEVDVWSAGVILYILLCGVPPFWAETEQGVALAILRGVLDFKRDPWSQISESAKSLVKQMLEP
DSTKRLTAQQVLDHPWIQNAKKAPNVPLGDIVRSRLKQFSMMNRLKKKALRVIAEHLSIQEVEVIRNMFTLMDDDNDGKISYLELRAGLRKVGSQLGEPE
IKLLMEVADVNGNGCLDYGEFVAVIIHLQKMENDEHFRQAFMFFDKDGSGYIESEELREALTDELGEPDNSVIIDIMREVDTDKDGKINYDEFVVMMKAG
TDWRKASRQYSRERFKSLSLNLMKDGSMHLHDALTGQSIAV
>AT1G76040.2 | Symbols:CPK29 | calcium-dependent protein kinase 29 |  Chr1:28537743-28540448 FORWARD
LENGTH=561
MLQNQHKTTKNQRNKNIGTKYFLRKKIMGFCFSKFGKSQTHEIPISSSSDSSPPHHYQPLPKPTVSQGQTSNPTSNPQPKPKPAPPPPPSTSSGSQIGPI
LNRPMIDLSALYDLHKELGRGQFGITYKCTDKSNGREYACKSISKRKLIRRKDIEDVRREVMILQHLTGQPNIVEFRGAYEDKDNLHLVMELCSGGELFD
RIIKKGSYSEKEAANIFRQIVNVVHVCHFMGVVHRDLKPENFLLVSNEEDSPIKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLHRNYGKEIDVWSAGV
MLYILLSGVPPFWGETEKTIFEAILEGKLDLETSPWPTISESAKDLIRKMLIRDPKKRITAAEALEHPWMTDTKISDKPINSAVLVRMKQFRAMNKLKKL
ALKVIAENLSEEEIKGLKQTFKNMDTDESGTITFDELRNGLHRLGSKLTESEIKQLMEAADVDKSGTIDYIEFVTATMHRHRLEKEENLIEAFKYFDKDR
SGFITRDELKHSMTEYGMGDDATIDEVINDVDTDNDGRINYEEFVAMMRKGTTDSDPKLIR
>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
MGNSCRGSFKDKIYEGNHSRPEENSKSTTTTVSSVHSPTTDQDFSKQNTNPALVIPVKEPIMRRNVDNQSYYVLGHKTPNIRDLYTLSRKLGQGQFGTTY
LCTDIATGVDYACKSISKRKLISKEDVEDVRREIQIMHHLAGHKNIVTIKGAYEDPLYVHIVMELCAGGELFDRIIHRGHYSERKAAELTKIIVGVVEAC
HSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFKDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKG
YIDFDTDPWPVISDSAKDLIRKMLCSSPSERLTAHEVLRHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALKVIAESLSEEEIAGLRAMFEAMDT
DNSGAITFDELKAGLRRYGSTLKDTEIRDLMEAADVDNSGTIDYSEFIAATIHLNKLEREEHLVSAFQYFDKDGSGYITIDELQQSCIEHGMTDVFLEDI
IKEVDQDNDGRIDYEEFVAMMQKGNAGVGRRTMKNSLNISMRDV
>AT2G31500.1 | Symbols:CPK24 | calcium-dependent protein kinase 24 |  Chr2:13414016-13416324 FORWARD
LENGTH=582
MGSCVSSPLKGSPFGKRPVRRRHSSNSRTSSVPRFDSSTNLSRRLIFQPPSRVLPEPIGDGIHLKYDLGKELGRGEFGVTHECIEISTRERFACKRISKE
KLRTEIDVEDVRREVEIMRCLPKHPNIVSFKEAFEDKDAVYLVMEICEGGELFDRIVSRGHYTERAAASVAKTILEVVKVCHEHGVIHRDLKPENFLFSN
GTETAQLKAIDFGLSIFFKPAQRFNEIVGSPYYMAPEVLRRNYGPEIDVWSAGVILYILLCGVPPFWAETEEGIAHAIVRGNIDFERDPWPKVSHEAKEL
VKNMLDANPYSRLTVQEVLEHPWIRNAERAPNVNLGDNVRTKIQQFLLMNRFKKKVLRIVADNLPNEEIAAIVQMFQTMDTDKNGHLTFEELRDGLKKIG
