

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

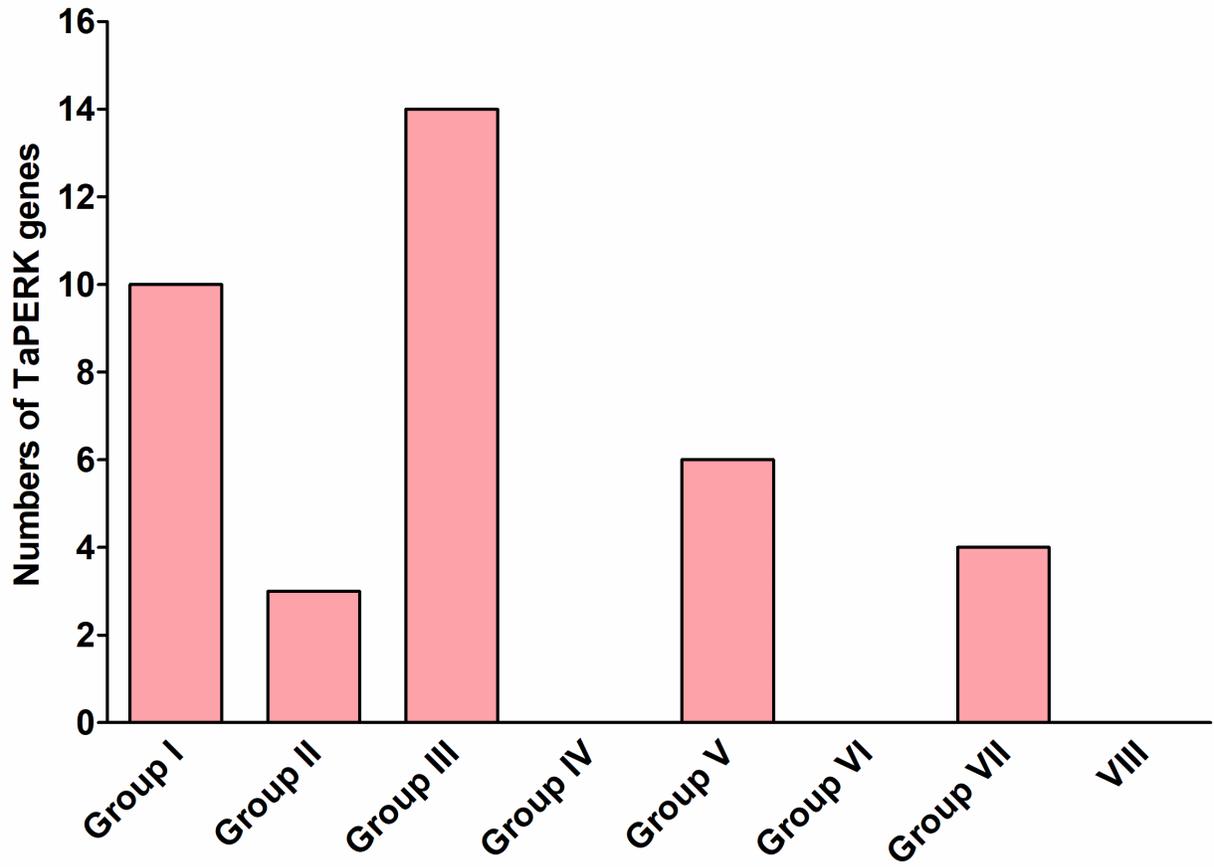


Figure S2. Distribution of TaPERKs in a different group of the phylogenetic tree.

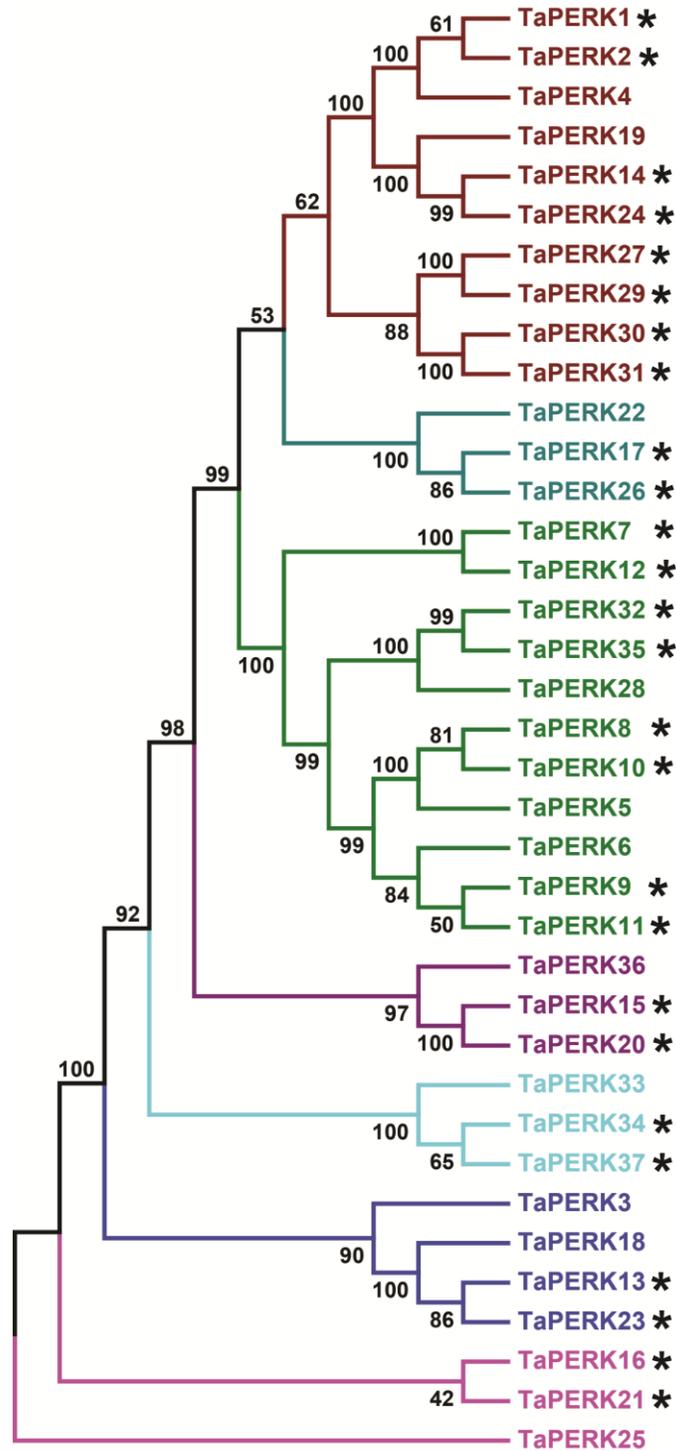


Figure S3. Phylogenetic analysis of TaPERK genes. A phylogenetic tree was constructed using MEGAX with the neighbor-joining (NJ) method and 1000 bootstrap replications. A black asterisk indicates the duplicated genes.

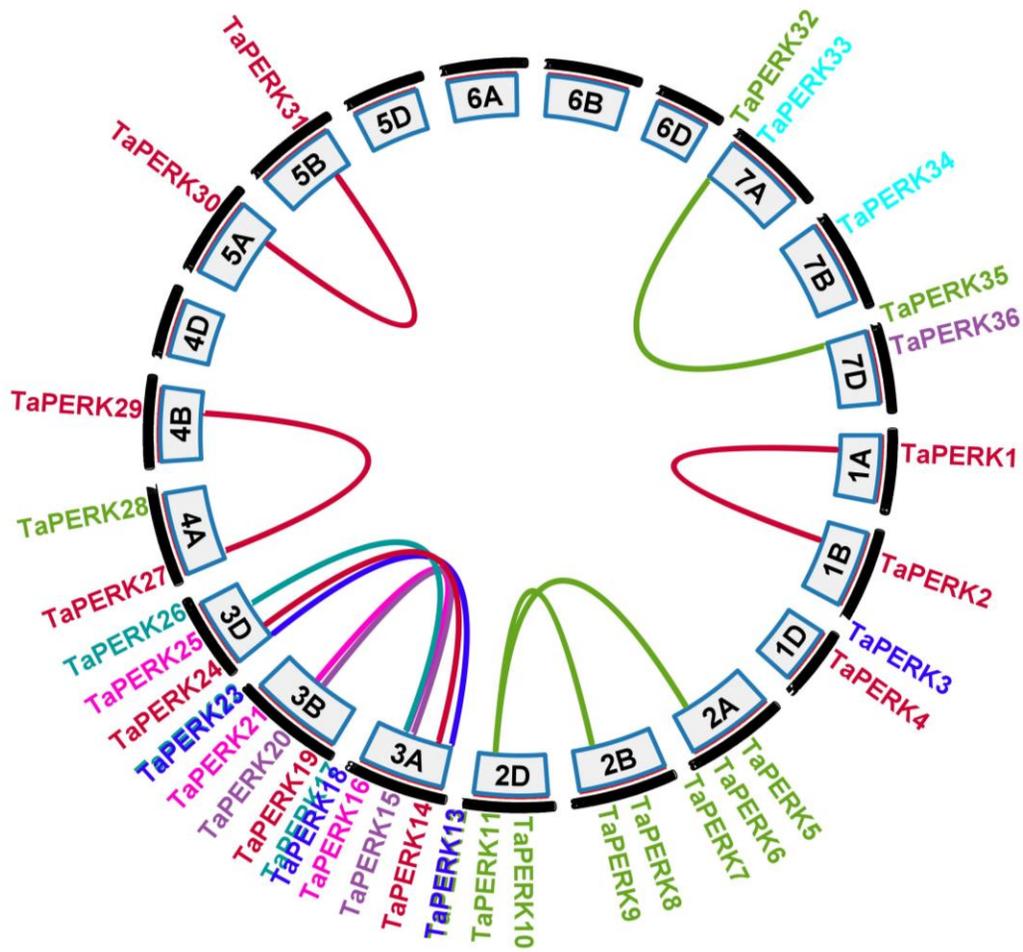


Figure S4. Chromosomal distribution and duplicated PERK gene pairs in wheat. Duplicated PERK gene pairs are connected with lines with distinct colors. The figure was generated using TB tools.

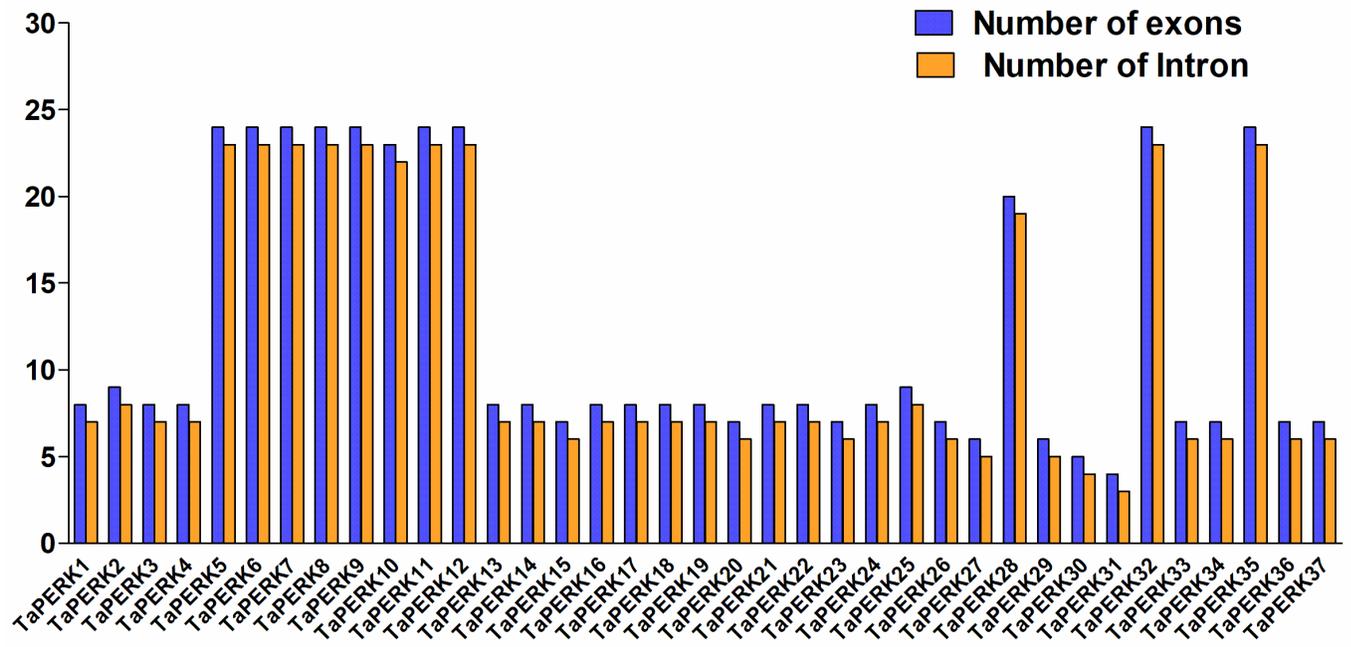


Figure S5. Distribution of exon and introns in TaPERKs gene family.

