

Catalytic domain of the Serine/Threonine Kinases

		93	100	110	120	138
AtSnRK2.4 At1g10940	(39)	-----	-----	-----	PKIDENVAREIINHRSLR	----
AtSnRK2.9 AT2G23030	(39)	-----	-----	-----	YKIDENVAREIINHRAIN	----
HsSnRK NP_001094064	(54)	-----	-----	-----	TLATGHLFQEVRCMKLVQ	----
MmSnRK NP_001158044.1	(54)	-----	-----	-----	TLATGHLFQEVRCMKLVQ	----
OsSnRK 1a Os05g0530500	(51)	-----	-----	-----	MEEEKVKKREIKILRIFM	----
OsSnRK1b Os08g0484600	(56)	-----	-----	-----	MEMEAKAKREIKILRIFI	----
ZmSnRK NP_001105673.1	(56)	-----	-----	-----	MEMEAKAKREFKILRIFI	----
TaCIPK20	(93)	RDQRDEASQPPQHSQDTRGSCSN	FHHSILLVAQASSLRTHAESNP			
TaCIPK17	(66)	-----	-----	-----	ADDQVRREIATITMLA	----
TaCIPK21	(54)	-----	-----	-----	IDEQIKTEIATLKLK	----
AtSOS2 AAF62923.1	(52)	-----	-----	-----	MVDQIKREISIMKIVR	----
TaCIPK24	(54)	-----	-----	-----	MIQQIKKEISIMKIVR	----
TaCIPK8	(57)	-----	-----	-----	MVDQIKREISIMKIVR	----
TaCIPK23	(66)	-----	-----	-----	MIAQIKREISIMKIVR	----
TaCIPK3	(60)	-----	-----	-----	LVEQIRREICTMKLIQ	----
TaCIPK31	(61)	-----	-----	-----	LVEQIRREICTMKLIK	----
TaCIPK32	(54)	-----	-----	-----	MVEQIKREIATMKLIK	----
TaCIPK9	(58)	-----	-----	-----	MVEQIKREIATMKLIR	----
TaCIPK22	(63)	-----	-----	-----	KAAAARRSVERELAAIRVQG	----
TaCIPK29	(73)	-----	-----	-----	EGSAGSAAIEREAAILARLR	----
TaCIPK4	(59)	-----	-----	-----	NAPRVLQEVAMRRLR	----
TaCIPK7	(61)	-----	-----	-----	MDARVLGEVAMRRLR	----
TaCIPK12	(87)	-----	-----	-----	LVPHIKREITILRRVR	----
TaCIPK19	(87)	-----	-----	-----	LVSHIKREIIVLRVR	----
TaCIPK25	(52)	-----	-----	-----	AWQQIKREIIVMRRLR	----
TaCIPK13	(78)	-----	-----	-----	ITAHIKREIIVLRVR	----
TaCIPK10	(54)	-----	-----	-----	LMDQVRREISVMKLVK	----
TaCIPK2	(54)	-----	-----	-----	ITDQIKREISVMKLVK	----
TaCIPK11	(54)	-----	-----	-----	LMEQIKREISVMRLVK	----
TaCIPK26	(53)	-----	-----	-----	LIVQIKREISIMGLVR	----
TaCIPK28	(52)	-----	-----	-----	LVDQIKREISIMRIVR	----
TaCIPK14	(63)	-----	-----	-----	ISEQIRREIVTMRIVA	----
TaCIPK15	(53)	-----	-----	-----	LAEQVRREITMRLVT	----
TaCIPK5	(53)	-----	-----	-----	MIDQIKREISIMRLVR	----
TaCIPK27	(57)	-----	-----	-----	MVEQIKREIIVMKMVS	----
TaCIPK6	(57)	-----	-----	-----	MVEQIKREIIVMKMVS	----
TaCIPK30	(57)	-----	-----	-----	TVEQVKREIVDMRVRH	----
TaCIPK16	(1)	-----	-----	-----	MVEQLRREISIMRIVR	----
Consensus	(93)				MVEQIKREISIMRLVR	