QVVPDGDVKMLMDAADTDGNGMLSCDEFVTLSIHLKRMGCDEHLQEAFKYFDKNGNGFIELDELKVALCDDKLGHANGNDQWIKDIFFDVDLNKDGRISF
DEFKAMMKSGTDWKMASRQYSRALLNALSIKMFKEDFGDNGPKSHSMEFPIARKRAKLLDAPKNKSMELQISKTYKPSGLRN
>AT2G35890.1 | Symbols:CPK25 | calcium-dependent protein kinase 25 |  Chr2:15067175-15069136 REVERSE
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KRKAHNVRRLMSAGLQAESVLKTKTGHLKEYYNLGSKLGHGQFGTTFVCVEKGTGEEYACKSIPKRKLENEEDVEDVRREIEIMKHLLGQPNVISIKGAY
EDSVAVHMVMELCRGGELFDRIVERGHYSERKAAHLAKVILGVVQTCHSLGVMHRDLKPENFLFVNDDEDSPLKAIDFGLSMFLKPGENFTDVVGSPYYI
APEVLNKNYGPEADIWSAGVMIYVLLSGSAPFWGETEEEIFNEVLEGELDLTSDPWPQVSESAKDLIRKMLERNPIQRLTAQQVLCHPWIRDEGNAPDTP
LDTTVLSRLKKFSATDKLKKMALRVIAERLSEEEIHELRETFKTIDSGKSGRVTYKELKNGLERFNTNLDNSDINSLMQIPTDVHLEDTVDYNEFIEAIV
RLRQIQEEEANDRLESSTKV
>AT2G41860.1 | Symbols:CPK14 | calcium-dependent protein kinase 14 |  Chr2:17467646-17469786 REVERSE
LENGTH=530
MGNCCGTAGSLIQDKQKKGFKLPNPFSNEYGNHHDGLKLIVLKEPTGHEIKQKYKLGRELGRGEFGVTYLCTEIETGEIFACKSILKKKLKTSIDIEDVK
REVEIMRQMPEHPNIVTLKETYEDDKAVHLVMELCEGGELFDRIVARGHYTERAAASVIKTIIEVVQMCHKHGVMHRDLKPENFLFANKKETASLKAIDF
GLSVFFKPGERFNEIVGSPYYMAPEVLRRSYGQEIDIWSAGVILYILLCGVPPFWAETEHGVAKAILKSVIDFKRDPWPKVSDNAKDLIKKMLHPDPRRR
LTAQQVLDHPWIQNGKNASNVSLGETVRARLKQFSVMNKLKKRALRVIAEHLSVEETSCIKERFQVMDTSNRGKITITELGIGLQKLGIVVPQDDIQILM
DAGDVDKDGYLDVNEFVAISVHIRKLGNDEHLKKAFTFFDKNKSGYIEIEELRDALADDVDTTSEEVVEAIILDVDTNKDGKISYDEFATMMKTGTDWRK
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ASRQYSRDLFKCLSLKLMQDGSLQSNGDTK
>AT2G46700.1 | Symbols:CRK3,ATCRK3 | CDPK-related kinase 3 |  Chr2:19182968-19186430 REVERSE LENGTH=595
MGQCYGKVNQSKQNGEEEANTTTYVVSGDGNQIQPLTPVNYGRAKNTPARSSNPSPWPSPFPHGSASPLPSGVSPSPARTSTPRRFFRRPFPPPSPAKHI
KASLIKRLGVKPKEGPIPEERGTEPEQSLDKSFGYGKNFGAKYELGKEVGRGHFGHTCSGRGKKGDIKDHPIAVKIISKAKMTTAIAIEDVRREVKLLKS
LSGHKYLIKYYDACEDANNVYIVMELCDGGELLDRILARGGKYPEDDAKAIVVQILTVVSFCHLQGVVHRDLKPENFLFTSSREDSDLKLIDFGLSDFIR
PDERLNDIVGSAYYVAPEVLHRSYSLEADIWSIGVITYILLCGSRPFWARTESGIFRTVLRTEPNYDDVPWPSCSSEGKDFVKRLLNKDYRKRMSAVQAL
THPWLRDDSRVIPLDILIYKLVKAYLHATPLRRAALKALAKALTENELVYLRAQFMLLGPNKDGSVSLENFKTALMQNATDAMRESRVPEILHTMESLAY
RKMYFEEFCAAAISIHQLEAVDAWEEIATAGFQHFETEGNRVITIEELARELNVGASAYGHLRDWVRSSDGKLSYLGFTKFLHGVTLRAAHARPR