A

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*      20      *      40      *      60      *      80
TaPERK1 : ----- : -
TaPERK2 : ----- : -
TaPERK3 : ----- : -
TaPERK4 : ----- : -
TaPERK5 : ---MGRRRQALHGAALSL--LLLAAA----AHAQQTDP----GDAALNAVFAKLGQKALSSWNISGDPCTGAATDNT : 65
TaPERK6 : ---MKLLHGAALAL--LLLAAA----AHAQRTPRTH---AGDAAALNAVFAKLGQKASSSWNISGNLCTGAAIDDT : 64
TaPERK7 : MGPPSPRWSSCLRHGSLVLLPLLLTALSSWRAAAQAQAPPPPSQTDPTAAAVNAIILGKLGSLAPASWNISGNPCSGAATDDT : 85
TaPERK8 : ---MGRRRQVILHGAALSL--LLLA AV----ADAQQTDP----GDAALNAVFAKLGQKALSSWNISGDPCTGAATDNT : 65
TaPERK9 : ---MKLLLGAALTLP LLLLTAA----AHAQRSPRTH---LGDAALNAVFAKLGQKASSSWNISGNLCTGAAIDDT : 66
TaPERK10 : ---MGRRSRLHGAALSL--LLLAAA----AHAQQTDP----GDAALNAVFAKLGQKALPSWNISGDPCTGAATDNT : 65
TaPERK11 : -----MSSQLSNVWVSLGQST----- : 16
TaPERK12 : MGRPSPGWSSCLRHGFLVLLPLLLSALCSSWRAAAQAQAPPPPP--QTEPTAAAVNAIILGKLGSLAPASWNISGNPCSGAATDDT : 84
TaPERK13 : ----- : -
TaPERK14 : ----- : -
TaPERK15 : ----- : -
TaPERK16 : ----- : -
TaPERK17 : ----- : -
TaPERK18 : ----- : -
TaPERK19 : ----- : -
TaPERK20 : ----- : -
TaPERK21 : ----- : -
TaPERK22 : ----- : -
TaPERK23 : ----- : -
TaPERK24 : ----- : -
TaPERK25 : ----- : -
TaPERK26 : ----- : -
TaPERK27 : ----- : -
TaPERK28 : ----- : -
TaPERK29 : ----- : -
TaPERK30 : ----- : -
TaPERK31 : ----- : -
TaPERK32 : ---MREMRLMILHGAALLL--LLAAV----AHAQQTRTTD---PADAAALHAVFAKLGQKAGPQWNISGDPCTGAAIDNT : 69
TaPERK33 : ----- : -
TaPERK34 : ----- : -
TaPERK35 : ---MRLMILHAVALLL--LLAAV----AHAQQTMRTD---PADAAALHAVFAKLGQKAGPQWNISGDPCTGAAIDNT : 66
TaPERK36 : ----- : -
TaPERK37 : ----- : -
AtPERK1 : ----- : -
AtPERK2 : ----- : -
AtPERK3 : ----- : -
AtPERK4 : ----- : -
AtPERK5 : ----- : -
AtPERK6 : ----- : -
AtPERK7 : ----- : -
AtPERK8 : ----- : -
AtPERK9 : ----- : -
AtPERK10 : ----- : -
AtPERK11 : ----- : -
AtPERK12 : ----- : -
AtPERK13 : ----- : -
AtPERK14 : ----- : -
AtPERK15 : ----- : -
OsPERK1 : ----- : -
OsPERK2 : ----- : -
OsPERK3 : ----- : -
OsPERK4 : ----- : -
OsPERK5 : ----- : -
OsPERK6 : ----- : -
OsPERK7 : ----- : -
OsPERK8 : ----- : -
GmPERK1 : ----- : -
GmPERK2 : ----- : -
GmPERK3 : ----- : -
GmPERK4 : ----- : -
GmPERK5 : ----- : -
GmPERK6 : ----- : -
GmPERK7 : ----- : -
GmPERK8 : ----- : -
GmPERK9 : ----- : -
GmPERK10 : ----- : -
GmPERK11 : ----- : -
GmPERK12 : ----- : -
GmPERK13 : ----- : -
GmPERK14 : ----- : -
GmPERK15 : ----- : -
GmPERK16 : ----- : -
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*      100      *      120      *      140      *      160      *
TaPERK1 : -----MS- : 2
TaPERK2 : ----- : -
TaPERK3 : -----MAAKAPA : 7
TaPERK4 : -----MS- : 2
TaPERK5 : NIDNPPFNPAIKCECSGG-NASVCRVTRLKIYALDAVGPIPEELRNLTALTNLDSLQNYLTGPLPSFIGELTRMQYMSFGINAL : 149
TaPERK6 : DIDNDPNFNPAIKCLCSTG-NASLCRITRLKIYALDAVGPIPEELWNLTSLTNLNLAQNYLTGPIPSFIGKLAQMQLYLSMGINAL : 148
TaPERK7 : PLDDNPNFNPAIKCDCTDQ-NGTLCHVTRLKINSLDAAGPIPEELRNLTSLIKLDFRKNLSLTGPLPAFIGELTALKYITVGTNAL : 169
TaPERK8 : NIDNPPFNPAIKCECTGG-NASVCRVTRLKIYALDAVGPIPEELRNLTALTNLDSLQNYLTGPLPSFIGELTRMQYMSFGINAL : 149
TaPERK9 : DIDNDPNFNPAIKCLCSTG-NASVCRITRLKIYALDAVGPIPEELWNLTSLTNLNLAQNYLTGPIPSFIEKLDQMQLYLSLGINAL : 150
TaPERK10 : NIDNPPFNPAIKCECTGG-NASVCRVTRLKIYALDAVGSPIPEELRNLTALTNLDSLQNYLTGPLPSFIGELTRMQYMSFGINAL : 149
TaPERK11 : -----VFQAPA-ELAVCR-----NLAQNYLTGPIPSFIGELTRMQYLSLGINAL : 59
TaPERK12 : PLDDNPNFNPAIKCDCTDQ-NGTLCHVTRLKINSLDAAGPIPEELRNLTSLIKLDFRKNLSLTGLLPAFIGELTSLKYITVGTNAL : 168
TaPERK13 : -----MASS : 4
TaPERK14 : -----MS- : 2
TaPERK15 : -----MPRILVESVEHLATAPV : 17
TaPERK16 : -----MGGYADPFMPPQPASSSSY : 19
TaPERK17 : -----MSGP : 4
TaPERK18 : -----MASS : 4
TaPERK19 : -----MS- : 2
TaPERK20 : -----MPRVFEVESVEHLANAPA : 17
TaPERK21 : -----MGGYADPFMPPQPASSSSY : 19
TaPERK22 : -----MSSSPDPDAGGSPFVTPSP : 19
TaPERK23 : ----- : -
TaPERK24 : -----MSS- : 3
TaPERK25 : -----MGGYADPFMPPQPASSSSY : 19
TaPERK26 : ----- : -
TaPERK27 : ----- : -
TaPERK28 : -----MKEMTFGINAL : 11
TaPERK29 : ----- : -
TaPERK30 : ----- : -
TaPERK31 : ----- : -
TaPERK32 : NIDNNDIFKAAIKCEVCTGGNTSVCRIITRLKIYALDAVGPIPEELRNLTALTDLDLQNYLTGPLPSFIGELTAMKSMTFGINAL : 154
TaPERK33 : -----MRTLLQAKGGGRGAGAG-----AADAADAADVTVTG-TTPPSSTD : 40
TaPERK34 : -----MRTLLQAKGGGRGPGGG-AAEAADAADAADVTVTGTTTPPSSTD : 44
TaPERK35 : NIDNNDIFKAAIKCEVCTGGNTSVCRIITRLKIYALDAVGPIPEELRNLTALTDLDLQNYLTGPLPSFIGELTDMKEMTFGINAL : 151
TaPERK36 : -----MPRLAPSPGSSSESDSS : 16
TaPERK37 : -----MRTLLQAKGGGRGGGGGGGAADAADAADVTVTGTTTPPSSTD : 45
AtPERK1 : -----MSTAPSPG- : 8
AtPERK2 : -----MSSAPPPGG : 9
AtPERK3 : -----MARSNR--- : 6
AtPERK4 : ----- : -
AtPERK5 : ----- : -
AtPERK6 : ----- : -
AtPERK7 : ----- : -
AtPERK8 : -----MSLVPLP--- : 8
AtPERK9 : -----MATFPVQPP---VS : 11
AtPERK10 : -----MTTPAQAPREVS : 13
AtPERK11 : -----MDKVQQQADLFGKTIISPFV : 19
AtPERK12 : -----MSDLGESPPSSPPAPPADT : 19
AtPERK13 : -----MSDSPTSSPPAPSADS : 16
AtPERK14 : -----MSLSPSSSP : 9
AtPERK15 : ----- : -
OsPERK1 : -----MS- : 2
OsPERK2 : ----- : -
OsPERK3 : ----- : -
OsPERK4 : ----- : -
OsPERK5 : ----- : -
OsPERK6 : -----MSSESQAPSPSPSSSSS : 19
OsPERK7 : ----- : -
OsPERK8 : ----- : -
GmPERK1 : -----MSAASPSPATST : 12
GmPERK2 : ----- : -
GmPERK3 : ----- : -
GmPERK4 : -----MSAVSPSPSTST : 12
GmPERK5 : ----- : -
GmPERK6 : -----MFAVAYYSPA : 10
GmPERK7 : -----MLAVAPYSPA : 10
GmPERK8 : -----MSTAPAPS- : 8
GmPERK9 : -----MTSTNPSFNASP : 12
GmPERK10 : -----MSTKHTEEDNDSSYLTIPNKDK : 22
GmPERK11 : -----MSTAPAPS- : 8
GmPERK12 : ----- : -
GmPERK13 : -----MSAPSPS---SS : 9
GmPERK14 : ----- : -
GmPERK15 : ----- : -
GmPERK16 : -----MASANPSFNASP : 12

