

Figure S1. Molecular weight (kDa) vs. isoelectric point plots of TaPERK genes.

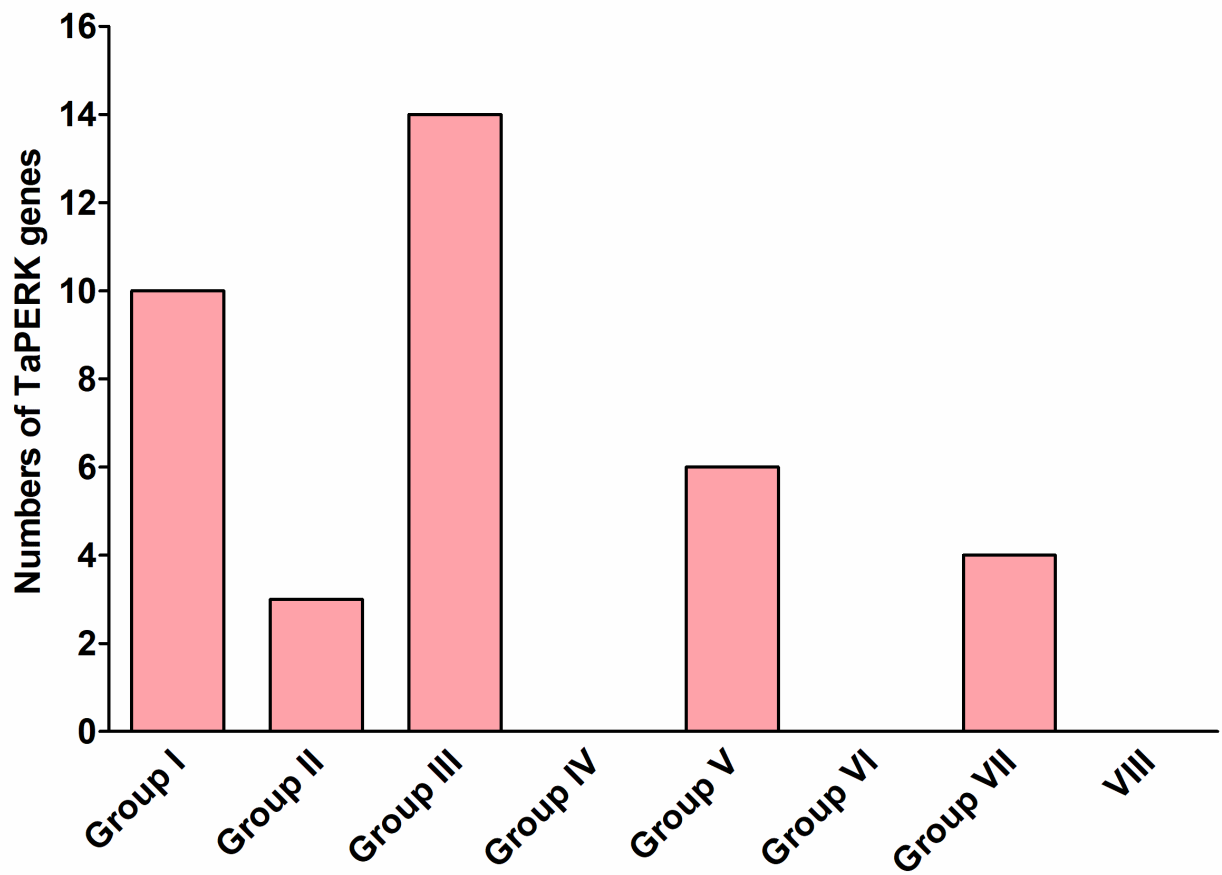


Figure S2. Distribution of TaPERKs in a different group of the phylogenetic tree.

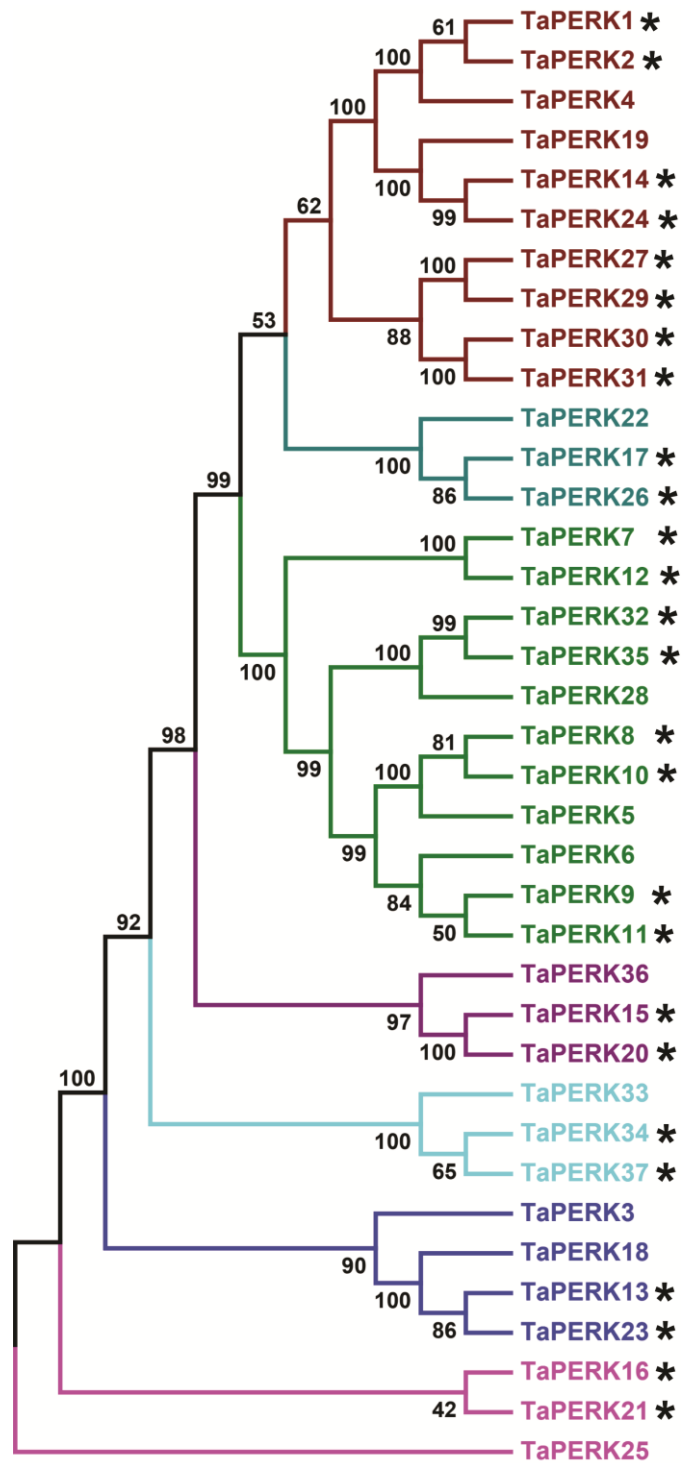


Figure S3. Phylogenetic analysis of TaPERK genes. A phylogenetic tree was constructed using MEGAX with the neighbor-joining (NJ) method and 1000 bootstrap replications. A black asterisk indicates the duplicated genes.

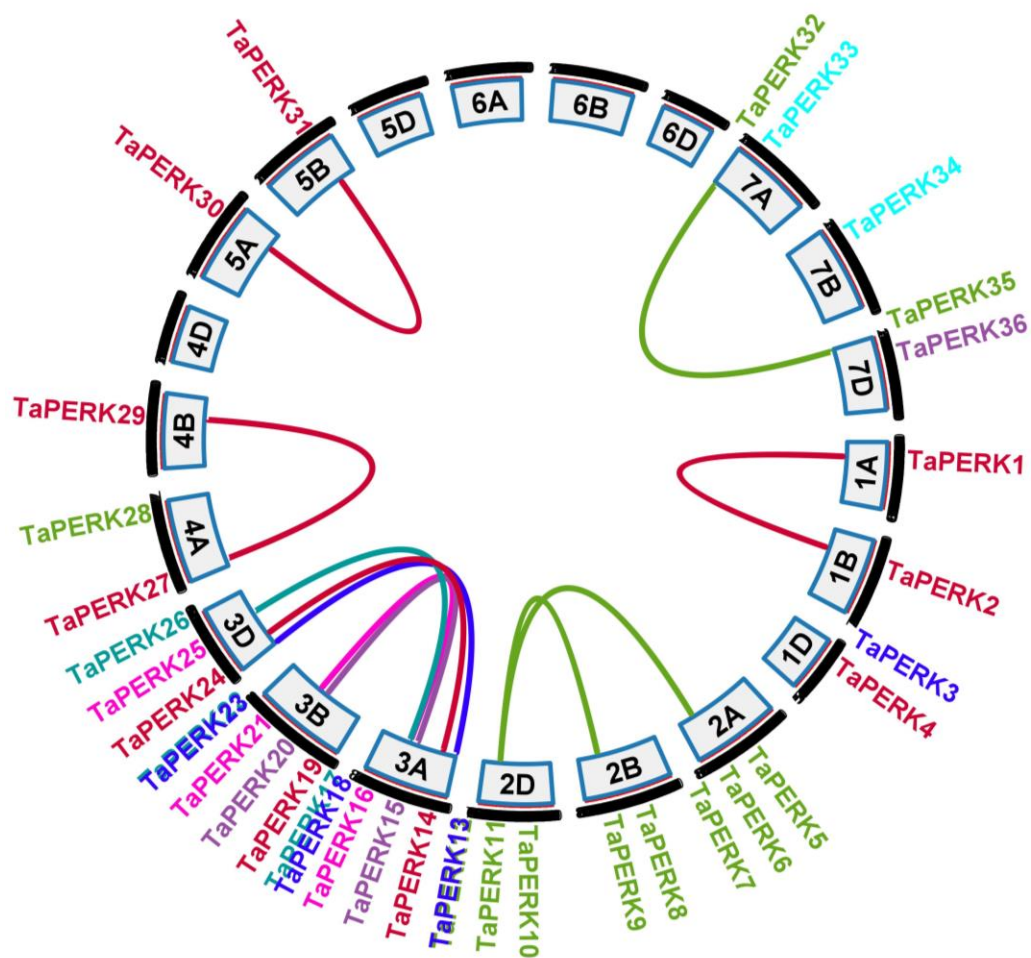


Figure S4. Chromosomal distribution and duplicated PERK gene pairs in wheat. Duplicated PERK gene pairs are connected with lines with distinct colors. The figure was generated using TB tools.

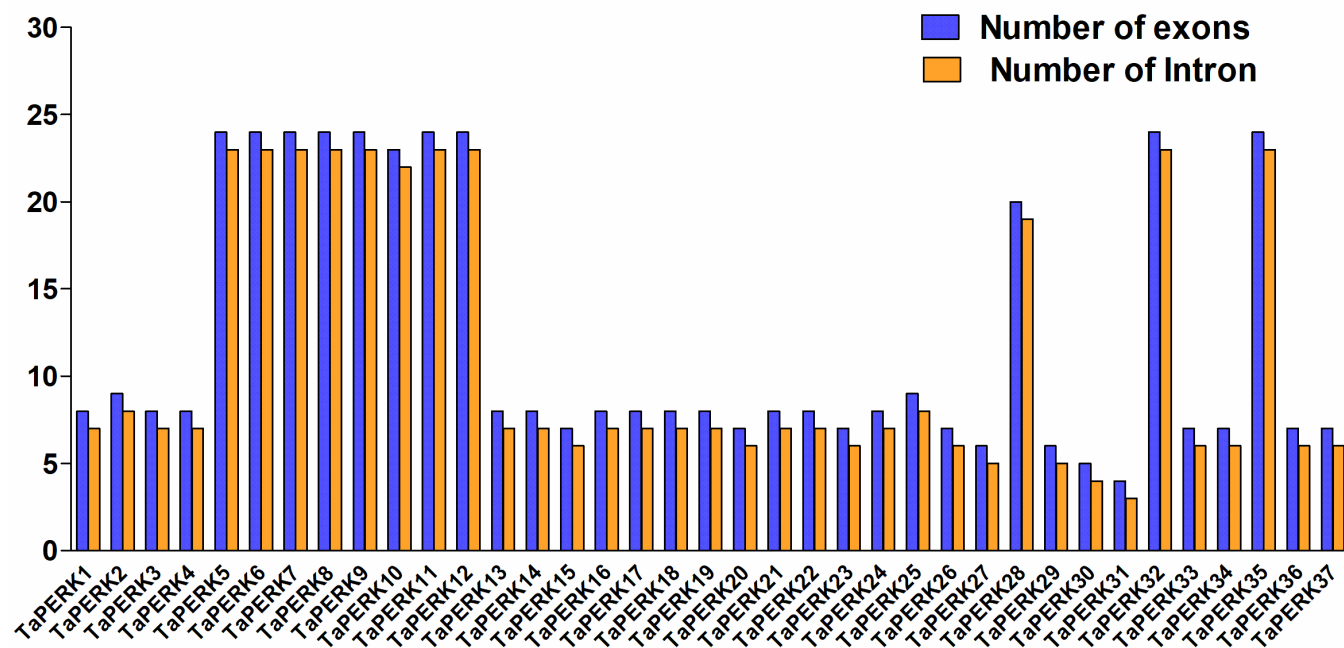


Figure S5. Distribution of exon and introns in TaPERKs gene family.

	*	20	*	40	*	60	*	80	
TaPERK1 :	- - - - -		- - - - -		- - - - -		- - - - -	:	-
TaPERK2 :	- - - - -		- - - - -		- - - - -		- - - - -	:	-
TaPERK3 :	- - - - -		- - - - -		- - - - -		- - - - -	:	-
TaPERK4 :	- - - - -		- - - - -		- - - - -		- - - - -	:	-
TaPERK5 :	--MGRRRQALHGAALS-	L-L-L-A-A-	A-H-A-Q-Q-T-D-P--	G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-L-S-S-W-N-I-S-G-D-P-C-T-G-A-A-T-D-N-T	: 65				
TaPERK6 :	--MKLLHGAALAL-	L-L-L-A-A-	A-H-A-Q-R-T-P-R-T-H--	A-G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-S-S-W-N-I-S-G-N-L-C-T-G-A-A-I-D-D-T	: 64				
TaPERK7 :	MGPPSPRWSSCLRHGSVILLPLLLTALSSSWRAAAQAQPFPSPQTDPTEAAA	VNAIILGKLGLSAPASWNISGNPCSGAATDDT	: 85						
TaPERK8 :	--MGRRRQVQLHGAALS-	L-L-L-A-A-V-	A-D-A-Q-Q-T-D-P--	G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-L-S-S-W-N-I-S-G-D-P-C-T-G-A-A-T-D-N-T	: 65				
TaPERK9 :	--MKLLLGAALTLPLLLLTA-	A-H-A-Q-R-S-P-R-T-H--	L-G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-S-S-W-N-I-S-G-N-L-C-T-G-A-A-T-D-D-T	: 66					
TaPERK10 :	--MGRRSRLHGAALS-	L-L-L-A-A-	A-H-A-Q-Q-T-D-P--	G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-L-P-S-W-N-I-S-G-D-P-C-T-G-A-A-T-D-N-T	: 65				
TaPERK11 :	- - - - -		- - - - -	M-S-S-Q-L-S-N-V-K-W-S-L-Q-Q-S-T- - - - -	: 16				
TaPERK12 :	MGRPSPGWSSCLRHGFVLLPLLLSALCSSWRAAAQAQAPPPP-QTEPTEAAAVNAILGKLGLSAPASWNISGNPCSGAATDDT	: 84							
TaPERK13 :	- - - - -		- - - - -		:	-			
TaPERK14 :	- - - - -		- - - - -		:	-			
TaPERK15 :	- - - - -		- - - - -		:	-			
TaPERK16 :	- - - - -		- - - - -		:	-			
TaPERK17 :	- - - - -		- - - - -		:	-			
TaPERK18 :	- - - - -		- - - - -		:	-			
TaPERK19 :	- - - - -		- - - - -		:	-			
TaPERK20 :	- - - - -		- - - - -		:	-			
TaPERK21 :	- - - - -		- - - - -		:	-			
TaPERK22 :	- - - - -		- - - - -		:	-			
TaPERK23 :	- - - - -		- - - - -		:	-			
TaPERK24 :	- - - - -		- - - - -		:	-			
TaPERK25 :	- - - - -		- - - - -		:	-			
TaPERK26 :	- - - - -		- - - - -		:	-			
TaPERK27 :	- - - - -		- - - - -		:	-			
TaPERK28 :	- - - - -		- - - - -		:	-			
TaPERK29 :	- - - - -		- - - - -		:	-			
TaPERK30 :	- - - - -		- - - - -		:	-			
TaPERK31 :	- - - - -		- - - - -		:	-			
TaPERK32 :	--MREMRLFIMLHGAALL-	- - L-L-A-A-V - - - -	A-H-A-Q-Q-T-R-T-D-T-D--	P-A-D-A-A-A-L-H-A-V-F-A-K-L-G-Q-K-A-G-P-Q-W-N-I-S-G-D-P-C-T-G-A-A-I-D-N-T	: 69				
TaPERK33 :	- - - - -		- - - - -		:	-			
TaPERK34 :	- - - - -		- - - - -		:	-			
TaPERK35 :	--MRLFIMLHAVALLL-	- - L-L-A-A-V - - - -	A-H-A-Q-Q-T-M-R-T-D-T-D--	P-A-D-A-A-A-L-H-A-V-F-A-K-L-G-Q-K-A-G-P-Q-W-N-I-S-G-D-P-C-T-G-A-A-I-D-N-T	: 66				
TaPERK36 :	- - - - -		- - - - -		:	-			
TaPERK37 :	- - - - -		- - - - -		:	-			
AtPERK1 :	- - - - -		- - - - -		:	-			
AtPERK2 :	- - - - -		- - - - -		:	-			
AtPERK3 :	- - - - -		- - - - -		:	-			
AtPERK4 :	- - - - -		- - - - -		:	-			
AtPERK5 :	- - - - -		- - - - -		:	-			
AtPERK6 :	- - - - -		- - - - -		:	-			
AtPERK7 :	- - - - -		- - - - -		:	-			
AtPERK8 :	- - - - -		- - - - -		:	-			
AtPERK9 :	- - - - -		- - - - -		:	-			
AtPERK10 :	- - - - -		- - - - -		:	-			
AtPERK11 :	- - - - -		- - - - -		:	-			
AtPERK12 :	- - - - -		- - - - -		:	-			
AtPERK13 :	- - - - -		- - - - -		:	-			
AtPERK14 :	- - - - -		- - - - -		:	-			
AtPERK15 :	- - - - -		- - - - -		:	-			
OsPERK1 :	- - - - -		- - - - -		:	-			
OsPERK2 :	- - - - -		- - - - -		:	-			
OsPERK3 :	- - - - -		- - - - -		:	-			
OsPERK4 :	- - - - -		- - - - -		:	-			
OsPERK5 :	--MGRRRQALHGAALS-	L-L-L-A-A-	A-H-A-Q-Q-T-D-P--	G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-L-S-S-W-N-I-S-G-D-P-C-T-G-A-A-T-D-N-T	: 65				
OsPERK6 :	--MKLLHGAALAL-	L-L-L-A-A-	A-H-A-Q-R-T-P-R-T-H--	A-G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-S-S-W-N-I-S-G-N-L-C-T-G-A-A-I-D-D-T	: 64				
OsPERK7 :	MGPSPRPWSSCLRHGGSVILLPLLLTALSSSWRAAAQAQPFPSPTDPTFAAAA	VNAILGKLGLSAPASWNISGNPCSGAATDDT	: 85						
OsPERK8 :	--MGRRRQVQLHGAALS-	L-L-L-A-A-V-	A-D-A-Q-Q-T-D-P--	G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-L-S-S-W-N-I-S-G-D-P-C-T-G-A-A-T-D-N-T	: 65				
GmPERK1 :	--MKLLLGAALTLPLLLLTA-	A-H-A-Q-R-S-P-R-T-H--	L-G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-S-S-W-N-I-S-G-N-L-C-T-G-A-A-T-D-D-T	: 66					
GmPERK2 :	--MGRRSRLHGAALS-	L-L-L-A-A-	A-H-A-Q-Q-T-D-P--	G-D-A-A-A-N-A-V-F-A-K-L-G-Q-K-A-L-P-S-W-N-I-S-G-D-P-C-T-G-A-A-T-D-N-T	: 65				
GmPERK3 :	- - - - -		- - - - -	M-S-S-Q-L-S-N-V-K-W-S-L-Q-Q-S-T- - - - -	: 16				
GmPERK4 :	MGRPSPGWSSCLRHGFVLLPLLLSALCSSWRAAAQAQAPPPP-QTEPTEAAAVNAILGKLGLSAPASWNISGNPCSGAATDDT	: 84							
GmPERK5 :	- - - - -		- - - - -		:	-			
GmPER									

