

Figure 2.

CPK1	-----MCNTCVGSPSRNGFLQSVSAAMWRPRDGDDSSASHMNGDIASEAVSGELRS-RLSDEVQN	57
CPK2	-----MCNACVGPNI SGNGLQTVTAAAMWRPRIGAEQASSSSHGNGQVSKAAASEPATDQVQN	58
CPK3	-----MCHRHSSKSSSDPPSSSSSSSSGNVVHVHKPA-----GERRGSSG	40
CPK4	-----	-
CPK5	-----MCNSCRGSF KDKLDEGDNKPEDYSKTSTTNLSSNSDHS PNAAD-----IIAQEF SK	52
CPK6	-----MCNSCRGSF KDKIYEGNHSRPEENSKSTTTTVSSVHSP-----TTDQDF SK	46
CPK7	-----MCN---CCGNPSSATNQSKQKPKNKNNPFYS-----NEYAT TDR	37
CPK8	-----MCN---CCASPGSETG-SKKGKPKIKSNPFYS-----EAYTTNG-	35
CPK9	-----MCNCFAKNHG-LMKPQQNGNTRSRVGVGTNQ-----DPPSYT PQ	39
CPK10	-----MCNACNACVR PDSKESKPSKPKKPNRDRKLN P-----FAG-DFTR	39
CPK11	-----	-
CPK12	-----	-
CPK13	-----MCN---CCRS PAAVAREDVKSNSYSGHDHARKD-----AAG---GK	34
CPK14	-----MCN---CCGTAGSLIQD--KQKGF KLPNPF S-----NEYGNHHD	35
CPK15	-----MC-CFSSKHRNTE SDIINGSVQSSI PTNQPEN-----HVS RDVLK	39
CPK16	-----MGLCFSSAAKSSGHNRSSRNPHPHPLTVVKS RPPRSPCFEMAVTIQKDHR TQPRRA	58
CPK17	-----MCNCCSHGRDSADNGDALENGAS----ASNA-----ANSTGPTA	35
CPK18	-----MCLCF S-SPKATRRGTGSRNPNPDSPTQ GKAS-----EKVSNKNKK	40
CPK19	-----MC-CLCINLKKKVKKPT PDISGEQNT EVKSRE-----ITPK EQPR	39
CPK20	-----MCNTCVGPNLNPNGFLQSVSAAVWRNQK PDDSIKSSKDESSRKKNDK---SVNGDDSN	55
CPK21	-----MC-CFSSKHRKTQN---DGG-EKSI PINPVQT-----HV V---PE	32
CPK22	-----MCNCCGSKPLTASD-----	14
CPK23	-----MC-CFSSKHRKTQN---DGGGERSI PII PVQT-----HIVDQV PD	36
CPK24	-----MCS---CVSSPLKGSPEGKR PVRRHSSNSRT-----SSVPRPDS	37
CPK25	-----MCNVCVHMVNVCVDTKNSWVRPTDLIMDHP LK PQLQDKPPQPMLMNKDDDKTKLNDT	58
CPK26	-----	-
CPK27	-----MC-CFSSKELQQS-----	12
CPK28	-----MCVCFS-AIRVTGASSRRSSQT KS-----KAAP-TPI	31
CPK29	MLQNQHKT TKNQRNKNIGTKYFLRKKIMCFCSKFGKSQTHEIPISSSSDSSPPHYQP-----LPKPTV SQ	67
CPK30	-----MCNCIACVKFDPDNSKPNQK-KKPPRGRQRNP-----YDDPDGLR	39
CPK31	-----MC-CYSSKNLQ S-----	12
CPK32	-----MCN---CCGTAGSLAQDNKPKKGRKKQNPF S-----IDYGLHHG	37
CPK33	-----MCNCLAKKYGLVMK PQQNG--ERSVIEIENRRR-----S-----	31
CPK34	-----MCNCCSHGRSDSDN---KEEPR---PENG-----GGGVG-AA	30
CPK1	KPPEQVTMPKPGTDVETK---DREIRTESK-----PETLEEISLE-----SKPETKQETKS-----ET	107
CPK2	KPPEPITMPSSKTNPETKLPDLLEIQPEEKKEKVLAEETKQKVVPBESKQEVPPBESKREV VVQPESAKPETKSESKPETTKPET	143
CPK3	SGTVGSSGSGTGSSRS	56
CPK4	-----	-
CPK5	DNNSNNNSKDPALVIPLR-----	70
CPK6	QNTN-----PALVI PVK-----	58
CPK7	SGAG-----	41
CPK8	SGTG-----	39
CPK9	ARTTQQPEKPGSVNSQPPFWRA-----	61
CPK10	SPAPIRV-----	46
CPK11	-----	-
CPK12	-----	-
CPK13	KSAPIR-----	40
CPK14	G-----	36
CPK15	PQKPPSPQI PTTTQSNHHHQESKPVNQI-----	69
CPK16	TAKKT PTRHT PPHGKVRKVIS-----	80
CPK17	EASVPQSKHAPSPPP-----	51
CPK18	NTKKIQLRHQG-----	51
CPK19	QRQP---APRAKFI VVQPHKLPLPLPQP-----	65
CPK20	GHVSSTVDPAPSTLPTPS-----TPPPPVKMANE-----EPPPKP-----	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	---THQDPSKISTGTNQPPFWRN-----	51
CPK34	EASVRASKHPPASPPP-----	46