Catalytic domain of the Serine/Threonine Kinases

		139	150	160	170	184
AtSnRK2.4 At1g10940	(57)	--HPNIIRFKEVVLTPTHLAIA	AMEYAAAGGELFERI	CSAGR--FSE	ED	
AtSnRK2.9 AT2G23030	(57)	--HPNIVRFKEVVLTPTHLGIV	MEYAAAGGELFERISSVGR	--FSE	EA	
HsSnRK NP_001094064	(72)	--HPNIVRLYEVIDTQTKLYL	LILELGDGDMFDYIMHEEG	--LNE	ED	
MmSnRK NP_001158044.1	(72)	--HPNIVRLYEVIDTQTKLYL	LILELGDGDMFDYIMHEEG	--LNE	ED	
OsSnRK 1a Os05g0530500	(69)	--HPHIIRLYEVIDTPADIVV	MEYVYKSGELFDYIIVEKGR	--LQE	ED	
OsSnRK1b Os08g0484600	(74)	--HPHIIRLYEVIYTPDIYV	MEYCKFGELFDYIIVEKGR	--LQE	ED	
ZmSnRK NP_001105673.1	(74)	--HPHIIRLYEVIYTPDIYV	MEYCKYKSGELFDYIIVEKGR	--LQE	ED	
TaCIPK20	(139)	LSRLTAVTFAQVIATKTKIC	LVMEYVGGQLSDKLSYLK	--RL	ED	
TaCIPK17	(82)	--HPNVVRLHEVAAASKTKIY	MVLEFVNGGELFDRIAMK	--GKL	SER	
TaCIPK21	(70)	--HPNVVRLHEVAAASKTKIY	MVLEFVNGGELFEKIALK	--GKL	SEK	
AtSOS2 AAF62923.1	(68)	--HPNIVRLHEVLAASPSKIY	IVLEFVTCGELFDRIVHK	--GRL	ES	
TaCIPK24	(70)	--HPNIIRLNEVLGGQTKIYI	IMELFTGGELFDKIIARQ	--GKL	REN	
TaCIPK8	(73)	--HPNVVRLHEVLASRKKIF	IILEFTTCGELFDKIIARH	--GRL	SEA	
TaCIPK23	(82)	--HPNIVIRMEVMASRTKIY	IVMELFTGGELFDKIIASR	--GRL	KED	
TaCIPK3	(76)	--HPNVVRLHEVMGSKARIF	VILEYVTCGELFDHIIAR	--GSL	KED	
TaCIPK31	(77)	--HPNVVRLHEVMGSKARIF	VILEYVTCGELFDHIIAR	--GSL	KED	
TaCIPK32	(70)	--HPNVVCLHEVMGSKTKIY	IVLEYVTCGELFDHIIAR	--GRM	RED	
TaCIPK9	(74)	--HPNVVQLHEVMASRSKIY	MVLEFVEGELFDHIIARS	--GKL	GED	
TaCIPK22	(84)	--HPHVMLLDVLAASRTVY	LVLELARGGTLSDAMDR	--GRF	ED	
TaCIPK29	(93)	--HRHVRLHEILGTRKQVH	FVLDLAAGGELFSLVDS	--GRM	TE	
TaCIPK4	(75)	--HPGVIRLHEVLATRASIV	YLVMEAPRGDLQSRLAAL	PSHRFSE	EK	
TaCIPK7	(77)	--HPNVIRLHEVLATRSKVY	LVMEAPRGDLQSRLAAL	PKRRLP	EH	
TaCIPK12	(103)	--HPNIVHLFEVMATKSKIY	FVMEYVGGELFDKIIAR	--GRL	KED	
TaCIPK19	(103)	--HPNIVHLFEVMATKTKIY	FVMEYVGGELFDKIIAR	--GRL	KED	
TaCIPK25	(68)	--HPNIVQLHKVMAACKSRI	FVMEYVGGELFDKIIAR	--GRL	KED	
TaCIPK13	(94)	--HPHIVQLYEVMATKTKIY	FVMEYVGGELFDKIIAR	--GRL	KED	
TaCIPK10	(70)	--HPNIVQLYEVMATKTKIY	FVMEYVGGELFDKIIAR	--GRL	KED	
TaCIPK2	(70)	--HPNIVQMYEVMATKTKIY	FVLEHVKGELFDKIIAR	--GRL	KED	
TaCIPK11	(70)	--HPNIVQLFEVMATKSKIY	FVLEYAKGELFDKIIAR	--GRL	KED	
TaCIPK26	(69)	--HPNVKLFEVMASRSKIY	FVLEYAKGELFDKIIAR	--GRL	KED	
TaCIPK28	(68)	--HPNIVQLFEVMATRSKIY	FVLEYAKGELFDKIIAR	--GRL	SE	
TaCIPK14	(79)	--HKNIVQLFEVMATRNKIY	FVMEYVGGELFDKIIAR	--GKL	AE	
TaCIPK15	(69)	--HKSIVQLFEVMATRSKIY	FVMEYVGGELFDKIIAR	--GKL	TE	
TaCIPK5	(69)	--HPNIVQLHEVMASRTKIY	FAMEYVGGELFDKIIAR	--GRL	KED	
TaCIPK27	(73)	--HPNIVQLHEVLATRTKIY	LALELVRGGELFDKIIAR	--GRL	RED	
TaCIPK6	(73)	--HPNIVELHEVLATRTKIY	LALELVRGGELFDKIIAR	--GRL	RED	
TaCIPK30	(73)	--HPNVVRLHEVMATRSRIY	FVMEYASGGELFDRLAK	--TRF	PEP	
TaCIPK16	(17)	--HPNVVGLREVLAASRQRF	VFVMEYVGGELFDKIIAR	--GRL	TE	
Consensus	(139)	HPNIVRLHEVMATKTKIYIV	LEVYVGGELFDKIIAR	GRL	ED	