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180          *          200          *          220          *          240          *
TaPERK1 : -----SPTAAPAPPTTPAPPAN-----ATAPPATPSAPPPAIPSPSPAPPANPPFVSV-- : 51
TaPERK2 : ----- : -
TaPERK3 : PSARSRALASASAPASSRRFNATPAA-----DTAAPSTSAT-----TSPPPSSPPSAPPKLAAS-PPPASPPP----- : 72
TaPERK4 : -----SPTAAPAPPTTPAPPAN-----ATAPPATPSAPPPAIPSPSPAPPANPPFASV-- : 51
TaPERK5 : SGPLPKELGNLTDIVLSVSSNNFSGSLPSELGNLAKLEQLYIDSAGFSGPLPSSLKLTMKMILWASDNDFGTQIPDYIGSWN- : 233
TaPERK6 : SGPLPKELGNLTNLVSLGIGSNKFNGLSPLLELGNLVKLEQMYIDSAGLSGPLPASLSRLTKMKILWASDNDFGTQIPDYIGSW- : 232
TaPERK7 : SGVPVKELWNLTDIVSVALGNSHFNGSLPDELGKLTQLQYIDSNDFTGPLEALSQLTNLSTLWASDNDFGTQIPDFLGLSLTN : 254
TaPERK8 : SGPLPKELRNLTDLVLSVSSNNFSGSLPSELGDLAKLEQLYIDSAGFSGPLPSSLKLTMKMILWASDNDFGTQIPDYIGTWN- : 233
TaPERK9 : SGPLPKELGNLTNLVSLGIGSNKFNGLSPLSELGNLAKLEQMYIDSAGLSGPLPASLSLTKMKILWASDNDFGTQIPDYIGSW- : 234
TaPERK10 : SGPLPKELGNLTDIVLSVSSNNFSGSLPSELGNLAKLEQLYIDSAGFSGPLPSTLSKLTMKMILWASDNDFGTQIPDYIGSWN- : 233
TaPERK11 : SGPLPKELGNLTNLVSLGIGSNKFNGLSPLSELGNLAKLEQMYIDSAGLTGPLPASLSKLTMKMILWASDNDFGTQIPDYIGSW- : 143
TaPERK12 : SGVPVKELWNLTDIVSLALGNSHFNGSLPDELGKLTQLQYIDSNDFTGPLPAALSQTLNLTSTLWASDNDFGTQIPDFLGLSLTN : 253
TaPERK13 : PPSPGATKASPADSVAPATSSPFPAP-----VKLPNDTPAD-----PPAAPAPSAAVPPQTPE-PPPPSPSP----- : 69
TaPERK14 : -----SPPAAPGPASPPGNRT-----APPPASAPPATNSTPPSPAP-----PPSSPL-- : 45
TaPERK15 : VGGPPPPPKSSASPTPARSSPPPTP-----PPKSPPPS-----SPPASSGNNQSANLPPGSPPAKKSAS----- : 81
TaPERK16 : AVPQGGHGQPQ--APRPPGCPYSSAS-----APPVTSY-----HSLPPAASPPFVSS-PPPASPPPELPS----- : 80
TaPERK17 : SPPVTFVS---PPADAGETPRVTPATPPVVTFVSPPPDA-----AGTPPPDASGTPEVTPPPPDAAATPPPVNPP : 76
TaPERK18 : PPSPGATKASPAASVAPATSSPASPAP-----VKLPNETPAD-----PPAAPAPSAAVPPQTPE-PPPPSPSP----- : 69
TaPERK19 : -----SPPAAPGPASPPGNRT-----APPPASAPPATNSTPPSPAPASSPPSSPL----- : 50
TaPERK20 : VGGPPAPPQPSASPPQARSPPPPTP-----PPKSPPPS-----SPPASSGNNQSFNLPPGSPPEKSPAS----- : 81
TaPERK21 : AVPQGGHGQPQPPAPRPPGCPYSSAS-----APPVTSY-----HSLPPAASPPFVSS-PPPASPPPELPS----- : 82
TaPERK22 : TSPVTFVTSPTFPVTFVTPSPDDNFVTPFVAFVNSPPPDTSMFNPPFVTPSPPPPEATPPPFVTPSPPPFVATPPTFTPTS : 104
TaPERK23 : ----- : -
TaPERK24 : -----SPPAAPGPASPPGNRT-----APPPASAPPATNSTPPSPAPPASPPSSPV----- : 51
TaPERK25 : AVPQGGHGQPQPPAPRPPGCPYSSAS-----APPVTSY-----HSLPPAASPPFVSS-PPPASPPPELPS----- : 82
TaPERK26 : ----- : -
TaPERK27 : -----MDSPLSRGFLGGLGSGPLDFSS-SAADSDGSGSSSADSDSSGGS---SSGSPSPSSSQ----- : 59
TaPERK28 : SGPLPKELGNLKNLKLGLGNNFSGSLPSELGNLAKLEELYIDSSGLSGPLPSSLQLTKMKLWASDNDFGTQIPDYIGTWSS : 96
TaPERK29 : -----MDSPLSRGLAPLLGSGPLDFSSAAADSDGSGSSSGADSSGES---SSGSPSPSGFQ----- : 60
TaPERK30 : ----- : 14
TaPERK31 : -----MSSNSSAAPPFSS----- : 14
TaPERK32 : SGVPVKELGNLKNLKLGLGNNFSGSLPTELGNLAKLEELYIDSSGLSGPLPSSLQLTKMKLWASDNDFGTQIPDYIGSWSS : 239
TaPERK33 : DSPPPASD---PPSPSSSSSSPPPS---PSSPDPPPS---PSSPPSPPLAPPSPASSPPFVPS : 102
TaPERK34 : DSPPPPTDSSSDPPSPSSSSPPPS---PSAPDPPPS---PSSPPSPPLAPPSPASSPPPEALP--- : 110
TaPERK35 : SGVPVKELGNLKNLKLGLGNNFSGSLPSELGNLAKLEELYIDSSGLSGPLPSSLQLTKMKVWASDNDFGTQIPDYIGSWSS : 236
TaPERK36 : DDRSDGSKSKSKKAPFRRSRSSGSSSDENDGSSSSPSPSS---DDEGGSRSSSSSDSDSPSDSKSSQSSRRS--- : 93
TaPERK37 : DSPPPASDSSSDPPSPSSSSPPPT---PSSPDPPPA---PSSPPSPPLAPPSPASSPPPEALP--- : 111
AtPERK1 : -----TTPSPSPSPTNSTTT-----TTPAASPPPTTTPSSPPSPSTNSTS : 53
AtPERK2 : TSPPPQLPIPIPPQLPVTTPPPPTAL-----PPALPPPPPTALPPALPPPPPTTVPFIPSTP : 72
AtPERK3 : -----CVPNSSIVQIIEEVE-----KTQLKSRWQITMSSASSPPQVVFV : 50
AtPERK4 : -----MAS-SPESAPP---TNSTSSPSPSNTN-----STSSPPA---PSPSPTPPQGS : 45
AtPERK5 : -----MADSFVDSAPETSNGTTPSNGTSPNESSPTPPSSPPSSISAPPPDISASFPFPATQ : 64
AtPERK6 : -----MAEQSPENSPPSP---TPSPSSDNQQSSPPSPSPAPPAPPDSSNGSPQPPSSDL : 61
AtPERK7 : -----MAEQSPENSPPAPPSPSPSPSSNDQQTSPSPSDNQETTSPPPP---SSPIAPPQQQ : 60
AtPERK8 : -----ILSPSS---NSSTAP---PPLQQT---TPSAPPVTP---PPS---PPQSPFVVS : 55
AtPERK9 : NSPVTSP---PPLN---NATSP---ATPPVTSPL---PPSAPPENRAPPFP---FVTSPPEVANGA : 67
AtPERK10 : LSPSLASPPMALPPQPSPFGDNATSPREPTNGNPETNTN-----AQSSPPETPLSPP-PEPSPPSLTP : 85
AtPERK11 : ASQP-TNVGGFTDQKIIGSETTQPATSP---SPSPDTQT---SPPATAAQPPFNQPP---NTTPTTPSS : 85
AtPERK12 : APPPETPSENSALPP-VDSFPP-SPPADSS---TPPLEPST---PPDSQLPPLPSILP---LTDSPPPSS : 85
AtPERK13 : APPPDTSSDGAAPPPTDSAPPSPPADSS---PPPALPSL---PPAVFSPPTVSSPPPPPLDSSPPPPDLT : 84
AtPERK14 : APATSPAMSLPPADSVPTDSSPPAPPLSPLPPLSSPPPLSPPPLSAPTASPPPLEVESPPSPPIESPPPLLESPPPPLES : 94
AtPERK15 : -----MSTDTPSLSSPPAPEF----- : 17
OsPERK1 : -----SPSSPP---PANQT-----ATP---PPANQTAAP----- : 25
OsPERK2 : -----MWAREWYSKPAERARP-----AAFVPPPPPTPPQYVPEEPSAFAKLYA : 45
OsPERK3 : -----MARP-----AAFVPPP---QYVPEEPSAFARLY : 27
OsPERK4 : ----- : 7
OsPERK5 : ----- : -
OsPERK6 : SSSGNGS---NKAPPEESDNSS---NGSSSSPTPSSQSSSDSDSGGSSSPSQGSSSPSPPPSGSSSEHSS : 89
OsPERK7 : ----- : -
OsPERK8 : ----- : -
GmPERK1 : AAPPLQTPSSNNTSPSPSTA--TTPPLQQTTPSTSPQPPASP-----PPSTPSFANPPSSP---PSSPPFMSGT : 80
GmPERK2 : -----MSS-PHNSPD---NETPDNSTPDDADNSSSPSSQSPSSPPPS---SPPSSPPSSFP : 54
GmPERK3 : -----MSS-PHNSAPH---NSSPDNSTPDD---ATFNN---SIPDNSTPDNSIP : 39
GmPERK4 : AAPPPQTSFASANTTSPSPSTV--TTPPPQQTPTSSTSPQPPASP-----PPTTSPFANPPSPSPSPSPSSPMSGT : 83
GmPERK5 : -----MASNSDKDSP---TPSPDSS---SQSPSSPPSSQDSSPPPS---SQDNSSPPSSFP : 52
GmPERK6 : ASPPLPP-FDITPPPSMYPTPPAPPVT---PPP---SAVTPLPLEFLLP---SPFVSLPPFP : 67
GmPERK7 : APPPLSLEDITPPPSMYPTPPAPPVT---PPPETLLVQDSSPPSSVTPLELLEFLLP---SPFVSLPPPLPSSTVT : 84
GmPERK8 : -----SPPPTNGTAPPSTPSA---PPPATPSAPPSTPSPPPATPSPPPATPSS : 57
GmPERK9 : VAVPPALGGILSPPSSSSPTNSKSPS---FPNSQFN---QTQTFNSPAPSSSAPP---SPSPQAVDT : 78
GmPERK10 : RKQKSSHDNDKESAPSKPPDLDTQESAPSN---SPPSPPPP---PPQLKPLPILSPRLKPSISLSPKDLGSGFSW : 97
GmPERK11 : -----SPPANNGTAPPSTP---ATPSAPPATPSAPPSTPSPPPATPSS : 52
GmPERK12 : -----MSS-PHNSPDSSPDNATPDNSTPDDSDSSPPS-QSPSSPPPS---SPPSSPPSSFP : 58
GmPERK13 : PAPP-----PELSSA---PPSSTPLPLP-----SPFSL : 38
GmPERK14 : -----MSS-PHNSAPH---NSTPDNSPDD---ATPDN---SIPDNSTPDDATP : 39
GmPERK15 : ----- : 10
GmPERK16 : VAVPPALGAILSPPSSSSPTNTSTPPS-----PPSSQFNQTQTQTFNSPAPSSPSDPSA--PPSPPPQAVPLT : 82