Figure 2.

	Kinase Domain		
CPK1	KPESKPDPPAKPKK-PKHMKRVS	SAGLRTE	SVLQRKTNFKEFYSLGRKLGOGQFGTTFLOVEXTGKEFACKSIARRKLLTDBE 191
CPK2	TSETKPETKAEPOK-PKHMRRVSS	SAGLRTE	SVLQRKTNFKEFYSLGRKLGOGQFGTTFLEKGTGNEYACKSISKRRLLTDBE 227
CPK3	-----	TTSTQONGRI	ILGRPMEEVRRTYEFGRLGRGQFGVTYLVTHKEKQOVACKSIPTRRIVHKDE 119
CPK4	-----	ME-KPNRRRPSNS	VLPEYTPRLRDHYLGRKLGOGQFGTTLCTEKSSSANYACKSIPKRRKLVCRE 66
CPK5	-----	EPIMRNPNQAYY	VLGHKTPNIRDIYTSRRLGOGQFGTTLCTEIASGVDYACKSISKRRLLSKED 138
CPK6	-----	EPIMRNVDNQSY	VLGHKTPNIRDIYTSRRLGOGQFGTTLCTDIATGVDYACKSISKRRLLSKED 126
CPK7	-----	FKLS---	VLKDPGTGHDISLQYDLGRBVGGRGEGFTYLCDEKTEGKEYACKSISKKRLTAVD 100
CPK8	-----	FKLS---	VLKDPGTGHDISLQYDLGRBVGGRGEGFTYLCDEKTEGKEYACKSISKKRLTAVD 98
CPK9	-----	AAAAPGLSPKTTTK	NSILENAFEDVQLFYTLGKBLGRGQFGVTYLCENSTGKKYACKSISKKRLVTKAD 132
CPK10	-----	LKD---	VI PMSNQTI SDKYLLGRBLGRGEGFTYLCDEKTEGKEYACKSISKKRLTAVD 104
CPK11	-----	METKPNRRRPSNT	VLPEYTPRLRDHYLGRKLGOGQFGTTLCTEKSSTANYACKSIPKRRKLVCRE 67
CPK12	-----	MANKRTR---	WVLPYKTKNVDENYFLGQVVGOGQFGTFLCTHKQTGQKLACKSIPKRRLLCQED 63
CPK13	-----	VLSDVPKENI	EDRYLLDRBLGRGEGFTYLCIERSSRDLLACKSISKKRLTAVD 95
CPK14	-----	LKLI---	VLKPTGHEIRKQYDLGRBLGRGEGFTYLCDEKTEGKEYACKSISKKRLTAVD 95
CPK15	-----	EKKHVLTPQLK	PVIFRETETILGKPEEIRKLYTLGKBLGRGQFGVTYLCENSTGNTYACKSIPKRRLTRKD 143
CPK16	-----	NNGRRHGETI	PIYGRVDFGYAKDFDHYTIGKLLGHGQFGVTYVATDKKIGDRVAVKLDIAKMTPIA 149
CPK17	-----	ATKQGP	IGPVLGRPMEDVRSYSLGRBLGRGQFGVTHLCTQKATGHOFACTIAKRRIVNKE 114