Catalytic domain of the Serine/Threonine Kinases

	(185)	185	190	200	210	220	230																																						
AtSnRK2.4 At1g10940 (99)	E	A	R	Y	F	Q	Q	L	I	S	G	V	S	Y	C	H	A	M	Q	I	C	H	R	D	L	K	L	K	L	---	E	N	T	L	L	D	G	S	P	A	P	R	L	K	I
AtSnRK2.9 AT2G23030 (99)	E	A	R	Y	F	Q	Q	L	I	C	G	V	H	L	H	A	L	Q	I	C	H	R	D	L	K	L	K	L	---	E	N	T	L	L	D	G	S	P	A	P	R	L	K	I	
HsSnRK NP_001094064 (115)	L	A	K	K	Y	F	A	Q	I	V	H	A	I	S	Y	C	H	K	L	H	V	V	H	R	D	L	K	F	---	E	N	V	V	F	F	F	E	K	Q	G	-	L	V	K	L
MmSnRK NP_001158044.1 (115)	L	A	K	K	Y	F	A	Q	I	V	H	A	I	S	Y	C	H	K	L	H	V	V	H	R	D	L	K	F	---	E	N	V	V	F	F	F	E	K	Q	G	-	L	V	K	L
OsSnRK 1a Os05g0530500 (111)	E	A	R	R	F	Q	Q	I	S	G	V	E	Y	C	H	R	N	M	V	V	H	R	D	L	K	F	---	E	N	L	L	L	D	S	K	C	N	---	V	K	I				
OsSnRK1b Os08g0484600 (116)	E	A	R	R	F	Q	Q	I	S	G	V	E	Y	C	H	R	N	M	V	V	H	R	D	L	K	F	---	E	N	L	L	L	D	S	K	Y	N	---	V	K	L				
ZmSnRK NP_001105673.1 (116)	E	A	R	R	F	Q	Q	I	S	G	V	E	Y	C	H	R	N	M	V	V	H	R	D	L	K	F	---	E	N	L	L	L	D	S	K	Y	N	---	V	K	L				
TaCIPK20 (128)	E	A	K	K	Y	F	Q	Q	L	I	D	A	V	D	Y	C	H	R	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	N	Q	Y	N	---	L	K	V		
TaCIPK17 (184)	E	G	R	R	L	F	Q	Q	L	I	D	G	V	S	Y	C	H	G	K	G	V	F	H	R	D	L	K	F	---	E	N	V	L	I	D	R	K	G	N	---	I	K	I		
TaCIPK21 (112)	E	G	R	R	L	F	Q	Q	L	M	D	A	I	S	Y	C	H	E	R	G	V	F	H	R	D	L	K	F	---	E	N	V	L	V	D	A	K	G	N	---	I	K	V		
AtSOS2 AAF62923.1 (110)	E	S	R	K	Y	F	Q	Q	L	V	D	A	V	A	H	C	H	C	K	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	T	N	G	N	---	L	K	V		
TaCIPK24 (112)	E	A	R	K	Y	F	Q	Q	L	I	D	A	I	N	Y	C	H	S	K	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	S	R	G	N	---	L	K	V		
TaCIPK8 (115)	D	A	R	K	Y	F	Q	Q	L	I	D	G	V	F	C	H	S	K	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	S	Q	G	N	---	L	K	I			
TaCIPK23 (124)	D	A	R	K	Y	F	Q	Q	L	I	N	A	V	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	A	N	G	T	---	L	K	V		
TaCIPK3 (118)	E	A	R	R	Y	F	Q	Q	L	I	N	A	V	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	L	---	E	N	L	L	L	D	T	A	G	N	---	L	K	V		
TaCIPK31 (119)	E	A	R	R	Y	F	Q	Q	L	I	N	A	V	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	L	---	E	N	L	L	L	D	A	A	G	N	---	L	K	V		
TaCIPK32 (112)	E	A	R	R	Y	F	Q	Q	L	I	N	A	V	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	S	C	G	N	---	L	K	V		
TaCIPK9 (116)	E	A	R	R	Y	F	H	Q	L	I	N	A	V	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	S	Y	G	A	---	L	K	V		
TaCIPK22 (126)	T	S	R	R	L	F	V	Q	L	V	S	A	L	A	V	H	S	R	G	V	F	H	R	D	V	K	F	---	E	N	L	L	L	D	E	H	G	D	---	L	K	L			
TaCIPK29 (135)	L	A	R	H	Y	F	R	Q	L	V	S	A	V	R	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	G	Q	D	---	L	K	V			
TaCIPK4 (119)	A	A	R	R	V	F	V	Q	L	T	V	A	L	A	H	C	H	A	R	G	V	T	H	R	D	L	K	F	---	Q	N	L	L	L	D	G	A	G	N	---	L	K	V		
TaCIPK7 (121)	A	A	R	R	V	F	L	Q	L	V	S	A	L	I	Y	C	H	A	R	G	V	F	H	R	D	V	K	F	---	Q	N	V	L	T	D	A	D	G	N	---	L	K	V		
TaCIPK12 (144)	T	A	R	R	V	F	Q	Q	L	I	S	A	V	G	F	C	H	A	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	V	D	E	R	G	D	---	L	K	V		
TaCIPK19 (142)	I	A	R	R	Y	F	Q	H	L	I	S	A	V	G	F	C	H	T	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	V	E	A	G	N	---	L	K	V			
TaCIPK25 (110)	E	T	R	R	I	F	Q	Q	L	V	S	A	L	T	F	C	H	A	Q	G	V	F	H	R	D	L	K	F	---	D	N	L	L	V	D	E	H	G	N	---	L	K	V		
TaCIPK13 (135)	E	A	R	R	Y	F	Q	Q	L	V	S	A	V	A	F	C	H	A	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	D	A	G	D	---	L	K	V		
TaCIPK10 (111)	V	A	R	R	Y	F	Q	Q	L	N	S	A	V	D	F	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	E	N	R	N	---	L	K	I		
TaCIPK2 (111)	A	A	R	R	Y	F	Q	Q	L	I	C	A	V	D	F	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	E	N	S	N	---	L	K	V		
TaCIPK11 (112)	A	A	R	R	Y	F	H	Q	L	I	S	A	I	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	E	N	E	N	---	L	K	V		
TaCIPK26 (110)	A	A	R	R	Y	F	H	Q	L	I	S	A	V	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	E	N	E	N	---	L	K	V		
TaCIPK28 (109)	G	A	R	T	F	F	Q	Q	L	I	S	A	I	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	V	D	E	Y	G	T	---	L	R	V		
TaCIPK14 (121)	A	A	H	K	Y	F	Q	Q	L	I	S	A	V	D	Y	C	H	S	Q	G	V	F	H	R	D	L	K	L	---	E	N	L	L	L	D	E	N	E	N	---	L	K	V		
TaCIPK15 (111)	A	A	H	K	Y	F	Q	Q	L	I	S	A	V	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	G	N	E	N	---	L	K	V		
TaCIPK5 (110)	A	A	R	R	Y	F	Q	Q	L	I	G	A	V	D	F	C	H	S	R	D	V	F	H	R	D	L	K	F	---	E	N	L	L	V	D	E	H	G	N	---	L	K	V		
TaCIPK27 (115)	V	A	R	R	Y	F	R	Q	L	I	S	A	V	D	F	C	H	G	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	E	A	G	N	---	L	K	V		
TaCIPK6 (115)	V	A	R	R	Y	F	R	Q	L	I	S	A	V	D	F	C	H	G	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	E	A	G	N	---	L	K	V		
TaCIPK30 (115)	V	A	R	R	Y	F	Q	Q	L	V	T	A	V	E	F	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	A	H	G	N	---	L	K	V		
TaCIPK16 (58)	A	A	R	R	Y	F	Q	Q	L	V	A	A	V	A	F	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	E	E	G	R	---	L	K	V		
Consensus (185)	A	R	R	Y	F	Q	Q	L	I	S	A	V	D	Y	C	H	S	R	G	V	F	H	R	D	L	K	F	---	E	N	L	L	L	D	G	N	---	L	K	V					

Activation loop

Catalytic domain of the Serine/Threonine Kinases

	(231)	231	240	250	260	276																																			
AtSnRK2.4 At1g10940 (142)	C	D	F	G	Y	S	K	S	L	L	H	S	R	---	---	P	K	S	T	V	G	T	-	P	A	Y	I	A	P	E	V	L	S	R	H	E	Y	D	G	K	M
AtSnRK2.9 AT2G23030 (142)	C	D	F	G	Y	S	K	S	V	L	H	S	N	---	---	P	K	S	T	V	G	T	-	P	A	Y	I	A	P	E	V	F	C	R	S	E	Y	D	G	K	S
HsSnRK NP_001094064 (157)	T	D	F	G	F	S	N	K	F	Q	P	G	K	---	---	L	T	T	S	C	G	S	-	L	A	S	A	P	E	I	L	G	D	E	Y	D	A	P	A		
MmSnRK NP_001158044.1 (157)</																																									