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260          *          280          *          300          *          320          *          340
TaPERK1 : -----PPPAAPASPP-----APSSPTPATP : 71
TaPERK2 : ----- : -
TaPERK3 : --TP-PAALPTPKP-----APSTSTPPPTTSTPPAPPKRSF-----AAAPPTTAPAPRP : 119
TaPERK4 : -----PPPAAPASPP-----APSSPTPATP : 71
TaPERK5 : LTDLRFQNSFGQPLPATLSNLVQLTSLRIGDILNGSSSSSLAFISNMTSLNSLVLNRCRISDTLLSVNFSKFTSLNLLDLSFNFI : 318
TaPERK6 : LTELRFQNSFEGPIPATLSNLAQLTSLRIGDILNGSSSSSLAFVNMNTSLSTLVLNRCRISDKLSSIDFSKLTSLNLLDLSFNFI : 317
TaPERK7 : MTQLRLQGNFQGPPIPRSLNLIKLTSLRIGDIVNGSSS-MEFGVNMNTSLGELVLRNSKISDTLASVDFSKFVNLTLLDLSFNFI : 338
TaPERK8 : LTDLRFQNSFGQPLPATLSNLIQLTSLRIGDIVNGSSSSSLAFISNMTSLNTLVLNRCRISDTLLSVNFSKFTSLNLLDLSFNFI : 318
TaPERK9 : LTELRFQNSFEGPIPATLSNLAQLTSLRIGDILNGSSSSSLAFVNMNTSLSTLVLNRCRISDKLSSIDFSKLTSLDLDLDSFNFI : 319
TaPERK10 : LTDLRFQNSFGQPLPATLSNLVQLTSLRIGDIVNGSSSSSLAFISNMTSLNTLVLNRCRISDTLLSVNFSKFTSLNLLDLSFNFI : 318
TaPERK11 : LTELRFQNSFEGPIPATLSNLAQLTSLRIGDILNGSSSSSLAFVNMNTSLSTLVLNRCRISDKLSSIDFSKLTSLNLLDLSFNFI : 228
TaPERK12 : MTQLRLQGNFQGPPIPRSLNLIKLTSLRIGDIVNGSSS-MAFGVNMNTSLGELVLRNSKISDTLASVDFSKFVNLTLLDLSFNFI : 337
TaPERK13 : --PPDFVASPPFVP-----VASPPPTP-PATMPPAQVPPPPA-----PAADPPKQSPLRP : 116
TaPERK14 : -----PPPSTPAATFP-----SPGATPATP : 65
TaPERK15 : --SPPPPASPPPST-----PPASRSPPPSSPPSPSPSQ-----QSSPPPAQSTPP : 124
TaPERK16 : --PPPALPSSPPPPALS-----PPPPDAPPPSLPPSPSPS-----PPPAEVQAPPPP : 126
TaPERK17 : PPD-----GASTPPP-----VNPFVNPFPPTPTP----- : 101
TaPERK18 : --PPDPTASPPFVP-----VASPPPAALPPSPPTAVPPPPA-----PAADPPKQSPLRP : 117
TaPERK19 : -----PPSTPAAPPP-----SSGTTPATP : 70
TaPERK20 : --SPPPPASPPPST-----PPASRSPPPSSPPSPSPSQ-----QSSPPPAQSTPP : 124
TaPERK21 : --PPPALPSSPPPPALS-----PPPPDAPPPSLPPSPSPS-----PPPAEVQAPPPP : 128
TaPERK22 : PPPPPVAIPPPSP-----VTAPPPPPVVAIPPSLPQVAAVPTTAKPPTIVNPPAPEPSVQPPVNSPPPPSPPPPPR : 179
TaPERK23 : ----- : -
TaPERK24 : -----PPPSTPAAPPP-----SSGTTPATP : 71
TaPERK25 : --PPPALPSSPPPPALS-----PPPPDAPPPSLPPSPSPS-----PPPAEVQAPPPP : 128
TaPERK26 : ----- : -
TaPERK27 : -----SST--QSTPPPG : 69
TaPERK28 : LTELRFQNSFGQPIPATLSNLGQLASLRIGDILNGSSSSSLAFISNLTSLNTLVLNRCRISDKLVSIDFSKFASLNLLDLSFNFI : 181
TaPERK29 : -----SST--QSTPPPG : 70
TaPERK30 : -----KSSPPPSAAPP : 26
TaPERK31 : -----KSSPPPSAAPP : 26
TaPERK32 : LTELRFQNSFGQPIPATLSNLSQLASLRIGDILGSSSSSLAFINNLTSINTLVLNRCRISDKLVSIDFSKFTSLNLLDLSFNFI : 324
TaPERK33 : --PPFFVASPPPPDAPPPPPSPVSAAPPPAD-AAPPPDNAPLPPD-----NAAAPPSPTQAA : 160
TaPERK34 : --PPFFVASPPPPDAPPPPPSPVSAAPPPADTAAPPPDNAPPPD-----NAAAPTSPTQAP : 169
TaPERK35 : LTELRLQGNFQGPPIPATLSNLGQLASLRIGDILNGSSSSSLAFVNMNTSLNTLVLNRCRISDKLVSIDFSKFTSLNLLDLSFNFI : 321
TaPERK36 : --PPFSKSKSSPSSSS-----PSRPPSSRRNGGKSDSPPPPTDESSG-----DGEDTSSPPPKRSPPEQ : 153
TaPERK37 : --PPFFVASPPPPDAPPPPPSPVSAAPPPAD-AAPPPDNTPPPPD-----NAAAPPSPTQAP : 169
AtPERK1 : -----PPSSPLPP-----SLPPSPPGS : 72
AtPERK2 : SPPPLTPSPPLPSPPTTPSPPLTPSPPTTPSPPLTPSPPPAITSPPLTPSPPLPSPPTTPSPPPSPSIPSPPLTPSPPPSSPLRP : 157
AtPERK3 : -----EPLFSEPP-----PPKAFVNV : 67
AtPERK4 : -----SSSPPDSTSP : 57
AtPERK5 : -----ETSPPTSPSSSP : 76
AtPERK6 : -----QSPSPQGNNNN : 73
AtPERK7 : -----ESPPPLPENSS : 72
AtPERK8 : --PPFFVSSPPPS-----SSPPSPFVITSPPTVASS-----PPFFVVIASPPP : 99
AtPERK9 : --PPPLPK--PESSS--PPQVIPSPP--PSTSPQVIPSPPP--SASPP--PALVPLPS--SPPPASVPPPR : 134
AtPERK10 : --PPTTIPVSPPEPSP--PPPLPTEAPPANVSSPPPESSPPPPPP--TEAPPTTPTITSPSPPT--NPPPPESPPSLP : 158
AtPERK11 : --PPPSITPPPSPP-----PQPQPPQPTTPTGDSVVVIP-----FPKPLPPPSLFP : 131
AtPERK12 : --PFVDSPTPSP-----PPFTSNESFPEDSETFP-----APFNESNDNNPPP : 126
AtPERK13 : --PPSSPPPPDA-----PPPIPIVFP-PPIDS-----PPES-TNSPPP : 120
AtPERK14 : PSPSPPH-----VSAPSGSPPLPFLPAKSPSPPS-----SPPSETVPPGNTISPPPSLPESTP : 149
AtPERK15 : -----PSTTPTDA : 25
OsPERK1 : -----PPASNSSSPP-----APG-SLSP : 44
OsPERK2 : -----VAGDVVGRA : 54
OsPERK3 : -----DVVDRA : 33
OsPERK4 : -----KSSPPLMAAS-P : 18
OsPERK5 : ----- : -
OsPERK6 : --PPAPPQSSSSSSSS-----SSSGGSKSSPEAPSPPESSGNGGG-----GGGGRSSPPFNWSPPPPQ : 149
OsPERK7 : ----- : -
OsPERK8 : -----SKS--PSPPSP : 35
GmPERK1 : --PPPLVPPSPPPSP--PSTPAAQPAVPPSSPPPPSPSPSVP--SSPPSNPNRNTSPPP--SPPQPAAPPQ : 150
GmPERK2 : -----PSSPPSSS--S : 64
GmPERK3 : -----DNSTPDNSTSNK : 51
GmPERK4 : --PPPLVPPSPPPSPSSPPSSPAAPPEVPPSSPPPP--SPSAEVPPNPNRNTSPPSPQPPQSPAPPPQPPAPPQ : 165
GmPERK5 : -----PSSPPPS-SSPP : 63
GmPERK6 : LSPSTP-----TAASQPPPLPFATA-----PATTTFPPFAVALSPP--TPTATFP : 110
GmPERK7 : PSPPTP-----TAESQPPPFATA-----PAPTTFPPFAVAPSP--TPTATFP : 127
GmPERK8 : -----PPPATPSSPPPS-----TPSSPPPATP : 79
GmPERK9 : --PPPSISLSPPP-----TLPPSP--DSPPPLPPAS-----PPSPPATAPP : 119
GmPERK10 : SPPPPPSRSPSPPS-----SLSLSSSSPPSPS-----SPPPPSPSP : 137
GmPERK11 : -----PPPATPSSPPPA-----TPSSPPPATP : 74
GmPERK12 : -----PSSPPSSPPPS : 70
GmPERK13 : -----PAN-PLP-----APPPQSFASISSP : 57
GmPERK14 : -----DNSIPDN : 46
GmPERK15 : --PPPSRPP--LPLPSPLRPPSPL-----PPSP--PPS : 41
GmPERK16 : --PPPSISLSPSSSTP-----PPTLPPSP--DSPPPLPASPTP-----FVTTSPSPFVTTSPSPPATTSPPP : 146

