

Arabidopsis CDPK Sequence Alignment

CPK1	-----MNTCVGSPSRNGFLQSVSAAMWRPRDGDDSSASMSNGDIASEAVSGELRS-RLSDEVQN	57
CPK2	-----MGNACVGPNISGNGLQTVTAAMWRPRIGAEQASSSSSHGNGQVSKAAASEPATDQVQN	58
CPK3	-----MCHRRHSKSKSSDPPPPSSSSSSSGNVVHVHVKPA-----GERRGSSG	40
CPK4	-----	-
CPK5	-----MNSCRGSPFKDKLDEGDNNKPEDYSKTSTTNLSNSDHSNAAD-----IIAQEF SK	52
CPK6	-----MNSCRGSPFKDKIYEGNHSRPEENSKSTTTTVSSVHSP-----TTDQDFSK	46
CPK7	-----MGN---CCGNPSSATNQSQKQKPKNKNNPFYS-----NEYATDR	37
CPK8	-----MGN---CCASPGSETG-SKKGKPKIKSNPFYS-----EAYTTNG-	35
CPK9	-----MGNCFAKNHG-LMKPQQNGNTRSRSEVGVNTQ-----DPPSYTPQ	39
CPK10	-----MGNCNACVRPDSKESKPSKPKKPNRDRKLNPE-----FAG-DETR	39
CPK11	-----	-
CPK12	-----	-
CPK13	-----MGN---CCRSAAVAREDVKSNSYSGHDHARKD-----AAG--GK	34
CPK14	-----MGN---CCGTAGSLIQD--KQKGFKLNPFS-----NEYGNHHD	35
CPK15	-----MG-CFSSKHRNTESDIINGSVQSSIPTNQPEN-----HVS RDVLK	39
CPK16	-----MGLCFSSAAKSSGHNRSRNPHPHPLTVVKSRRPPSPCFEMAVTIQKDHRTQPRRA	58
CPK17	-----MGNCCSHGRDSADNGDALENGAS---ASNA-----ANSTGPTA	35
CPK18	-----MGLCFSS-SPKATRRTGSRNPNPDSPTQ GKAS-----EKVSNKNKK	40
CPK19	-----MG-CLCINLKKKVKKPTPDISGEQNTQTEVKSRE-----ITPKQPR	39
CPK20	-----MNTCVGPNLNPNGLQSVSAAVWRNPKPDDSIKSSKDESSRKKNDK---SVNGDDSN	55
CPK21	-----MG-CFSSKHRKTQN---DGG-EKSIPI NPVQT-----HVV---PE	32
CPK22	-----MGNCCGSKPLTASD-----	14
CPK23	-----MG-CFSSKHRKTQN---DGGGERSIPII PVQT-----HIVDQVPD	36
CPK24	-----MGS---CVSSPLKGSPPGKRPVRRRHSSNSRT-----SSVPRPDS	37
CPK25	-----MGNVVCVHMVNVCVDTKSNVWRPTDLIMDHPKPLQDKPPQPLMKNKDDDKTKLNDT	58
CPK26	-----	-
CPK27	-----MG-CFSSKELQSS-----	12
CPK28	-----MGVCFSS-AIRVTGASSRRSSQTKS-----KAAP-TPI	31
CPK29	MLQNQHKTTRNQRNKNIGTKYFLRKKIMGFCFSKFGKSQTHEIPISSSSDSSPPHHYQP-----LPKPTVSQ	67
CPK30	-----MGNCIACVKFDPDNSKPNQK-KKPPRGRQRNP-----YDDPDGLR	39
CPK31	-----MG-CYSSKNLQSS-----	12
CPK32	-----MGN---CCGTAGSLAQNDNPKKGRKKQNPFS-----IDYGLHHG	37
CPK33	-----MGNCLAKKYGLVMKPPQNG--ERSVEIENRRR-----S-----	31
CPK34	-----MGNCCSHGRSDSDN---KEEPR---PENG-----GGGVG-AA	30