	(277)	277	290	300	310	322																																						
AtSnRK2.4 At1g10940 (181)	ADV	W	S	G	G	V	T	L	V	M	L	V	G	A	Y	P	F	E	D	Q	E	D	P	K	N	F	R	K	T	I	Q	K	I	M	A	V	Q	Y	K	I	P	D	Y	
AtSnRK2.9 AT2G23030 (181)	V	D	V	W	S	C	G	V	A	L	V	M	L	V	G	A	Y	P	F	E	D	P	K	P	R	N	F	R	K	T	V	Q	K	I	M	A	V	N	Y	K	I	P	G	Y
HsSnRK NP_001094064 (196)	V	D	I	W	S	L	G	V	I	L	F	M	L	V	C	Q	P	P	F	Q	E	A	N	D	S	E	T	L	T	M	I	M	D	C	K	Y	T	V	F	S	-----			
MmSnRK NP_001158044.1 (196)	V	D	I	W	S	L	G	V	I	L	F	M	L	V	C	Q	P	P	F	Q	E	A	N	D	S	E	T	L	T	M	I	M	D	C	K	Y	T	V	F	S	-----			
OsSnRK 1a Os05g0530500 (191)	V	D	V	W	S	C	G	V	I	L	F	M	L	V	C	Q	P	P	F	D	D	E	N	I	P	N	L	F	F	K	K	I	K	G	G	I	Y	T	L	F	S	-----		
OsSnRK1b Os08g0484600 (196)	V	D	V	W	S	C	G	V	I	L	F	M	L	V	C	Q	P	P	F	D	D	E	N	I	P	N	L	F	F	K	K	I	K	G	G	I	Y	T	L	F	S	-----		
ZmSnRK NP_001105673.1 (196)	V	D	V	W	S	C	G	V	I	L	F	M	L	V	C	Q	P	P	F	D	D	E	N	I	P	N	L	F	F	K	K	I	K	G	G	I	Y	T	L	F	S	-----		
TaCIPK20 (249)	A	D	I	W	S	C	G	V	I	L	F	E	L	L	A	G	Y	L	P	F	Q	D	C	S	L	H	L	Y	R	R	Y	A	L	P	Q	W	I	T	L	F	P	-----		
TaCIPK17 (248)	S	D	I	W	S	C	G	V	I	L	Y	I	M	L	I	C	Q	L	P	F	D	R	N	M	V	V	L	Y	Q	K	I	F	K	G	D	T	K	V	H	E	-----			
TaCIPK21 (195)	S	D	V	W	S	C	G	V	I	L	V	M	L	T	G	N	L	P	F	D	D	E	N	M	V	L	Y	Q	K	I	L	K	G	D	Y	R	I	F	K	-----				
AtSOS2 AAF62923.1 (191)	A	D	I	W	S	C	G	V	I	L	F	V	L	A	G	Y	L	P	F	S	E	T	D	L	P	L	G	L	Y	R	K	I	N	A	A	E	F	S	C	F	P	-----		
TaCIPK24 (191)	A	D	I	W	S	C	G	V	I	L	V	L	M	A	G	Y	L	P	F	E	E	N	D	L	P	T	L	Y	D	K	I	T	A	A	H	F	S	C	F	D	-----			
TaCIPK8 (196)	A	D	T	W	S	C	G	V	I	L	V	L	L	A	G	Y	L	P	F	D	E	V	D	L	T	T	L	Y	G	K	I	E	T	A	E	Y	S	F	H	A	-----			
TaCIPK23 (207)	A	D	L	W	S	C	G	V	I	L	F	V	L	M	A	C	Y	L	P	F	E	D	S	N	L	M	A	L	Y	K	K	I	Y	K	A	D	F	S	C	F	S	-----		
TaCIPK3 (201)	A	D	L	W	S	C	G	V	I	L	F	V	L	M	A	G	Y	L	P	F	E	D	N	S	A	L	Y	K	K	I	S	G	A	Q	T	F	C	F	S	-----				
TaCIPK31 (202)	A	D	L	W	S	C	G	V	I	L	F	I	L	L	A	G	Y	L	P	F	E	D	E	N	L	I	L	Y	K	K	I	S	E	A	Q	T	F	C	F	S	-----			
TaCIPK32 (195)	A	D	L	W	S	C	G	V	I	L	F	V	L	L	A	G	Y	L	P	F	E	D	S	N	L	M	A	L	Y	K	K	I	S	D	A	E	F	T	F	P	-----			
TaCIPK9 (199)	A	D	V	W	S	C	G	I	L	F	V	L	M	A	G	Y	L	P	F	D	D	P	N	L	M	T	L	Y	K	L	I	S	R	A	N	V	S	C	F	P	-----			
TaCIPK22 (210)	V	D	V	W	S	S	G	V	A	L	F	S	L	T	A	G	Y	L	P	F	N	D	G	N	L	M	G	M	R	K	I	F	S	G	R	F	R	C	F	P	-----			
TaCIPK29 (214)	V	D	I	W	S	C	G	V	I	L	F	V	L	A	G	S	L	P	F	N	D	A	S	L	N	M	Y	R	K	I	Y	A	C	R	F	R	C	F	N	-----				
TaCIPK4 (202)	A	D	A	W	S	C	G	V	T	L	F	V	L	A	G	R	L	P	F	D	D	A	N	I	P	D	M	C	R	K	A	C	R	R	Q	V	V	P	P	-----				
TaCIPK7 (204)	A	D	A	W	S	C	G	V	I	L	V	L	L	A	G	R	L	P	F	D	D	S	N	L	A	E	M	C	M	K	A	H	R	R	E	Y	T	L	F	E	-----			
TaCIPK12 (227)	A	D	I	W	S	C	G	V	I	L	F	V	L	M	A	G	Y	L	P	F	H	D	Q	N	L	M	A	M	Y	R	K	I	Y	R	G	E	F	R	C	F	P	-----		
TaCIPK19 (227)	A	D	I	W	S	C	G	V	I	L	F	V	L	M	A	G	Y	L	P	F	H	D	Q	N	L	M	A	M	Y	R	K	V	Y	K	G	E	F	R	C	F	P	-----		
TaCIPK25 (193)	A	D	A	W	S	C	G	I	V	L	F	V	L	A	G	R	K	P	F	R	D	D	D	F	T	L	Y	R	T	I	C	R	G	D	Y	R	C	F	P	-----				
TaCIPK13 (218)	A	D	L	W	S	C	G	V	I	L	F	V	L	A	G	Y	L	P	F	Q	D	R	N	L	M	G	M	Y	R	K	I	H	R	G	D	F	R	C	F	P	-----			
TaCIPK10 (194)	A	D	L	W	S	C	G	V	I	L	V	L	L	A	G	Y	L	P	F	Q	D	K	N	L	M	Y	K	K	I	Y	K	A	E	L	K	W	F	S	-----					
TaCIPK2 (194)	A	D	I	W	S	C	G	V	I	L	F	V	L	L	A	G	Y	L	P	F	Q	D	K	N	L	M	Y	K	K	I	G	K	A	E	F	K	C	F	S	-----				
TaCIPK11 (195)	A	D	I	W	S	S	G	V	I	L	V	L	V	A	G	Y	L	P	F	H	E	A	N	L	I	E	M	Y	R	R	I	S	K	A	D	F	K	C	F	P	-----			
TaCIPK26 (193)	A	D	I	W	S	C	G	V	I	L	F	V	L	A	G	Y	L	P	F	H	D	T	N	L	I	E	M	Y	R	K	I	S	R	A	E	Y	R	C	F	P	-----			
TaCIPK28 (192)	A	D	I	W	S	C	G	V	I	L	F	V	L	A	G	Y	L	P	F	H	E	R	N	L	M	V	L	Y	R	K	I	A	K	A	E	L	K	W	F	C	P	-----		
TaCIPK14 (204)	S	D	I	W	S	C	G	V	I	L	F	V	L	A	G	Y	L	P	F	H	G	S	N	L	M	D	M	Y	R	K	I	E	Q	G	D	F	R	C	F	S	-----			
TaCIPK15 (194)	S	D	I	W	S	C	G	V	I	L	F	V	L	A	G	Y	L	P	F	Q	G	Q	N	L	I	E	M	Y	R	K	I	E	K	G	D	F	R	C	F	G	-----			
TaCIPK5 (193)	A	D	I	W	S	C	G	V	I	L	F	V	L	L	A	G	Y	L	P	F	Q	D	S	N	L	M	E	M	Y	R	K	I	S	K	G	D	V	R	H	Q	-----			
TaCIPK27 (198)	A	D	I	W	S	C	G	V	I	L	V	L	L	V	G	A	L	P	F	Q	D	E	N	L	M	S	M	Y	R	K	M	Q	R	G	G	F	L	C	F	S	-----			
TaCIPK6 (198)	A	D	I	W	S	C	G	V	I	L	V	L	L	V	G	A	L	P	F	Q	D	E	N	L	M	S	M	Y	R	K	M	Q	R	G	G	F	L	C	F	S	-----			
TaCIPK30 (202)	A	D	I	W	S	C	G	V	I	L	F	V	L	L	A	G	R	L	P	F	H	D	T	N	L	M	L	L	Y	K	R	I	A	R	S	D	Y	K	C	F	A	-----		
TaCIPK16 (141)	A	D	M	W	S	C	G	V	I	L	V	L	L	C	G	L	P	F	Q	H	D	N	Y	K	M	Y	Q	K	I	F	K	G	E	Y	Q	M	P	-----						
Consensus (277)	AD	I	W	S	C	G	V	I	L	F	V	L	L	A	G	Y	L	P	F	D	N	L	M	L	Y	R	K	I	K	G	E	F	C	P	-----									