>AT3G10660.1 | Symbols:ATCPK2,CPK2 | calmodulin-domain protein kinase cdpk isoform 2 |  Chr3:3331599-
3334268 REVERSE LENGTH=646
MGNACVGPNISGNGFLQTVTAAMWRPRIGAEQASSSSHGNGQVSKEAASEPATDQVQNKPPEPITMPSSKTNPETKLKPDLEIQPEEKKEKVLAEETKQK
VVPEESKQEVPPEESKREVVVQPESAKPETKSESKPETTKPETTSETKPETKAEPQKPKHMRRVSSAGLRTESVLQRKTENFKEFYSLGRKLGQGQFGTT
FLCLEKGTGNEYACKSISKRKLLTDEDVEDVRREIQIMHHLAGHPNVISIKGAYEDVVAVHLVMELCSGGELFDRIIQRGHYTERKAAELARTIVGVLEA
CHSLGVMHRDLKPENFLFVSREEDSLLKTIDFGLSMFFKPDEVFTDVVGSPYYVAPEVLRKRYGPESDVWSAGVIVYILLSGVPPFWAETEQGIFEQVLH
GDLDFSSDPWPSISESAKDLVRKMLVRDPKRRLTAHQVLCHPWVQIDGVAPDKPLDSAVLSRMKQFSAMNKFKKMALRVIAESLSEEEIAGLKQMFKMID
ADNSGQITFEELKAGLKRVGANLKESEILDLMQAADVDNSGTIDYKEFIAATLHLNKIEREDHLFAAFSYFDKDESGFITPDELQQACEEFGVEDARIEE
MMRDVDQDKDGRIDYNEFVAMMQKGSIMGGPVKMGLENSISISLKH
>AT3G20410.1 | Symbols:CPK9 | calmodulin-domain protein kinase 9 |  Chr3:7116388-7118824 FORWARD
LENGTH=541
MGNCFAKNHGLMKPQQNGNTTRSVEVGVTNQDPPSYTPQARTTQQPEKPGSVNSQPPPWRAAAAAPGLSPKTTTKSNSILENAFEDVKLFYTLGKELGRG
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NVVKICHFMGVLHRDLKPENFLLSSKDEKALIKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRRYGKEVDIWSAGIILYILLSGVPPFWAETEKGIF
DAILEGHIDFESQPWPSISSSAKDLVRRMLTADPKRRISAADVLQHPWLREGGEASDKPIDSAVLSRMKQFRAMNKLKKLALKVIAENIDTEEIQGLKAM
FANIDTDNSGTITYEELKEGLAKLGSKLTEAEVKQLMDAADVDGNGSIDYIEFITATMHRHRLESNENLYKAFQHFDKDSSGYITIDELESALKEYGMGD
DATIKEVLSDVDSDNDGRINYEEFCAMMRSGNPQQQQPRLF
>AT3G51850.1 | Symbols:CPK13 | calcium-dependent protein kinase 13 |  Chr3:19232667-19235526 FORWARD
LENGTH=528
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REVAIMKHLPKSSSIVTLKEACEDDNAVHLVMELCEGGELFDRIVARGHYTERAAAGVTKTIVEVVQLCHKHGVIHRDLKPENFLFANKKENSPLKAIDF
GLSIFFKPGEKFSEIVGSPYYMAPEVLKRNYGPEIDIWSAGVILYILLCGVPPFWAESEQGVAQAILRGVIDFKREPWPNISETAKNLVRQMLEPDPKRR
LTAKQVLEHPWIQNAKKAPNVPLGDVVKSRLKQFSVMNRFKRKALRVIAEFLSTEEVEDIKVMFNKMDTDNDGIVSIEELKAGLRDFSTQLAESEVQMLI
EAVDTKGKGTLDYGEFVAVSLHLQKVANDEHLRKAFSYFDKDGNGYILPQELCDALKEDGGDDCVDVANDIFQEVDTDKDGRISYEEFAAMMKTGTDWRK
ASRHYSRGRFNSLSIKLMKDGSLNLGNE
>AT3G57530.1 | Symbols:ATCPK32,CPK32,CDPK32 | calcium-dependent protein kinase 32 |  Chr3:21296898-