CPK1	KPPEQVTMPKPGTDVETK---DREIRTESK-----PETLEEISLE-----SKPETKQETKS-----ET	107
CPK2	KPPEPITMPSSKTNPETKLPDLEIQPEEKKEKVLAEETKQKVVPBESKQEVPPBESKREVVVQPESAKPETKSEKPKETTKPET	143
CPK3	SGTVGSSGSGTGSSRS	56
CPK4	-----	-
CPK5	DNNSNNNSKDPALVIPLR-----	70
CPK6	QNTN-----PALVIPK-----	58
CPK7	SGAG-----	41
CPK8	SGTG-----	39
CPK9	ARTTQQPEKPGSVNSQPPPPRA-----	61
CPK10	SPAPIRV-----	46
CPK11	-----	-
CPK12	-----	-
CPK13	KSAPIR-----	40
CPK14	G-----	36
CPK15	PQKPPSPQIPTTTQSNHHHQESKPVNQI-----	69
CPK16	TAKKTPTRHTPPHGKVRKVIS-----	80
CPK17	EASVPQSKHAPPPPPP-----	51
CPK18	NTKKIQLRHQG-----	51
CPK19	QRQP---APRAKFIIVVQPHKLPLPLPQP-----	65
CPK20	GHSVSTVDPAPSTLPTPS-----T PPPPVKMANE-----E PPPPKP-----	90
CPK21	HRKP---QTPTPKPMTQPIHQQ-----	51
CPK22	-----	-
CPK23	HRKP---QIPSP-----	45
CPK24	STNLSRRL-----	45
CPK25	HGDPKLLLEGKPKPAQKQTSQ-----GQGGKCSDE-----	88
CPK26	-----	-
CPK27	-----	-
CPK28	DTKASTKRRTG-----	42
CPK29	GQTSNPTSNPQPKPKPAPPPPP-----	89
CPK30	THAPLR-----	45
CPK31	-----	-
CPK32	GGDGGGRP-----	45
CPK33	--THQDPSKISTGTNQP PPWRN-----	51
CPK34	EASVRASKHPPASPPP-----	46