Catalytic domain of the Serine/Threonine Kinases

	(323)	323	330	340	350	368																																								
AtSnRK2.4 At1g10940 (227)	V	H	I	S	Q	D	C	K	N	L	I	S	R	I	F	V	A	N	S	L	K	R	I	T	I	A	E	T	K	-	K	H	S	W	F	L	K	N	L	P	R	E	L	T	E	T
AtSnRK2.9 AT2G23030 (227)	V	H	I	S	E	D	C	R	K	L	L	S	R	I	F	V	A	N	L	H	R	S	T	L	K	E	I	K	-	S	H	A	W	F	L	K	N	L	P	R	E	L	K	E	P	
HsSnRK NP_001094064 (237)	-	H	V	S	K	C	K	D	L	I	T	R	M	L	Q	R	D	P	K	R	R	A	S	L	E	E	I	E	-	N	H	P	W	L	Q	G	V	D	P	S	P	A	T	K	Y	
MmSnRK NP_001158044.1 (237)	-	R	V	S	A	G	C	R	D	L	I	T	R	M	L	Q	R	D	P	K	R	R	A	S	L	E	E	I	-	S	H	P	W	L	Q	G	V	D	P	S	P	A	T	K	Y	
OsSnRK 1a Os05g0530500 (232)	-	H	L	S	P	L	A	R	D	L	I	P	R	M	L	V	V	D	P																											

	(553)	553	560	570	580	598
AtSnRK2.4 At1g10940 (364)	-----					
AtSnRK2.9 AT2G23030 (340)	-----					
HsSnRK NP_001094064 (411)	AKK	DLPELAGPA	STV	PPASLKPTASGRKCLFR	VEEDEEE	DEEDK
MmSnRK NP_001158044.1 (411)	AKK	ELPELAGPA	STV	PPASMKPAASGRKCLFR	VEEDEEE	DEEDK
OsSnRK 1a Os05g0530500 (393)	AHPRE	IITEVLKAL	QEL	NVCWKKIGHY	NMKCRWSPSPSH	ESMMHN
OsSnRK1b Os08g0484600 (398)	AQPRE	IMTEVLKALE	ED	NVCWKKNGQ	NMKCRWS	VGYPQATDMLDV
ZmSnRK NP_001105673.1 (398)	AHPRE	IMVEVLKAL	QEL	NVRWKKNGHY	NVKCRWCPGFP	EVNDTLDA
TaCIPK20 (463)	LSAEV	IQVTPAHC	VVEVSK	SSGDLRAYKEVC	QYGNMNA	WCSFQSDL
TaCIPK17 (399)	VCAEV	FVVLGPSLH	VVELRK	SQGD	TAVYKKLCDR-	ISSDLGIDN--I
TaCIPK21 (389)	LSAEV	FEINESLY	VVELKR	SCGDCSL	YRQLCAT-	LSDDLGICKSQQ
AtSOS2 AAF62923.1 (387)	VVIEI	YEVAPSLF	MVDVR	KAAGET	LEYHKFY	KK-LCSKLENI
TaCIPK24 (387)	VVLEI	FEVAPALF	MVDVR	KVAGDS	LEYHRYKS-	LCSKLESTIWRP
TaCIPK8 (390)	IMLQI	FEVAPSI	FVVELER	SAGDT	SEYKNFV	NN-YCSKLEDDI
TaCIPK23 (401)	LATEV	FEVTPSLY	VVELRK	NSGDT	LEFHKFY	HS-LSNGLKDV
TaCIPK3 (393)	VATEV	FQVAPSLF	VVELKK	AKGDT	LEFQKFY	KT-LSAQTKD
TaCIPK31 (394)	VATEV	FQVAPSLH	VVELKK	AKGDT	LEFQMFY	RS-LSTQTKD
TaCIPK32 (387)	VATEI	LRVGPLSH	MVEVR	KAAGDT	LEFHKFY	KN-LSNLTKD
TaCIPK9 (392)	VATEV	FEVAPTLH	VVELRK	TGDDT	LEFHSFY	KN-FSSELEK
TaCIPK22 (392)	AMVRV	SRLLEEM	LMVEVER	AS--S	SDAPNL	LWERLQQGLKFSND---
TaCIPK29 (395)	AKVTV	FRADTVS	VVEVVK	GH--G	PEAAA	FNDWLEPA
TaCIPK4 (378)	ISV	ISELELPL	LLVEMR	LEM-DD	GEVRF	SWDQLRVE
TaCIPK7 (380)	MSMEM	SEVAPPL	MLVELR	LEAGD	DEEVQAF	GWDELRT
TaCIPK12 (379)	IGAEI	FELTPSL	LVLEVKK	KAGDKAE	YDDF	CNKELKPG
TaCIPK19 (462)	ICAEI	FELTPSL	VVEVKK	KAGDKE	EYDD	CNKELKPG
TaCIPK25 (430)	ISTK	IFQLTPEL	VVMVQ	VCKKAGD	TAEYRQ	FCGSELEK
TaCIPK13 (463)	MAATE	IYELTPEL	VVVEVRR	KSGGAA	EYEE	FRARLKP
TaCIPK10 (389)	IDTEI	FRJAPNF	HLEIR	KTNGD	TEYQK	VK-HDMRPA
TaCIPK2 (394)	IDAEI	FEVTPDF	HLELKK	TNGDT	IYEQK	VLNQEMRPA
TaCIPK11 (391)	LDAEI	FDVAPS	FLLVELK	KTNGD	TFEYQ	KLVKEEVRPA
TaCIPK26 (390)	FDAEV	FEFAPSL	HLELKK	TNGDT	IYEQK	LMKDEIRPA
TaCIPK28 (377)	FEAEI	FELASS	FLLVELK	KTNGD	IYEQK	LLKEDIRPS
TaCIPK14 (400)	LDMEI	FEIITPS	HHLEEM	QTSGD	PLEYREL	LED-IRPAL
TaCIPK15 (390)	FDSI	FEIITPS	YHLEEM	QTSGD	SLEYQ	KLLEESIRPA
TaCIPK5 (392)	IDAEI	FEVTPSF	YVVEV	VKSA	GDTLEYER	FCKMGLRPS
TaCIPK27 (386)	VAAE	FFSVAPS	VLVVDV	VKDG	GDTMEY	RSFCSDEL
TaCIPK6 (386)	VAAE	FFSVAPS	VLVVDV	VKDG	GDTMEY	RSFCSDEL
TaCIPK30 (412)	LEAEI	FEVAPSV	HVVEMR	KTGDS	LEFHD	FYKQELKPS
TaCIPK16 (332)	VTAEV	FEVAAD	VTVE	FAHDG	GDALD	ANKFCAED
Consensus (553)	V	EIFEV	PSL	LVELKK	GDT	EY F L DIVW