	*	100	*	120	*	140	*	160	*	
TaPERK1	:	-----	-----	-----	-----	-----	-----	-----	MS-	2
TaPERK2	:	-----	-----	-----	-----	-----	-----	-----	-----	-
TaPERK3	:	-----	-----	-----	-----	-----	-----	-----	MAAKAPA	7
TaPERK4	:	-----	-----	-----	-----	-----	-----	-----	MS-	2
TaPERK5	:	NIDNPPFNPAIKCECSGG-NASVCRVTRLKIYALDAVGPIPEELRNLTALTNLDSLQNYLTGPLPSFIGELTRMQYMSFGINAL	:	149						
TaPERK6	:	DIDNDPFNFNPAIKCLCSTG-NASLCRITRLKIYALDAVGPIPEELWNLTSLTNLNLAQNYLTGPIPSFIGKLAQMQLYSMGINAL	:	148						
TaPERK7	:	PLDDNPFNFNPAIKCDCTDQ-NGTLCHVTRLKINSLDAAGPIPEELRNLTALIKLDFRKNLSLTGPLPAFIGELTALKYITVGTNAL	:	169						
TaPERK8	:	NIDNPPFNPAIKCECTGG-NASVCRVTRLKIYALDAVGPIPEELRNLTALTNLDSLQNYLTGPLPSFIGELTRMQYMSFGINAL	:	149						
TaPERK9	:	DIDNDPFNFNPAIKCLCSTG-NASVCRITRLKIYALDAVGPIPEELWNLTSLTNLNLAQNYLTGPIPSFIGELDKMQYLSLGINAL	:	150						
TaPERK10	:	NIDNPPFNPAIKCECTGG-NASVCRVTRLKIYALDAVGSIPEELRNLTALTNLDSLQNYLTGPLPSFIGELTRMQYMSFGINAL	:	149						
TaPERK11	:	-----VFQAPA-ELAVCR-----	:	59					NLAQNYLTGPIPSFIGELTRMQYLSLGINAL	
TaPERK12	:	PLDDNPFNFNPAIKCDCTDQ-NGTLCHVTRLKINSLDAAGPIPEELRNLTALIKLDFRKNLSLTGLLPAFIGELTSLKYITVGTNAL	:	168						
TaPERK13	:	-----	:	4					MASS	
TaPERK14	:	-----	:	2					MS-	
TaPERK15	:	-----	:	17					MPRIIVESVEHLATAPV	
TaPERK16	:	-----	:	19					MGGYADPFMPQPASSSSY	
TaPERK17	:	-----	:	4					MSGP	
TaPERK18	:	-----	:	4					MASS	
TaPERK19	:	-----	:	2					MS-	
TaPERK20	:	-----	:	17					MPRVFVESVEHLANAPA	
TaPERK21	:	-----	:	19					MGGYADPFMPQPASSSSY	
TaPERK22	:	-----	:	19					MSSSPPDAGGSFPVTPSP	
TaPERK23	:	-----	:	-					-----	
TaPERK24	:	-----	:	3					MSS-	
TaPERK25	:	-----	:	19					MGGYADPFMPQPASSSSY	
TaPERK26	:	-----	:	-					-----	
TaPERK27	:	-----	:	-					-----	
TaPERK28	:	-----	:	11					MKEMTFGINAL	
TaPERK29	:	-----	:	-					-----	
TaPERK30	:	-----	:	-					-----	
TaPERK31	:	-----	:	-					-----	
TaPERK32	:	NIDNNDIFKAAIKCEVCTGGNTSVCRIITRLKIYALDAVGPIPEELRNLTALTDLGQNYLTGPLPSFIGELTAMKSMTFGINAL	:	154						
TaPERK33	:	-----MRTLLQAKGGGRGAGAG-----	:	40					AADAADAVDTVTG-TTPPSSSTD	
TaPERK34	:	-----MRTLLQAKGGGRGPGGG-AAEADEADAVDTVTGTITPPSSSTD	:	44						
TaPERK35	:	NIDNNDIFKAAIKCEVCTGGNTSVCRIITRLKIYALDAVGPIPEELRNLTALTDLGQNYLTGPLPSFIGELTDMKEMTFGINAL	:	151						
TaPERK36	:	-----	:	16					MPRLAPSPGSSSEDS	
TaPERK37	:	-----MRTLLQAKGGGRGGGGGGGAADAADAVDTVTGTITPPSSSTD	:	45						
AtPERK1	:	-----	:	8					MSTAPSPG-	
AtPERK2	:	-----	:	9					MSSAPPPGG	
AtPERK3	:	-----	:	6					MARSNR---	
AtPERK4	:	-----	:	-					-----	
AtPERK5	:	-----	:	-					-----	
AtPERK6	:	-----	:	-					-----	
AtPERK7	:	-----	:	-					-----	
AtPERK8	:	-----	:	8					MSLVPLP---	
AtPERK9	:	-----	:	11					MATTFVQPP---VS	
AtPERK10	:	-----	:	13					MTTPAQAPREEVS	
AtPERK11	:	-----	:	19					MDKVQQQADLFKGTISPFV	
AtPERK12	:	-----	:	19					MSDLGESPPSSFPAPPADT	
AtPERK13	:	-----	:	16					MSDSPTSSFPAPSADS	
AtPERK14	:	-----	:	9					MSLSPSSSP	
AtPERK15	:	-----	:	-					-----	
OsPERK1	:	-----	:	2					MS-	
OsPERK2	:	-----	:	-					-----	
OsPERK3	:	-----	:	-					-----	
OsPERK4	:	-----	:	-					-----	
OsPERK5	:	-----	:	-					-----	
OsPERK6	:	-----	:	19					MSSESQAPSPSPSSSSS	
OsPERK7	:	-----	:	-					-----	
OsPERK8	:	-----	:	-					-----	
GmPERK1	:	-----	:	12					MSAASFPSTST	
GmPERK2	:	-----	:	-					-----	
GmPERK3	:	-----	:	-					-----	
GmPERK4	:	-----	:	12					MSAVSPSTST	
GmPERK5	:	-----	:	-					-----	
GmPERK6	:	-----	:	10					MFAVAYYSPA	
GmPERK7	:	-----	:	10					MLAVAPYSPA	
GmPERK8	:	-----	:	8					MSTAPAPS-	
GmPERK9	:	-----	:	12					MTSTNPSFNASP	
GmPERK10	:	-----	:	22					MSTKHTEEDNDSSYLTIPNKDK	
GmPERK11	:	-----	:	8					MSTAPAPS-	
GmPERK12	:	-----	:	-					-----	
GmPERK13	:	-----	:	9					MSAPSPS---SS	
GmPERK14	:	-----	:	-					-----	
GmPERK15	:	-----	:	-					-----	
GmPERK16	:	-----	:	12					MASANPSFNASP	

	180	*	200	*	220	*	240	*		
TaPERK1	: -----SPTAAPATTPPAPPAN-----						ATAPPATPSAPPPAIPSPSPAPPANPPFVS-		51	
TaPERK2	:								-	
TaPERK3	:	PSARSRALASASAPASSRRFNATPAA-----	DTAAPSTSAT-----				TSPPPSSPPSAPPKLAAS-PPPASPPP-		72	
TaPERK4	:	-----SPTAAPATTPPAPPAN-----					ATAPPATPSAPPPAIPSPSPAPPANPPFVS-		51	
TaPERK5	:	SGPLPKELGNLTDIVLSVSSNNFSGSLPSELGNLAKLEQLYIDSAGFSGPLPSSLSKLTMMKTLWASDNDFGTQIPDYIGSWN-							233	
TaPERK6	:	SGPLPKELGNLTNLVSLGIGSNKFNGSLPSELGNLAKLEQLYIDSAGLSGPLPASLSRLTKMKILWASDNDFGTQIPDYIGSWN-							232	
TaPERK7	:	SGFVPKELWNLTDIVSVALGSNHFNGLPDELGKLTQLQQLYIDSNDFGTGLPEALSQLTNLSTLWASDNSTFTQIPDFLGLSLTN							254	
TaPERK8	:	SGPLPKELGNLTDIVLSVSSNNFSGSLPSELGDLAKLEQLYIDSAGFSGPLPSSLSKLTMMKTLWASDNDFGTQIPDYIGTWN-							233	
TaPERK9	:	SGPLPKELGNLTNLVSLGIGSNKFNGSLPSELGNLAKLEQLYIDSAGLSGPLPASLSRLTKMKILWASDNDFGTQIPDYIGSWN-							234	
TaPERK10	:	SGPLPKELGNLTDIVLSVSSNNFSGSLPSELGNLAKLEQLYIDSAGFSGPLPSTLSKLTMMKTLWASDNDFGTQIPDYIGSWN-							233	
TaPERK11	:	SGPLPKELGNLTNLVSLGIGSNKFNGSLPSELGNLAKLEQLYIDSAGLTGPLPASLSKLTMMKILWASDNDFGTQIPDYIGSWN-							143	
TaPERK12	:	SGFVPKELWNLTDIVSVALGSNHFNGLPDELGKLTQLQQLYIDSNDFGTGLPAALSQTLNLSTLWASDNSTFTQIPDFLGLSLTN							253	
TaPERK13	:	PSPSPGATKASPADSVAPATSSPSPAP-----	VKLFNDTPAD-----				PFAAPPAPSAAVPPQTPEP-PPPPSPSP-		69	
TaPERK14	:	-----SPPAAPGPASPPGNRT-----					APPPASAPPATNSTPSPSPAP-----	PPSSSL-	45	
TaPERK15	:	VGGPPPPPKSSASPTPARSSPPPTTP-----	PPKSPPPS-----				SPPPASSGNNQSANLPPGSPPAKKSAS-		81	
TaPERK16	:	AVPQGGHGQQPQ--APRPPGCPYSSAS-----	APFVSTSY-----				HSLPPAASPPFVSS-PPPASPPPELPS-		80	
TaPERK17	:	SPFVTFVS-----PPAPDAGETPRVTPAPTFFVTVFSPPPDA-----					AGTTPPPDASGTPEVTPPPPDAAATPPFVNPF		76	
TaPERK18	:	PSPSPGATKASPAASVAPATSSPSPAP-----	VKLFNETPAD-----				PFAAPPAPSAAVPPQTPEP-PPPPSPSP-		69	
TaPERK19	:	-----SPPAAPGPASPPGNRT-----					APPPASAPPATNSTPSPSPAPASPPSSSL-		50	
TaPERK20	:	VGGPPAPPQPSASPPQARSPPPPTTP-----	PPKSPPPS-----				SPPPASSGNNQSFNLPPGSPPEKSPAS-		81	
TaPERK21	:	AVPQGGHGQQPQPPAPRPPGCPYSSAS-----	APFVSTSY-----				HSLPPAASPPFVSS-PPPASPPPETLPS-		82	
TaPERK22	:	TPPFTVTPSPPTFFVTFVTPSPPDNFVVTFFVAFVNSPPPDTSMFNPPFVTPSPPPPEATPPPFVTPFVTPFVTPS							104	
TaPERK23	:								-	
TaPERK24	:	-----SPPAAPGPASPPGNRT-----					APPPASAPPATNSTPSPSPAPPASPPSSSV-		51	
TaPERK25	:	AVPQGGHGQQPQPPAPRPPGCPYSSAS-----	APFVSTSY-----				HSLPPAASPPFVSS-PPPASPPPELPS-		82	
TaPERK26	:								-	
TaPERK27	:	-----MDDSPLSRGFLGGLGSGPLDFSS--SAADSDGSGGSSSADSDSSGGS--					SSGSPSPSSSQ-----		59	
TaPERK28	:	SGPLPKELGNLKNLKLGLGNNFSGSLPSELGNLAKLEELYIDSSGLSGPLPSSLSQTLTKMKLWASDNDFGTQIPDYIGTWSS							96	
TaPERK29	:	-----MDDSPLSRGLAPLLGSGPLDFSSAAADSDGSGGSSSGADSSGES--					SSGSPSPSPSGFQ-----		60	
TaPERK30	:							MSSNSSSAAPPPPS-----	14	
TaPERK31	:							MSSNSSSAAPPPPS-----	14	
TaPERK32	:	SGFVPKELGNLKNLKLGLGNNFSGSLPTELGNLAKLEELYIDSSGLSGPLPSSLSQTLTKMKLWASDNDFGTQIPDYIGSWSS							239	
TaPERK33	:	DSPPPPASD-----PPSPSSSSSSPPPPS-----	PSSPSDFPPS-----				PSSPPSPPLAPPSPPAASSPPFVEVP-		102	
TaPERK34	:	DSPPPPASDSSDDPPSPSSSSSSPPPPS-----	PSAPSDPPPS-----				PSSPPSPQLAPPSPPAASSPPFVEALP-		110	
TaPERK35	:	SGFVPKELGNLKNLKLGLGNNFSGSLPSELGNLAKLEELYIDSSGLSGPLPSSLSQTLTKMKVWASDNDFGTQIPDYIGSWSS							236	
TaPERK36	:	DDSDGSKSKSKSKAPPPRRSSSSSSDENDDDSSSPSPSS--	DDSDGSSRSSSSSSSDSDSDSKSSQSSRRS--						93	
TaPERK37	:	DSPPPPASDSSDDPPSPSSSSSSPPPT-----	PSSPSDFPPA-----				PSSPPSPPLAPPSPPAASSPPFVEALP-		111	
AtPERK1	:	-----TTPSPSPSPPTNSTTT-----					TPPPAASSPPPTTTPSPSPSPSTNSTT-		53	
AtPERK2	:	TPSPPPQLPIPPPPQLFVTPPPPTTAL-----					PPALPPPPPTTALPPALPPPPPTTVPFIPSTP		72	
AtPERK3	:	-----CVPNSSIVQIIEEVE-----					KTQLKSRWQQTITMSSASPPFQVFVP-		50	
AtPERK4	:	-----MAS-SPESAPP-----	TNSTSSPSPSNTN-----				STTSSPPA-----	PSPSPPTPPQGS-----	45	
AtPERK5	:	-----MADSFVDSAPAPETSGTNGTSPSNESSTPPSPSSSIAPPPDISAFSPFPAPTQ-----							64	
AtPERK6	:	-----MAEQSPENSPPSP-----	TPSPSSSDNQSSPPSSSPSPAPPDDSSNGSPQPPSSDS-----						61	
AtPERK7	:	-----MAEQSPENSPPAPPSPSPSSNDQQTTSPPPSDNQETTSPPFP-----					SSPDIAFPQQQ-----		60	
AtPERK8	:	-----ILSPSS-----	NSSTTAP-----				PPLQQT-----	TPSAPFVTP--PPS--	PPQSPFVVS-----	55
AtPERK9	:	NSPFTVTS-----	PPPLN-----	NATSP-----	ATPPFVTSPL-----		PPSAPPENRAPPPPP-FVTSPPFVANGA-----		67	
AtPERK10	:	LSPSLASPPMALPPPPQSPFGDNATSPTREPTNGNPETNTNP-----					AQSSPPPETPLSPP-PEPSPSPSLTGP-----		85	
AtPERK11	:	ASQP--TNVGGFTDQKIIGSETTQPPATSP-----	SPSPDTQT-----				SPPATAAQPPFNQPP--NTTPTPTPSS-----		85	
AtPERK12	:	APPPTPSENSALPP--VDSSPP--SPPADSSS-----	TPPLESP-----				PPDSQLPPLPSILPP--LTDSPPPSDS-----		85	
AtPERK13	:	APPPTSSDGSAAAPPPTSAPPSPPADSS-----	PPPALPSL-----				PPAVFSPPPTVSSPPPPPLDSSPPPPDLT-----		84	
AtPERK14	:	APATSPPPAMSLPPADSVPTDSSPPAPPLSPLPPPLSSPPPLSPPPPLSAPTASPPPLEVESPPSPPIESPPPLLESPPPPPLES							94	
AtPERK15	:	-----MSTDTPISLSSPPAPEF-----							17	
OsPERK1	:	-----SPSSPP-----	PANQT-----				ATP-----	PPANQTAAP-----		25
OsPERK2	:	-----MWAREFWSKPAERARP-----					AAFVPPPPPTPPQYVPEEPSAFAKLYA-----		45	
OsPERK3	:	-----MARP-----					AAFVPPPP-----	QYVPEEPSAFARLY-----		27
OsPERK4	:							MSIVPPP-----		7
OsPERK5	:									-
OsPERK6	:	SSSGNGS-----	NKAPPPESDNSSS-----				NGSSSSSPTPSSQSSSDSGGSSSPSQGSSSPSPPPSGSSSESHS-----		89	
OsPERK7	:									-
OsPERK8	:						MAASPESSPSAN-----	STTPSAPSPSSSL-----		26
GmPERK1	:	AAPPLQTTPSSNNTSPSPSTA--TTPPLQQTTPSTSPQQPASP-----					PPSTPSFANPPSSP-----	PSSPPFMSGT-----		80
GmPERK2	:	-----MSS-PHNSSPD-----	NETPDNSTPDDADNSSSPSSQSPSSPPPS-----				SPPSPSPSSPP-----			54
GmPERK3	:	-----MSS-PHNSAPH-----	NSSPDNSTPDD-----				ATFNN-----	SIPDNSTPDNSIP-----		39
GmPERK4	:	AAPPQTSPSANTTSPSPSTV--TTPPPQQTPTSSTSPQQPASP-----					PPTTPSFANPPSPSPSPSPSPSPMSGT-----			83
GmPERK5	:	-----MASNSDKDSP-----	TPSPSSDS--SSQSPSSPPSSQDSSPPPS-----				SQDNSSPPSSPP-----			52
GmPERK6	:	ASPLPP--FDITPPSPSMYPTTPAPFVT-----	PPP-----				SAVTPLPLTEPLLP--SPSFVSLPPFP-----			67
GmPERK7	:	APPPLSLFDITPPSPSMYPTTPAPFVT-----	PPPETLLVQDSPPSSVTPLPLTEPLLP--SPSPESLPLPLPSSTVT							84
GmPERK8	:	-----SPPPTNGTAPPSTPSA-----					PPPATPSAPPSTPSSPPPATPSSPPPATPSS--			57
GmPERK9	:	VAVPPALGGILSPSSSSSPTNSSKSPS-----	PFNSPQFN-----				QTQTFNSPAPSSSPAPP--SPSPSQAVVT-----			78
GmPERK10	:	RKQKSSHDNDKESAPSKPPDLDQESAPSN-----	SPPSPPPP-----				PPQLKLPLSPRLKPSISLSLSPSSQLDLSGSPSW			97
GmPERK11	:	-----SPPANNGTAPPSTP-----					ATPSAPPATPSAPPSTPSSPPPATPSS--			52
GmPERK12	:	-----MSS-PHNSSPDSSPDNATPDNSTPDDSDSSSPSS--	QSPSSPPSPS-----				SPPSSPPSSPP-----			58
GmPERK13	:	PAPP-----	PELSSA-----				PPSSTSLPLP-----	SPFSLS-----		38
GmPERK14	:	-----MSS-PHNSAPH-----	NSTPDNSPD-----				ATPDN-----	SIPDNSTPDATP-----		39
GmPERK15	:						MSPP-----	PSKYL-----		10
GmPERK16	:	VAVPPALGAILSPSSSSSPTNSTTPPS-----					PPSSSQFNQTQTQTQTFNSPAPSSPSDPSA--PPSPPPQAVPLT-----			82