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*          440          *          460          *          480          *          500          *
TaPERK1 : G---GGSGVSTSVVVGVAVGGFVLLLLATFVCLCCLRKKRRRQ-----PPPPHYGY-----PP : 181
TaPERK2 : -----MFCLT----- : 5
TaPERK3 : --TQSAGERGRKASPSFGSSNGGASNGVVI--AVGAVLAFVLVTLIAAAVLYTKRRRRGRDDYRAGFRSPPYSELPE----- : 255
TaPERK4 : -----GSGVSTSVVVGVAVGGFVLLLLATFVCLCCLRKKRRRQ-----PPPPHYGY-----PP : 177
TaPERK5 : QRNTPCFGLGPHSSSFVAVDCGSDRPIGSDNSLYQDDAATLGAASYVVTGAPTGWASNVGREMDASNGSSIIYSSHQFLINTLDTE : 485
TaPERK6 : QRNTPCFGLGPHSSSFVAVDCGSDRPIGSDNSLYQDDAATLGAASYVVTGAPTGWASNVGREMDASNGSSIIYSSHQFLINTLDTE : 485
TaPERK7 : QRNTPCSLGSPHSSSLAVDCGSSRTISGSDNAMYQADNANLGAASYVVTGAPTGWASNVGREMDASNVSSIIYSSHQFLINTLDSE : 508
TaPERK8 : QRNTPCFGLGSPKSSSFVAVDCGSDRPIGSDNSLYQDDAATLGAASYVVTGAPTGWASNVGREMDASNGSSIIYSSHQFLINTLDTE : 486
TaPERK9 : QRNTPCFGLGSPKSSSFVAVDCGSDRPIGSDNSLYQDDAATLGAASYVVTGAPTGWASNVGREMDASNGSSIIYSSHQFLINTLDTE : 487
TaPERK10 : QRNTPCFGLGSPKSSSFVAVDCGSDRPIGSDNSLYQDDAATLGAASYVVTGAPTGWASNVGREMDASNVSSIIYSSHQFLINTLDTE : 486
TaPERK11 : QRNTPCFGLGSPKSSSFVAVDCGSDRPIGSDNSLYQDDAATLGAASYVVTGAPTGWASNVGREMDASNGSSIIYSSHQFLINTLDTE : 396
TaPERK12 : QRNTPCSLGSPKSSSLAVDCGSSRTISGSDNAMYQADNANLGAASYVVTGAPTGWASNVGREMDASNVSSIIYSSHQFLINTLDSE : 507
TaPERK13 : --SPTFVDPTTPTAPTTPSPPTPGFGPPS--VPTPTTTPPTPIAFN-----IPQVPSWQDS----- : 233
TaPERK14 : -----SSALNTATVAGIAGVGLIALLLASLLCFCMFKKRRRHHPHHPPPP-----PPPPHLLHYGHPPPPP : 166
TaPERK15 : ----AGTSPPIETPTPTSPVAAAGQVPAAPGTPSAASLLPSSIMPAS-----RPPPGTWQSPPPGPAVARASPPSLAP : 257
TaPERK16 : ----VAVYSPPPRIASPPPPRHFFK-----PHYAPP-----RSPGRPHSNSTR-----S : 222
TaPERK17 : LPDATPP--PPEDVPSSPPFPNDAPAAAAPPSPPLTSPPPPPQASASAP-----STSAKSSSSSGTAV--G : 228
TaPERK18 : --SPT--SPTVPATPTAPSPPTPGFGPPS--VPSATTTTPTPIGPN-----MPQDPSWQDS----- : 232
TaPERK19 : ----SSALNTATVAGIAGVGLIALLLASLLCFCMFKKRRRHHPHHPPPP-----PPPPHLLHYGHPPPPP : 170
TaPERK20 : ----AGTSPPIETPTPTSPVAAAGQVPAAPGTPSAASLLPSSIMPAS-----GRPPGSWQSPPPGPAVARASPPSLAP : 257
TaPERK21 : ----VAVYSPPPRIASPPPPRHFFK-----PHYAPP-----RSPGRPHSNSTR-----S : 224
TaPERK22 : PPDATPP--PPEDVPYSPAPNDAPAEQAPPSALTWSSPPPLSTDVVP-----ATLAKSSSSSRTTVGLG : 311
TaPERK23 : -----SAHYS----- : 5
TaPERK24 : ----SSALNTATVAGIAGVGLIALLLASLLCFCMFKKRRRHHPHHPPPP-----PPPPHLLHYGHPPPPP : 171
TaPERK25 : ----VAVYSPPPRVASPPPP--RHHTK-----PHYAPP-----RSPGRSHLNSTR-----S : 223
TaPERK26 : ----- : -
TaPERK27 : -----SSESGGSKGGGGSSGRGKGGKQDDSPFVEAVVVG-----V : 162
TaPERK28 : QRNTPCFLDSPKSSSFVAVDSG--KSIIVGPDNSVYEPDRASLGAASLYVTGAPTGWASNVGKEMEANNGSYIIHSPGQFLINLEPE : 347
TaPERK29 : -----SSESGGSKGGGGSS--KGGKGGKQDGSPPFVEAVVVG-----V : 158
TaPERK30 : -----RSGDSSRSSQTSABRVV-----FNNTAEIIFA-----A : 100
TaPERK31 : -----RGDESSRSSSSQASHRVV-----SNTAEIIFA-----A : 104
TaPERK32 : QRNTPCFLDSPKSSSFVAVDSG--KSIIVGPDNSVYEPDRASLGAASLYVTGAPTGWASNVGKEMEANNGSYIIHSPGQFLINLEPE : 490
TaPERK33 : --VTPTADRSTAPAPPSTGGMSSGATAGVAVVAVIAFLCFAGVVFVCLTKRRRKRYSQYYPGFAAPPYTPQHMSGEAPFLRV : 306
TaPERK34 : --VTPTADRSTAPAPPSTGGMSSGATAGVAVVAVIAFLCFAGVVFVCLTKRRRKRYSQYYPGFAAPPYTPQHMSGEAPFLRV : 315
TaPERK35 : QRNTPCFLDSPKSSSFVAVDSG--KSIIVGPDNSVYEPDRASLGAASLYVTGAPTGWASNVGKEMEANNGSYIIHSPGQFLINLEPE : 487
TaPERK36 : VNHSFGAP--PGLVSIAPPGTGVMSAQLPGAQG--GATGAGGMQAAGSSAS--SSTNGAGGSSAASASAQQ : 286
TaPERK37 : --VTPTADRSTAPAPPSTGG--MSSGATAGVAVVAVIAFLCFAGVVFVCLTKRRRKRYSQYYPGFAAPPYTPQHMSGEAPFLRV : 314
AtPERK1 : -----SDGLSTGVVVGIAIGGVA--ILVILTLCLLCKKRRRRHDEAA-----YYVP-----PP : 181
AtPERK2 : -----SKELSKGAMVGIAGGGFVLLVALALIFFLCKKRRR--DNEA----- : 260
AtPERK3 : -----PSRLSTGAVVGISIGGG--VEVLTLLFFLCKKRRR--DDKA----- : 155
AtPERK4 : -----PPGDTGGSRSNDNPPSSGGSSGGGGGRSNTNTAIIVG-----V : 156
AtPERK5 : -RTSGDGGSPSPRSISPPQNSGSDSSSSGNHP--QANIGLIIG-----V : 193
AtPERK6 : -RNS--DRNSPSPRALAPRSPSSGGSSSSGN--EPTAAIVG-----I : 191
AtPERK7 : -KTS--DHSHSQPRSLAPP--TSNSGSSSSND--GLNIGAVIG-----L : 179
AtPERK8 : -TTTTSPPPPATSASPPSSNP-----TDPSTLAPPPT-----PLEVVPREKPIAKPTGPASNNGN--NTLP : 224
AtPERK9 : -PSPSP--SDRPSQ--SPPPPEDTKQP--PRRSPNSPPTIFSSP-----PRSPPEILVPGSNNPQNNPTLRPLDA : 267
AtPERK10 : TSPSPSPDSKRFVHPSPSPPEETLPPPKSPDPLPSNSSPPTLLPSS--SVVSPSPPRKSVSGPDNPSFNNPTP--V : 316
AtPERK11 : ---SPGNLQPLDSPLGGENRVSSSSSPSPSLGSSNHSGGSSNRH-----NANSNGDGGTQQSSNESN : 257
AtPERK12 : ---PPANAPP--SPFPTVPPKTPSSGFVVS--PSLTSFKSTPTFNQG-----NGDGGGGGGG : 241
AtPERK13 : ---PPAPPNAPPNSSHALPPKSTAAG--GPLTSPSRGVPPSSGNS-----VPPANSGGG : 230
AtPERK14 : PAAVTLPPFFGAGQLPDGTVAPPVIEPKTSPAESISPTP--QPLVP-----KSLFVTTTSHRSSAGFL : 282
AtPERK15 : ---RNVALTGLITGVVVGATEVLLGVCIFVCYKRRKRRKLLK----- : 93
OsPERK1 : -----SSGLTFVVVGVIVGGLVLLVLTILLVCLFKKRRRHHHHPPPP-----PPPPHLLHYGHPPPPP : 130
OsPERK2 : -----SSGLSSTAVVWIIVAAGVVGAVLALCVLTLWIRRCRRQ----- : 134
OsPERK3 : -----PSFLNSVAVK--VAAGVVGLVGLCLVALWIRRRR----- : 120
OsPERK4 : -----SGSEDVARSALASARRGG-----YNAMVEIVFA-----A : 97
OsPERK5 : -----MSP--TSPLS----- : 8
OsPERK6 : PQSPPSAANQSVVFIIVFVANSPPGMLPPPQVIDATPSGALSSTNFPGG-----RNSTAGSNTSLSQQQHT : 285
OsPERK7 : -----SHASRRLSTSITFAGG-----LDVTSELVIA-----A : 34
OsPERK8 : -----KSGGSS-----RGESGRYRQDVTVAGVFLF-----V : 107
GmPERK1 : APSTPPSRTSPPTPSSQPAPPSNSTPRSSPPSPSTINLAPS-----PPSRILSSPPPPPAQNGTE--NS : 286
GmPERK2 : -----KSLDSPSSRNSSGSDSGSRDSSNGGGDDSSKAIVG-----A : 159
GmPERK3 : -----SGKDSSNKLSNEKSLGSSN--DSSNKVAMG-----A : 123
GmPERK4 : EPSTPPSRTSTPTPSSQAPPTSNSSTPRSSPPSPSTINLAPP-----PPSRVLSSPLPSPAQNGTK--NP : 301
GmPERK5 : -----HRLSPPKSSSSG--SSDGLKDSSEH--SLSMFVIIG-----I : 156
GmPERK6 : -----SGSLP-----VA-----VNVQKPSIFHVSSG--L : 183
GmPERK7 : -----GGSLP-----VA-----VDVQKPSIFHVSSG--L : 202
GmPERK8 : S---SSSSSISTGVVVGIAVAVVLLVLSILCICRKKRRRDEEYAP-----PPQ-----P : 199
GmPERK9 : ---SVSEFPKPPSSDVHPPSTLP--SDTSGSSPATLDPPTNTTAAQGPVTVSLPSLPEKPTARPTNDGNTSMSS--NNTP : 267
GmPERK10 : ---SLRNPASNDSTPRTSDK--PRSGHGHGGGATSSHTNSTGSSFN-----QTSDDNSEK----- : 241
GmPERK11 : SPPSSSSSISTGVVVGIAVAVVLLVLSILCICRKKRRRDEEYHAP-----PPQQQQ-----P : 192
GmPERK12 : -----KSLDSPSSRNSSGSDSGSRDSSNGGGDDSSKAIVG-----A : 166
GmPERK13 : -----PPTTRKNPFDSSHSTP-----SHTSGLAPP-----PPS-----AQN----- : 115
GmPERK14 : -----SGKDSFNKSLN--AKSSGSSN--DSGDKAAMG-----A : 112
GmPERK15 : ---PSSRRNAPSNDSTQGTSEK--SRSGHH--KHG--VAHSTNSTGSSFN-----QTSDDNSEK----- : 149
GmPERK16 : ---SVSETPPKPPSSDVHPPSTLPSTPPSDPSGSSPPASLDPPTNKTVVGGPKVSLPSLPEKPTARPTNDGNTSMSS--NNTP : 298

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Protein tyrosine kinase domain