Arabidopsis CDPK Sequence Alignment

Kinase Domain

CPK1	KPESKDPDPAKPKK-PKHMKRVS SAGLRTE SVLQRKTE NFKEFYSLGRKLGQGQFGTTFLOVEKT	TGKEEACKSIAKRKLLTDBD	191
CPK2	TSETKPETKAE POK-PKHMRVSS SAGLRTE SVLQRKTE NFKEFYSLGRKLGQGQFGTTFLOVEKT	TGNEYACKSISKRRLLTDBD	227
CPK3	-----TTSTQONGRILGRPMEEVRRTYEFCRBLGRGQFGVTYLVTHKE	TKQOVACKSIPTRRIVHKDD	119
CPK4	-----ME-KPNRRRPSNSVLPYETPRLRDHYLLGKRLGQGQFGTTFLOVEKT	SSANYACKSIPKRKLVCRE	66
CPK5	-----EPIMRNPDNQAYYVLGHKTPNIRDIYTLRRLGQGGQFGTTFLOVEKT	SGVDYACKSISKRRLLSKBD	138
CPK6	-----EPIMRNVDNQSYVVLGHKTPNIRDIYTLRRLGQGGQFGTTFLOVEKT	SGVDYACKSISKRRLLSKBD	126
CPK7	-----FKLS---VLKDPGTGHDISLQYDLGRBVGREBFGTTFLOVEKT	TGKEYACKSISKKLDRTAVD	100
CPK8	-----FKLS---VLKDPGTGHDISLQYDLGRBVGREBFGTTFLOVEKT	TGKEYACKSISKKLDRTAVD	98
CPK9	-----AAAAPGLSPKTTTKNSILENAFEDVLFYTLGKBLGRGQFGVTYLVCTENST	TGKKYACKSISKKLVTKAD	132
CPK10	-----LKD---VLPMSNQQTSDKYLLGRBLGRGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	104
CPK11	-----METKPNRRRPSNTVLPYQTPRLRDHYLLGKRLGQGQFGTTFLOVEKT	TGKEYACKSISKKLDRTAVD	67
CPK12	-----MANKPRTR---WVLPYKTKNVDENYFLGQVLLGQGGQFGTTFLOVEKT	TGQKLACKSIPKRKLLCQED	63
CPK13	-----VLSDPVKENIEDRYLLDRBLGRGQFGTTFLOVEKT	SRDLLACKSISKKLDRTAVD	95
CPK14	-----LKLI---VLKPEPTGHEIRKQYKRLGRBLGRGQFGTTFLOVEKT	TGGEIFACKSISKKLLTRSD	95
CPK15	-----EKKHVLTPQLKPIVRETETILGKPEEIRKLYTLGKBLGRGQFGTTFLOVEKT	TGNTYACKSIPKRKLRKQD	143
CPK16	-----NNGRRHGETIPYGRVDFGYAKDFDHYRTIGKLLGHGQGGQFGTTFLOVEKT	TGDRVAVKKLDKAKMTPIA	149
CPK17	-----ATKQGPPIGVLGRPMEDVRSYSLGKBLGRGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	114
CPK18	-----GIPYGRVDFGYAKDFDHYRTIGKLLGHGQGGQFGTTFLOVEKT	TGDRVAVKKLDKAKMTPIA	112
CPK19	-----QEKQKLINHQKQSTLQOPEPILGRPFEDIKKYSLGRBLGRGQGGQFGTTFLOVEKT	ISSGKNEACKSILKRRLLIRTKD	139
CPK20	ITENKEDPNSK POKKEAHMKRMASAGLQIDSVLGRKTE NFKEFYSLGRKLGQGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	175
CPK21	-----ISTPSSNPVSVRDPDTILGKPEEIRKLYTLGKBLGRGQGGQFGTTFLOVEKT	TGNTYACKSIPKRKLLSKQD	121
CPK22	-----IVSDQKQETILGKPLEDILKHYSLGKBLGRGQGGQFGTTFLOVEKT	TGKEYACKSIPKRKLSSEE	77
CPK23	-----SIPISVRDPETILGKPEEIRKLYTLGKBLGRGQGGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	110
CPK24	-----IFQPPSRVLEPIGDGILHLKYLGRBLGRGQGGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	107
CPK25	EYKKRAIACANSKRKAHVRRRLMSAGLQAE SVLKTKTGHLKEYYSLGKBLGRGQGGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	173
CPK26	-----MKHSGNQACYVLLGQKPSIRDLYSGLGKBLGRGQGGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	65
CPK27	-----KRTILEKPLVDITKIVYLLGKBLGRGQGGQFGTTFLOVEKT	TGTRKVEKSTGKTFACKTILKTKKDEBC	69
CPK28	-----SIPCGKRTDFGYSKDFHDHYRTIGKLLGHGQGGQFGTTFLOVEKT	TGDRVAVKKLDKAKMTPIA	103
CPK29	-----STSSGSGTGPILNRPMDLSALYDLGRBLGRGQGGQFGTTFLOVEKT	TGDRVAVKKLDKAKMTPIA	153
CPK30	-----VLPMSHQQTSDKYLLGRBLGRGQGGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	100
CPK31	-----KRTILEKPEVDITKIVYLLGKBLGRGQGGQFGTTFLOVEKT	TGTRKVEKSTGKTYACKTILKTNLKSRE	69
CPK32	-----LKLI---VLNDPTGREITKQYKRLGRBLGRGQGGQFGTTFLOVEKT	TGDDVFACKSISKKLLTRSD	104
CPK33	-----PAKHSG---AAALEKPYEDVLFYTLGKBLGRGQGGQFGTTFLOVEKT	TGKRFACKSISKKLVTKAD	114
CPK34	-----ATKQGPPIGVLGRPMEDVRSYSLGKBLGRGQGGQFGTTFLOVEKT	TGHEALACKSISKKLDRTAVD	109