21299351 REVERSE LENGTH=538
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TAVDIEDVRREVEIMRHMPEHPNVVTLKETYEDEHAVHLVMELCEGGELFDRIVARGHYTERAAAAVTKTIMEVVQVCHKHGVMHRDLKPENFLFGNKKE
TAPLKAIDFGLSVFFKPGERFNEIVGSPYYMAPEVLKRNYGPEVDIWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVLDFRRDPWPKVSENAKDLIRK
MLDPDQKRRLTAQQVLDHPWLQNAKTAPNVSLGETVRARLKQFTVMNKLKKRALRVIAEHLSDEEASGIREGFQIMDTSQRGKINIDELKIGLQKLGHAI
PQDDLQILMDAGDIDRDGYLDCDEFIAISVHLRKMGNDEHLKKAFAFFDQNNNGYIEIEELREALSDELGTSEEVVDAIIRDVDTDKDGRISYEEFVTMM
KTGTDWRKASRQYSRERFNSISLKLMQDASLQVNGDTR
>AT4G04695.1 | Symbols:CPK31 | calcium-dependent protein kinase 31 |  Chr4:2381634-2383996 REVERSE
LENGTH=484
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SVHIVMEYCGGGELFKKIEALSKDGKSYSEKEAVEIIRPIVNVVKNCHYMGVMLRDLKPENFLLSSTDKNATVKAIDFGCSVFIEEGEVHRKFAGSAYYI
APEVLQGKYGKEADIWSAGIILYILLCGKPPFVTEPEAQMFSEIKSAKIDVDSESWKFIDVKAKHLVNRMLNRNPKERISAAEVLGHPWMKDGEASDKPI
DGVVLSRLKQFRDMNKLKKVALKVIAANLSEEEIKGLKTLFTNIDTDKSGTITLEELKTGLTRLGSNLSKTEVEQLMEAADVDGNGTIDIDEFISATMHR
YRLDRDDHVYQAFQHFDKDNDGHITKEELEMAMKEHGVGDEVSIKQIITEVDTDNDGKINFEEFRTMMRSGSSLQPQRELLPIK
>AT4G04700.1 | Symbols:CPK27 | calcium-dependent protein kinase 27 |  Chr4:2385276-2387986 REVERSE
LENGTH=485
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SVHIVMEYCGGGELYDKILALYDVGKSYSEKEAAGIIRSIVNVVKNCHYMGVMHRDLKPENFLLTSNDDNATVKVIDFGCSVFIEEGKVYQDLAGSDYYI
APEVLQGNYGKEADIWSAGIILYILLCGKSPFVKEPEGQMFNEIKSLEIDYSEEPWPLRDSRAIHLVKRMLDRNPKERISAAEVLGHPWMKEGEASDKPI
DGVVLSRLKRFRDANKFKKVVLKFIAANLSEEEIKGLKTLFTNIDTDKSGNITLEELKTGLTRLGSNLSKTEVEQLMEAADMDGNGTIDIDEFISATMHR
YKLDRDEHVYKAFQHFDKDNDGHITKEELEMAMKEDGAGDEGSIKQIIADADTDNDGKINFEEFRTMMRTESSLQPEGELLPIIN
>AT4G04710.1 | Symbols:CPK22 | calcium-dependent protein kinase 22 |  Chr4:2390497-2392887 REVERSE
LENGTH=498
MGNCCGSKPLTASDIVSDQKQETILGKPLEDIKKHYSFGDELGKGNFGTTYLCKENSTGKSYACKSIPKRTLSSEEEKEAVKTEIQIMDHVSGQPNIVQI
KGSYEDNNSIHIVMELCGGGELFDKIDALVKSHSYYSEKDAAGIFRSIVNAVKICHSLDVVHRDLKPENFLFSSKDENAMLKAIDFGCSVYIKEGKTFER
VVGSKYYIAPEVLEGSYGKEIDIWSAGVILYILLSGVPPFQTGIESIIVSTLCIVDAEIKECRLDFESQPWPLISFKAKHLIGKMLTKKPKERISAADVL
EHPWMKSEAPDKPIDNVVLSRMKQFRAMNKLKKLALKVIAEGLSEEEIKGLKTMFENMDMDKSGSITYEELKMGLNRHGSKLSETEVKQLMEAADVDGNG