	260	*	280	*	300	*	320	*	340	
TaPERK1	:	----	----	----	PPPAAPASPP	----	----	----	APSSPTATP	: 71
TaPERK2	:	----	----	----	----	----	----	----	----	: -
TaPERK3	:	----	TP-PAALPTPKP	----	APSTSTPPTTTSPAPPPKRS	----	----	----	AAAPPTAPAPRP	: 119
TaPERK4	:	----	----	----	PPPAAPASPP	----	----	----	APSSPTATP	: 71
TaPERK5	:	LTDLRFQNSFGGPIPATLSNLVQLTNLRIGDILNGSSSSSLAFISNMTSLNSIVLRNCRISDTLLSVNFSKFTSLNLLDLSFN	NI	:	318					
TaPERK6	:	LTELRFQNSFGGPIPATLSNLQALTSRIGDILNGSSSSSLAFVNMTSLSTIVLRNCRISDKLSSIDFSKLTSLNLLDLSFN	NI	:	317					
TaPERK7	:	MTQLRLQNSFGGPIPRSLNLIKLSRIGDIVNGSSS-MEFVGNMTSLGELVLRNSKISDTLASVDFSKFVNLTLLDLSFN	NI	:	338					
TaPERK8	:	LTDLRFQNSFGGPIPATLSNLQALTSRIGDILNGSSSSSLAFISNMTSLNTIVLRNCRISDTLLSVNFSKFTSLNLLDLSFN	NI	:	318					
TaPERK9	:	LTELRFQNSFGGPIPATLSNLQALTSRIGDILNGSSSSSLAFVNMTSLSTIVLRNCRISDKLSSIDFSKLTSLDLDLSFN	NI	:	319					
TaPERK10	:	LTDLRFQNSFGGPIPATLSNLVQLTSRIGDILNGSSSSSLAFISNMTSLNTIVLRNCRISDTLLSVNFSKFTSLNLLDLSFN	NI	:	318					
TaPERK11	:	LTELRFQNSFGGPIPATLSNLQALTSRIGDILNGSSSSSLAFVNMTSLSTIVLRNCRISDKLSSIDFSKLTSLNLLDLSFN	NI	:	228					
TaPERK12	:	MTQLRLQNSFGGPIPRSLNLIKLSRIGDIVNGSSS-MAFVGNMTSLGELVLRNSKISDTLASVDFSKFVNLTLLDLSFN	NI	:	337					
TaPERK13	:	----	PPDFVASPPFVP	----	VASPPPTP-PATMPPAQVPPPPA	----	----	PAADPPKQSP	LRP	: 116
TaPERK14	:	----	----	----	PPSTPAATPP	----	----	----	SPGATPATP	: 65
TaPERK15	:	----	SPPPASPPST	----	PPASRSPPPSSPPSPSQ	----	----	----	QSSPPPAQSTPP	: 124
TaPERK16	:	----	PPPALPSSPPPPALS	----	PPPPDAPPPSLPPSPSPS	----	----	----	PPPAEVQAPPPP	: 126
TaPERK17	:	PPD	----	----	GASTPPP	----	----	VNPFVNPPPPPRTP	----	: 101
TaPERK18	:	----	PPDPTASPPFVP	----	VASPPPPAALPPSPPTAVPPPPA	----	----	PAADPPKQSP	LRP	: 117
TaPERK19	:	----	----	----	PPSTPAATPP	----	----	SSGTTTATP	----	: 70
TaPERK20	:	----	SPPPASPPST	----	PPASRSPPPSSPPSPSQ	----	----	QSSPPPAQSTPP	----	: 124
TaPERK21	:	----	PPPALPSSPPPPALS	----	PPPPDAPPPSLPPSPSPS	----	----	PPPAEVQAPPPP	----	: 128
TaPERK22	:	PPPPFVAIPSP	----	----	VTAPPPPPVAIPSPLPQVAAVPPTAKPPTIVNPPAFEPSPVQPFVNSPPPPSPPPPP	----	----	----	----	: 179
TaPERK23	:	----	----	----	----	----	----	----	----	: -
TaPERK24	:	----	----	----	PPSTPAATPP	----	----	SSGTTTATP	----	: 71
TaPERK25	:	----	PPPALPSSPPPPALS	----	PPPPDAPPPSLPPSPSPS	----	----	PPPAEVQAPPPP	----	: 128
TaPERK26	:	----	----	----	----	----	----	----	----	: -
TaPERK27	:	----	----	----	----	----	----	SST-QSTPPPG	----	: 69
TaPERK28	:	LTELRFQNSFGGPIPATLSNLGQLASLRIGDILNGSSSSSLAFISNLTSLNTIVLRNCRISDKLVSIDFSKFASLNLLDLSFN	NI	:	181					
TaPERK29	:	----	----	----	----	----	----	SST-QSTPPPG	----	: 70
TaPERK30	:	----	----	----	----	----	----	KSSPPPSAAPP	----	: 26
TaPERK31	:	----	----	----	----	----	----	KSSPPPSAAPP	----	: 26
TaPERK32	:	LTELRFQNSFGGPIPATLSNLGQLASLRIGDILNGSSSSSLAFINLTSLNTIVLRNCRISDKLVSIDFSKFTSLNLLDLSFN	NI	:	324					
TaPERK33	:	----	PPPFVASPPPPDAPPPPPSPVSAAPPPAD-AAPPPDNAPLPD	----	----	----	----	NAAAPPSPTQAA	----	: 160
TaPERK34	:	----	PPPFVASPPPPDAPPPPPSPVSAAPPPADTAAPPPDNAPPPD	----	----	----	----	NAAAPTSPTQAP	----	: 169
TaPERK35	:	LTELRLQNSFGGPIPATLSNLGQLASLRIGDILNGSSSSSLAFVNLTSLNTIVLRNCRISDKLVSIDFSKFTSLNLLDLSFN	NI	:	321					
TaPERK36	:	----	PPPSKSKSSSPSSS	----	PSRPPSSRNKGKSDSSPPPTDESSG	----	----	DGEDTSSPPPKRSSPPEQ	----	: 153
TaPERK37	:	----	PPPFVASPPPPDAPPPPPSPVSAAPPPAD-AAPPPDNTPPPD	----	----	----	----	NAAAPTSPTQAP	----	: 169
AtPERK1	:	----	----	----	PPSSPLPP	----	----	SLPPSPPGS	----	: 72
AtPERK2	:	SPPPPLTPSPLPSPPTTPSPPLTPSPPTTPSPPLTPSPFPAPITPSPLTPSPPLTPSPPPSPSIPSPPLTPSPPPSSPLRP	:	:	157					
AtPERK3	:	----	----	----	ELFSEPP	----	----	PPKAFVNV	----	: 67
AtPERK4	:	----	----	----	----	----	----	SSSPPDSTSP	----	: 57
AtPERK5	:	----	----	----	----	----	----	ETSPPTSPSSSP	----	: 76
AtPERK6	:	----	----	----	----	----	----	QSPSPQGNNN	----	: 73
AtPERK7	:	----	----	----	----	----	----	ESPPPLPENSS	----	: 72
AtPERK8	:	----	PPPFVVSPPPS	----	SSPPSPFVITSPPTVASS	----	----	PPPFVVIASPP	----	: 99
AtPERK9	:	----	PPPLPK-PESSS-PPQFVIPSPP	----	PSTSPPPQFVIPSPP	----	SASPP-PALVPPLPS	----	SPPPASVPPPP	: 134
AtPERK10	:	----	PPPTTIVSPPPEPSP	----	PPPLPTEAPPANVSSPPPESSPPPPPP	----	TEAPPTTPTSPSPPT	----	NPPPPESPPSLP	: 158
AtPERK11	:	----	PPPSITPPSP	----	PQPQPPQSTPTGDSFVVIP	----	----	FPKQLPPPSLFP	----	: 131
AtPERK12	:	----	PPVDSPTSP	----	PPPTSNESSPPEDSETPP	----	----	APFNENNNPP	----	: 126
AtPERK13	:	----	PPSSPPPPDA	----	PPPIPIVFP-PPIDS	----	----	PPPS-TNSPP	----	: 120
AtPERK14	:	PSPPSPH	----	----	VSAPSGSPPLPFLPAKPSPPPS	----	----	SPPSETVPPGNTISPPPSLPSESTP	----	: 149
AtPERK15	:	----	----	----	----	----	----	PSTTDPDA	----	: 25
OsPERK1	:	----	----	----	PPASNSSSP	----	----	APG-SLSP	----	: 44
OsPERK2	:	----	----	----	----	----	----	VAGDVVGRA	----	: 54
OsPERK3	:	----	----	----	----	----	----	DVVDR	----	: 33
OsPERK4	:	----	----	----	----	----	----	KSSPPLMAAS-P	----	: 18
OsPERK5	:	----	----	----	----	----	----	----	----	: -
OsPERK6	:	----	PPAPQSSSSSSS	----	SSSGGSKSSPEAPSPSESSGNGG	----	----	GGGGGRSSPPFNWSPPPQ	----	: 149
OsPERK7	:	----	----	----	----	----	----	----	----	: -
OsPERK8	:	----	----	----	----	----	----	SKS-PSPPSP	----	: 35
GmPERK1	:	----	PPPLVPPSPPPSP	----	PSTPAAQPAVPSSPPPPSPSPSPV	----	SSPPSNPRNNTSP	----	SPPPQPAAPPQ	: 150
GmPERK2	:	----	----	----	----	----	----	PSSPPSSS-S	----	: 64
GmPERK3	:	----	----	----	----	----	----	DNSTPDNSTSNK	----	: 51
GmPERK4	:	----	PPPLVPPSPPPSPSPSSPPSPSPAAPFVPPSSPPPP	----	SPSAFVPFNPNNTSPPPSQPPQSPAPPPQPAAPPQ	----	----	PPPPPPS-SSPP	: 63	
GmPERK5	:	----	----	----	----	----	----	----	----	: 63
GmPERK6	:	LSPSTP	----	----	TAASQPPPLPFATA	----	----	PATTTFFPPFAVALSP	----	: 110
GmPERK7	:	PSPTP	----	----	TAESQPPPPFFATA	----	----	PAPTTFPPFAVAPSP	----	: 127
GmPERK8	:	----	----	----	PPPATSSPPPS	----	----	TPSSPPPATP	----	: 79
GmPERK9	:	----	PPPSISLSP	----	TLPPSP-DSPPPLPPAS	----	----	PPSPPATAPP	----	: 119
GmPERK10	:	SPPPPSRSPSPS	----	----	SLSLSSSPSPS	----	----	SPPPSPSP	----	: 137
GmPERK11	:	----	----	----	PPPATSSPPPA	----	----	TPSSPPPATP	----	: 74
GmPERK12	:	----	----	----	----	----	----	PSSPPSSPPS	----	: 70
GmPERK13	:	----	----	----	PAN-PLP	----	----	APPPQSPASISSP	----	: 57
GmPERK14	:	----	----	----	----	----	----	DNSIPDN	----	: 46
GmPERK15	:	----	PPPSRPP	----	----	----	----	PPSP-PPS	----	: 41
GmPERK16	:	----	PPPSISLSPSPSTP	----	PPTLPPSP-DSPPPLPPASFTP	----	----	FVTTSPPSPFVTTSPPSPPATTSPP	----	: 146

[illegible]

