

● N-myristoylation
● ▼ palmitoylation

St CDPK4	1	MGNTCRG--SIGGKTFQGY-----T-QEDSSCSTN-----HNPSSGNSYSSSDNFSPTS-----NA	49
St CDPK5	1	MGNACRG--SFGGKTFQGY-----P-QPDDHSESNS-----NPKHN-----SDSPFK-----40	40
Cm CPK2	1	MGNTCRG--SFKGNIFQGY-----YSQPEESSTPNF-----KRNING-----SSDHSPTSINTNLLIS	50
Ca CDPK3	1	MGNACRG--SFRKTFQGS-----YQNHSTSKH-----SKVEE-----EQQDPAP-----LV	42
At CPK6	1	MGNACRG--SFKDKIYECN-----HSRPEENSKS-----TTTTV-----SSVHSP-----TD	41
Nt CDPK2	1	MGNTCVGPSISKNGLEQSVSAAMWRTRADDSGSTTNGDSARGETTESGKDPDLVVQNKPEQITMPKSE	70

Variable domain ← → Kinase domain

St CDPK4	50	QONSNHKKEHSLSLVSPRKASMNRSGSN--QAYVVMGHMTPNIRDLYTLGRKLGQGGFGTTYLCTENSIG	117
St CDPK5	40	-----KEQQPLVDMNRSTN--QSYVVLGHKTPNIRDLYTLGRKLGQGGFGTTYLCTELSSIG	95
Cm CPK2	51	QAFAEENKTKSKDNDCKDYTMKSAEN--QAYVVLGHKTPNIRDLYTLGRKLGQGGFGTTYLCTEIMIG	118
Ca CDPK3	43	VKD-----HSTSTKKNMNRSSAN--QSCCVLGHKTPNIRDLYTLGRKLGQGGFGTTYLCTELSPIC	100
At CPK6	42	QDFSQN--NPNALVIPVKEPIIMRRNVDN--QSYVVLGHKTPNIRDLYTLGRKLGQGGFGTTYLCTDIAPIC	108
Nt CDPK2	71	QKEEPAKKEEGPVKPKKPEEMKRVGSAGLRDTSVLQKKTGNLKEFFSTGKKGQGGFGTTFKQVQKATIG	140

★ ATP-binding site

St CDPK4	118	AEYACKSIKRRKLSKEDVEDVRREIQIMHHLGAGHKNIVTKGAYEDPLYVHVMEICSGGELFDRIIQR	187
St CDPK5	96	IDYACKSIKRRKLSKEDVEDVRREIQIMHHLGAGHKNIVTKGAYEDPLYVHVMEICSGGELFDRIIQR	165
Cm CPK2	119	IEYACKSIKRRKLSKEDVEDVRREIQIMHHLGAGHKNIVTKGAYEDPLYVHVMEICSGGELFDRIIQR	188
Ca CDPK3	101	IDYACKSIKRRKLSKEDVEDVRREIQIMHHLGAGHKNIVTKGAYEDPLYVHVMEICSGGELFDRIIQR	170
At CPK6	109	VDYACKSIKRRKLSKEDVEDVRREIQIMHHLGAGHKNIVTKGAYEDPLYVHVMEICAGGELFDRIIQR	178
Nt CDPK2	141	KEYACKSIKRRKLSKEDVEDVRREIQIMHHLGAGHKNIVTKGAYEDVAVHVHVMEICAGGELFDRIIQR	210

St CDPK4	188	GHYSERKAAELTKIIVGVVEACHSLGVMHRDLKPENFLVNKDDDFSLKAIIDFGLSVFFKPGQIFTDVVG	257
St CDPK5	166	GHYTERKAAELTKIIVGVVEACHSLGVMHRDLKPENFLVNKDDDFSLKAIIDFGLSVFFKPGQIFTDVVG	235
Cm CPK2	189	GHYSERKAAELTKIIVGVVEACHSLGVMHRDLKPENFLVNKDDDFSLKAIIDFGLSVFFKPGQIFTDVVG	258
Ca CDPK3	171	GHYTERKAAELTKIIVGVVEACHSLGVMHRDLKPENFLVNKDDDFSLKAIIDFGLSVFFKPGQIFTDVVG	237
At CPK6	179	GHYSERKAAELTKIIVGVVEACHSLGVMHRDLKPENFLVNKDDDFSLKAIIDFGLSVFFKPGQIFTDVVG	248
Nt CDPK2	211	GHYTERKAAELTKIIVGVVEACHSLGVMHRDLKPENFLVNKDDDFSLKAIIDFGLSVFFKPGQIFTDVVG	280