CPK18	-----	GI	PYGKRIDFGYAKDFDNRYPITGKLLGHGQFGVTYVATDNNNGNRVAVKRIIDAKMTQPIE 112
CPK19	-----	QEQK	LINHQQSTLQPEPILGRPFEDIKKYSLGRBLGRGQFGVTYLCDEISSGKNFACKSILKRRKLRTRK 139
CPK20	ITENKEDPNSK	PQKKEAHKRMASAGLQIDS	VLGRKTNELRDIYSLGRKLGOGQFGTTFLOVDDKKTGKEFACKSIAKRRIVNKE 175
CPK21	-----	ISTPSSNPVSV	VRDPTDILGKPFEDIRKPYSLGRBLGRGQFGVTYMCKEICGTGNTYACKSIPKRRLLSKED 121
CPK22	-----	IVSDQKQET	ILGKPLEDITKHYSEDELGRGEGFTYLCENSTGKSYACKSIPKRRLLSSEE 77
CPK23	-----	SIPISVRDPET	ILGKPFEDIRKPYSLGRBLGRGEGFTYMCKEICGTGNTYACKSIPKRRLLSELG 110
CPK24	-----	IFOPPSRV	LEPIGDGILHLYDLGRBLGRGEGFTYVTHEIETSTRERFACKRISSEKLRTEID 107
CPK25	EYKKRAIACAN	SKRKAHVRRRLMSAGLQAES	VLKTKTGHLEKYYNLSGLGHGQFGTTFVQVEKGTGEEYACKSIPKRRLENE 173
CPK26	-----	MKHSGNQAC	YVLGQKTPSIDLYSLGHKLGOGQFGVTYMCKEISTGREYACKSIPKRRLLSKED 65
CPK27	-----	KRTILEK	PVLDITKIYLLGEBLGRGEGFTYTRKVEKSTGKTEFACTILKTRLEKDEBC 69
CPK28	-----	SIPCGKRT	DFGYSKDFHDHYTIGKLLGHGQFGVTYVAIHRPNGDRVAVKRLDMSKMLPIA 103
CPK29	-----	STSSGSQIG	PIHLGRPMEDVRSYSLGRBLGRGQFGVTYKCTDKSNGREYACKSIPKRRIVNKE 153
CPK30	-----	VI	PMSHQSI SDKYLLGRBLGRGEGFTYLCDEKTEGKEYACKSISKKRLTAVD 100
CPK31	-----	KRTILEK	PFVDITKVIYLLGEBLGRGEGFTYTRKVEKSTGKTYFACTILKTRLEKDEBC 69
CPK32	-----	LKLI---	VLNDPTGREISEKYLGRBLGRGEGFTYLCDEKTEGKEYACKSISKKRLTAVD 104
CPK33	-----	PAKHSG---	AAALEKPYEDVQLFYTLGKBLGRGQFGVTYLCDEKTEGKEYACKSISKKRLVTKED 114
CPK34	-----	ATKQGP	IGPVLGRPMEDVRSYSLGRBLGRGQFGVTHLCTQKATGHOFACTIAKRRIVNKE 109