TIDYIEFISATMHRHRLERDEHLYKAFQYFDKDGSGHITKEEVEIAMKEHGMGDEANAKDLISEFDKNNDGKIDYEEFCTMMRNGILQPQGKLVGIHI
>AT4G04720.1 | Symbols:AtCPK21,CPK21 | calcium-dependent protein kinase 21 |  Chr4:2394817-2397631
REVERSE LENGTH=531
MGCFSSKHRKTQNDGGEKSIPINPVQTHVVPEHRKPQTPTPKPMTQPIHQQISTPSSNPVSVRDPDTILGKPFEDIRKFYSLGKELGRGQFGITYMCKEI
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VHRDLKPENFLLSSKEENAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRSYGKEIDIWSAGVILYILLSGVPPFWAENEKGIFDEVIKGEIDFV
SEPWPSISESAKDLVRKMLTKDPKRRITAAQVLEHPWIKGGEAPDKPIDSAVLSRMKQFRAMNKLKKLALKVIAESLSEEEIKGLKTMFANIDTDKSGTI
TYEELKTGLTRLGSRLSETEVKQLMEAADVDGNGTIDYYEFISATMHRYKLDRDEHVYKAFQHFDKDNSGHITRDELESAMKEYGMGDEASIKEVISEVD
TDNDGRINFEEFCAMMRSGSTQPQGKLLPFH
>AT4G04740.2 | Symbols:CPK23,ATCPK23 | calcium-dependent protein kinase 23 |  Chr4:2404883-2408493
REVERSE LENGTH=533
MGCFSSKHRKTQNDGGGERSIPIIPVQTHIVDQVPDHRKPQIPSPSIPISVRDPETILGKPFEDIRKFYSLGRELGRGGLGITYMCKEIGTGNIYACKSI
LKRKLISELGREDVKTEIQIMQHLSGQPNVVEIKGSYEDRHSVHLVMELCAGGELFDRIIAQGHYSERAAAGTIKSIVDVVQICHLNGVIHRDLKPENFL
FSSKEENAMLKVTDFGLSAFIEEGKIYKDVVGSPYYVAPEVLRQSYGKEIDIWSAGVILYILLCGVPPFWADNEEGVFVEILKCKIDFVREPWPSISDSA
KDLVEKMLTEDPKRRITAAQVLEHPWIKGGEAPEKPIDSTVLSRMKQFRAMNKLKKLALKVSAVSLSEEEIKGLKTLFANMDTNRSGTITYEQLQTGLSR
LRSRLSETEVQQLVEASDVDGNGTIDYYEFISATMHRYKLHHDEHVHKAFQHLDKDKNGHITRDELESAMKEYGMGDEASIKEVISEVDTDNALSPVEIM
REVALEIGVPVNTFKQNNVQEDGLYLPVLNNAA
>AT4G09570.1 | Symbols:CPK4,ATCPK4 | calcium-dependent protein kinase 4 |  Chr4:6049560-6052184 FORWARD
LENGTH=501
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IVMEVCEGGELFDRIVSKGCFSEREAAKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPSDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK
CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKIDFKSDPWPTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDEHAAPDKPLDPAVLS
RLKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHINKMERE
ENLVVAFSYFDKDGSGYITIDELQQACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMKKGDGVGRSRTMRNNLNFNIAEAFGVEDTSSTAKSDDSP
K
>AT4G21940.2 | Symbols:CPK15 | calcium-dependent protein kinase 15 |  Chr4:11640847-11643487 FORWARD
LENGTH=561