		440		460		480		500				
TaPERK1	:	G----	GGSGVSTSVVVGAVGGFVLLLLATFVCLCCLRRKKRRRQ	-----	-----	-----	-----	PPPPHYGY	-----	PP : 181		
TaPERK2	:	-----	-----	-----	-----	-----	-----	-----	-----	5		
TaPERK3	:	---	TQSAGERGRKASPSGSSNGGASNGVVI	---	---	AVGAVLAFIVLTLLIAAAVLYTKRRRRGRDDYRAGFRSPPYSEL	-----	-----	-----	255		
TaPERK4	:	-----	GGSGVSTSVVVGAVGGFVLLLLATFVCLCCLRRKKRRRQ	-----	-----	-----	-----	PPPPHYGY	-----	PP : 177		
TaPERK5	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	GREMDASNGSSI	IIYSSHQ	FINTL	485	
TaPERK6	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	GREMDASNGSSI	IIYSSHQ	FINTL	485	
TaPERK7	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	GREMDASNGSSI	IIYSSHQ	FINTL	508	
TaPERK8	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	GREMDASNGSSI	IIYSSHQ	FINTL	486	
TaPERK9	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	GREMDASNGSSI	IIYSSHQ	FINTL	487	
TaPERK10	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	GREMDASNGSSI	IIYSSHQ	FINTL	486	
TaPERK11	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	GREMDASNGSSI	IIYSSHQ	FINTL	396	
TaPERK12	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	GREMDASNGSSI	IIYSSHQ	FINTL	507	
TaPERK13	:	---	SPTFVDPTTPTAPT	TPSPSTPGFGPPS	---	VPTSTTTTPTPIAPN	-----	---	IPQVPSWQDS	-----	233	
TaPERK14	:	-----	SSALNTATVAGI	AVGGGLIALLLASLLCFCMFKKKRRHHHPHPP	-----	-----	-----	PPPPHLLHYGHPPPP	-----	166		
TaPERK15	:	---	AGTSPPPPIET	PTPTSPVAAAGQVPAAPGT	PSAASLLPSSIMPAS	-----	---	RPPTGTWQSP	PPGPAVARASPPSLAP	-----	257	
TaPERK16	:	---	VAVYSPPPPRIAS	PPPPPRHFK	---	PHYAPP	-----	---	RSPGRPHSNSTR	-----	222	
TaPERK17	:	LPDATPP	---	PPEDVPSSPP	PPNDAPAAAPPSPLT	LSPPPPQ	QSASAP	-----	---	STSAKSSSSSGTAV	---	228
TaPERK18	:	---	SPT	---	SPTVPATPTAPSP	STPGFGPPS	---	VPSAPT	TTTTPTPIGPN	-----	232	
TaPERK19	:	---	SSALNTATVAGI	AVGGGLIALLLASLLCFCMFKKKRRHHHPHPP	-----	-----	-----	PPPPHLLHYGHPPPP	-----	170		
TaPERK20	:	---	AGTSPPPPIET	PTPTSPVAAAGQVPAAPGT	PSSSSLLPSSGIMPAS	-----	---	GRPPGSWQSP	PPGPAARASPPSLAP	-----	257	
TaPERK21	:	---	VAVYSPPPPRIAS	PPPPPRHFK	---	PHYAPP	-----	---	RSPGRPHSNSTR	-----	224	
TaPERK22	:	PPDATPP	---	PPEDVPYSP	PPAPNDAPAEQAPPSALT	WSPPPPL	STDVP	-----	---	ATLAKSSSSSRTTVGLG	---	311
TaPERK23	:	-----	-----	-----	-----	-----	-----	---	SAHYS	-----	5	
TaPERK24	:	---	SSALNTATVAGI	AVGGGLIALLLASLLCFCMFKKKRRHHHPHPP	-----	-----	-----	PPPPHLLHYGHPPPP	-----	171		
TaPERK25	:	---	VAVYSPPPPRV	ASPPPPRHHTK	---	PHYAPP	-----	---	RSPGRSHLNSTR	-----	223	
TaPERK26	:	-----	-----	-----	-----	-----	-----	-----	-----	-----	-	
TaPERK27	:	---	SSESGGGSKGGGSS	GRGKGGSKQDDSP	PFVEAVVVG	-----	-----	---	---	---	162	
TaPERK28	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	KEMEANNNGSYI	IHSPGQ	FINTLE	347	
TaPERK29	:	---	SSESGGGSKGGGSS	GRGKGGSKQDDSP	PFVEAVVVG	-----	-----	---	---	---	158	
TaPERK30	:	---	RGSGDSSRSSQ	SAHRVS	---	FNNTAEIIFA	-----	---	---	---	100	
TaPERK31	:	---	RGDESSRSSSSQ	ASHRVS	---	FNNTAEIIFA	-----	---	---	---	104	
TaPERK32	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	KEMEANNNGSYI	IHSPGQ	FINTL	490	
TaPERK33	:	---	VTPPTADRSV	TAPAPPSTGGG	MSSGATAGVAVVAVIA	FLCFAGV	FVCLTKRRKRKYSDQ	YYPGFA	APPYTPQHMSGE	APFLRV	306	
TaPERK34	:	---	VTPPTADRSV	TAPAPPSTGGG	MSSGATAGVAVVAVIA	FLCFAGV	FVCLTKRRKRKYSDQ	YYPGFA	APPYTPQHMSGE	APFLRV	315	
TaPERK35	:	QRNTPCFGLSPKSSSF	AVDCGSDRPI	SGSDNSLYQ	PDAAATLGAASYVVT	GEPTW	GASNVG	KEMEANNNGSYI	IHSPGQ	FINTL	487	
TaPERK36	:	VNSHPGAP	---	PGLVSI	APPPTGTVGMSAQLPGAQ	---	GATGAGGMQAAGSSAS	-----	---	TSSTNGAGGSAASASAQ	---	286
TaPERK37	:	---	VTPPTADRSV	TAPAPPSTGGG	MSSGATAGVAVVAVIA	FLCFAGV	FVCLTKRRKRKYSDQ	YYPGFA	APPYTPQHMSGE	APFLRV	314	
AtPERK1	:	---	SDGLSTG	VVVGIAIGGVA	---	ILVLTLLCCLCKKKRRRRHDEAA	-----	---	---	---	181	
AtPERK2	:	---	SKELSKGAM	VGIAIGGGFVLLVALALIFFLCKKKRRR	---	DNEA	-----	---	---	---	260	
AtPERK3	:	---	PSRLSTG	AVVGISIGGG	---	VEVLTLLIFFLCKKKRRR	---	DDKA	-----	---	155	
AtPERK4	:	---	PPGDTGG	SRSDNPPSSGGSSGGGGGRS	NTNTAIIVG	-----	---	---	---	---	156	
AtPERK5	:	---	RTSGDGGSP	SPPSRISPPQNSGDS	SSSSGNHF	---	QANIGLIIG	-----	---	---	193	
AtPERK6	:	---	DRNSPSP	PRALAPPRSSGGGSSN	SGNN	---	EPNTAIVG	-----	---	---	191	
AtPERK7	:	---	KTS	DHSSHSQPRSLAPP	---	TSNSGSSNSND	---	GLNIGAVIG	-----	---	179	
AtPERK8	:	---	TTTTSPPPP	PATASPPSSNP	---	TDPTSLAPPT	-----	---	PLFVVPREKPIAKPTGPAS	NNGN	224	
AtPERK9	:	---	PSPPSP	---	SDRPSQ	---	SPPPPPEDTKPQ	---	PRSPNSPPTTFSSP	---	PRSPPEILVPGSNNPSQNNPTLRPLDA	267
AtPERK10	:	---	TPSPSPSDSKRFV	HPSPSPPEETLPPKPS	PDPLSNSSSPPTLLPS	---	---	---	SVVSPPSPPRKSVSGPDNPS	PNNPTP	316	
AtPERK11	:	---	SPGNFLQ	PLDSPLGGS	NRVPSSSSSPSPSLSGSNHSGGSNRH	-----	---	---	NANSNGDGGTQ	QSSNESN	257	
AtPERK12	:	---	PPANFNAPP	---	SPFTVPKTPSSG	FVVS	---	PSLTSPSKGTPTFNQG	-----	---	NGDGGGGGGG	241
AtPERK13	:	---	PPAPPNAPP	PRNSSHALLPKSTAAG	---	---	---	---	---	---	230	
AtPERK14	:	---	PAAVTLFP	FGPAGQLPDGT	VAPPIGVIEPKTSPAESIS	SGTP	---	QPLVP	-----	---	282	
AtPERK15	:	---	RNAVLTGLITG	VVLGATEFVLLGV	CI	FCVFKYKRRKKLK	-----	---	---	---	93	
OsPERK1	:	---	SSGLTTF	VVVVGIVGGIVLLV	LTILLVCLF	KKKKRRHHHHHPHPP	-----	---	PPPPHLLHYGHPPPP	-----	130	
OsPERK2	:	---	SSGLSTAV	VWII	VAGVVGAVLALCVLTI	WIRRCRRQ	-----	---	---	---	134	
OsPERK3	:	---	PSFLNS	VAVK	---	VAGVVGIVLGLCVLALWIRRWRR	-----	---	---	---	120	
OsPERK4	:	---	SGSED	VARSALASARRGG	---	---	---	---	---	---	97	
OsPERK5	:	---	-----	-----	-----	-----	-----	---	---	---	8	
OsPERK6	:	---	QSPPSAANQ	SVVFI	VPVVASNSPPGM	LEPPQVIDATPSGAISSTN	FPGG	-----	---	---	285	
OsPERK7	:	---	SHASRL	STSTITFAGG	---	LDVTSELVIA	-----	---	---	---	34	
OsPERK8	:	---	-----	-----	-----	-----	-----	---	---	---	107	
GmPERK1	:	---	APSTPPSR	STPPTSSQ	PAPPSNSTPRSSPPSP	ITNLAPS	-----	---	PPSRLLSSPPPPPAQNGTE	---	NS : 286	
GmPERK2	:	---	KSLS	PPSSRN	SGSGSDSGSRDS	NGGGGDDSSKAIVG	-----	---	---	---	159	
GmPERK3	:	---	SGKDSS	SNKSLS	NEKSLGSNN	---	---	---	---	---	123	
GmPERK4	:	---	EPSTPPSR	STSTPPTSSQ	PAPPSNSTPRSSPPSP	ITNLAPP	-----	---	PPSRVLS	SSPLPSPAQNGTK	---	NP : 301
GmPERK5	:	---	---	---	---	---	---	---	---	---	156	
GmPERK6	:	---	---	---	---	---	---	---	---	---	183	
GmPERK7	:	---	---	---	---	---	---	---	---	---	202	
GmPERK8	:	---	SSSSS	ISTGVVVGIAV	GAVALLVLSILCICCRKKRRRDEEYAP	---	---	---	---	---	199	
GmPERK9	:	---	SVSE	SPPKPPSSDV	HPPTLP	---	---	---	---	---	267	
GmPERK10	:	---	---	---	---	---	---	---	---	---	241	
GmPERK11	:	---	SPSSSSSS	ISTGVVVGIAV	GAVALLVLSILCICCRKKRRRDEEYHAP	---	---	---	---	---	192	
GmPERK12	:	---	KSLS	PPSSRN	SGSGSDSGSRDS	NGGGGDDSSKAIVG	-----	---	---	---	166	
GmPERK13	:	---	---	---	---	---	---	---	---	---	115	
GmPERK14	:	---	---	---	---	---	---	---	---	---	112	
GmPERK15	:	---	---	---	---	---	---	---	---	---	149	
GmPERK16	:	---	SVSET	PPKPPSSDV	VPPTLPSTPPSD	PSGSSPPASLPDPPTNKT	VVGGPKVSLPSLPT	---	---	---	298	

	600	*	620	*	640	*	660	*	680	
TaPERK1	:	-----	-----	-----	PPPPPPPMINSSGSGSNYS	SG	-EI	-----	LP	: 255
TaPERK2	:	-----	-----	-----	PPPPPPPMINSSGSGSVSNYS	SG	-EI	-----	LP	: 73
TaPERK3	:	-----	-----	-----	ADPSVHTNYS	-AG	-----	-----	SP	: 286
TaPERK4	:	-----	-----	-----	PPPPPPPMINSSGSGSNYS	SG	-EI	-----	LP	: 250
TaPERK5	:	KNFLEIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRSAVAKKND	SKTG	VIAGVVVGIAVLGLVVL	LAGIFLWRRRQ	KRRK	:	655		
TaPERK6	:	KNFLEIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRNAAAKKNGS	KTG	VIAGVVVGIAVLGLVVA	FAAIFVWR	-QKRRK	:	653		
TaPERK7	:	KNFLEIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRNAAAKKNGS	KTG	VIAGVVVGIAVLGLVVA	FAAIFVWR	-QKRRK	:	676		
TaPERK8	:	KNFLEIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRSAVAKKND	SKTG	VIAGVVVGIAVLGLVVL	LAGIFLWRRRQ	KRRK	:	654		
TaPERK9	:	KNFLEIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRNAAAKKNGS	KTG	VIAGVVVGIAVLGLVVA	FAAIFVWR	-QKRRK	:	655		
TaPERK10	:	KNFLEIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRSAVAKKND	SKTG	VIAGVVVGIAVLGLVVL	LAGIFLWRRRQ	KRRK	:	656		
TaPERK11	:	KNFLEIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRNAAAKKNGS	KTG	VIAGVVVGIAVLGLVVA	FAAIFVWR	-QKRRK	:	564		
TaPERK12	:	KNFLEIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRNAAAKKNGS	KTG	VIAGVVVGIAVLGLVVA	FAAIFVWR	-QKRRK	:	675		
TaPERK13	:	-----	ASPQVLLG	-----	HSEKTKTNY	-AG	-----	-----	SP	: 312
TaPERK14	:	-----	ASPQVLLG	-----	KQPPFPVNVNSSGSGSHFSG	GEN	-----	-----	RP	: 225
TaPERK15	:	-----	-----	-----	TMVVPARAPDSYPPS	NG	-----	-----	PA	: 326
TaPERK16	:	PPPNYIPSSAGSSLAS	-----	-----	DGFYLRSPGYPFMR	STG	-----	-----	SH	: 317
TaPERK17	:	-----	-----	-----	TTPLQQSHALSTPSSTP	PLMHSWAQ	-----	-----	SS	: 299
TaPERK18	:	-----	ASPQVLLG	-----	GHSEKTKANY	-AG	-----	-----	SP	: 312
TaPERK19	:	-----	-----	-----	KPPFPFVNVNSSGSGSHFSG	GEN	-----	-----	RP	: 229
TaPERK20	:	-----	-----	-----	TMVVLAPAPDSYPPS	NG	-----	-----	FV	: 326
TaPERK21	:	PPPNYIPSSAGSSLAS	-----	-----	DGFYLRSPGYPFMR	STG	-----	-----	SH	: 319
TaPERK22	:	-----	-----	-----	TTPLQQSHALSTPSSTP	PLMHSWAQ	-----	-----	SS	: 384
TaPERK23	:	-----	-----	-----	HSEKTKTNY	-AG	-----	-----	SP	: 26
TaPERK24	:	-----	-----	-----	KLPPFPVNVNSSGSGSHFSG	GEN	-----	-----	RP	: 230
TaPERK25	:	PPPNYIPSSAGSSLAS	-----	-----	DGFYLRSPGYPFMR	STG	-----	-----	SH	: 318
TaPERK26	:	-----	-----	-----	-----	MHSWAQ	-----	-----	SS	: 8
TaPERK27	:	-----	QSGGP	-----	VDGHG	-----	-----	-----	MSGSG	-TGS : 253
TaPERK28	:	KNFLDIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRNAAVKKNGS	KTG	VIAGAIIVGVVVLGLLAF	VGIFVWR	-QKRRK	:	515		
TaPERK29	:	-----	QSGGP	-----	SDGHG	-----	-----	-----	MSGSG	-SGS : 250
TaPERK30	:	-----	AGSTYYTGGPQPQ	-----	-----	-----	-----	-----	MNSGVYSSPRDQ	: 194
TaPERK31	:	HGVATTASSTYYTGGPQPQ	-----	-----	WQSGTGAGPSTSTDP	PGGFW	-----	-----	HNSGVHSSPRDQ	: 234
TaPERK32	:	KNFLDIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRNAVVKK	-GSKTG	VIAGAIIVGVVVLGLLAF	VGIFVWR	-QKRRK	:	657		
TaPERK33	:	-----	-----	-----	PPQFASANYSSSTMGS	QC	-----	-----	PA	: 365
TaPERK34	:	-----	-----	-----	PPQFASANYSSSTMGS	QC	-----	-----	PA	: 372
TaPERK35	:	KNFLDIHLFWAGKGTCCIPDQGYGPAISALSATPNFTPTVRNAVVKK	-GSKTG	VIAGAIIVGVVVLGLLAF	VGIFVWR	-QKRRK	:	654		
TaPERK36	:	-----	MHSGQLTGSNHPGAF	-----	YGPPPPGASGGFSYGS	STPG	-----	-----	PTD	: 380
TaPERK37	:	-----	-----	-----	PPQFASANYSSSTMGS	QC	-----	-----	PA	: 371
AtPERK1	:	-----	-----	-----	PRKPPPPPPPAFMSSSGSDYS	DL	-----	-----	FV	: 251
AtPERK2	:	-----	-----	-----	PPRPPHFMSSSGSDYS	SNYSQSV	-----	-----	LP	: 325
AtPERK3	:	-----	-----	-----	-----	-----	-----	-----	-----	: -
AtPERK4	:	-----	SQG	-----	QNQQSTG	-----	-----	-----	SSMYSGPSRP	: 254
AtPERK5	:	-----	YKGTQDQHVNNMAGQ	-----	-----	GGGNWGPQ	-----	-----	QFVSG	-----
AtPERK6	:	-----	QGGYNNQSDHVMNLSQQY	-----	PGSNGNNNMNSPPPP	PPGWSQPSPPPP	PPVSGGMGNSS	-----	PHSDASNLGTGRT	: 283
AtPERK7	:	-----	QGGYNNQSDHVMNLSQQY	-----	PGSNGNNNMNSPPPP	PPGWSQPSPPPP	PPVSGGMGNSS	-----	DFSSNYS-GPHGP	: 307
AtPERK8	:	-----	QGGYNNQSDHVMNLSQQY	-----	PGSNGNNNMNSPPPP	PPGWSQPSPPPP	PPVSGGMGNSS	-----	GEMSSNFSGPGYAP	: 306
AtPERK9	:	-----	SSPGSDVV	-----	-----	LFNSRSSAPPMRSHSG	-----	-----	SD	: 309
AtPERK10	:	-----	SSPRSDSA	-----	-----	FFRMQSSAP-VGAKRS	-----	-----	G	: 349
AtPERK11	:	-----	SSPRSDSA	-----	-----	LLKTQSSAP-LVGNRSS	-----	-----	NR	: 400
AtPERK12	:	-----	YRQKPGNGNSSAQNS	-----	-----	SPDTNSLGNPKHGRG	-----	-----	CD	: 344
AtPERK13	:	-----	YQDPGKGYSSGPN GSM	-----	-----	YNNSSQQQSSMGNSTAGGKY	PHH	-----	QM	: 341
AtPERK14	:	-----	YQNPTKGYS-GPGG	-----	-----	YNS	-----	-----	RS	: 325
AtPERK15	:	-----	-----	-----	-----	NAGTNQAHVITMPPPIHAKY	ISSGG	-----	CD	: 359
OsPERK1	:	-----	-----	-----	-----	KKKKEDIEASINRDSLD	PKDDSN	-----	LQ	: 119
OsPERK2	:	-----	-----	-----	-----	PPPPAPLVHSGSGSNYS	SG	-----	QD	: 196
OsPERK3	:	-----	-----	-----	-----	FIQHGHPTTPQTSG	-TFSDAG	-----	S	: 197
OsPERK4	:	-----	-----	-----	-----	HHHHTAPQTSGGT	TFSDAG	-----	S	: 178
OsPERK5	:	-----	GGGGRDTS	-----	-----	GGPKP	-----	-----	PPPPFW	-----
OsPERK6	:	-----	-----	-----	-----	LDPSFKTNY	-AG	-----	SP	: 39
OsPERK7	:	-----	VPSSQFGGSSR	-----	-----	NHHPPPSA	IMLNSGGASADGGGY	-----	NSG	: 381
OsPERK8	:	-----	YHHTGGARPQ	-----	-----	WAATKTGAPSTP	PNMMHPTN	-----	MTGPHVVVRPP	: 124
GmPERK1	:	-----	QHGSSNYSIPPPP	-----	-----	PPGWHMSSSAGG	-FSGEMG	-----	MGYSSGPGYGP	: 203
GmPERK2	:	-----	ASSPESDSS	-----	-----	FFKTHSSAP-LVQSGSG	-----	-----	SD	: 368
GmPERK3	:	-----	PHG-DHVVVMQNG	-----	-----	MGPGGGG-WGAPPPPP	PFMMSSAE	-----	FSSNYSTGPA	: 261
GmPERK4	:	-----	SGPHGGDHVMRIQQQ	-----	-----	MGMGMG	-----	-----	MGPHSGG-WGAP	-----
GmPERK5	:	-----	ASSPESDSS	-----	-----	FFKTHSSAP-LVQSGSG	-----	-----	MSSNYSIG-M	: 235
GmPERK6	:	-----	YNNNGEHLNIPPP	-----	-----	PGAGWGAAQP	PP-QMISS	-----	DMSNSSFSGSHGP	: 253
GmPERK7	:	-----	-----	-----	-----	NPKLPPRP-LTEGGG	ASCFSNVS	-----	VK	: 254
GmPERK8	:	-----	-----	-----	-----	NPTLPPPLTEGGG	ASCFSNVS	-----	VK	: 285
GmPERK9	:	-----	-----	-----	-----	PPPPPPPIISSGSGSNYS	SG	-----	EF	: 272
GmPERK10	:	-----	TSSHNSGTL	-----	-----	FLRSQSPAN-FLGSGSG	-----	-----	SD	: 346
GmPERK11	:	-----	YVQQP	-----	-----	IPSP	-----	-----	PLANNYNGNNSMHL	: 322
GmPERK12	:	-----	PHG-DHVVVMQNG	-----	-----	MGPGGGGWGAPPP	PFMMSSAD	-----	FSSNYSTGPP	: 259
GmPERK13	:	-----	PESDMP	-----	-----	LHKIRSSAP-LIERASG	-----	-----	G	: 188
GmPERK14	:	-----	SGPHGGDHVMRIQQQ	-----	-----	MGMGMG	-----	-----	MGPHSGG-WGAP	-----
GmPERK15	:	-----	YVQQP	-----	-----	IPSP	-----	-----	PLANNYNGNNSMHL	: 230
GmPERK16	:	-----	TSSHNSGTL	-----	-----	FLRPQSPAN-FLGSGSG	-----	-----	SD	: 378