	(599)	599	610	620	630	644
AtSnRK2.4 At1g10940 (364)	-----					
AtSnRK2.9 AT2G23030 (340)	-----					
HsSnRK NP_001094064 (457)	KPMSL	STQVVLRR	KPSVTN	NRLTSRKS	APVLNQ	IFEEGESD
MmSnRK NP_001158044.1 (457)	KPVS	LSTQVVLRR	KPSVTN	NRLTSRKS	APVLNQ	IFEEGESD
OsSnRK 1a Os05g0530500 (439)	NHGF	GAEASAI	IETD	SE----	KSTHT	VKFEIQLYKTR
OsSnRK1b Os08g0484600 (444)	NHSF	VDDSI	IMDNG	DVNG----	RLPA	VIKFEIQLYKSR
ZmSnRK NP_001105673.1 (444)	SNSF	FLGDST	IMDND	DANG----	RLPT	VIKFEFQLYKTR
TaCIPK20 (509)	ISRK	HDAQFT	DEQC	NCIVNT	CSSAQ	ACPD
TaCIPK17 (442)	FGM	GSLFDEN	LPN	FDSRA	ATPL	VAL
TaCIPK21 (434)	LLKN	DSIRQ	ELYR	FNS	SS	
AtSOS2 AAF62923.1 (432)	TEGI	PKSEI	LR	TIT	F	
TaCIPK24 (432)	IEV	SAKS	ALLR	TTT	C	
TaCIPK8 (435)	SAE	KGSR	TSR	LSKR		
TaCIPK23 (446)	EGS	IAEG	DETR	HR	RS	
TaCIPK3 (438)	ESE	AEER	G	ST		
TaCIPK31 (439)	GGE	VED	N	ST	V	
TaCIPK32 (432)	DDL	QIQ	PS			
TaCIPK9 (437)	ESN	TI	AK			
TaCIPK22 (433)	-----					
TaCIPK29 (437)	-----					
TaCIPK4 (423)	WDS	REDL	Q	Q	V	
TaCIPK7 (425)	WHG	CEEL				
TaCIPK12 (425)	QGS	ARN	V	PS	D	T
TaCIPK19 (508)	VP	-VP	N	T	P	T
TaCIPK25 (476)	PED	GL	P	P	T	L
TaCIPK13 (509)	PAP	R	V	G	S	K
TaCIPK10 (434)	QGE	Q	P			
TaCIPK2 (440)	QGE	Q	Q	P	P	P
TaCIPK11 (437)	QGD	Q	Q	R	S	E
TaCIPK26 (436)	QGE	S	H	L	P	E
TaCIPK28 (423)	HGD	V	Q	Q	A	A
TaCIPK14 (445)	HGD	D	H	H	Q	L
TaCIPK15 (436)	AWG					
TaCIPK5 (438)	PSE	E	K	L	P	S
TaCIPK27 (432)	AAAA	AAAA	AS	PG	D	P
TaCIPK6 (432)	AAAA	AAAA	AS	PG	D	P
TaCIPK30 (458)	QGD	S	P	P	P	T
TaCIPK16 (378)	QGD	V	P	A	L	P
Consensus (599)	S	Q	P	P	P	P

	(645)	645	650	660	670	680	690
AtSnRK2.4 At1g10940 (364)		-----	-----	-----	-----	-----	-----
AtSnRK2.9 AT2G23030 (340)		-----	-----	-----	-----	-----	-----
HsSnRK NP_001094064 (503)		ENLPPKLSRLKMN	IASPGTVHKRYHR	RKSQGRGSSCSS	SETSDDDS		
MmSnRK NP_001158044.1 (503)		ENLPPKLSRLKMN	IASPGTVHKRYHR	RKSQGRGSSCSS	SETSDDDS		
OsSnRK 1a Os05g0530500 (479)		LQRVSGPQLLFL	DLCFAFLTQLRV	L			
OsSnRk1b Os08g0484600 (485)		MQRVTGPGQLL	FLDFCAAFLTK	LRVL			
ZmSnRK NP_001105673.1 (485)		MQRVTGPGQLL	FLDFCAAFLTK	LRVL			
TaCIPK20 (539)		-----	-----	-----	-----	-----	-----
TaCIPK17 (467)		-----	-----	-----	-----	-----	-----
TaCIPK21 (452)		-----	-----	-----	-----	-----	-----
AtSOS2 AAF62923.1 (447)		-----	-----	-----	-----	-----	-----
TaCIPK24 (447)		-----	-----	-----	-----	-----	-----
TaCIPK8 (450)		-----	-----	-----	-----	-----	-----
TaCIPK23 (462)		-----	-----	-----	-----	-----	-----
TaCIPK3 (448)		-----	-----	-----	-----	-----	-----
TaCIPK31 (450)		-----	-----	-----	-----	-----	-----
TaCIPK32 (440)		-----	-----	-----	-----	-----	-----
TaCIPK9 (444)		-----	-----	-----	-----	-----	-----
TaCIPK22 (433)		-----	-----	-----	-----	-----	-----
TaCIPK29 (437)		-----	-----	-----	-----	-----	-----
TaCIPK4 (433)		-----	-----	-----	-----	-----	-----
TaCIPK7 (432)		-----	-----	-----	-----	-----	-----
TaCIPK12 (437)		-----	-----	-----	-----	-----	-----
TaCIPK19 (526)		-----	-----	-----	-----	-----	-----
TaCIPK25 (488)		-----	-----	-----	-----	-----	-----
TaCIPK13 (523)		-----	-----	-----	-----	-----	-----
TaCIPK10 (439)		-----	-----	-----	-----	-----	-----
TaCIPK2 (457)		-----	-----	-----	-----	-----	-----
TaCIPK11 (483)		LQPQEQQNLQE	QPPLPPQNGFK	HQD			
TaCIPK26 (482)		QQPQE					
TaCIPK28 (468)		APPPQ					
TaCIPK14 (455)		-----	-----	-----	-----	-----	-----
TaCIPK15 (439)		-----	-----	-----	-----	-----	-----
TaCIPK5 (465)		-----	-----	-----	-----	-----	-----
TaCIPK27 (448)		-----	-----	-----	-----	-----	-----
TaCIPK6 (448)		-----	-----	-----	-----	-----	-----
TaCIPK30 (479)		-----	-----	-----	-----	-----	-----
TaCIPK16 (390)		-----	-----	-----	-----	-----	-----
Consensus (645)		-----	-----	-----	-----	-----	-----