MGCFSSKHRNTESDIINGSVQSSIPTNQPENHVSRDVLKPQKPPSPQIPTTTQSNHHHQQESKPVNQQIEKKHVLTQPLKPIVFRETETILGKPFEEIRK
LYTLGKELGRGQFGITYTCKENSTGNTYACKSILKRKLTRKQDIDDVKREIQIMQYLSGQENIVEIKGAYEDRQSIHLVMELCGGSELFDRIIAQGHYSE
KAAAGVIRSVLNVVQICHFMGVIHRDLKPENFLLASTDENAMLKATDFGLSVFIEEGKVYRDIVGSAYYVAPEVLRRSYGKEIDIWSAGIILYILLCGVP
PFWSETEKGIFNEIIKGEIDFDSQPWPSISESAKDLVRKLLTKDPKQRISAAQALEHPWIRGGEAPDKPIDSAVLSRMKQFRAMNKLKKLALKVIAESLS
EEEIKGLKTMFANMDTDKSGTITYEELKNGLAKLGSKLTEAEVKQLMEAADVDGNGTIDYIEFISATMHRYRFDRDEHVFKAFQYFDKDNSGFITMDELE
SAMKEYGMGDEASIKEVIAEVDTDNDGRINYEEFCAMMRSGITLPQQGKILPPCKRVADLN
>AT4G23650.1 | Symbols:CDPK6,AtCDPK6,CPK3 | Calcium dependent protein kinase 3,calcium-dependent
protein kinase 6 |  Chr4:12324967-12327415 REVERSE LENGTH=529
MGHRHSKSKSSDPPPSSSSSSSGNVVHHVKPAGERRGSSGSGTVGSSGSGTGGSRSTTSTQQNGRILGRPMEEVRRTYEFGRELGRGQFGVTYLVTHKET
KQQVACKSIPTRRLVHKDDIEDVRREVQIMHHLSGHRNIVDLKGAYEDRHSVNLIMELCEGGELFDRIISKGLYSERAAADLCRQMVMVVHSCHSMGVMH
RDLKPENFLFLSKDENSPLKATDFGLSVFFKPGDKFKDLVGSAYYVAPEVLKRNYGPEADIWSAGVILYILLSGVPPFWGENETGIFDAILQGQLDFSAD
PWPALSDGAKDLVRKMLKYDPKDRLTAAEVLNHPWIREDGEASDKPLDNAVLSRMKQFRAMNKLKKMALKVIAENLSEEEIIGLKEMFKSLDTDNNGIVT
LEELRTGLPKLGSKISEAEIRQLMEAADMDGDGSIDYLEFISATMHMNRIEREDHLYTAFQFFDNDNSGYITMEELELAMKKYNMGDDKSIKEIIAEVDT
DRDGKINYEEFVAMMKKGNPELVPNRRRM
>AT4G35310.1 | Symbols:CPK5,ATCPK5 | calmodulin-domain protein kinase 5 |  Chr4:16802436-16804628
FORWARD LENGTH=556
MGNSCRGSFKDKLDEGDNNKPEDYSKTSTTNLSSNSDHSPNAADIIAQEFSKDNNSNNNSKDPALVIPLREPIMRRNPDNQAYYVLGHKTPNIRDIYTLS
RKLGQGQFGTTYLCTEIASGVDYACKSISKRKLISKEDVEDVRREIQIMHHLAGHGSIVTIKGAYEDSLYVHIVMELCAGGELFDRIIQRGHYSERKAAE
LTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFTDVVGSPYYVAPEVLLKRYGPEADVWTAGVILYILLSGVPPFWAE
TQQGIFDAVLKGYIDFESDPWPVISDSAKDLIRRMLSSKPAERLTAHEVLRHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALKVIAESLSEEEI
AGLREMFQAMDTDNSGAITFDELKAGLRKYGSTLKDTEIHDLMDAADVDNSGTIDYSEFIAATIHLNKLEREEHLVAAFQYFDKDGSGFITIDELQQACV
EHGMADVFLEDIIKEVDQNNDGKIDYGEFVEMMQKGNAGVGRRTMRNSLNISMRDA
>AT4G38230.2 | Symbols:CPK26,ATCPK26 | ARABIDOPSIS THALIANA CALCIUM-DEPENDENT PROTEIN KINASE
26,calcium-dependent protein kinase 26 |  Chr4:17928994-17931101 REVERSE LENGTH=514