Protein tyrosine kinase domain

[illegible]

Protein tyrosine kinase domain

	*	780	*	800	*	820	*	840	*	
TaPERK1	ELVSLVGYG	ISGGKRLVYE	VTNTTEFSL	LGK---	GRPTLE	PIRLIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 419
TaPERK2	ELVSLVGYG	ISGGKRLVYE	VTNTTEFSL	LGK---	GRPTLE	PIRLIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 237
TaPERK3	ELVSLVGYG	IANSQRLVYD	VVSNTDTHYSL	---	QGGRFVLE	SANVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 450
TaPERK4	ELVSLVGYG	ISGGKRLVYE	VTNTTEFSL	LGK---	GRPTLE	PIRLIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 414
TaPERK5	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 820	
TaPERK6	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 818	
TaPERK7	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 841	
TaPERK8	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 819	
TaPERK9	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 820	
TaPERK10	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 821	
TaPERK11	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 729	
TaPERK12	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 840	
TaPERK13	ELVSLVGYG	ISGDQRLVYD	VVNTDTHYSL	---	GRGVFVLE	PANVKISAS	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 476
TaPERK14	ELVTLVGYG	ISEDKRLVYE	VEVTNTTEFSL	LGK---	RGPTMD	PSIRIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 388
TaPERK15	ELVTLVGYG	VTENHRLVYE	VVSNTDTEHSL	---	GEGLFVMD	PKMKIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 491
TaPERK16	ELVSLVGYG	VSEGQRILVYD	VVNTDTHYSL	---	VN-EVPLD	RTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 481
TaPERK17	NLVSLVGYG	IHAEQRLVYE	VEKTESQL	LGK---	GSARATD	PRWIKVGS	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 464
TaPERK18	ELVSLVGYG	ISGDQRLVYD	VVNTDTHYSL	---	GRGVFVLE	PANVKISAS	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 476
TaPERK19	ELVTLVGYG	ISEDKRLVYE	VEVTNTTEFSL	LGK---	RGPTMD	PSIRIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 392
TaPERK20	ELVTLVGYG	VTENHRLVYE	VVSNTDTEHSL	---	GEGLFVMD	PKMKIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 491
TaPERK21	ELVSLVGYG	VSEGQRILVYD	VVNTDTHYSL	---	VN-EVPLD	RTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 483
TaPERK22	NLVSLVGYG	IHAEQRLVYE	VEKTESQL	LGK---	GSARATD	PRWIKVGS	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 548
TaPERK23	ELVSLVGYG	ISGDQRLVYD	VVNTDTHYSL	---	GRGVFVLE	PANVKISAS	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 190
TaPERK24	ELVTLVGYG	ISEDKRLVYE	VEVTNTTEFSL	LGK---	RGPTMD	PSIRIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 393
TaPERK25	ELVSLVGYG	VSEGQRILVYD	VVNTDTHYSL	---	VN-EVPLD	RTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 482
TaPERK26	NLVSLVGYG	IHAEQRLVYE	VEKTESQL	LGK---	GSARATD	PRWIKVGS	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 175
TaPERK27	ELVSLVGYG	IAGASQRLVYE	VVNTDTEHSL	---	GKGLFVMD	PKMKIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 418
TaPERK28	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 680	
TaPERK29	ELVSLVGYG	IAGSSQRLVYE	VVNTDTEHSL	---	GKGLFVMD	PKMKIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 415
TaPERK30	ELVSLVGH	IAGASQRLVYE	VVNTDTEHSL	---	GKGLFVMD	PKMKIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 359
TaPERK31	ELVSLVGH	IAGTSRLVYE	VVNTDTEHSL	---	GKGLFVMD	PKMKIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 399
TaPERK32	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 822	
TaPERK33	ELVSLVGYG	ISEDKRLVYD	VVNTDTHHNL	---	GRGVFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 529
TaPERK34	ELVSLVGYG	ISEDKRLVYD	VVNTDTHHNL	---	GRGVFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 536
TaPERK35	NLVKLYGC	LEGNKPLVYE	LENGSDHAF	FG---	KGKSSLD	PTFEICLV	ARGLS	FLHESSI	RVVHRDIKASNILLDEK : 819	
TaPERK36	ELVSLVGYG	IAQQHRLVYE	VEVTGTEHSL	---	GRGVFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 545
TaPERK37	ELVSLVGYG	ISEDKRLVYD	VVNTDTHHNL	---	GRGVFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 535
AtPERK1	ELVSLVGYG	MAGVQRLVYE	VEVTNTTEFSL	LGK---	GRPTLE	PIRLIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 415
AtPERK2	ELVSLVGYG	IADAQRLVYE	VEVTNTTEFSL	LGK---	GRPTLE	PIRLIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 489
AtPERK3	NLVSLVGYG	IAGAQRILVYE	VEVTNTTEFSL	LGK---	GRPTLE	PIRLIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 318
AtPERK4	NLVSLVGYG	IADGQRLVYE	VEVTNTTEFSL	---	GKGLFVMD	PKMKIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 419
AtPERK5	ELVSLVGYG	ISGGQRLVYE	VEVTNTTEFSL	---	GKGLFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 447
AtPERK6	ELVSLVGYG	IAGGQRLVYE	VEVTNTTEFSL	---	GKSGKVLMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 472
AtPERK7	ELVSLVGYG	SNAGGQRLVYE	VEVTNTTEFSL	---	GKSGTVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 472
AtPERK8	ELVTLVGYG	ISEQRLVYD	VVNTDTHYSL	---	APGREVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 474
AtPERK9	ELVSLVGH	ISGDRRLVYD	VVNTDTHYSL	---	GE-KSVLD	ATVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 511
AtPERK10	NLVSLVGYG	ISGDRRLVYD	VVNTDTHYSL	---	AGTPTMD	ATVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 565
AtPERK11	ELVSLVGYG	ISEQRLVYD	VVNTDTHYSL	---	GKGLFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 505
AtPERK12	ELVSLVGYG	ISDQRLVYD	VVNTDTHYSL	---	GKGLFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 506
AtPERK13	ELVSLVGYG	IADSERILVYE	VEVTNTTEHSL	---	GRGVFVMD	ARVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 488
AtPERK14	ELVSLVGYG	INGDKRLVYE	VEVTNTTEHSL	---	RGSVLEMD	EMIRIVGA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 524
AtPERK15	ELVSLVGYG	ITGAQRLVYE	VEVTNTTEHSL	---	ERFVLEMD	SKMIRIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 278
OsPERK1	ELVTLVGYG	ISGGQRLVYE	VEVTNTTEFSL	---	GRPTLE	PIRLIALG	AAKGLAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 358
OsPERK2	NLVSLVGYG	ISGNERILVYE	VEVTNTTEFSL	---	GKGLFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 362
OsPERK3	NLVSLVGYG	ISGNERILVYE	VEVTNTTEFSL	---	GKGLFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 338
OsPERK4	ELVSLVGYG	IAGARRLVYE	VEVTNTTEFSL	---	GKGLFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 329
OsPERK5	ELVSLVGYG	ISNNQRLVYD	VVNTDTHYSL	---	QGGRFVLE	SANVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 203
OsPERK6	ELVSLVGYG	IAAHHRLVYE	VEVTNTTEHSL	---	GRGMFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 545
OsPERK7	ELVPLVGYG	IAGAQRILVYD	VVNTDTEHSL	---	EKGLFVMD	TTIRIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 289
OsPERK8	ELVSLVGYG	IAAN-QRLVYE	VEVTNTTEHSL	---	GKGLFVMD	SAIRIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 371
GmPERK1	ELVSLVGYG	IEDNKRLVYD	VVNTDTHYSL	---	GKGLFVMD	ANVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 533
GmPERK2	ELVSLVGS	ISGGQRLVYE	VEVTNTTEFSL	---	GKGRPTMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 426
GmPERK3	ELVSLVGYG	ICGGQRLVYE	VEVTNTTEHSL	---	GKGMPTMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 400
GmPERK4	ELVSLVGYG	IEDSRRLVYD	VVNTDTHYSL	---	GKGMPTMD	ANVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 548
GmPERK5	ELVSLVGYG	IESKRLVYE	VEVTNTTEFSL	---	GKGRFVMD	NTIRIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 418
GmPERK6	ELVEFVGS	SDTRAERILVYE	VEVTNTTEFSL	---	LG-----	NTIRIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 390
GmPERK7	ELVEFVGYG	ITRAERILVYE	VEVTNTTEFSL	---	LG-----	SMIRIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 450
GmPERK8	ELVSLVGYG	ITGSQRLVYE	VEVTNTTEFSL	---	GRPTMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 434
GmPERK9	ELVSLVGYG	ISEHQRILVYD	VVNTDTHYSL	---	GENRFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 511
GmPERK10	ELVSLVGYG	ICEQRLVYE	VEVTNTTEHSL	---	ASGMFVMD	DKIRIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 484
GmPERK11	ELVSLVGYG	ITGSQRLVYE	VEVTNTTEFSL	---	GRPTMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 427
GmPERK12	ELVSLVGS	ISGGQRLVYE	VEVTNTTEFSL	---	GKGRPTMD	ATVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 424
GmPERK13	ELVSLVGYG	ISDNRLVYD	VVNTDTHYSL	---	GRGVFVMD	TKVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 348
GmPERK14	ELVSLVGYG	ICGGQRLVYE	VEVTNTTEHSL	---	GKGMPTMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 391
GmPERK15	ELVSLVGYG	ICEQRLVYE	VEVTNTTEHSL	---	ESGMFVMD	AKIRIALG	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 392
GmPERK16	ELVSLVGYG	ISEHQRILVYD	VVNTDTHYSL	---	GENRFVMD	PTVVKIAA	AAARGIAYL	HEEDCH	PKI	IHRDIKSSNILLDEK : 543

Protein tyrosine kinase domain

	860	*	880	*	900	*	920	*	
TaPERK1	FEARVADFLGAKFT--S--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		TQTYM : 491
TaPERK2	FEARVADFLGAKFT--S--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		TQTYM : 309
TaPERK3	FDALVADFLGAR--A--LAV--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SRPLG : 522
TaPERK4	FEARVADFLGAKFT--S--NS--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		TQTYM : 486
TaPERK5	INPKISDFGLAKY--D--QK--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPN-YSTED		E : 890
TaPERK6	INPKISDFGLAKY--D--QK--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPN-YSTKD		E : 888
TaPERK7	INPKISDFGLAKY--D--KK--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		VAGESNHHTTLE		E : 912
TaPERK8	INPKISDFGLAKY--D--QK--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPN-YSTED		E : 889
TaPERK9	INPKISDFGLAKY--D--QK--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPN-YSTKD		E : 890
TaPERK10	INPKISDFGLAKY--D--QK--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPN-YSTED		E : 891
TaPERK11	INPKISDFGLAKY--D--QK--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPN-YSTKD		E : 799
TaPERK12	INPKISDFGLAKY--D--KK--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		VAGESNHHTTLE		E : 911
TaPERK13	FEARVADFLGAR--A--MFA--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDA-		SNPLG : 548
TaPERK14	CEARVADFLGAKT--S--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVSS-		KQAHM : 460
TaPERK15	FEARVADFLGAKT--N--SM--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SQPLG : 563
TaPERK16	FEARVADFLGAR--A--ASN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SQPLG : 553
TaPERK17	FEPRVADFLGACQ--EAEH--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVSS-		SSDHQ : 536
TaPERK18	FEARVADFLGAR--A--MFA--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDA-		SNPLG : 548
TaPERK19	CEARVADFLGAKT--S--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVSS-		KQAHM : 464
TaPERK20	FEARVADFLGAKT--N--SM--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SQPLG : 563
TaPERK21	FEARVADFLGAR--A--ASN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SQPLG : 555
TaPERK22	FEPRVADFLGACQ--EAEH--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVSS-		SSDHQ : 620
TaPERK23	FEARVADFLGAR--A--MFA--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDA-		SNPLG : 262
TaPERK24	CEARVADFLGAKT--S--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVSS-		KQAHM : 465
TaPERK25	FEARVADFLGAR--A--ASN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SQPLG : 554
TaPERK26	FEPRVADFLGACQ--EAEH--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVSS-		SSDHQ : 247
TaPERK27	FEARVADFLGAKT--T--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDP-		SNYM : 489
TaPERK28	INPKISDFGLAKY--D--QE--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPNYYTTED		Q : 751
TaPERK29	FEARVADFLGAKT--T--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDP-		SNYM : 486
TaPERK30	FEARVADFLGAKT--Y--GI--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDA-		TAHLVL : 432
TaPERK31	FEARVADFLGAKT--Y--GI--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDA-		TAHLVL : 472
TaPERK32	INPKISDFGLAKY--D--QE--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPNYYTTED		Q : 893
TaPERK33	FEARVADFLGAR--A--EDV--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SRPLG : 601
TaPERK34	FEARVADFLGAR--A--EDV--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SRPLG : 608
TaPERK35	INPKISDFGLAKY--D--QE--		TVSTKVAGTFGYLAPEYAS		MRCHMTBKIDVFAAGVVVLELI		AGFPNYYTTED		Q : 890
TaPERK36	FEARVADFLGAKS--N--TH--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDDQ-		DRPLG : 617
TaPERK37	FEARVADFLGAR--A--EDV--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDS-		SRPLG : 607
AtPERK1	FEARVADFLGAKT--S--TN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDA-		NNVYV : 487
AtPERK2	FEARVADFLGAKT--S--TN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDV-		NNVHA : 561
AtPERK3	FEARVADFLGAKT--L--TN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVDA-		NNVYA : 390
AtPERK4	FDAMVADFLGAKT--S--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDN-		SITM : 490
AtPERK5	FEPRVADFLGAKS--Q--NY--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDL-		TGEM : 518
AtPERK6	FEARVADFLGAKS--Q--NV--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDL-		TGEM : 543
AtPERK7	FEARVADFLGAKS--Q--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDL-		SGDM : 543
AtPERK8	FEALVADFLGAKAQEL--LN--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDT-		SQPLG : 548
AtPERK9	FDARVADFLGAR--A--LCN--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDT-		SQPLG : 583
AtPERK10	FEARVADFLGAKT--L--CN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDA-		SQPLG : 637
AtPERK11	FEARVADFLGAR--N--DTAQ--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDT-		SQPLG : 577
AtPERK12	FEARVADFLGAR--N--DTQ--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDQ-		TQPLG : 578
AtPERK13	FEARVADFLGAKN--D--STQ--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDQ-		YQPLG : 560
AtPERK14	FEARVADFLGAKFF--S--TNSSET		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDQ-		KDSST : 599
AtPERK15	FEARVADFLGARSS--L--TD--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDK-		SQPPA : 350
OsPERK1	FEARVADFLGAKT--S--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVRS-		NQSQM : 430
OsPERK2	FEPRVADFLGAKYQ--PGNH--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVRS-		SESYM : 434
OsPERK3	FEPRVADFLGAKYQ--PGNH--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVRS-		SESYM : 410
OsPERK4	FEARVADFLGAKT--S--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDA		AADHPWPASFME : 409
OsPERK5	FEARVADFLGAR--A--LAV--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDA-		SRPLG : 275
OsPERK6	FEARVADFLGAKT--N--TH--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDQ-		TQPLG : 617
OsPERK7	FEPLVADFGMAKT--S--ENV--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVADR		SSYG : 360
OsPERK8	FEARVADFLGAKT--T--TN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDT-		SNYM : 442
GmPERK1	FEARVADFLGAKT--L--AN--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDA-		SQPLG : 605
GmPERK2	FEARVADFLGAKT--T--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDH-		TNAM : 497
GmPERK3	FEARVADFLGAKT--N--TN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDL-		TNAM : 471
GmPERK4	FEARVADFLGAKT--L--AN--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDA-		SQPLG : 620
GmPERK5	FEARVADFLGAKS--Q--TN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVNNN-		TGEY : 489
GmPERK6	FEPRVADFLGAKF--P--NDSCIS		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDT		AGS-R : 464
GmPERK7	FEPRVADFLGAKF--P--NDSCIS		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDT		AGS-R : 524
GmPERK8	FEARVADFLGAKS--S--VN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDK-		NQTFM : 506
GmPERK9	FEARVADFLGAKT--L--SN--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDA-		SQPIG : 583
GmPERK10	FEARVADFLGAR--A--DASN--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDQ-		TQPLG : 556
GmPERK11	FEARVADFLGARFS--S--VN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDK-		NQTYM : 499
GmPERK12	FEARVADFLGAKT--T--NN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDH-		TNAM : 495
GmPERK13	FEARVADFLGAKT--V--AN--		TVSTRVMGTFGYVAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDI-		SQFVG : 420
GmPERK14	FEARVADFLGAKT--N--TN--		TVSTRVMGTFGYLAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDL-		TNAM : 462
GmPERK15	FEARVADFLGAR--A--DAAN--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDQ-		TQPLG : 464
GmPERK16	FEARVADFLGAKT--L--SN--		TVSTRVMGTFGYMAPEYAS		SGLTBKSDFVSSGVMLELI		GRRVIDQ-		SQPIG : 615