	*	700	*	720	*	740	*	760																																																				
TapERK1	:	PPSP-GTALGFTNSK	T	T	D	L	V	R	A	T	D	G	F	S	D	A	L	L	G	G	G	F	Y	H	G	V	P	-	N	G	R	E	I	A	V	K	L	L	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		338		
TapERK2	:	PPSP-GTALGFSNSK	T	T	D	L	V	R	A	T	D	G	F	S	D	A	L	L	G	G	G	F	Y	H	G	V	P	-	N	G	R	E	I	A	V	K	L	L	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		156		
TapERK3	:	RLKACVSDMSVGNRS	F	T	T	Q	M	Y	Q	I	D	G	F	S	P	R	L	L	G	G	G	F	Y	H	G	V	P	-	E	S	R	D	V	A	V	K	L	L	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		369		
TapERK4	:	PPSP-GTALGFTNSK	T	T	D	L	V	R	A	T	D	G	F	S	D	A	L	L	G	G	G	F	Y	H	G	V	P	-	N	G	R	E	I	A	V	K	L	L	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		333		
TapERK5	:	LSLEQEELYSIVGRF	V	L	S	G	L	R	S	A	T	D	N	F	S	P	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	A	S	H	G	K	E	E	A	T	E	T	I	S	F	V	H	R		739		
TapERK6	:	LSLEQEELYSIVGRF	V	L	S	G	L	R	S	A	T	D	N	F	S	P	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	K	S	H	G	K	E	E	A	T	E	T	I	S	F	V	H	R		737		
TapERK7	:	ILLELEELYTIVGRF	V	L	S	G	L	R	S	A	T	E	N	D	S	S	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	S	S	N	G	E	K	L	E	A	T	E	T	I	S	F	V	H	R		760	
TapERK8	:	LSLEQEELYSIVGRF	V	L	S	G	L	R	S	A	T	D	N	F	S	P	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	A	S	H	G	K	E	E	A	T	E	T	I	S	F	V	H	R		738		
TapERK9	:	LSLEQEELYSIVGRF	V	L	S	G	L	R	S	A	T	D	N	F	S	P	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	K	S	H	G	K	E	E	A	T	E	T	I	S	F	V	H	R		739		
TapERK10	:	LSLEQEELYSIVGRF	V	L	S	G	L	R	S	A	T	D	N	F	S	P	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	A	S	H	G	K	E	E	A	T	E	T	I	S	F	V	H	R		740		
TapERK11	:	LSLEQEELYSIVGRF	V	L	S	G	L	R	S	A	T	D	N	F	S	P	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	K	S	H	G	K	E	E	A	T	E	T	I	S	F	V	H	R		648		
TapERK12	:	MLELEELYTIVGRF	V	L	S	G	L	R	S	A	T	E	N	D	S	S	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	S	S	N	G	E	K	L	E	A	T	E	T	I	S	F	V	H	R		759	
TapERK13	:	EFKDITMSEYSMGNCR	F	T	T	E	M	H	N	I	N	G	F	S	D	A	L	L	G	G	G	F	Y	H	G	V	P	-	E	S	R	V	A	I	K	L	L	D	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		395		
TapERK14	:	LQSPFGNALSFSS--K	T	T	T	E	L	V	A	N	E	F	D	A	L	L	L	G	G	G	F	Y	H	G	V	P	-	D	T	E	V	A	V	K	L	L	D	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		307			
TapERK15	:	ASPSDINSYEFTGYK	C	M	D	L	A	G	I	G	C	F	S	A	A	V	I	G	G	F	G	V	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	L	A	G	G	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		410	
TapERK16	:	GFPYSPADSGIGYSRI	L	A	P	E	N	L	A	G	I	N	D	E	D	E	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	I	K	L	L	I	N	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		401		
TapERK17	:	GGGDPGGPPLPAMTG	T	L	G	D	L	A	A	A	D	G	F	S	E	A	L	L	G	G	F	G	V	Y	H	G	V	P	-	N	G	E	V	A	I	K	L	L	A	G	S	G	G	H	E	R	E	E	I	I	S	F	V	H	R		382			
TapERK18	:	EFKDITMSEYSMGNCR	F	T	T	E	M	H	N	I	N	G	F	S	D	A	L	L	G	G	G	F	Y	H	G	V	P	-	E	S	R	V	A	I	K	L	L	D	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		395		
TapERK19	:	LQSPFGNALSFSS--K	T	T	T	E	L	V	A	N	E	F	D	A	L	L	L	G	G	G	F	Y	H	G	V	P	-	D	T	E	V	A	I	K	L	L	D	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		311			
TapERK20	:	APPSDINSYEFTGYK	C	M	D	L	A	G	I	G	C	F	S	A	A	V	I	G	G	F	G	V	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	L	A	G	G	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		410	
TapERK21	:	GFPYSPADSGIGYSRI	L	A	P	E	N	L	A	G	I	N	D	E	D	E	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	I	K	L	L	I	N	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		403		
TapERK22	:	GG-DPGGPPLPAMTG	T	L	G	D	L	A	A	A	D	G	F	S	E	A	L	L	G	G	F	G	V	Y	H	G	V	P	-	N	G	E	V	A	I	K	L	L	A	G	S	G	G	H	E	R	E	E	I	I	S	F	V	H	R		466			
TapERK23	:	SMPPPPP--AIFGSQ	S	T	T	E	L	A	S	A	T	G	C	F	S	K	A	L	L	G	G	F	Y	H	G	V	P	-	E	S	R	V	A	I	K	L	L	D	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		109		
TapERK24	:	LQSPFGNALSFSS--K	T	T	T	E	L	V	A	N	E	F	D	A	L	L	L	G	G	G	F	Y	H	G	V	P	-	D	T	E	V	A	V	K	L	L	D	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		312			
TapERK25	:	GFPYSPADSGIGYSRI	L	A	P	E	N	L	A	G	I	N	D	E	D	E	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	I	K	L	L	I	N	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		402		
TapERK26	:	GGGDPGGPPLPAMTG	T	L	G	D	L	A	A	A	D	G	F	S	E	A	L	L	G	G	F	G	V	Y	H	G	V	P	-	N	G	E	V	A	I	K	L	L	A	G	S	G	G	H	E	R	E	E	I	I	S	F	V	H	R		91			
TapERK27	:	SMPPPPP--AIFGSQ	S	T	T	E	L	A	S	A	T	G	C	F	S	K	A	L	L	G	G	F	Y	H	G	V	P	-	E	S	R	V	A	V	K	L	L	A	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		336		
TapERK28	:	LSLEQEELYSIVGRF	V	L	S	G	L	R	S	A	T	E	N	D	S	S	L	L	G	G	G	F	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	S	E	T	S	H	G	K	E	E	A	T	E	T	I	S	F	V	H	R		599		
TapERK29	:	SMPPPPP--AIFGSQ	S	T	T	E	L	A	S	A	T	G	C	F	S	K	A	L	L	G	G	F	Y	H	G	V	P	-	E	S	R	V	A	V	K	L	L	A	G	S	G	G	H	E	R	E	E	I	I	S	F	V	H	R		333				
TapERK30	:	PTSPAPQETLGLGR	T	T	T	E	L	A	A	T	G	C	F	S	Q	S	L	L	G	G	F	Y	H	G	V	P	-	S	R	A	V	A	V	K	L	L	A	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		278			
TapERK31	:	PTSPAPQETLGLGR	T	T	T	E	L	A	A	T	G	C	F	S	Q	S	L	L	G	G	F	Y	H	G	V	P	-	S	R	A	V	A	V	K	L	L	A	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		318			
TapERK32	:	LQSPFGNALSFSS--K	T	T	T	E	L	V	A	N	E	F	D	A	L	L	L	G	G	G	F	Y	H	G	V	P	-	D	T	E	V	A	V	K	L	L	D	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		741			
TapERK33	:	RSMATSGDLSVGNK	S	F	R	D	L	Y	E	I	G	C	F	R	D	K	L	L	G	G	F	G	V	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	L	A	G	G	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		448
TapERK34	:	RSVATSGDLSVGNK	S	F	R	D	L	Y	E	I	G	C	F	R	D	K	L	L	G	G	F	G	V	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	L	A	G	G	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		455
TapERK35	:	LQSPFGNALSFSS--K	T	T	T	E	L	V	A	N	E	F	D	A	L	L	L	G	G	G	F	Y	H	G	V	P	-	D	T	E	V	A	V	K	L	L	D	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		738			
TapERK36	:	SFRGAGYPSGSMESK	S	F	R	E	L	T	S	I	T	S	N	F	R	D	V	I	G	G	F	G	V	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	L	A	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		464
TapERK37	:	RSVATSGDLSVGNK	S	F	R	D	L	Y	E	I	G	C	F	R	D	K	L	L	G	G	F	G	V	Y	H	G	V	P	-	D	G	R	F	V	A	V	K	L	L	A	G	G	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		454
AtPERK1	:	LPPP-SPGLVIGFSK	T	T	T	E	L	S	R	A	N	G	F	S	E	A	L	L	G	G	F	Y	H	G	V	P	-	N	G	E	V	A	V	K	L	L	A	G	S	G	G	E	R	E	F	Q	E	E	I	I	S	F	V	H	R		334			
AtPERK2	:	PPSP-GLALGLGIYQ	T	N	E	L	S	R	A	N	G	F	S	E	A	L	L	G	G	F	Y	H	G	V	P	-	N	G</																																