	(691)	691	700	710	720	736
AtSnRK2.4 At1g10940 (364)		-----	-----	-----	-----	-----
AtSnRK2.9 AT2G23030 (340)		-----	-----	-----	-----	-----
HsSnRK NP_001094064 (549)		ESRRRLDKD	SGFTYSWHR	RRDSSEGGPP	PGSEGDDGGG	QSKPSNASGGVD
MmSnRK NP_001158044.1 (549)		ESRRRLDKD	SGFAYSWHR	RRDSSEGGPP	PGSEGDDGGG	QSKPS-SGGGVD
OsSnRK 1a Os05g0530500 (504)		-----	-----	-----	-----	-----
OsSnRk1b Os08g0484600 (510)		-----	-----	-----	-----	-----
ZmSnRK NP_001105673.1 (510)		-----	-----	-----	-----	-----
TaCIPK20 (539)		-----	-----	-----	-----	-----
TaCIPK17 (467)		-----	-----	-----	-----	-----
TaCIPK21 (452)		-----	-----	-----	-----	-----
AtSOS2 AAF62923.1 (447)		-----	-----	-----	-----	-----
TaCIPK24 (447)		-----	-----	-----	-----	-----
TaCIPK8 (450)		-----	-----	-----	-----	-----
TaCIPK23 (462)		-----	-----	-----	-----	-----
TaCIPK3 (448)		-----	-----	-----	-----	-----
TaCIPK31 (450)		-----	-----	-----	-----	-----
TaCIPK32 (440)		-----	-----	-----	-----	-----
TaCIPK9 (444)		-----	-----	-----	-----	-----
TaCIPK22 (433)		-----	-----	-----	-----	-----
TaCIPK29 (437)		-----	-----	-----	-----	-----
TaCIPK4 (433)		-----	-----	-----	-----	-----
TaCIPK7 (432)		-----	-----	-----	-----	-----
TaCIPK12 (437)		-----	-----	-----	-----	-----
TaCIPK19 (526)		-----	-----	-----	-----	-----
TaCIPK25 (488)		-----	-----	-----	-----	-----
TaCIPK13 (523)		-----	-----	-----	-----	-----
TaCIPK10 (439)		-----	-----	-----	-----	-----
TaCIPK2 (457)		-----	-----	-----	-----	-----
TaCIPK11 (508)		-----	-----	-----	-----	-----
TaCIPK26 (487)		-----	-----	-----	-----	-----
TaCIPK28 (473)		-----	-----	-----	-----	-----
TaCIPK14 (455)		-----	-----	-----	-----	-----
TaCIPK15 (439)		-----	-----	-----	-----	-----
TaCIPK5 (465)		-----	-----	-----	-----	-----
TaCIPK27 (448)		-----	-----	-----	-----	-----
TaCIPK6 (448)		-----	-----	-----	-----	-----
TaCIPK30 (479)		-----	-----	-----	-----	-----
TaCIPK16 (390)		-----	-----	-----	-----	-----
Consensus (691)		-----	-----	-----	-----	-----

	(737)	737	750	760	770	782
AtSnRK2.4 At1g10940 (364)	-----					
AtSnRK2.9 AT2G23030 (340)	-----					
HsSnRK NP_001094064 (595)	KASPSENNAGGGSPSSGSGGNPTNTSGTTRRCAGPSNS-----MQL					
MmSnRK NP_001158044.1 (594)	KASPGEQGTGGGS-QGGSGGTPSGTAGSSRRRCAGPDSSSPSPASAS					
OsSnRK 1a Os05g0530500 (504)	-----					
OsSnRk1b Os08g0484600 (510)	-----					
ZmSnRK NP_001105673.1 (510)	-----					
TaCIPK20 (539)	-----					
TaCIPK17 (467)	-----					
TaCIPK21 (452)	-----					
AtSOS2 AAF62923.1 (447)	-----					
TaCIPK24 (447)	-----					
TaCIPK8 (450)	-----					
TaCIPK23 (462)	-----					
TaCIPK3 (448)	-----					
TaCIPK31 (450)	-----					
TaCIPK32 (440)	-----					
TaCIPK9 (444)	-----					
TaCIPK22 (433)	-----					
TaCIPK29 (437)	-----					
TaCIPK4 (433)	-----					
TaCIPK7 (432)	-----					
TaCIPK12 (437)	-----					
TaCIPK19 (526)	-----					
TaCIPK25 (488)	-----					
TaCIPK13 (523)	-----					
TaCIPK10 (439)	-----					
TaCIPK2 (457)	-----					
TaCIPK11 (508)	-----					
TaCIPK26 (487)	-----					
TaCIPK28 (473)	-----					
TaCIPK14 (455)	-----					
TaCIPK15 (439)	-----					
TaCIPK5 (465)	-----					
TaCIPK27 (448)	-----					
TaCIPK6 (448)	-----					
TaCIPK30 (479)	-----					
TaCIPK16 (390)	-----					
Consensus (737)	-----					

	(783)	783	790	800	810	828
AtSnRK2.4 At1g10940 (364)	-----					
AtSnRK2.9 AT2G23030 (340)	-----					
HsSnRK NP_001094064 (636)	ASRSAGELVESLKLMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQE					
MmSnRK NP_001158044.1 (639)	AAPRGAELVQSLKLVSLCLGSQLHG- AKYILDPQK-ALFSSVKVQE					
OsSnRK 1a Os05g0530500 (504)	-----					
OsSnRk1b Os08g0484600 (510)	-----					
ZmSnRK NP_001105673.1 (510)	-----					
TaCIPK20 (539)	-----					
TaCIPK17 (467)	-----					
TaCIPK21 (452)	-----					
AtSOS2 AAF62923.1 (447)	-----					
TaCIPK24 (447)	-----					
TaCIPK8 (450)	-----					
TaCIPK23 (462)	-----					
TaCIPK3 (448)	-----					
TaCIPK31 (450)	-----					
TaCIPK32 (440)	-----					
TaCIPK9 (444)	-----					
TaCIPK22 (433)	-----					
TaCIPK29 (437)	-----					
TaCIPK4 (433)	-----					
TaCIPK7 (432)	-----					
TaCIPK12 (437)	-----					
TaCIPK19 (526)	-----					
TaCIPK25 (488)	-----					
TaCIPK13 (523)	-----					
TaCIPK10 (439)	-----					
TaCIPK2 (457)	-----					
TaCIPK11 (508)	-----					
TaCIPK26 (487)	-----					
TaCIPK28 (473)	-----					
TaCIPK14 (455)	-----					
TaCIPK15 (439)	-----					
TaCIPK5 (465)	-----					
TaCIPK27 (448)	-----					
TaCIPK6 (448)	-----					
TaCIPK30 (479)	-----					
TaCIPK16 (390)	-----					
Consensus (783)	-----					