Protein tyrosine kinase domain

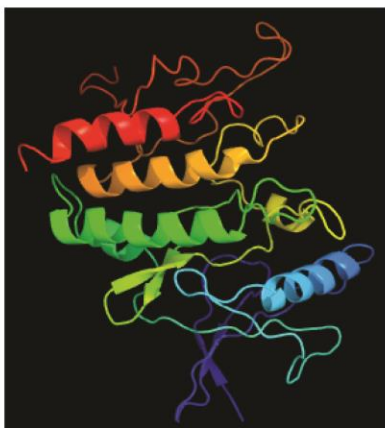
	940	*	960	*	980	*	1000	*	1020										
TaPERK1	DD- SLVDWARFL MRALEDGN----	YDE	VDA	LGKDFNPN	EA	AMT	ACAA	ACVH	SAAR	RR	SM	SV	VRA	EG	---	DVSLDD	: 567		
TaPERK2	DD- SLVDWARFL MRALEDGN----	YDE	VDA	LGKDFNPN	EA	AMT	ACAA	ACVH	SAAR	RR	SM	SV	VRA	EG	---	DVSLDD	: 385		
TaPERK3	DE- SLVDWARFL SRALETGK----	LEG	VDP	LEKNE	NE	VE	FM	ES	AA	AC	IN	HS	SS	RR	SM	SV	VRA	: 597	
TaPERK4	DD- SLVDWARFL MRALEDGN----	YDE	VDA	LGKDFNPN	EA	AMT	ACAA	ACVH	SAAR	RR	SM	SV	VRA	EG	---	DVSLDD	: 562		
TaPERK5	NKVYF FEV WVEIYENNHP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 959
TaPERK6	NKVYF FEV WVEIYEDNHP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 957
TaPERK7	ETTY FEK VWDY Y ENGNNP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 981
TaPERK8	NKVYF FEV WVEIYENNHP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 958
TaPERK9	NKVYF FEV WVEIYEDNRA-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 959
TaPERK10	NKVYF FEV WVEIYENNHP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 960
TaPERK11	NKVYF FEV WVEIYEDNRP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 868
TaPERK12	ETTY FEK VWDY Y ENGNNP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 980
TaPERK13	DE- SLVDWARFL TQALETGN----	AGE	LD	P	LD	KN	NE	VE	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 623
TaPERK14	DD- SLVDWARFL TQALEDGN----	HDA	VDP	HL	GID	FN	DN	EA	AMT	ACAA	ACVH	SAAR	RR	SM	SV	VRA	EG	---	: 536
TaPERK15	EE- SLVDWARFL VDALETDD----	FRE	AD	P	LE	CR	YS	KI	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 639
TaPERK16	DE- SLVDWARFL SQAIEHRD----	FGD	P	DP	LE	KN	KE	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 628
TaPERK17	PE- SLVDWARFL TKALEEEN----	YEE	LD	P	EL	GT	NY	DA	YD	AA	LV	CA	AA	AV	Q	AR	SR	PM	: 612
TaPERK18	DE- SLVDWARFL TQALETGN----	AGE	LD	P	LD	KN	NE	VE	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 623
TaPERK19	DD- SLVDWARFL TQALEDGN----	HDA	VDP	HL	GID	FN	DN	EA	AMT	ACAA	ACVH	SAAR	RR	SM	SV	VRA	EG	---	: 540
TaPERK20	EE- SLVDWARFL VDALETDD----	FRE	AD	P	LE	CR	YS	KI	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 639
TaPERK21	DE- SLVDWARFL SQAIEHRD----	FGD	P	DP	LE	KN	KE	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 630
TaPERK22	PE- SLVDWARFL TKALEEEN----	YEE	LD	P	EL	GT	NY	DA	YD	AA	LV	CA	AA	AV	Q	AR	SR	PM	: 696
TaPERK23	DE- SLVDWARFL TQALETGN----	VGE	LD	P	LD	KN	NE	VE	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 337
TaPERK24	DD- SLVDWARFL TQALEDGN----	HDA	VDP	HL	GID	FN	DN	EA	AMT	ACAA	ACVH	SAAR	RR	SM	SV	VRA	EG	---	: 541
TaPERK25	DE- SLVDWARFL SQAIEHRD----	FGD	P	DP	LE	KN	KE	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 629
TaPERK26	PE- SLVDWARFL TKALEEEN----	YEE	LD	P	EL	GT	NY	DA	YD	AA	LV	CA	AA	AV	Q	AR	SR	PM	: 623
TaPERK27	ED- SLVDWARFL ARALSEGGS----	FDE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 566
TaPERK28	NKVYF FEV WVEIYEDGQP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 820
TaPERK29	ED- SLVDWARFL ARALSEGNN----	FDE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 563
TaPERK30	ED- SLVDWARFL ARALADG----	DYDA	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 508
TaPERK31	ED- SLVDWARFL ARALADG----	DYDA	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 548
TaPERK32	SKVYF FEV WVEIYEDGQP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 962
TaPERK33	DE- SLVDWARFL NRAIDEQE-----	FEE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 678
TaPERK34	DE- SLVDWARFL NRAIDEQE-----	FEE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 685
TaPERK35	SKVYF FEV WVEIYEDGQP-----	LD	VDP	LE	EF	DS	ET	LA	AA	KV	LL	CT	QG	PH	CR	SS	SR	V	: 959
TaPERK36	EE- SLVDWARFL ADAIETGN----	HDE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 696
TaPERK37	DE- SLVDWARFL NRAIDEQE-----	FEE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 684
AtPERK1	DD- SLVDWARFL NRAIEEGD----	FE	GA	S	MG	NE	YD	RE	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 563
AtPERK2	DN- SLVDWARFL NQVSELGN----	FE	V	V	K	L	N	E	Y	D	R	E	EN	FM	EA	AA	AC	IN	: 637
AtPERK3	DD- SLVDWARFL VQALEESN----	FE	GA	S	MG	NE	YD	RE	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 466
AtPERK4	DD- SLVDWARFL ARALE-DGN----	FNE	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 566
AtPERK5	ED- SLVDWARFL CLKAAQ-DGD----	YNQ	AD	P	LE	LN	YD	RE	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 594
AtPERK6	ED- SLVDWARFL CLNAAQ-DGD----	YSE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 619
AtPERK7	ED- SLVDWARFL CMRVAQ-DGE----	YGE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 619
AtPERK8	DE- SLVDWARFL GQAINEE-----	FDE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 624
AtPERK9	DE- SLVDWARFL SHAITEE-----	FDS	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 658
AtPERK10	DE- SLVDWARFL SNATEET-----	FTA	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 712
AtPERK11	EE- SLVDWARFL IEAIEKGD-----	ISE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 653
AtPERK12	EE- SLVDWARFL LKAIEETGD-----	LSE	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 654
AtPERK13	EE- SLVDWARFL LKAIEETGD-----	FSE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 636
AtPERK14	NQ- SLVDWARFL TKAISGES-----	FDF	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 674
AtPERK15	DD- SLVDWARFL IQAINDGN----	FDG	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 427
OsPERK1	DD- SLVDWARFL MRAADDGN----	YDA	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 506
OsPERK2	DS- SLVDWARFL SEATEEGN----	FDI	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 510
OsPERK3	DS- SLVDWARFL SEAMEEGN----	FDI	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 486
OsPERK4	DD- SLVDWARFL ARALADG----	DYGG	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 485
OsPERK5	DE- SLVDWARFL TQAIETGN----	LEE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 350
OsPERK6	EE- SLVDWARFL ADAVETGD----	LSE	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 692
OsPERK7	AD- SLVDWARFL PRMAAGGG--GGYDD	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 439	
OsPERK8	ED- SLVDWARFL ARLVAGGEEGLIRE	VDS	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 519
GmPERK1	DE- SLVDWARFL SHALDTEE-----	FDS	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 680
GmPERK2	DD- SLVDWARFL TRGLEEDGN----	FGE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 574
GmPERK3	ED- SLVDWARFL NKGLD-DGN----	FGE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 547
GmPERK4	DE- SLVDWARFL SHALDTEE-----	FDS	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 695
GmPERK5	ED- SLVDWARFL CTKAME-NGT----	FE	G	V	D	P	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	: 565
GmPERK6	NE- SLVDWARFL AQALQDGD----	FDN	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 540
GmPERK7	NE- SLVDWARFL AQALQDGD----	FDN	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 600
GmPERK8	ED- SLVDWARFL TRALEEDD----	FDS	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 582
GmPERK9	DE- SLVDWARFL TEALDNE-----	FEI	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 659
GmPERK10	DE- SLVDWARFL LRAIETRD-----	FSD	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 632
GmPERK11	ED- SLVDWARFL TRALEEDD----	FDS	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 575
GmPERK12	DD- SLVDWARFL TRGLEEDGN----	FGE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 572
GmPERK13	EE- SLVDWARFL TDALDSEE-----	FES	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 495
GmPERK14	DE- SLVDWARFL NKGLD-DGN----	FRE	VDP	LE	KN	YD	RQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	SV	: 538
GmPERK15	DE- SLVDWARFL LRAIETRD-----	FSD	AD	P	LE	GR	NY	PQ	EN	FM	EA	AA	AC	IN	HS	SS	RR	SM	: 540
GmPERK16	DE- SLVDWARFL TEALDNE-----	FEI	VDP	LE	KN	YD	RQ	EN	FM	EA	AA								

	*	1040	*	1060	*	1080	*	1100	
TaPERK1	:	-EGVRP----	GHSRFFGSYS--SSDYDSGGQYNEDMKKKFK--MAFTTNDY-----	T	SQYSAPTS---EYGQIPS-	: 625			
TaPERK2	:	-EGVRP----	GHSRFFGSYS--SSDYDSGGQYNEDMKKKFK--MAFTTNDY-----	T	SQYSAPTS---EYGQIPS-	: 443			
TaPERK3	:	-NGVQP----	GQSELEN-----VANTADIRMFQQMVQNQDD-----	D	SAFSQYS---WISRSRAD-	: 645			
TaPERK4	:	-EGVRP----	GHSRFFGSYS--SSDYDSGGQYNEDMKKKFK--MAFTTNDY-----	T	SQYSAPTS---EYGQIPS-	: 620			
TaPERK5	:	-DVVTK----	PSYITEWQITGG-NTTYMT-----	DV	GQSSAPRPNSPSSRTSSP-	: 1005			
TaPERK6	:	-DVVTK----	PSYITEWQIKGG-NTTYMST-----	DV	GQSSAPRPNSSTSQTTSP-	: 1003			
TaPERK7	:	GEEVIK----	PSYITEWQVKGSSSYTGTSQAGLSSSSTTQQS	---	GGGHAAGGDATPATGNPSP-	: 1042			
TaPERK8	:	-DVVTK----	PSYITEWQITGG-NTTYMT-----	DV	GQSSAPRPNSPSSRTSSP-	: 1004			
TaPERK9	:	-DVVTK----	PSYITEWQIKGG-NTTYMST-----	DV	GQSSAPRPNSSTSQTTSP-	: 1005			
TaPERK10	:	-DVVTK----	PSYITEWQITGG-NTTYMST-----	DV	GQSSAPRPNSSTSSRTSSP-	: 1006			
TaPERK11	:	-DVVTK----	PSYITEWQIKGG-NTSYMST-----	DV	GQSSAPRPNSSTSQTTSP-	: 914			
TaPERK12	:	GEEVIK----	PSYITEWQVKGSSSYTGTSQAGLSSSSTTQQS	---	GGGHAAGGDATPATGNPSP-	: 104			
TaPERK13	:	-NGVQP----	GMSEMEN-----	AFNTAEIRLFQRMAFGSQDF-	TDFIQSSS---WNSSRQGG-	: 672			
TaPERK14	:	-EGVRP----	GHSRFMGSHA--SSEYDTSQYNEDLKRRK--MALGTSSF-----	Q	SQLPIDSGGEHEQHNPSP-	: 597			
TaPERK15	:	-NGVKL----	GHSTAYDS-----	GQYSADIELFRMGFEADLDT	AEYGLSDGGVLPGNMSGQLLD-	: 694			
TaPERK16	:	-NGIQP----	GRSEVEL-----	EPRTEEIRLFQLREFGSRE-C	DELSQLAS---WRSRDL-	: 675			
TaPERK17	:	-GGMAP----	GQSAMHRSGGG--NTDEVRLLRMAFGPGTG--TAGGTISEY-----	A	SEMSAPTS---EYGLNPS-	: 672			
TaPERK18	:	-NGVQP----	GMSEMEN-----	AFNTAEIRLFQRMAFGSQDF-	TDFIQSSS---WNSSRQGG-	: 672			
TaPERK19	:	-EGVRP----	GHSRFMGSHA--SSEYDTSQYNEDLKRRK--MALGTSSF-----	Q	SQLPSSD--EHERRQDPS-	: 599			
TaPERK20	:	-NGVKL----	GHSTAYDS-----	GQYSADIELFRMGFEADLDT	AEYGLSDQDELPPGSGRQQR-	: 693			
TaPERK21	:	-NGIQP----	GRSEVEL-----	EPRTEEIRLFQLREFGSRE-C	DELSQLAS---WRSRDL-	: 677			
TaPERK22	:	-GGMAP----	GQSAMHRSGGG--NTDEVRLLRMAFGPGTG--TAGGTISEY-----	A	SEMSAPTS---EYGLNPS-	: 756			
TaPERK23	:	-NGVQP----	GMSEMEN-----	AFNTAEIRLFQRMAFGSQDF-	TDFIQSSS---WNSSRQGG-	: 386			
TaPERK24	:	-EGVRP----	GHSRFMGSHA--SSEYDTSQYNEDLKRRK--MALGTSSF-----	Q	SQLPSSG--EHEHQEPS-	: 600			
TaPERK25	:	-NGIQP----	GRSEVEL-----	EPRTEEIRLFQLREFGSRE-C	DELSQLAS---WRSRDL-	: 676			
TaPERK26	:	-GGMAP----	GQSAMHRSGGG--NTDEVRLLRMAFGPGTG--TAGGTISEY-----	A	SEMSARTS---EYGLNPS-	: 683			
TaPERK27	:	-EGMKP----	GQSMIYS-----	SDESGSYAANIRNLRVAFESS-GEY	NEYS-----GTGESG-	: 314			
TaPERK28	:	-DWVPK----	PSYITEWHIKGGDTSYMSS-----	EVNGQSSVFP-----	AP	: 857			
TaPERK29	:	-EGMKP----	GQSMIYS-----	SDESGSYAANIRNLRVAFESS-EYY	NEYS-----GTGESG-	: 611			
TaPERK30	:	-DGVRP----	GQSRLEF-----	EEAGSCSSDNRLTKVVVV--ASPEY	GRFGRPSFV--SSDRPIDSD-	: 561			
TaPERK31	:	-DGVRP----	GQSRLEG-----	EEAGSYSSDNRAKEVAV--ASPEY	GRSGRPSFV--SSDRPIDSD-	: 601			
TaPERK32	:	-DWVPK----	PSYITEWQIKGGDTSYMSS-----	EVNGQSSSEP-----	AP	: 999			
TaPERK33	:	-NGVQP----	GKSQMEN-----	AANTADIRQFQRMAFGSQDFS	SEYQSKA---SLSGRRDL-	: 728			
TaPERK34	:	-NGVQP----	GKSQMEN-----	AANTADIRQFQRMAFGSQEFT	SEYAQSKA---SLSGRRDL-	: 735			
TaPERK35	:	-DWVPK----	PSYITEWQIKGGDTSYMSS-----	EVNGQSSSEP-----	AP	: 996			
TaPERK36	:	-NGVKV----	GQSQVENN-----	SQQAALQLRTPSPPPRSSRGSS	SSRPGSSS---RPGSTVP-	: 747			
TaPERK37	:	-NGVQP----	GKSQMEN-----	AANTADIRQFQRMAFGSQDFS	SEYQSKA---SLSGRRDL-	: 734			
AtPERK1	:	-EGMRP----	GHSNVYSSYGG--STDYDTSQYNDDMKRRK--MALGTQEYG-----	T	GEYSNPTS---DYGLYPS-	: 623			
AtPERK2	:	-QGITP----	GHSNVYSSGGG--STDYDSSQDNEMKNKERK--VGL-----E	H	TQDLYNPIS--EYDLYPS-	: 693			
AtPERK3	:	-QGITP----	GHSNVYSSXRG--STYYDTRTMXYTRKRI--KMG-----H	H	GKGEYSNPTS---DYRLYPG-	: 522			
AtPERK4	:	-EGMRP----	GHSNVYSSL--GASSDYSQTSYNADMKKERQIALS	---	QEFFVSDCB--GTSNDSR-	: 622			
AtPERK5	:	-EGTRP----	GQSTYLSFG--SVSEYDASSYTADMKKKKLALENKEY-Q	---	SEYGGTSEYGLNPSASSSE-	: 657			
AtPERK6	:	-EGGKA----	GQSSFLGRG--SSS-DYDSSTYSADMKKRKVALDSHEYGA	---	SEYGNTSEYGLDPSSSSSE-	: 682			
AtPERK7	:	-DGVRP----	KQSSSGGEG--SS--DYEMGTGYAEMKKERKVTLERSDYGA	---	SEYGATSEYGLDPSSSSSE-	: 681			
AtPERK8	:	-NGVRP----	GQSQVEDS-----	RQQAQIRMERQMAFGSQDYS	DDFDRSQSHSSWGSRDQ--	: 676			
AtPERK9	:	-NGVRL----	GESEVFNS-----	AQQAQAEIRLERMAFGSQNYS	DDFSHSS---YNSRDANV-	: 708			
AtPERK10	:	-NGVRL----	GESEIINS-----	AQQAQAEIRLERMAFGSQNYS	DSLTRNS---YISKDENL-	: 762			
AtPERK11	:	-NGVKV----	GQSRVYDS-----	GQYSNEIRIERRAS-----EDSSDLG	TN GYPSQ---DYATS	: 701			
AtPERK12	:	-NGVKI----	GQSTTYDS-----	GQYNEDIMKKERMAFGGDNSVESG	LY GNYSAK-----SSSDF	: 705			
AtPERK13	:	-NGNKV----	GQSSAYS-----	GQYNNDIMKKERMAFGFDDSSDSG	MY GDYVQDSRKSGSNAGASSEF	: 695			
AtPERK14	:	-EETGN----	S---VTYSSSE--NENDITP-----RYGTNKRREDTG	---	GDY---TS---EYGVNPS-	: 720			
AtPERK15	:	-EGAAP----	GQSTIYSLDG--SSDYSSSTQYKEDMKKKFK--MAFESKTF-----	G	SECGLTS---DNGQNPS-	: 48			