St CDPK4	258	SPYYVAPEVLLKHYGPEADVNTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSDPWPLISESAKD	327
St CDPK5	236	SPYYVAPEVLLKHYGPEADVNTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSDPWPLISESAKD	305
Cm CPK2	259	SPYYVAPEVLLKHYGPEADVNTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSDPWPLISESAKD	328
Ca CDPK3	238	SPYYVAPEVLLKHYGPEADVNTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSDPWPLISESAKD	307
At CPK6	249	SPYYVAPEVLLKHYGPEADVNTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSDPWPLISESAKD	318
Nt CDPK2	281	SPYYVAPEVLLKHYGPEADVNTAGVILYILLSGVPPFWAETQQGIFDAVLKGHIDFSDPWPLISESAKD	350

← → Junction domain ← → Calmodulin-like domain

St CDPK4	328	LIRKMLCMQPSERLTAHEVLCHPWICENGVPADRALDPAVLSRLKQFSAMNKLKMMALRVIAESLSEEEI	397
St CDPK5	306	LIRKMLCMRPSERLTAHEVLCHPWICENGVPADRALDPAVLSRLKQFSAMNKLKMMALRVIAESLSEEEI	375
Cm CPK2	329	LIRKMLCSRPSERLTAHEVLCHPWICENGVPADRALDPAVLSRLKQFSAMNKLKMMALRVIAESLSEEEI	398
Ca CDPK3	308	LIRKMLCMRPSERLTAHEVLCHPWICENGVPADRALDPAVLSRLKQFSAMNKLKMMALRVIAESLSEEEI	377
At CPK6	319	LIRKMLCSSPSERLTAHEVLCHPWICENGVPADRALDPAVLSRLKQFSAMNKLKMMALRVIAESLSEEEI	388
Nt CDPK2	351	LVRRMLVRDEKRRLTAHEVLCHRWVQVDGVAPDKPLDSAVLSRMKQFSAMNKLKMMALRVIAESLSEEEI	420

St CDPK4	398	AGLREMFKAMDTSAGAITFDELKAGLRKRVGSLKDTIEIRELMDAADVNSGTYDGEFFIAATVHLNKLE	467
St CDPK5	376	AGLREMFKAMDTSAGAITFDELKAGLRKRVGSLKDTIEIRELMDAADVNSGTYDGEFFIAATVHLNKLE	445
Cm CPK2	399	AGLREMFKAMDTSAGAITFDELKAGLRKRVGSLKDTIEIRELMDAADVNSGTYDGEFFIAATVHLNKLE	468
Ca CDPK3	378	AGLREMFKAMDTSAGAITFDELKAGLRKRVGSLKDTIEIRELMDAADVNSGTYDGEFFIAATVHLNKLE	447
At CPK6	389	AGLREMFKAMDTSAGAITFDELKAGLRKRVGSLKDTIEIRELMDAADVNSGTYDGEFFIAATVHLNKLE	458
Nt CDPK2	421	AGLREMFRIIDTNSGQITFDELKAGLRKRVGSLKDTIEIRELMDAADVNSGTYDGEFFIAATVHLNKLE	490

St CDPK4	468	REEHLMAAFQYFDKDGSGYITVDELOQACAEHNMIDTVYFEDIIREVDQDNDGRIDYGEFVAMMOKGNPFI	537
St CDPK5	446	REEHLMAAFQYFDKDGSGYITVDELOQACAEHNMIDTVYFEDIIREVDQDNDGRIDYGEFVAMMOKGNPFI	515
Cm CPK2	469	REEHLMAAFQYFDKDGSGYITVDELOQACAEHNMIDTVYFEDIIREVDQDNDGRIDYGEFVAMMOKGNPFI	538
Ca CDPK3	448	REEHLMAAFQYFDKDGSGYITVDELOQACAEHNMIDTVYFEDIIREVDQDNDGRIDYGEFVAMMOKGNPFI	517
At CPK6	459	REEHLMAAFQYFDKDGSGYITVDELOQACAEHNMIDTVYFEDIIREVDQDNDGRIDYGEFVAMMOKGNPFI	528
Nt CDPK2	491	REDHLMAAFQYFDKDGSGYITVDELOQACAEHNMIDTVYFEDIIREVDQDNDGRIDYGEFVAMMOKGNPFI	560

St CDPK4	538	G--RRTMRNSLNFSMRDAPGAQ	557
St CDPK5	516	G--RRTMRNSLNFSMRDAPGAH	535
Cm CPK2	539	G--RRTMRNSLNFSMRDAPGAL	558
Ca CDPK3	518	G--RRTMRNSLNFSMRDAPGAH	537
At CPK6	529	G--RRTMRNSLNFSMRDAPV	544
Nt CDPK2	561	GGGKGLHESFSTGFRALRL	581

Supplemental Figure 1. Alignment of the Predicted Amino Acid Sequences of St CDPK4, St CDPK5, Cm CPK2, Ca CDPK3, At CPK6 and Nt CDPK2.

Amino acids that are conserved are boxed in black. Multiple alignment of the protein sequence was made using the CLISTAL W program (Thompson et al., 1994).