• ATP Binding

Kinase Domain

CPK1	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	272
CPK2	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	308
CPK3	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	LYSERAADLGRMVMVHCHSLSMGVHM	200
CPK4	YEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	CFSERBAAKLTKTIIVGVVEACHSLGVMH	147
CPK5	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	219
CPK6	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	207
CPK7	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	181
CPK8	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	179
CPK9	KEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	213
CPK10	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	185
CPK11	YEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HSERBAAKLTKTIIVGVVEACHSLGVMH	148
CPK12	YEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERBAAKLTKTIIVGVVEACHSLGVMH	144
CPK13	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	176
CPK14	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	176
CPK15	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSEKAAAGVIRSVVQICHEFMGVH	224
CPK16	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	SRYSERDAAVVROMIKVAEACHLGLVH	232
CPK17	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	195
CPK18	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	SRYTEKDAAVVROMIKVAEACHLGLVH	195
CPK19	REDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSEKAAAGVIRSVVQICHEFMGVH	220
CPK20	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	256
CPK21	KEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	202
CPK22	KEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	162
CPK23	REDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	191
CPK24	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	188
CPK25	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	254
CPK26	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	146
CPK27	EEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	154
CPK28	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	NRYSERDAAVVROMIKVAEACHLGLVH	186
CPK29	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	SYSEKAAAGVIRSVVQICHEFMGVH	234
CPK30	VEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	181
CPK31	EEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	154
CPK32	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYTERKAABELARTIIVGVVEACHSLGVMH	185
CPK33	KEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	195
CPK34	IEDVRRREI OIMHHLAAGHPNVIITKGAIEDVAVHVLVMECCAGGELFDRIIQRC	HYSERKAABELARTIIVGVVEACHSLGVMH	190

Arabidopsis CDPK Sequence Alignment

Kinase Domain

CPK1	RDLKPENFLVSKHED-SLTKTIDFGLSMFFKPDDEVDVVGSPYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	356
CPK2	RDLKPENFLVSKHED-SLTKTIDFGLSMFFKPDDEVDVVGSPYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	392
CPK3	RDLKPENFLVSKDEN-SLTKTIDFGLSVFFKPKDKDKDLVGSAYYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	284
CPK4	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQYLYDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETES	231
CPK5	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	303
CPK6	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	291
CPK7	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	265
CPK8	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	263
CPK9	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	297
CPK10	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	269
CPK11	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETES	232
CPK12	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETES	228
CPK13	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETES	260
CPK14	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETES	260
CPK15	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	308
CPK16	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	316
CPK17	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEN	279
CPK18	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	279
CPK19	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	305
CPK20	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	340
CPK21	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	286
CPK22	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETES	246
CPK23	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEN	275
CPK24	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	272
CPK25	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	338
CPK26	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEQ	230
CPK27	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	238
CPK28	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	270
CPK29	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	318
CPK30	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	265
CPK31	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	237
CPK32	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	269
CPK33	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEK	279
CPK34	RDLKPENFLVSKHED-SLTKTIDFGLSVFFKPKQIETDVVGSFYVAPEVLRRKRCPEADVWSAGVIVYLLSGVPPFAETEN	274

Active Site

Kinase Domain

Autoinhibitory

CPK1	GIFE-----QVHGDIDFSSDPEWESI SESAKDLVRKMLVRDPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	433
CPK2	GIFE-----QVHGDIDFSSDPEWESI SESAKDLVRKMLVRDPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	469
CPK3	GIFD-----AIHQGLDFEADPEEALSDGAKDLVRKMLYDPPKDRITAAEVLN-HPWREDGEASEKPLDPAVLSRLKQESAM	361
CPK4	GIFR-----QIQGKIDFESDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	308
CPK5	GIFD-----AVLKGYIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	380
CPK6	GIFE-----AVLKGYIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	368
CPK7	GVAQ-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	342
CPK8	GVAQ-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	340
CPK9	GIFD-----AIEGHIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	374
CPK10	GVAL-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	346
CPK11	GIFR-----QIQGKIDFESDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	309
CPK12	GIFR-----KIIQGLDFEADPEEALSDGAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	305
CPK13	GVAQ-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	337
CPK14	GVAK-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	337
CPK15	GIFN-----EIIKGEIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	384
CPK16	GIFK-----EVLKKNKDFEADPEEALSDGAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	393
CPK17	GIFN-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	356
CPK18	GIFN-----EVIKGGIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	356
CPK19	GIFE-----EIIKGEIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	382
CPK20	GIFE-----QVHGDIDFSSDPEWESI SESAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	417
CPK21	GIFD-----EVIKGGIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	362
CPK22	IIVSTLCIVDAEIKKCRIDFESDPEWETI SFKAKHLIKKMLPKPKRRITAAQVLE-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	328
CPK23	GVEV-----EIIKCKIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	351
CPK24	GIAH-----AIIERSVIDFKRDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	349
CPK25	EIFN-----EVIKGGIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	415
CPK26	GIFD-----AVLKGYIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	307
CPK27	QMEN-----EIKSLEIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	314
CPK28	EIFK-----EVLKKNKDFEADPEEALSDGAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	347
CPK29	TIFE-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	394
CPK30	GVAL-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	342
CPK31	QMSF-----EIKSLEIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	314
CPK32	GVAQ-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	346
CPK33	GIFD-----AIEGHIDFESDPEWETI SDSAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	356
CPK34	GIFN-----AIIERSVIDFKRDPEWETI SEAKDLVRKMLVDRPKRRITAHQVLC-HPWVQVDGVAPEKPLDPAVLSRLKQESAM	351