	(829)	829	840	850	860	874
AtSnRK2.4 At1g10940 (364)		-----	-----	-----	-----	-----
AtSnRK2.9 AT2G23030 (340)		-----	-----	-----	-----	-----
HsSnRK NP_001094064 (682)		KSTWKMCISSTGNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLK				
MmSnRK NP_001158044.1 (683)		KSTWKMCISAPG-----PS-----P-SADLDPVVRTKKLR				
OsSnRK 1a Os05g0530500 (504)		-----	-----	-----	-----	-----
OsSnRk1b Os08g0484600 (510)		-----	-----	-----	-----	-----
ZmSnRK NP_001105673.1 (510)		-----	-----	-----	-----	-----
TaCIPK20 (539)		-----	-----	-----	-----	-----
TaCIPK17 (467)		-----	-----	-----	-----	-----
TaCIPK21 (452)		-----	-----	-----	-----	-----
AtSOS2 AAF62923.1 (447)		-----	-----	-----	-----	-----
TaCIPK24 (447)		-----	-----	-----	-----	-----
TaCIPK8 (450)		-----	-----	-----	-----	-----
TaCIPK23 (462)		-----	-----	-----	-----	-----
TaCIPK3 (448)		-----	-----	-----	-----	-----
TaCIPK31 (450)		-----	-----	-----	-----	-----
TaCIPK32 (440)		-----	-----	-----	-----	-----
TaCIPK9 (444)		-----	-----	-----	-----	-----
TaCIPK22 (433)		-----	-----	-----	-----	-----
TaCIPK29 (437)		-----	-----	-----	-----	-----
TaCIPK4 (433)		-----	-----	-----	-----	-----
TaCIPK7 (432)		-----	-----	-----	-----	-----
TaCIPK12 (437)		-----	-----	-----	-----	-----
TaCIPK19 (526)		-----	-----	-----	-----	-----
TaCIPK25 (488)		-----	-----	-----	-----	-----
TaCIPK13 (523)		-----	-----	-----	-----	-----
TaCIPK10 (439)		-----	-----	-----	-----	-----
TaCIPK2 (457)		-----	-----	-----	-----	-----
TaCIPK11 (508)		-----	-----	-----	-----	-----
TaCIPK26 (487)		-----	-----	-----	-----	-----
TaCIPK28 (473)		-----	-----	-----	-----	-----
TaCIPK14 (455)		-----	-----	-----	-----	-----
TaCIPK15 (439)		-----	-----	-----	-----	-----
TaCIPK5 (465)		-----	-----	-----	-----	-----
TaCIPK27 (448)		-----	-----	-----	-----	-----
TaCIPK6 (448)		-----	-----	-----	-----	-----
TaCIPK30 (479)		-----	-----	-----	-----	-----
TaCIPK16 (390)		-----	-----	-----	-----	-----
Consensus (829)		-----	-----	-----	-----	-----

	(875)	875	880	890	900	912
AtSnRK2.4 At1g10940 (364)		-----	-----	-----	-----	-----
AtSnRK2.9 AT2G23030 (340)		-----	-----	-----	-----	-----
HsSnRK NP_001094064 (728)		NNVLQLPLCEKTISVNIQRNPKEGLLCASSPASCCHVI				
MmSnRK NP_001158044.1 (711)		NNALQLPLCEKTISVNIQRSRKEGLLCASSPASCCHVI				
OsSnRK 1a Os05g0530500 (504)		-----	-----	-----	-----	-----
OsSnRk1b Os08g0484600 (510)		-----	-----	-----	-----	-----
ZmSnRK NP_001105673.1 (510)		-----	-----	-----	-----	-----
TaCIPK20 (539)		-----	-----	-----	-----	-----
TaCIPK17 (467)		-----	-----	-----	-----	-----
TaCIPK21 (452)		-----	-----	-----	-----	-----
AtSOS2 AAF62923.1 (447)		-----	-----	-----	-----	-----
TaCIPK24 (447)		-----	-----	-----	-----	-----
TaCIPK8 (450)		-----	-----	-----	-----	-----
TaCIPK23 (462)		-----	-----	-----	-----	-----
TaCIPK3 (448)		-----	-----	-----	-----	-----
TaCIPK31 (450)		-----	-----	-----	-----	-----
TaCIPK32 (440)		-----	-----	-----	-----	-----
TaCIPK9 (444)		-----	-----	-----	-----	-----
TaCIPK22 (433)		-----	-----	-----	-----	-----
TaCIPK29 (437)		-----	-----	-----	-----	-----
TaCIPK4 (433)		-----	-----	-----	-----	-----
TaCIPK7 (432)		-----	-----	-----	-----	-----
TaCIPK12 (437)		-----	-----	-----	-----	-----
TaCIPK19 (526)		-----	-----	-----	-----	-----
TaCIPK25 (488)		-----	-----	-----	-----	-----
TaCIPK13 (523)		-----	-----	-----	-----	-----
TaCIPK10 (439)		-----	-----	-----	-----	-----
TaCIPK2 (457)		-----	-----	-----	-----	-----
TaCIPK11 (508)		-----	-----	-----	-----	-----
TaCIPK26 (487)		-----	-----	-----	-----	-----
TaCIPK28 (473)		-----	-----	-----	-----	-----
TaCIPK14 (455)		-----	-----	-----	-----	-----
TaCIPK15 (439)		-----	-----	-----	-----	-----
TaCIPK5 (465)		-----	-----	-----	-----	-----
TaCIPK27 (448)		-----	-----	-----	-----	-----
TaCIPK6 (448)		-----	-----	-----	-----	-----
TaCIPK30 (479)		-----	-----	-----	-----	-----
TaCIPK16 (390)		-----	-----	-----	-----	-----
Consensus (875)		-----	-----	-----	-----	-----

Additional file 6: Analysis of SnRK proteins of representative species. Multiple sequence alignment was performed using the ClustalX1.83. Identical amino acids are shaded in yellow, conservative amino acids are shaded in wathet blue and similar amino acids are shaded in green. The PKC domain and NAD/FISL motifs are indicated in the figure.