Protein tyrosine kinase domain

	*	780	*	800	*	820	*	840	*				
TapERK1	ELVSLVGYC	ISGGKRLVYE	VTNTEFFSL	LGK---	GRPTLE	PIRLRLGSA	ARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 419	
TapERK2	ELVSLVGYC	ISGGKRLVYE	VTNTEFFSL	LGK---	GRPTLE	PIRLRLGSA	ARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 237	
TapERK3	ELVSLVGYC	IANSQRILVVD	VVSDTTHYSL	---	QGGRFVLE	SAPVRLIAA	AARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 450	
TapERK4	ELVSLVGYC	ISGGKRLVYE	VTNTEFFSL	LGK---	GRPTLE	PIRLRLGSA	ARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 414	
TapERK5	NLVK YGC	IEGNKPLVYE	LELGSDDHAF	FG---	KGKSSLD	PTFETCLV	ARGLS	FLB	ESSI	VVHRDIKASNILL	DN	: 820	
TapERK6	NLVK YGC	IEGNKPLVYE	LELGSDDHAF	FG---	KGKSSLD	PTFETCLV	ARGLS	FLB	ESSI	VVHRDIKASNILL	DN	: 818	
TapERK7	NLVK YGC	IESKTPLVYE	CLELGSDDHAF	FG---	KGGLNLD	PRFETCLV	ARGIAYL	B	ESSV	IVHRDIKASNILL	DD	: 841	
TapERK8	NLVK YGC	IEGNKPLVYE	CLELGSDDHAF	FG---	KGKSSLD	PTFETCLV	ARGLS	FLB	ESSI	VVHRDIKASNILL	DN	: 819	
TapERK9	NLVK YGC	IEGNKPLVYE	LELGSDDHAF	FG---	KGKSSLD	PTFETCLV	ARGLS	FLB	ESSI	VVHRDIKASNILL	DN	: 820	
TapERK10	NLVK YGC	IEGNKPLVYE	CLELGSDDHAF	FG---	KGKSSLD	PTFETCLV	ARGLS	FLB	ESSI	VVHRDIKASNILL	DN	: 821	
TapERK11	NLVK YGC	IEGNKPLVYE	LELGSDDHAF	FG---	KGKSSLD	PTFETCLV	ARGLS	FLB	ESSI	VVHRDIKASNILL	DN	: 729	
TapERK12	NLVK YGC	IESKTPLVYE	CLELGSDDHAF	FG---	KGGLNLD	PRFETCLV	ARGIAYL	B	ESSV	IVHRDIKASNILL	DD	: 840	
TapERK13	ELVSLVGYC	ISGDQRILVVD	VVSDTTHYSL	---	GRGVFVLE	PAVRLISA	SARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 476	
TapERK14	ELVTLVGYC	ISEDKRLVYE	VVNTTEFFSL	GR---	RGFTMD	PSLRILGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DR	: 388	
TapERK15	ELVTLVGYC	VTEHRLVYE	VVSDTEHSL	---	GEGLFVMD	PKMLIAG	SARGL	T	FLBEDCH	PKI	IHRDIKASNILL	DA	: 491
TapERK16	ELVSLVGYC	VSEGQRILVVD	VVNTTYFSL	---	VN-EVPLD	RTVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 481	
TapERK17	NLVSLVGYC	IHAEQRLVYE	VPKTESSL	HLH---	GSGRATL	PRWRLVGS	SARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 464	
TapERK18	ELVSLVGYC	ISGDQRILVVD	VVSDTTHYSL	---	GRGVFVLE	PAVRLISA	SARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 476	
TapERK19	ELVTLVGYC	ISEDKRLVYE	VVNTTEFFSL	GR---	RGFTMD	PSLRILGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DR	: 392	
TapERK20	ELVTLVGYC	VTEHRLVYE	VVSDTEHSL	---	GEGLFVMD	PKMLIAG	SARGL	T	FLBEDCH	PKI	IHRDIKASNILL	DA	: 491
TapERK21	ELVSLVGYC	VSEGQRILVVD	VVNTTYFSL	---	VN-EVPLD	RTVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 483	
TapERK22	NLVSLVGYC	IHAEQRLVYE	VPKTESSL	HLH---	GSARATL	PRWRLVGS	SARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 548	
TapERK23	ELVSLVGYC	ISGDQRILVVD	VVSDTTHYSL	---	GRGVFVLE	PAVRLISA	SARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 190	
TapERK24	ELVTLVGYC	ISEDKRLVYE	VVNTTEFFSL	GR---	RGFTMD	PSLRILGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DR	: 393	
TapERK25	ELVSLVGYC	VSEGQRILVVD	VVNTTYFSL	---	VN-EVPLD	RTVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 482	
TapERK26	NLVSLVGYC	IHAEQRLVYE	VPKTESSL	HLVSGS	GRATL	PRWRLVGS	SARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 175	
TapERK27	ELVSLVGYC	IAGASQRILVYE	VVADTEHSL	---	GKGLFVMD	PKLALGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 418	
TapERK28	NLVK YGC	IEGNKPLVYE	LELGSDDHAF	FG---	KGKSSLD	STFETCLV	ARGIAYL	B	ESSI	VVHRDIKASNILL	DN	: 680	
TapERK29	ELVSLVGYC	IAGSSQRILVYE	VVADTEHSL	---	GKGVFVMD	PKLALGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 415	
TapERK30	ELVSLVGH	IAGASQRILVYE	VVADTEHSL	---	GKGLFVMD	PKLALGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 359	
TapERK31	ELVSLVGH	IAGTSRILVYE	VVADTEHSL	---	GEGSFA	ATLRLIAA	AARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 399	
TapERK32	NLVK HGC	IEGNKPLVYE	LELGSDDHAF	FG---	KGKSSLD	STFETCLV	ARGIAYL	B	ESSI	VVHRDIKASNILL	DN	: 822	
TapERK33	ELVSLVGYC	ISEDHRLVVD	VVADTHHNL	---	GRGVFVMD	PTVRLISA	SARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 529	
TapERK34	ELVSLVGYC	ISEDHRLVVD	VVADTHHNL	---	GRGVFVMD	PTVRLISA	SARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 536	
TapERK35	NLVK HGC	IEGNKPLVYE	LELGSDDHAF	FG---	KGKSSLD	STFETCLV	ARGIAYL	B	ESSI	VVHRDIKASNILL	DN	: 819	
TapERK36	ELVSLVGYC	IAQQHRLVYE	VVGTEDHSL	---	GRGVFVMD	PTLRLIAA	AARGLAYL	BEDCH	PKI	IHRDIKASNILL	DS	: 545	
TapERK37	ELVSLVGYC	ISEDHRLVVD	VVADTHHNL	---	GRGVFVMD	PTVRLISA	SARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 535	
AtPERK1	ELVSLVGYC	IAGVQRILVYE	VVNTTEFFSL	LGK---	GRPTLE	PIRLRLGSA	ARGLS	FLB	EDCH	PKI	IHRDIKASNILL	DK	: 415
AtPERK2	ELVALVGYC	IADAQRILVYE	VVNTTEFFSL	LGK---	GRPTLE	SSLRILVGS	ARGLS	FLB	ENCP	PKI	IHRDIKASNILL	DK	: 489
AtPERK3	NLVSLVGYC	IAGAQRILVYE	VVNTTEFFSL	LGK---	GRPTLE	SLRLILVSS	ARGLS	FLB	ENCP	PKI	IHRDIKASNILL	DK	: 318
AtPERK4	YLVSLVGYC	IADGQRILVYE	VVKTTEYSL	---	GKNLEFVMD	STLRILGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 419	
AtPERK5	ELVSLVGYC	ISGGQRILVYE	IPNTEFFSL	---	GKGRFVMD	PTVRLISA	SARGLAYL	BEDCH	PKI	IHRDIKASNILL	DS	: 447	
AtPERK6	ELVSLVGYC	IAGGQRILVYE	IPNTEFFSL	---	GKSGKVL	PTLRLIALGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DS	: 472	
AtPERK7	ELVSLVGYC	ISNAGGQRILVYE	IPNTEFFSL	---	GKSGTVMD	PTLRLIALGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 472	
AtPERK8	ELVTLVGYC	ISEQRILVVD	VVNTTHYSL	---	APGRFVMD	ETVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DS	: 474	
AtPERK9	ELVSLVGH	ISGDRRILVVD	VVNDTYFSL	---	GE-KSVLD	ATVRLIAA	AARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 511	
AtPERK10	NLLSLVGYC	ISENRRLVVD	VVNDTYFSL	---	AAGTFGLD	ATVRLIAA	AARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 565	
AtPERK11	ELVSLVGYC	ISEQRILVYE	VVNTTYFSL	---	GKNLEFVMD	SRVRLIAA	AARGLAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 505	
AtPERK12	ELVSLVGYC	ISDQRILVYE	VVQTEHSL	---	GKGLFVLE	SKVRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 506	
AtPERK13	ELVSLVGYC	IADSERILVYE	VVQTEHSL	---	GKGLFVMD	AKVRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 488	
AtPERK14	ELVSLVGYC	INGDKRILVYE	VVKDTEFFSL	EN---	RGSVLE	EMLRILVGS	AARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 524	
AtPERK15	ELVSLVGYC	ITGAQRILVYE	VVKTTEFFSL	LEK---	ERFVMD	SKMLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 278	
OsPERK1	ELVTLVGYC	ISGGKRLVYE	VVNTTEFFSL	GR---	GRPTLE	PIRLRLGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DR	: 358	
OsPERK2	NLVSLVGYC	ISGNERILVYE	VVKTEDTSL	---	GKNGFVMD	QQWRLVGS	AARGLAYL	B	DCS	PKI	IHRDVKASNILL	DD	: 362
OsPERK3	NLVSLVGYC	ISGNDRILVYE	VVKTEDTSL	---	GDKWFLD	QQWRLVGS	AARGLAYL	B	DCS	PKI	IHRDVKASNILL	DD	: 338
OsPERK4	ELVSLVGYC	IAGARILVYE	VVKTTEFFSL	---	GKGLFVMD	PTLRLIALGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 329	
OsPERK5	ELVSLVGYC	ISNNQRILVVD	VVNTTHYSL	---	QGGRFVMD	SAPVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 203	
OsPERK6	ELVSLVGYC	IAAHRRLVYE	VVGTTEHSL	---	GRGMFVMD	PTLRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DS	: 545	
OsPERK7	ELVPLVGYC	IAGAQRILVVD	VVQTEHSL	---	EKGLFVMD	TTLRILVGS	ARGLAYL	B	ENP	PKI	IHRDIKASNILL	DK	: 289
OsPERK8	ELVSLVGYC	IAANQRILVYE	VVGTTEHSL	YRG---	GNGDRVMD	SAPVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 371	
GmPERK1	ELVSLVGYC	ISEDNRILVVD	VVNTTYFSL	---	GEGQFVLE	ANVRLIAA	AARGL	T	FLBEDCH	PKI	IHRDIKSSNILL	DK	: 533
GmPERK2	ELVSLVGS	ISGGQRILVYE	IPNTEFFSL	---	GKGRFVMD	PTMRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 426	
GmPERK3	ELVSLVGYC	ICGGQRILVYE	VVSTTEHSL	---	GKGMFVMD	PTMRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 400	
GmPERK4	ELVSLVGYC	IEDSRILVVD	VVNDTYFSL	---	GEGQFVLE	ANVRLIAA	AARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 548	
GmPERK5	ELVSLVGYC	ISESKRILVYE	VVKGTEFFSL	---	GKGRFVMD	NTLRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 418	
GmPERK6	ELVEFVGS	SDTRAERILVYE	VVNTTEFFSL	LG---	GRPTLE	PIRLRLGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 390	
GmPERK7	ELVEFVGS	VTRAERILVYE	VVNTTEFFSL	GE---	GNTFLE	SMPLRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 450	
GmPERK8	ELVSLVGYC	ITGSQRILVYE	VVNTTEFFSL	GR---	GRPTLE	PIRLRLGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 434	
GmPERK9	ELVSLVGYC	ISEQRILVVD	VVNTTHYSL	---	GENRFVMD	PTVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 511	
GmPERK10	ELVSLVGYC	ISEQRILVYE	VVGTTEHSL	---	ASGMFVMD	DKLRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 484	
GmPERK11	ELVSLVGYC	ITGSQRILVYE	VVNTTEFFSL	LGK---	GRPTLE	PIRLRLGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 427	
GmPERK12	ELVSLVGS	ISGGQRILVYE	IPNTEFFSL	---	GKGRFVMD	ATMRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 424	
GmPERK13	ELVSLVGYC	ISDNRRILVVD	VVNDTYFSL	---	GEGRFVMD	TKVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 348	
GmPERK14	ELVSLVGYC	ICGGQRILVYE	VVSTTEHSL	---	GKGMFVMD	PTMRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 391	
GmPERK15	ELVALVGYC	ICEQRILVYE	VVGTTEHSL	---	ESGMFVMD	AKLRLIAGSA	ARGLAYL	BEDCH	PKI	IHRDIKASNILL	DK	: 392	
GmPERK16	ELVSLVGYC	ISEQRILVVD	VVNTTHYSL	---	GENRFVMD	PTVRLIAA	AARGIAYL	BEDCH	PKI	IHRDIKSSNILL	DK	: 543	