Arabidopsis CDPK Sequence Alignment

Domain	Calmodulin-Like Domain	
CPK1	NRFKKMALRVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	516
CPK2	NRFKKMALRVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	552
CPK3	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	444
CPK4	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	391
CPK5	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	463
CPK6	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	451
CPK7	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	425
CPK8	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	424
CPK9	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	457
CPK10	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	429
CPK11	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	392
CPK12	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	388
CPK13	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	420
CPK14	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	420
CPK15	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	467
CPK16	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	477
CPK17	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	439
CPK18	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	440
CPK19	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	465
CPK20	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	500
CPK21	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	445
CPK22	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	411
CPK23	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	434
CPK24	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	432
CPK25	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	499
CPK26	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	390
CPK27	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	397
CPK28	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	431
CPK29	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	477
CPK30	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	425
CPK31	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	397
CPK32	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	429
CPK33	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	439
CPK34	NRIKKMALKVIAEASLSEBETIAGLREMFNMIDAKKSGOITFEBELRAGLKRVC-ANLKESELDLDMQA-ADVNSGTDYREFFIAT	434

EF Hand 1 Calmodulin-Like Domain EF Hand 2

CPK1	LHLNKIEREDH-----FAAFYFDKDKGSGYITPDELQOACE-EFG---VED-VRTEELMRDVEDQNDGRIIDYBEFVAMMKQGS	590
CPK2	LHLNKIEREDH-----FAAFYFDKDKGSGYITPDELQOACE-EFG---VED-ARTEEMMRDVEDQNDGRIIDYBEFVAMMKQGS	626
CPK3	MHRNRTEREDH-----LYTARQFPDNDNSGYITMBELSLAMK-KYN---MGDDKSHKEILIAEVDTRDGGKINYEFEFVAMMKRGN	519
CPK4	LHLNKMEREBN-----LVVARSYFDKDKGSGYITIDELQOACE-EFG---LCD-TPIDDMIKEIDLDNDGKIDFSEFTAMMKKGD	465
CPK5	IHLNKLEREBH-----LVVARSYFDKDKGSGYITIDELQOACE-EHG---MAD-VFEDIILKEVDQNDGRIIDYBEFVAMMKQGN	537
CPK6	IHLNKLEREBH-----LVVARSYFDKDKGSGYITIDELQOACE-EHG---MTD-VFEDIILKEVDQNDGRIIDYBEFVAMMKQGN	525
CPK7	VHLKKMANDEH-----VHKARQFPDQNSGYITIDELSLRALDELND-TSSEEVAAIMQDVEDTKDGRISYBEFVAMMKAGT	502
CPK8	VHLKKMANDEH-----VHKARQFPDQNSGYITIDELSLRALDELND-TSSEEVAAIMQDVEDTKDGRISYBEFVAMMKAGT	500
CPK9	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLAMK-EYG---MGDDATHKEVLSVDVSDNDGRIIDYBEFVAMMKRGN	532
CPK10	IHLQKTEENDEL-----FKLAEAFDQNSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKAGT	505
CPK11	LHLNKMEREBN-----LVVARSYFDKDKGSGYITIDELQOACE-EFG---LCD-TPIDDMIKEIDLDNDGKIDFSEFTAMMKKGD	466
CPK12	IHLNKLEREBN-----LVVARSYFDKDKGSGYITIDELQOACE-EFG---IND-SNIDEIKKIDQNDGRIIDYBEFVAMMKRGN	462
CPK13	LHLQKVANDEH-----VHKARQFPDQNSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKAGT	496
CPK14	VHLRKLGNDEH-----VHKARQFPDQNSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKAGT	496
CPK15	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLAMK-EYG---MGDEASHKEVIAEVDTRDGGKINYEFEFVAMMKRGN	542
CPK16	LHVNOLEEHDEKQQRRAAEKEDLDLQDGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKAGT	553
CPK17	MHRNRTEREDH-----LYSARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	514
CPK18	LHVNOLEEHDEKQQRRAAEKEDLDLQDGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	521
CPK19	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	540
CPK20	VHLNKIEKEDH-----LFTARSYFDQDGSYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	574
CPK21	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	520
CPK22	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	485
CPK23	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	509
CPK24	IHLKRNQDDEH-----LQEARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	511
CPK25	VHLRQLEEEE-----ANDRESSTK-V-----	520
CPK26	IHLNKLEREBH-----LVVARSYFDKDKGSGYITIDELQOACE-EHG---MSD-VFEDIILKEVDQNDGRIIDYBEFVAMMKQGI	464
CPK27	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	472
CPK28	LHVNOLEEHDEKQQRRAAEKEDLDLQDGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	507
CPK29	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	542
CPK30	IHLQKTEENDEL-----FKLAEAFDQNSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	501
CPK31	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	472
CPK32	VHLRKLGNDEH-----VHKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	504
CPK33	MHRNRTEREDH-----LYKARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	514
CPK34	MHRNRTEREDH-----LYSARQHPDKDSSGYITIDELSLRALDELND-EEDASVSDIMREVDTKDGRINYEFEFVAMMKRGN	509