MGLALFSSDGKLIWKGSTQTGKRRPQEEATMKHSGGNQACYVLGQKTPSIRDLYSLGHKLGQGQFGTTYMCKEISTGREYACKSITKRKLISKEDVEDVR
REIQIMHHLAGYKNIVTIKGAYEDPLYVHIVMELCSGGELFDRIIQRGHYSERKAAELIKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDF
GLSVFFKPGQIFEDVVGSPYYVAPEVLLKHYGPEADVWTAGVILYILVSGVPPFWAETQQGIFDAVLKGHIDFDSDPWPLISDSAKNLIRGMLCSRPSER
LTAHQVLRHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKQMALRVIAESLSEEEIAGLKEMFKAMDTDNSGAITFDELKAGLRRYGSTLKDTEIRDLM
EAADIDKSGTIDYGEFIAATIHLNKLEREEHLLSAFRYFDKDGSGYITIDELQHACAEQGMSDVFLEDVIKEVDQDNDGRIDYGEFVAMMQKGIVGRTMR
KSINMSIRNNAVSQ
>AT5G04870.1 | Symbols:ATCPK1,CPK1 | calcium dependent protein kinase 1 |  Chr5:1417015-1419877 REVERSE
LENGTH=610
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QETKSETKPESKPDPPAKPKKPKHMKRVSSAGLRTESVLQRKTENFKEFYSLGRKLGQGQFGTTFLCVEKTTGKEFACKSIAKRKLLTDEDVEDVRREIQ
IMHHLAGHPNVISIKGAYEDVVAVHLVMECCAGGELFDRIIQRGHYTERKAAELTRTIVGVVEACHSLGVMHRDLKPENFLFVSKHEDSLLKTIDFGLSM
FFKPDDVFTDVVGSPYYVAPEVLRKRYGPEADVWSAGVIVYILLSGVPPFWAETEQGIFEQVLHGDLDFSSDPWPSISESAKDLVRKMLVRDPKKRLTAH
QVLCHPWVQVDGVAPDKPLDSAVLSRMKQFSAMNKFKKMALRVIAESLSEEEIAGLKEMFNMIDADKSGQITFEELKAGLKRVGANLKESEILDLMQAAD
VDNSGTIDYKEFIAATLHLNKIEREDHLFAAFTYFDKDGSGYITPDELQQACEEFGVEDVRIEELMRDVDQDNDGRIDYNEFVAMMQKGSITGGPVKMGL
EKSFSIALKL
>AT5G12180.1 | Symbols:CPK17 | calcium-dependent protein kinase 17 |  Chr5:3937136-3939323 FORWARD
LENGTH=528
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CKTIAKRKLVNKEDIEDVRREVQIMHHLTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIVHTCHSMGVIHRDLKP
ENFLLLNKDENSPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLKRKYGPEADIWSIGVMLYILLCGVPPFWAESENGIFNAILRGHVDFSSDPWPSI
SPQAKDLVKKMLNSDPKQRLTAAQVLNHPWIKEDGEAPDVPLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDSSGTITLEELR
QGLAKQGTRLSEYEVQQLMEAADADGNGTIDYGEFIAATMHINRLDREEHLYSAFQHFDKDNSGYITMEELEQALREFGMNDGRDIKEIISEVDGDNDGR
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>AT5G12480.1 | Symbols:CPK7 | calmodulin-domain protein kinase 7 |  Chr5:4047817-4050035 REVERSE
LENGTH=535
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IEDVRREVEIMKHMPKHPNVVSLKDSFEDDDAVHIVMELCEGGELFDRIVARGHYTERAAAAVMKTIVEVVQICHKQGVMHRDLKPENFLFANKKETSAL