• ATP Binding

	Kinase Domain																						
CPK1	VEDVRRREI	QIMHHL	AGHPNVI	SIKGA	EDVVA	HLVME	CCAGG	ELFDR	IIRQC	----	HYTER	KAAEL	ARTI	IVGV	EACH	SLGVMH	272						
CPK2	VEDVRRREI	QIMHHL	AGHPNVI	SIKGA	EDVVA	HLVME	CCAGG	ELFDR	IIRQC	----	HYTER	KAAEL	ARTI	IVGV	EACH	SLGVMH	308						
CPK3	IEDVRRREI	QIMHHL	SGHRN	IVDL	KGA	EDRHS	VNL	IMEL	CBGGE	LFDR	IISK	----	LYSERA	AADL	CRVM	VMVH	CHSM	GVMH	200				
CPK4	YEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	CF	SERBA	AKL	IKTI	IGV	EACH	SLGVMH	147		
CPK5	VEDVRRREI	QIMHHL	AGHGS	IVT	IKGA	EDSLY	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSER	KAAEL	ARTI	IVGV	EACH	SLGVMH	219				
CPK6	VEDVRRREI	QIMHHL	AGHRN	IVT	IKGA	EDPLY	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSER	KAAEL	ARTI	IVGV	EACH	SLGVMH	207				
CPK7	IEDVRRREI	QIMHHL	PKHPN	VVSL	KDSE	DDAV	H	VME	LCB	GGEL	FDRI	VARG	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	181	
CPK8	IEDVRRREI	QIMHHL	PKHPN	VVSL	KDSE	DDAV	H	VME	LCB	GGEL	FDRI	VARG	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	179	
CPK9	KEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	213		
CPK10	IEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	185	
CPK11	YEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	148	
CPK12	YEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	144	
CPK13	IEDVRRREI	QIMHHL	PKHPN	VVSL	KDSE	DDAV	H	VME	LCB	GGEL	FDRI	VARG	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	176	
CPK14	IEDVRRREI	QIMHHL	PKHPN	VVSL	KDSE	DDAV	H	VME	LCB	GGEL	FDRI	VARG	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	176	
CPK15	IEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSEK	AAAG	VIR	SV	VM	QI	CH	SM	GVH	224	
CPK16	VEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	SRYSER	DA	AV	V	QI	CH	SM	GVH	232	
CPK17	IEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	195		
CPK18	VEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	SRYTE	KDA	AV	V	QI	CH	SM	GVH	195	
CPK19	REDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSEK	AAAG	VIR	SV	VM	QI	CH	SM	GVH	220	
CPK20	VEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	256	
CPK21	KEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	202		
CPK22	KEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSEK	AAAG	VIR	SV	VM	QI	CH	SM	GVH	162	
CPK23	REDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	191		
CPK24	VEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	188	
CPK25	VEDVRRREI	QIMHHL	AGYKN	IVT	IKGA	EDSV	VH	VME	LCR	GGEL	FDRI	VERG	----	HYSER	KAA	HL	AKVI	IGV	QI	CH	SM	GVH	254
CPK26	VEDVRRREI	QIMHHL	AGYKN	IVT	IKGA	EDPLY	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSER	KAA	HL	AKVI	IGV	QI	CH	SM	GVH	146	
CPK27	EEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSEK	AAAG	VIR	SV	VM	QI	CH	SM	GVH	154	
CPK28	VEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	NRYSEK	DA	AV	V	QI	CH	SM	GVH	186	
CPK29	IEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	SYSEK	BA	AV	V	QI	CH	SM	GVH	284		
CPK30	IEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	181	
CPK31	EEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	154		
CPK32	IEDVRRREI	QIMHHL	SEHPN	VVR	IKGT	MED	SVFV	HVME	VOB	GGEL	FDRI	VS	----	HYTER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	185	
CPK33	KEDVRRREI	QIMHHL	SGQPN	IVV	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	195		
CPK34	IEDVRRREI	QIMHHL	AGYKN	IVT	IKGA	EDRHS	VH	VME	LCAGG	ELFDR	IIRQC	----	HYSER	AAA	AVM	KTI	VEV	QI	CHK	QVMH	190		

Figure 2.