EF Hand 3 EF Hand 4

Arabidopsis CDPK Sequence Alignment

CPK1	ITGG-----PVKMGLEKSF SIALKL-----	610
CPK2	IMGG-----PVKMGLENSI SLSLKH-----	646
CPK3	PELVPNRRRM-----	529
CPK4	GVGR---SRTMNNLNFNIAEAFGVEDTSSTAKSDDSPK---	501
CPK5	AGVG---RRTMNRSLNISRDA-----	556
CPK6	AGVG---RRTMKNSLNISRMDV-----	544
CPK7	DWRKASRQYSRERFNSLSLKLMD-----GSLQLE-----GET-----	535
CPK8	DWRKASRQYSRERFNSLSLKLMD-----GSLQLE-----GEN-----	533
CPK9	PQQQQPRLF-----	541
CPK10	DWRKASRQYSRERFNSLSLNLMKD-----GSLHLH-----DALTGQTVPV-----	545
CPK11	GVGR---SRTMMKNLNFNIAEAFGVDE---KSD-----	495
CPK12	GTGGGIGRRMNRSLNFGTTLPEDESMNV-----	490
CPK13	DWRKASRHYSRGRFNSLSIKLMD-----GSLNLG-----NE-----	528
CPK14	DWRKASRQYSRDLFKCLS LKLMQD-----GSLQS-----NGDTK-----	530
CPK15	TLPQQGKILPVQ-----	554
CPK16	IKSRNVRSPPGYLISRKV-----	571
CPK17	PDPIPKKRRELSFK-----	528
CPK18	LKSKNVKSPPGYQLSQKM-----	539
CPK19	QSHQSKLVQPN-----	551
CPK20	FG-----KMGLKVS-----	583
CPK21	TQPQ-GKLLPFH-----	531
CPK22	ILQPQKLVGIHI-----	498
CPK23	TQPK-GKQYPFH-----	520
CPK24	DWKMASRQYSRALLNALS IKMFKEDFGDNGPKSHSMEFPIAR---KRAKLLDAPKNKSMELQISKTYKPSGLRN	582
CPK25	-----	-
CPK26	VG-----RTMRKSNMIRNNAVSQ-----	484
CPK27	SLQPEGELLPIIN-----	485
CPK28	ISSQRAPSPAGHRNLR-----	523
CPK29	-----	-
CPK30	DWRKASRQYSRERFNSLSLNLMKD-----GSMHLH-----DALTGQSI AV-----	541
CPK31	SLQFQRELLPIK-----	484
CPK32	DWRKASRQYSRERFNSLSLKLMD-----ASLQSCVFDILANERAEYGDQERKTVLAFGCV-----	560
CPK33	PQ--QPRLF-----	521
CPK34	PDENPKKRRELSFK-----	523