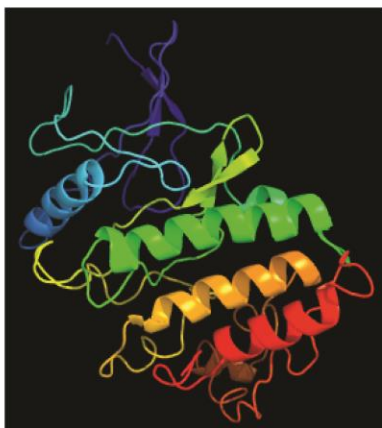
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TaPERK2	:	-ASSSEG--QQTQ-EIETGTMKKGGHSG--YSSGYSGPS-----					476
TaPERK3	:	AEATSSNSRIL-----					656
TaPERK4	:	-ASSSEG--QQTQ-EIETGTMKKGGHSG--YSSGYSGPS-----					653
TaPERK5	:	FLSSVIDEGR-----					1015
TaPERK6	:	FLSSVIDEGR-----					1013
TaPERK7	:	MFTSIIDEGR-----					1052
TaPERK8	:	FLSSVMDEGR-----					1014
TaPERK9	:	FLSSVIDEGR-----					1015
TaPERK10	:	FLSSVIDEGR-----					1016
TaPERK11	:	FLSSVIDEGR-----					924
TaPERK12	:	IFTSIIDEGR-----					1051
TaPERK13	:	-DADASGGFMHSQQLQP-----					687
TaPERK14	:	-VPSSDGH-QQTQ-EVELGTSTKRDDGD--VESQASMR-----					630
TaPERK15	:	GEAHQINQLGSPAGRLNPPATLHRTF-----					720
TaPERK16	:	-----					-
TaPERK17	:	-SEYTASSAADTEDMTDFPHRAGAGRGSAGGSGEAGRGTTEGFSRRTTVRRTRGRG					727
TaPERK18	:	GDVDASGGPRQSQP-----					686
TaPERK19	:	-VQSSDGH-RQTQ-EVELGTT-KRDDGD--VESQTSMR-----					631
TaPERK20	:	-----TAAGR-----					698
TaPERK21	:	-----					-
TaPERK22	:	-SEYTASSAADTEDMTDFPHRAGTGRGAAGASGEAGRGTTEGFSRRTTGRRTSRG					811
TaPERK23	:	-DVDASGGPRHPQSQP-----					401
TaPERK24	:	-VPSSDGH-QQTQ-EVELGTR-KRDDGD--VESQASMR-----					632
TaPERK25	:	-----					-
TaPERK26	:	-SEYTASSAADTEDMTDFPHRAGTGRGAAGVSGEAGRGTTEGFSRRTTVRRTRGRG					438
TaPERK27	:	ETTQRHH-----					621
TaPERK28	:	FLGSVIDQGR-----					867
TaPERK29	:	ETTQRHH-----					618
TaPERK30	:	EMSPAERQQPHL-----					573
TaPERK31	:	EMSPAERQPPHL-----					613
TaPERK32	:	FLGSVIDQGR-----					1009
TaPERK33	:	-----					-
TaPERK34	:	-----					-
TaPERK35	:	FLGSVIDQGR-----					1006
TaPERK36	:	PFVL-----					751
TaPERK37	:	-----					-
AtPERK1	:	-GSSSEGGQ-ATREM--EMGKIKKTGGQY---SGPSL-----					652
AtPERK2	:	-WSSDGGQ-TTQ GK--ATGNIKRPGQGY---G-----					717
AtPERK3	:	GRSSSEGQ-ATRGNGFEMGKIKRTAQRY---GGDSL-----					554
AtPERK4	:	DMGTKSPTPPK-----					633
AtPERK5	:	EMNRGSMKRNQPL-----					670
AtPERK6	:	EIRRGGANNNKTPSRDH-----					700
AtPERK7	:	EMHIGGSTSKTTTNRGI-----					699
AtPERK8	:	-SREVP-----					681
AtPERK9	:	-----					-
AtPERK10	:	-----					-
AtPERK11	:	HEYESERAFNTSHRNH-----					718
AtPERK12	:	SGNESETRPFNNRRF-----					720
AtPERK13	:	TRNETENRNFNRRY-----					710
AtPERK14	:	-QSSSEHQVNT-----					731
AtPERK15	:	-GSSSITEGQRTTQEIPEKNTKDT-----					509
OsPERK1	:	-VSMGDAR-QIPETEMEMGSLKKDGDSNGTRDSQAS-----					597
OsPERK2	:	NRSFAKGR-----					568
OsPERK3	:	TKQFNYYR-----					520
OsPERK4	:	EMSAEWKQPPHRVSR-----					555
OsPERK5	:	-----					-
OsPERK6	:	E-----					748
OsPERK7	:	NASSGEHDNQWRKAHR-----					517
OsPERK8	:	HSSRLPPKR-----					568
GmPERK1	:	-----					-
GmPERK2	:	EVSQKQQL-----					634
GmPERK3	:	ELSSKEMGYH-----					608
GmPERK4	:	-----					-
GmPERK5	:	QSSAEYARRTTGGGRMHTP-----					645
GmPERK6	:	-----					-
GmPERK7	:	-GSSSEAQQSFRDIV-----					673
GmPERK8	:	-GSSSEAQSRQTTREMEMRKMNSQGFS-----GSS-----					671
GmPERK9	:	NTMFSQKGTGFWNV-----					724
GmPERK10	:	LIRHSSSGSLNLELSTCIGVVLNENRD-----					718
GmPERK11	:	-GSSSEAQSRQTTREMEMRKMNNQGFS-----GSS-----					664
GmPERK12	:	EVSQKQQL-----					632
GmPERK13	:	-----					-
GmPERK14	:	ELSSKEMSYH-----					599
GmPERK15	:	LIQHSSSGEFDSRDINMHRSSIE-----					622
GmPERK16	:	TTVFSQNKTGHNV-----					756

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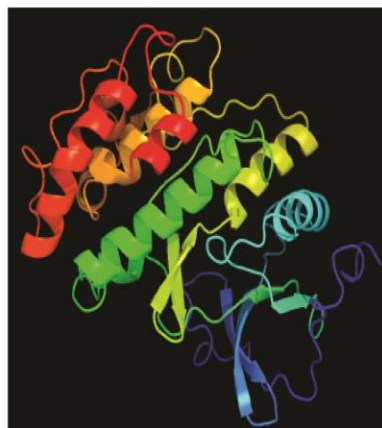
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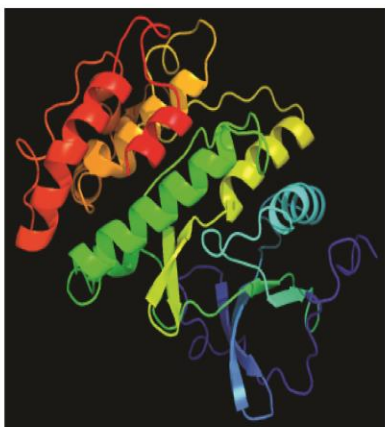
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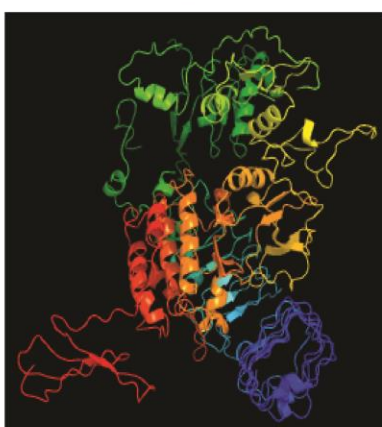
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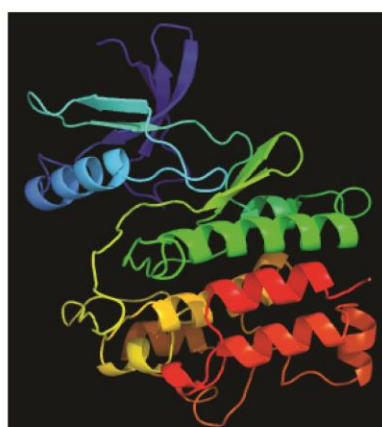
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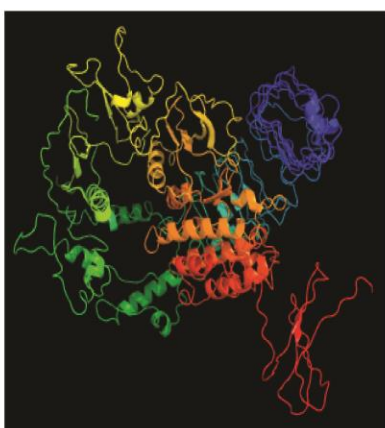
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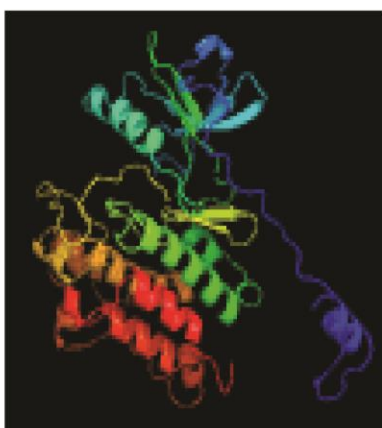
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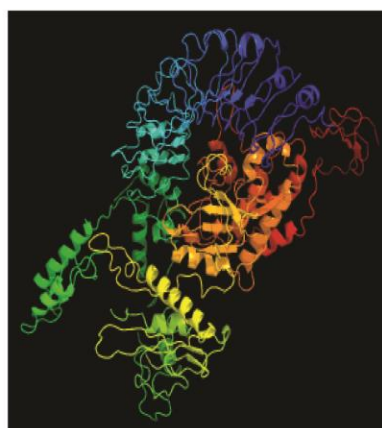
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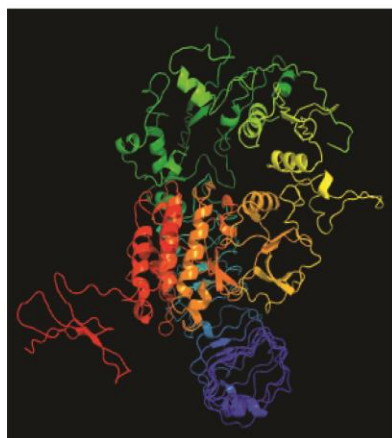
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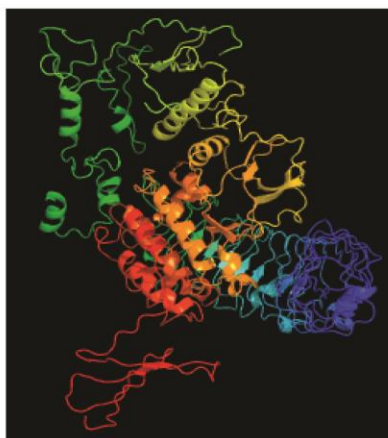
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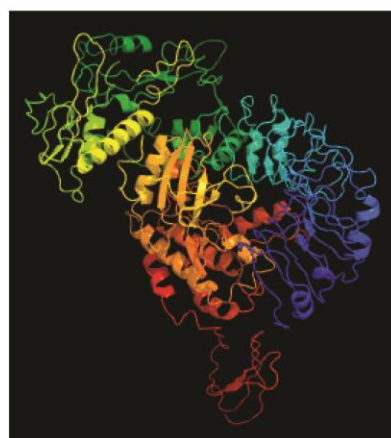
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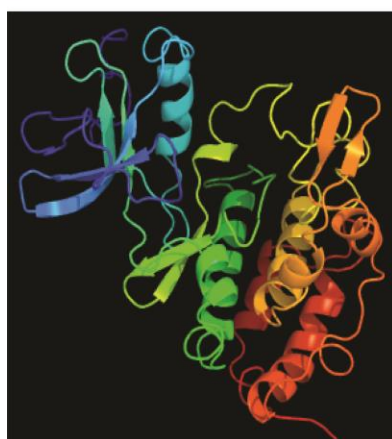
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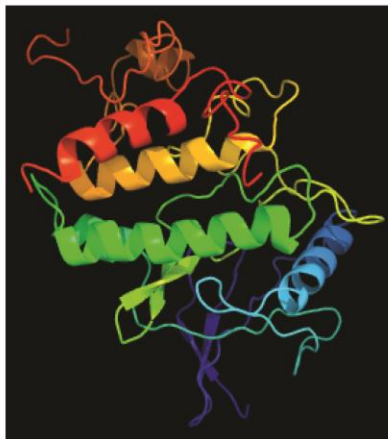
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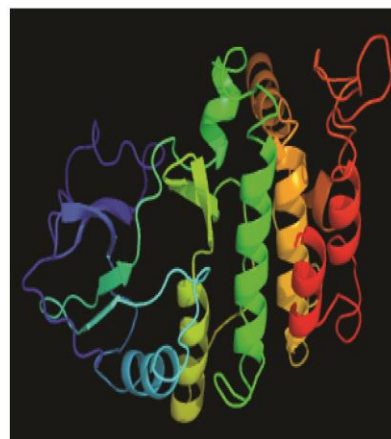
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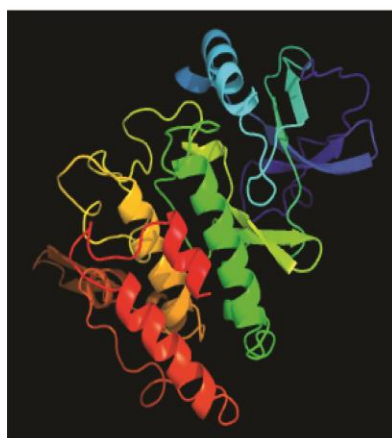
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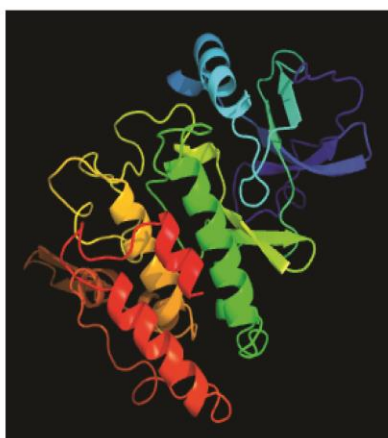
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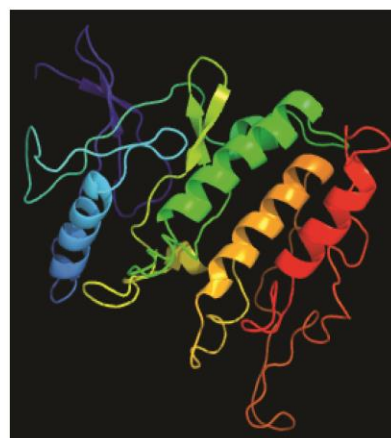
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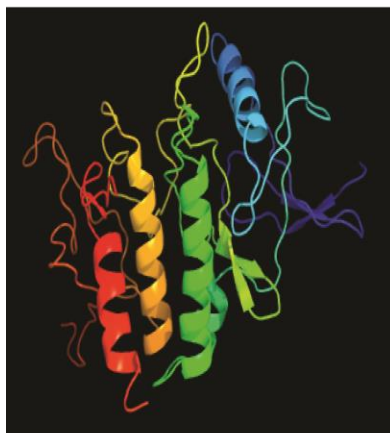
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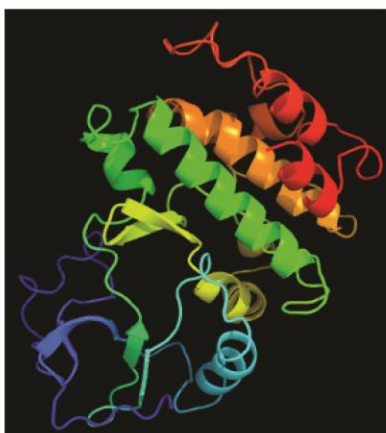
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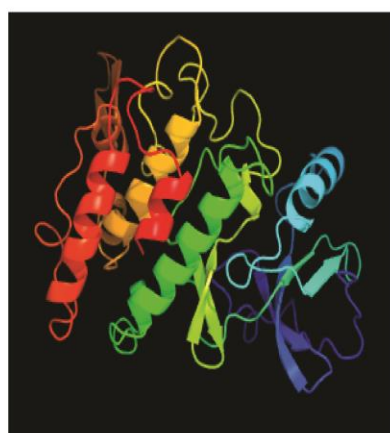
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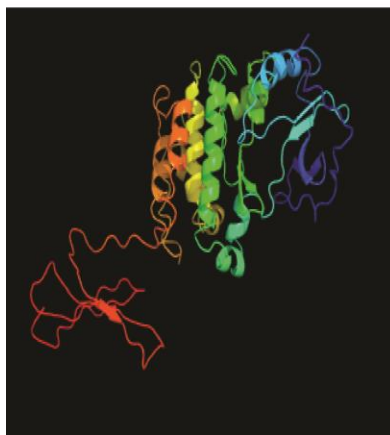
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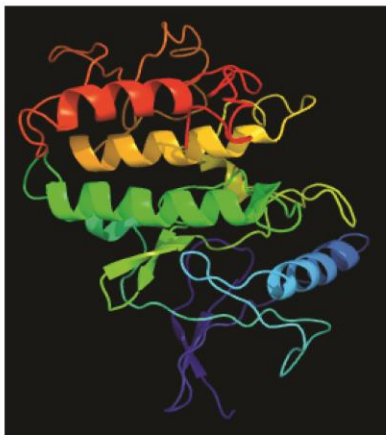
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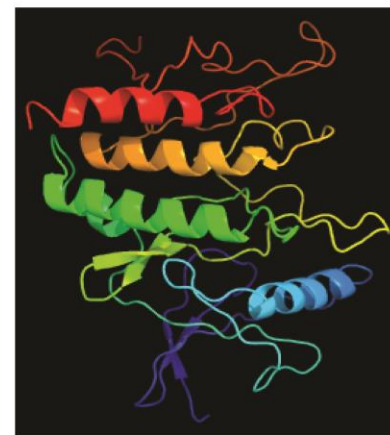
TaPERK22