KAIDFGLSVFFKPGEQFNEIVGSPYYMAPEVLRRNYGPEIDVWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPRVSDSAKDLVRKMLEP
DPKKRLTAAQVLEHTWILNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSVEEAAGIKEAFEMMDVNKRGKINLEELKYGLQKAGQQIADTD
LQILMEATDVDGDGTLNYSEFVAVSVHLKKMANDEHLHKAFNFFDQNQSGYIEIDELREALNDELDNTSSEEVIAAIMQDVDTDKDGRISYEEFVAMMKA
GTDWRKASRQYSRERFNSLSLKLMRDGSLQLEGET
>AT5G19360.1 | Symbols:CPK34,AtCPK34 | calcium-dependent protein kinase 34 |  Chr5:6521716-6523780
REVERSE LENGTH=523
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KRKLVNKEDIEDVRREVQIMHHLTGQPNIVELKGAYEDKHSVHLVMELCAGGELFDRIIAKGHYSERAAASLLRTIVQIIHTCHSMGVIHRDLKPENFLL
LSKDENSPLKATDFGLSVFYKPGEVFKDIVGSAYYIAPEVLRRKYGPEADIWSIGVMLYILLCGVPPFWAESENGIFNAILSGQVDFSSDPWPVISPQAK
DLVRKMLNSDPKQRLTAAQVLNHPWIKEDGEAPDVPLDNAVMSRLKQFKAMNNFKKVALRVIAGCLSEEEIMGLKEMFKGMDTDNSGTITLEELRQGLAK
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FVAMMRKGNPDPNPKKRRELSFK
>AT5G19450.1 | Symbols:CPK8,CDPK19 | calcium-dependent protein kinase 19 |  Chr5:6558672-6561471
REVERSE LENGTH=533
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DVRREVEIMKHMPRHPNIVSLKDAFEDDDAVHIVMELCEGGELFDRIVARGHYTERAAAAVMKTILEVVQICHKHGVMHRDLKPENFLFANKKETSALKA
IDFGLSVFFKPGEGFNEIVGSPYYMAPEVLRRNYGPEVDIWSAGVILYILLCGVPPFWAETEQGVAQAIIRSVIDFKRDPWPRVSETAKDLVRKMLEPDP
KKRLSAAQVLEHSWIQNAKKAPNVSLGETVKARLKQFSVMNKLKKRALRVIAEHLSVEEVAGIKEAFEMMDSKKTGKINLEELKFGLHKLGQQQIPDTDL
QILMEAADVDGDGTLNYGEFVAVSVHLKKMANDEHLHKAFSFFDQNQSDYIEIEELREALNDEVDTNSEEVVAAIMQDVDTDKDGRISYEEFAAMMKAGT
DWRKASRQYSRERFNSLSLKLMREGSLQLEGEN
>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
MANKPRTRWVLPYKTKNVEDNYFLGQVLGQGQFGTTFLCTHKQTGQKLACKSIPKRKLLCQEDYDDVLREIQIMHHLSEYPNVVRIESAYEDTKNVHLVM
ELCEGGELFDRIVKRGHYSEREAAKLIKTIVGVVEACHSLGVVHRDLKPENFLFSSSDEDASLKSTDFGLSVFCTPGEAFSELVGSAYYVAPEVLHKHYG
PECDVWSAGVILYILLCGFPPFWAESEIGIFRKILQGKLEFEINPWPSISESAKDLIKKMLESNPKKRLTAHQVLCHPWIVDDKVAPDKPLDCAVVSRLK
KFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDKSGTITFEELKDSMRRVGSELMESEIQELLRAADVDESGTIDYGEFLAATIHLNKLEREENL
VAAFSFFDKDASGYITIEELQQAWKEFGINDSNLDEMIKDIDQDNDGQIDYGEFVAMMRKGNGTGGGIGRRTMRNSLNFGTTLPDESMNV
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