Kinase Domain

Table showing Kinase Domain sequences for CPK1 through CPK34. Each row represents a protein and its sequence. The sequences are aligned, with asterisks indicating conserved residues. The table ends with a row of asterisks: ** * * * * * *

Active Site

Kinase Domain

Autoinhibitory

Table showing Kinase Domain and Autoinhibitory sequences for CPK1 through CPK34. The Kinase Domain sequences are aligned, with asterisks indicating conserved residues. The Autoinhibitory sequences are also aligned. The table ends with a row of asterisks: * * * * * *

Figure 2.

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

EF Hand 1 **EF Hand 2**

Calmodulin-Like Domain

CPK1	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	590
CPK2	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	626
CPK3	MHNRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	519
CPK4	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	465
CPK5	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	537
CPK6	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	525
CPK7	VHLKKNWANDH-----VHKAQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	502
CPK8	VHLKKNWANDH-----VHKAQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	500
CPK9	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	532
CPK10	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	505
CPK11	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	466
CPK12	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	462
CPK13	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	496
CPK14	VHLKKNWANDH-----VHKAQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	496
CPK15	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	542
CPK16	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	553
CPK17	MHLNRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	514
CPK18	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	521
CPK19	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	540
CPK20	VHLKKNWANDH-----VHKAQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	574
CPK21	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	520
CPK22	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	485
CPK23	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	509
CPK24	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	511
CPK25	VHLKKNWANDH-----VHKAQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	520
CPK26	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	464
CPK27	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	472
CPK28	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	507
CPK29	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	542
CPK30	LHLNKIEREDH-----FAAFTYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	501
CPK31	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	472
CPK32	VHLKKNWANDH-----VHKAQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	504
CPK33	MHRRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	514
CPK34	MHLNRLEREDH-----YTARQYFDKDGSGYITPDELQOACE-EFG---VED-VREELMRDVEDQNDGRIDYEFVAMMQKGS	509

EF Hand 3 **EF Hand 4**

Figure 2.

CPK1	ITGG-----PVKMGLEKSF SIALKL-----	610
CPK2	IMGG-----PVKMGLENSI SISKH-----	646
CPK3	PELVPNRRRM-----	529
CPK4	GVGR---SRTMNNLNFNIAEAFGVEDTSSTAKSDDSPK---	501
CPK5	AGVG---RRTMNSLNISMRDA-----	556
CPK6	AGVG---RRTMKNSLNISMRDV-----	544
CPK7	DWRKASRQYSRERFNSLSLKLMRD-----GSLQLE-----GET-----	535
CPK8	DWRKASRQYSRERFNSLSLKLMRD-----GSLQLE-----GEN-----	533
CPK9	PQQQQPRLF-----	541
CPK10	DWRKASRQYSRERFNSLSLNLMKD-----GSLHLH-----DALTGQTVPV-----	545
CPK11	GVGR---SRTMMKNLNFNIAADAFGVDGE---KSD-----	495
CPK12	GTGGGIGRRTMNSLNFGTTL PDESMNV-----	490
CPK13	DWRKASRHYSRGRFNSLSIKLMKD-----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 IKMFKEDFGDNGPKSHSMEF PIAR---KRAKLLDAPKNKSMELQISKTYKPSGLRN	582
CPK25	-----	-
CPK26	VG-----RTMRKINMSIRNNAVSQ-----	484
CPK27	SLQPEGELLPIIN-----	485
CPK28	ISSQRAPSPAGHRNLR-----	523
CPK29	-----	-
CPK30	DWRKASRQYSRERFNSLSLNLMKD-----GSMHLH-----DALTGQSI AV-----	541
CPK31	SLQPQRELLPIK-----	484
CPK32	DWRKASRQYSRERFNSLSLKLMD-----ASLQSCVFDILANERAEYGDQERKTVLAFGCV-----	560
CPK33	PQ--QPRLF-----	521
CPK34	PDPNPKKRRELSFK-----	523