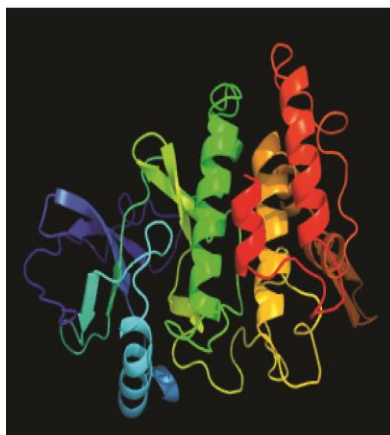
TaPERK23



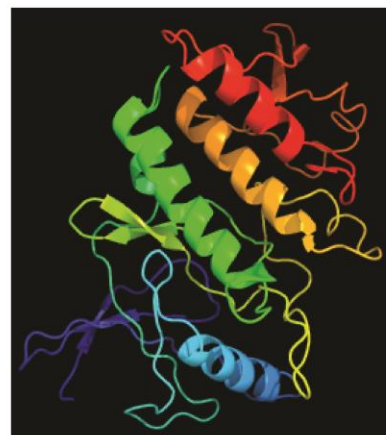
TaPERK24



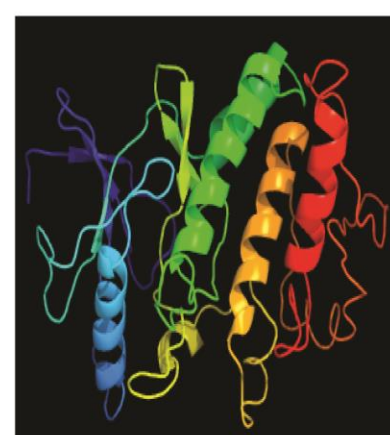
TaPERK25



TaPERK26



TaPERK27



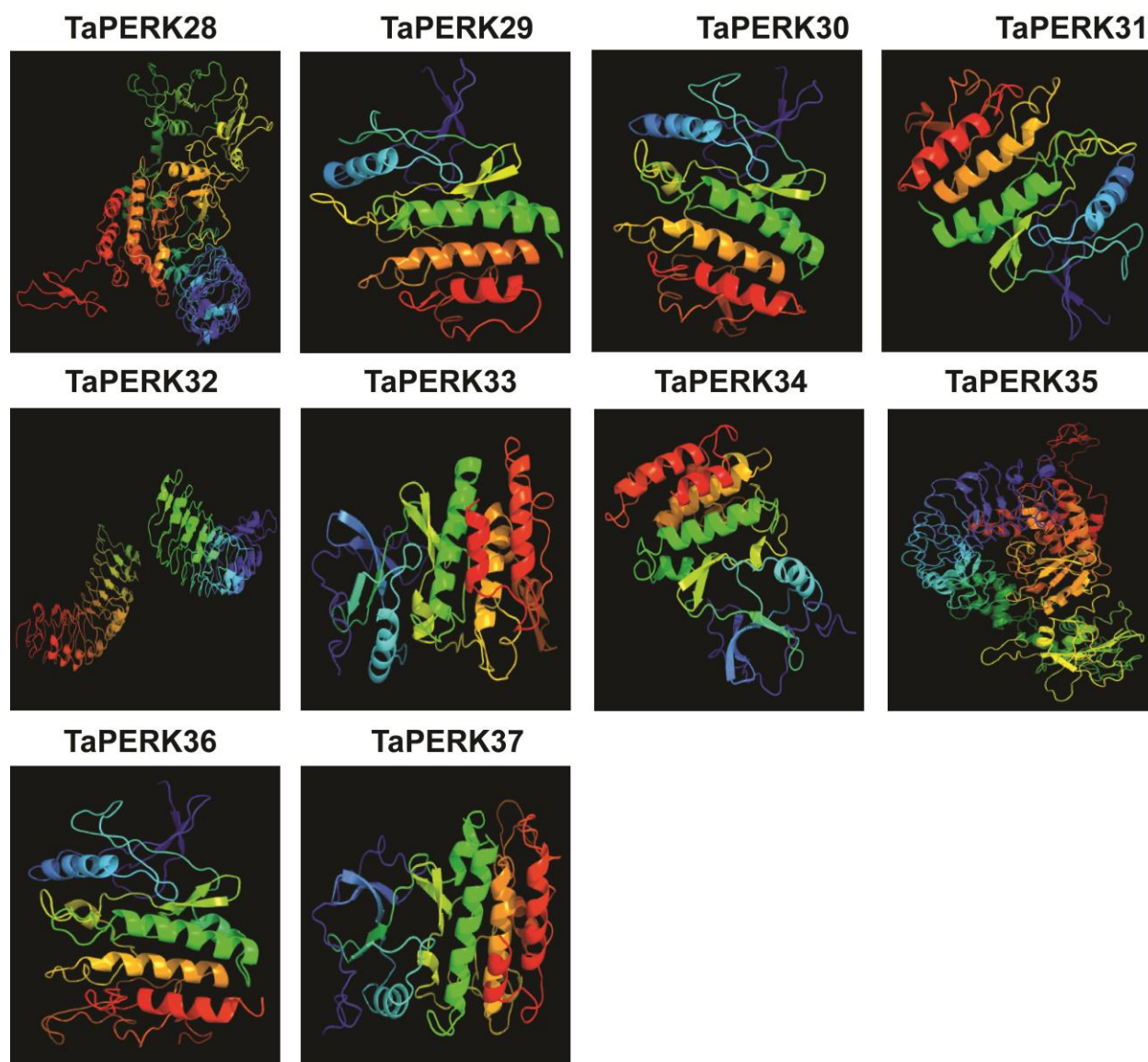
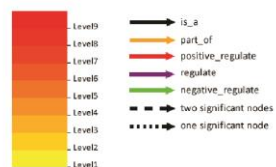
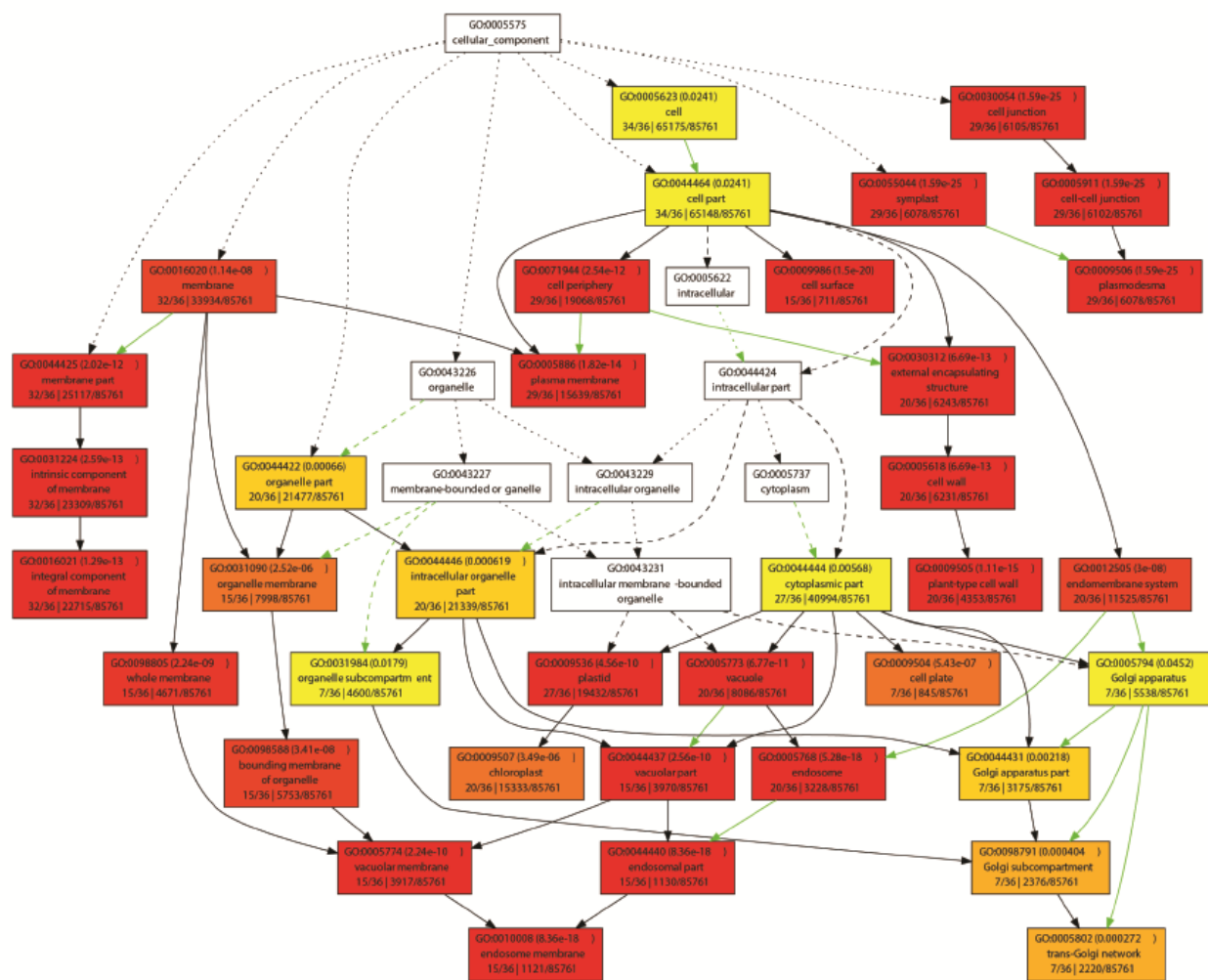


Figure S6. Alignment and 3-dimensional structure of the TaPERK protein sequences. **A.** The conserved protein tyrosine kinase domain is boxed with red color. Colored and shaded amino acids are chemically similar residues. Dashes indicate gaps introduced to maximize the alignment of the homologous region. **B.** Predicted 3D structures TaPERK proteins.



B



C

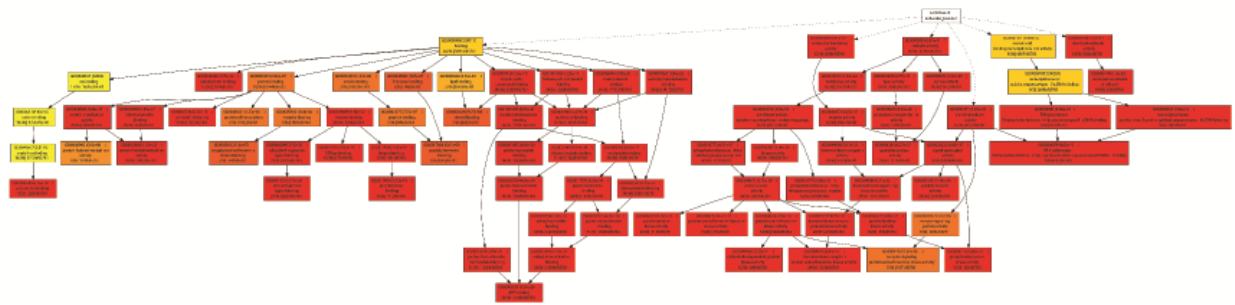


Figure S7. Gene ontology term distribution TaPERK gene family predicted using AgriGO **A.** Biological Process. **B.** Cellular component. **C.** Molecular function.

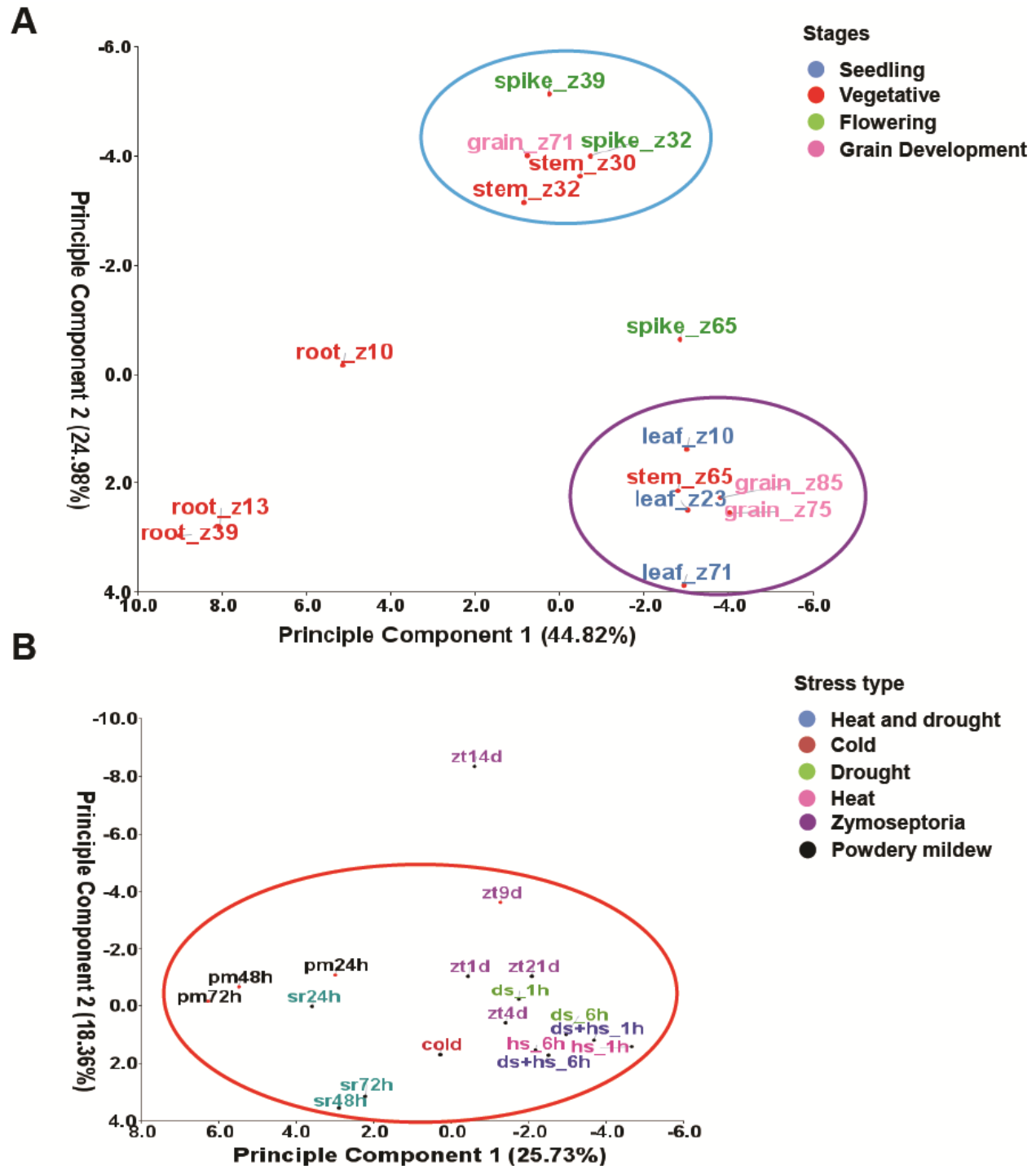


Figure S8. PCA plots displaying grouping of different (A) Developmental stages (B) Biotic and abiotic stress conditions based on the TaPERK expression pattern. DS: Drought stress, HS: Heat stress, Zt: *Zymoseptoria tritici*, PM: Powdery mildew; SR: Stripe rust, h: hour and d: days.

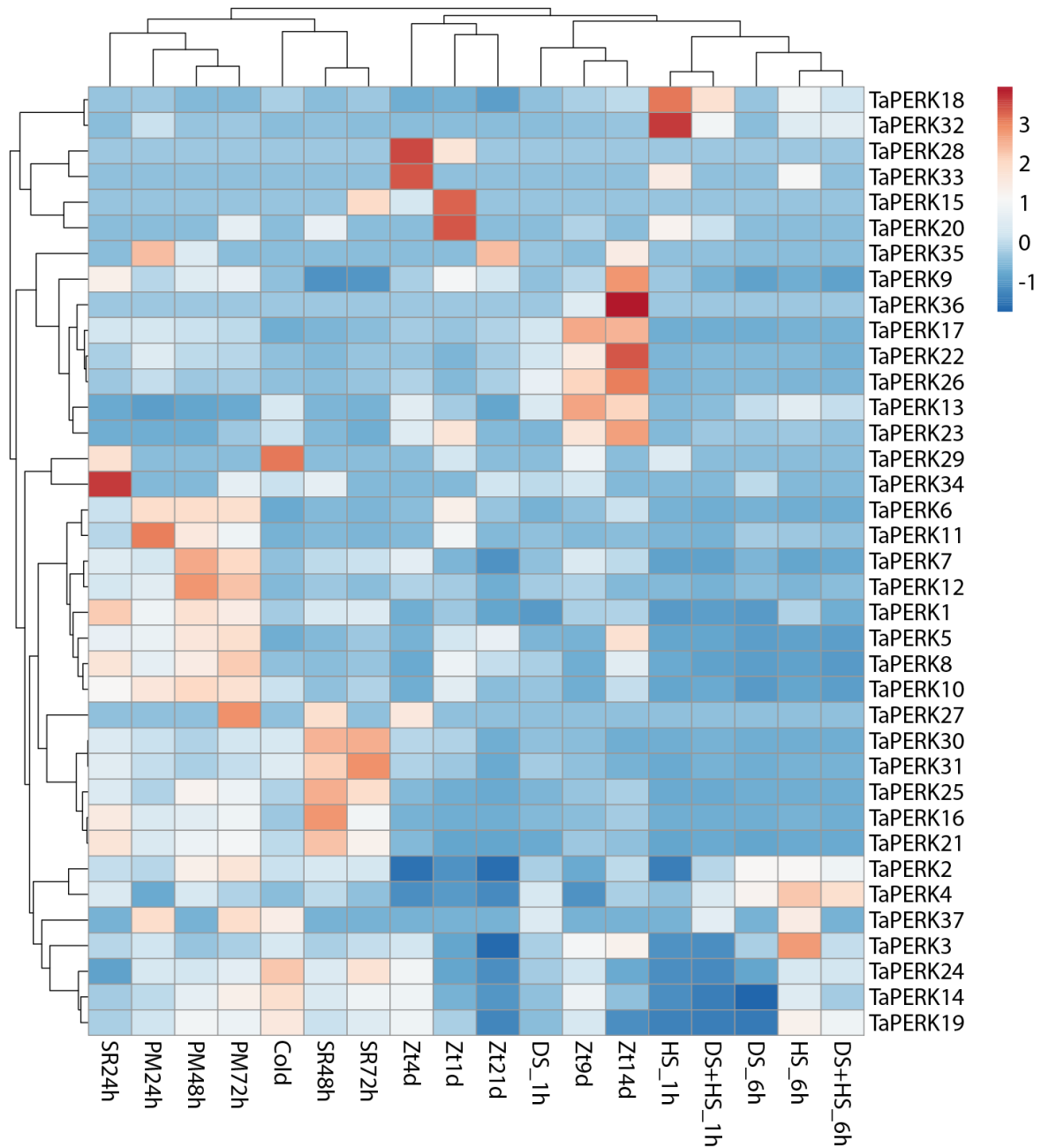


Figure S9. Heatmaps representing the expression pattern of TaPERK genes in different stress conditions. TPM values were directly used to construct the heatmaps. DS: Drought stress, HS: Heat stress, Zt: *Zymoseptoria tritici*, PM: Powdery mildew; SR: Stripe rust, h: hour and d: days.