Protein tyrosine kinase domain

	860	*	880	*	900	*	920	*									
TaPERK1	FEARV	ADFLGAK	FT--S	INN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDS	-----	TQTYM	: 491		
TaPERK2	FEARV	ADFLGAK	FT--S	INN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDS	-----	TQTYM	: 309		
TaPERK3	FDALV	ADFLGAR	A--L	AV--	T	VTRTV	MGTFGYMAPEY	SS	GLTEKSDVFS	GVM	LELM	GKRVDS	-----	SRPLG	: 522		
TaPERK4	FEARV	ADFLGAK	FT--S	INS--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDS	-----	TQTYM	: 486		
TaPERK5	LNPKS	SDFGLAK	Y--D	QK--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	-YST	ED	-----	E	: 890
TaPERK6	LNPKS	SDFGLAK	Y--D	QK--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	-YST	KD	-----	E	: 888
TaPERK7	LNPKS	SDFGLAK	Y--D	KK--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGVAGES	NHHTT	LE	-----	E	: 912
TaPERK8	LNPKS	SDFGLAK	Y--D	QK--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	-YST	ED	-----	E	: 889
TaPERK9	LNPKS	SDFGLAK	Y--D	QK--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	-YST	KD	-----	E	: 890
TaPERK10	LNPKS	SDFGLAK	Y--D	QK--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	-YST	ED	-----	E	: 891
TaPERK11	LNPKS	SDFGLAK	Y--D	QK--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	-YST	KD	-----	E	: 799
TaPERK12	LNPKS	SDFGLAK	Y--D	KK--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGVAGES	NHHTT	LE	-----	E	: 911
TaPERK13	FEARV	ADFLGAR	A--M	FA--	T	VTRTV	MGTFGYMAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDA	-----	SNPLG	: 548		
TaPERK14	FEARV	ADFLGAK	T--S	INN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVSS	-----	KQAHM	: 460		
TaPERK15	FEARV	ADFLGAK	T--N	SM--	T	VSTRV	MGTFGYMAPEY	SS	GLTDRSDVFS	GVM	LELI	GKRVDS	-----	SQPLG	: 563		
TaPERK16	FEARV	SDFGLAR	A--A	SN--	T	VTRTV	MGTFGYLAPEY	L	GLTAKSDLYS	GVM	LELI	GKRVDS	-----	SQPLG	: 553		
TaPERK17	FEPRV	ADFLGAR	CQ--E	AEH--	T	VSTRV	MGTFGYLAPEY	YA	GVADRSDVYS	GVM	LELI	GKRVDA	-----	SSDHQ	: 536		
TaPERK18	FEARV	ADFLGAR	A--M	FA--	T	VTRTV	MGTFGYMAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDA	-----	SNPLG	: 548		
TaPERK19	FEARV	ADFLGAK	T--S	INN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVSS	-----	KQAHM	: 464		
TaPERK20	FEARV	ADFLGAK	T--N	SM--	T	VSTRV	MGTFGYMAPEY	SS	GLTDRSDVFS	GVM	LELI	GKRVDS	-----	SQPLG	: 563		
TaPERK21	FEARV	SDFGLAR	A--A	SN--	T	VTRTV	MGTFGYLAPEY	L	GLTAKSDLYS	GVM	LELI	GKRVDS	-----	SQPLG	: 555		
TaPERK22	FEPRV	ADFLGAR	CQ--E	AEH--	T	VSTRV	MGTFGYLAPEY	YA	GVADRSDVYS	GVM	LELI	GKRVDA	-----	SSDHQ	: 620		
TaPERK23	FEARV	ADFLGAR	A--M	FA--	T	VTRTV	MGTFGYMAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDA	-----	SNPLG	: 262		
TaPERK24	FEARV	ADFLGAK	T--S	INN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVSS	-----	KQAHM	: 465		
TaPERK25	FEARV	SDFGLAR	A--A	SN--	T	VTRTV	MGTFGYLAPEY	L	GLTAKSDLYS	GVM	LELI	GKRVDS	-----	SQPLG	: 554		
TaPERK26	FEPRV	ADFLGAR	CQ--E	AEH--	T	VSTRV	MGTFGYLAPEY	YA	GVADRSDVYS	GVM	LELI	GKRVDA	-----	SSDHQ	: 247		
TaPERK27	FEARV	ADFLGAK	T--T	INN--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELI	GRRVDP	-----	SNYM	: 489		
TaPERK28	LNPKS	SDFGLAK	Y--D	QE--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	YYTT	ED	-----	Q	: 751
TaPERK29	FEARV	ADFLGAK	T--T	INN--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELI	GRRVDP	-----	SNYM	: 486		
TaPERK30	FEARV	ADFLGAK	T--Y	GI--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVYS	GVM	VELI	GRRVDA	-----	TAHLVL	: 432		
TaPERK31	FEARV	ADFLGAK	T--Y	GI--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVYS	GVM	MEDI	GRRVDA	-----	TAHLVL	: 472		
TaPERK32	LNPKS	SDFGLAK	Y--D	QE--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	YYTT	ED	-----	Q	: 893
TaPERK33	FEARV	ADFLGAR	A--E	DV--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDS	-----	SRPLG	: 601		
TaPERK34	FEARV	ADFLGAR	A--E	DV--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDS	-----	SRPLG	: 608		
TaPERK35	LNPKS	SDFGLAK	Y--D	QE--	T	VSTKV	AGTFGYLAPEY	MR	GHVTEKIDVFA	GVM	LETL	AGFPN	YYTT	ED	-----	Q	: 890
TaPERK36	FEARV	ADFLGAK	S--N	TH--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELI	GKRVDD	-----	DRPLG	: 617		
TaPERK37	FEARV	ADFLGAR	A--E	DV--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDS	-----	SRPLG	: 607		
AtPERK1	FEARV	ADFLGAK	T--S	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDA	-----	NNVYV	: 487		
AtPERK2	FEARV	ADFLGAK	A--S	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVID	-----	NNVHA	: 561		
AtPERK3	FEARV	ADFLGAK	A--L	TN--	T	VSTRV	MGTFGYLAPEY	AA	GLTEKSDVYS	GVM	LELI	GRRVDA	-----	NNVYA	: 390		
AtPERK4	FDAMV	ADFLGAK	T--S	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDN	-----	SITM	: 490		
AtPERK5	FEPRV	ADFLGAK	S--Q	NY--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELI	GSPLED	-----	TGEM	: 518		
AtPERK6	FEARV	ADFLGAK	S--Q	NV--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELV	GRRVDD	-----	TGEM	: 543		
AtPERK7	FEARV	ADFLGAK	S--Q	NN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDD	-----	SGDM	: 543		
AtPERK8	FEALV	ADFLGAK	AQEL	LN--	T	VSTRV	MGTFGYMAPEY	T	GLTDRSDVYS	GVI	LELI	GKRVDT	-----	SQPLG	: 548		
AtPERK9	FDARV	SDFGLAR	A--L	CN--	T	ITTRV	MGTFGYMAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDT	-----	SQPLG	: 583		
AtPERK10	FEARV	ADFLGAK	A--L	CN--	T	ITTRV	MGTFGYMAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDA	-----	SQPLG	: 637		
AtPERK11	FEARV	ADFLGAR	N--D	TAQ--	S	ISTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELI	GKRVDT	-----	SQPLG	: 577		
AtPERK12	FEARV	ADFLGAR	N--D	TQ--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELV	GKRVDD	-----	TQPLG	: 578		
AtPERK13	FEARV	ADFLGAK	N--D	STQ--	T	VSTRV	MGTFGYLAPEY	Q	GLTDRSDVFS	GVM	LELI	GKRVDD	-----	YQPLG	: 560		
AtPERK14	FEARV	SDFGLAK	FF--S	TNSSE	T	ISTRV	MGTFGYMAPEY	SS	GLTDRSDVYS	GVM	LELI	GSPSFA	-----	KDSST	: 599		
AtPERK15	FEAKV	ADFLGAR	SS--L	TD--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	I	GVM	LELI	GRRVDD	-----	SQPPA	: 350	
OsPERK1	FEARV	ADFLGAK	T--S	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVRS	-----	NQSQM	: 430		
OsPERK2	FEPRV	ADFLGAK	YQ--P	GNH--	T	VSTRV	MGTFGYIAP	ELLS	GLTDRKADVFA	GVM	LELI	GLLVQS	-----	SESYM	: 434		
OsPERK3	FEPRV	ADFLGAK	YQ--P	GNH--	T	VSTRV	MGTFGYIAP	ELLS	GLTDRKADVFA	GVM	LELI	GLLVQS	-----	SESYM	: 410		
OsPERK4	FEARV	ADFLGAK	T--S	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELV	GRRVDA	-----	AADHPWP	ASFM	: 409	
OsPERK5	FEARV	ADFLGAR	A--L	AV--	T	VTRTV	MGTFGYMAPEY	SS	GLTEKSDVFS	GVM	LELI	GKRVDA	-----	SRPLG	: 275		
OsPERK6	FEARV	ADFLGAK	A--N	TH--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELI	GKRVDD	-----	TQPLG	: 617		
OsPERK7	FEPLV	ADFGMAK	T--S	ENV--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELI	GRRADR	-----	SSYG	: 360		
OsPERK8	FEARV	ADFLGAK	T--T	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDT	-----	SNYM	: 442		
GmPERK1	FEARV	SDFGLAK	A--L	AN--	T	ITTRV	MGTFGYMAPEY	SS	GLTEKSDVYS	GVM	LELI	GKRVDA	-----	SQPLG	: 605		
GmPERK2	FEARV	ADFLGAK	T--T	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDD	-----	TNAM	: 497		
GmPERK3	FEARV	SDFGLAK	T--N	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDD	-----	TNAM	: 471		
GmPERK4	FEARV	SDFGLAK	A--L	AN--	T	ITTRV	MGTFGYMAPEY	SS	GLTEKSDVYS	GVM	LELI	GKRVDA	-----	SQPLG	: 620		
GmPERK5	FEARV	ADFLGAK	S--Q	TN--	T	VSTRV	MGTFGYMAPEY	SS	GLTDRSDVFS	GIM	LELI	GRRVNN	-----	TGEY	: 489		
GmPERK6	FEPRV	SDFGLAK	F--P	NDSCIS	L	TRTV	MGTFGYLAPEY	SS	GLTDRSDLYS	GIM	LELI	GSPITTT	-----	AGS-R	: 464		
GmPERK7	FEPRV	SDFGLAK	F--P	NDSCIS	L	TRTV	MGTFGYLAPEY	SS	GLTDRSDVYS	GIM	LELI	GHPITTT	-----	AGS-R	: 524		
GmPERK8	FEARV	ADFLGAK	S--S	VN--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GVM	LELI	GRRVDD	-----	NQTFM	: 506		
GmPERK9	FEARV	SDFGLAR	A--L	SN--	T	VTRTV	MGTFGYMAPEY	T	GLTEKSDVYS	GVM	LELI	GKRVDA	-----	SQPIG	: 583		
GmPERK10	FEARV	ADFLGAR	A--D	ASN--	T	VSTRV	MGTFGYMAPEY	T	GLTDRSDVFS	GVM	LELV	GKRVDD	-----	TQPLG	: 556		
GmPERK11	FEARV	ADFLGAK	S--S	VN--	T	VSTRV	MGTFGYLAPEY	SS	GLTDRSDVFS	GIM	LELI	GRRVDD	-----	NQTYM	: 499		
GmPERK12	FEARV	ADFLGAK	T--T	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDD	-----	TNAM	: 495		
GmPERK13	FEARV	SDFGLAK	A--V	AN--	T	VTRTV	MGTFGYMAPEY	SS	GLTEKSDVYS	GVM	LELI	GKRVDD	-----	SQFVG	: 420		
GmPERK14	FEARV	SDFGLAK	T--N	TN--	T	VSTRV	MGTFGYLAPEY	SS	GLTEKSDVFS	GVM	LELI	GRRVDD	-----	TNAM	: 462		
GmPERK15	FEARV	ADFLGAR	A--D	ASN--	T	VSTRV	MGTFGYMAPEY	T	GLTDRSDVFS	GVM	LELV	GKRVDD	-----	TQPLG	: 464		
GmPERK16	FEARV	SDFGLAK	A--L	SN--	T	VTRTV	MGTFGYMAPEY	T	GLTEKSDVYS	GVM	LELI	GKRVDA	-----	SQPIG	: 615		

Protein tyrosine kinase domain

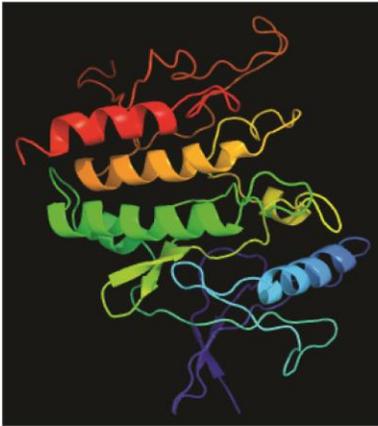
	940	*	960	*	980	*	1000	*	1020																																			
TapERK1	DD	LD	WARFL	MRALEDGN	----	YDE	VEA	LGKDFN	FN	EA	AM	ACAS	ACVH	EAR	RR	SM	SCV	VRA	EG	---	DVSL	DD	:	567																				
TapERK2	DD	LD	WARFL	MRALEDGN	----	YDE	VEA	LGKDFN	FN	EA	AM	ACAS	ACVH	EAR	RR	SM	SCV	VRA	EG	---	DVSL	DD	:	385																				
TapERK3	DE	LD	WARFL	SRALETGK	----	LEG	VD	PE	LEK	N	NE	VE	F	FM	ES	AA	AC	I	H	SS	RR	SM	SCV	VV	D	---	SLA	--	DID	M	:	597												
TapERK4	DD	LD	WARFL	MRALEDGN	----	YDE	VEA	LGKDFN	FN	EA	AM	ACAS	ACVH	EAR	RR	SM	SCV	VRA	EG	---	DVSL	DD	:	562																				
TapERK5	NK	VY	FE	VWEI	YENNH	P	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	CT	Q	PH	CR	SS	SR	V	A	M	TG	----	DVEA	I	:	959											
TapERK6	NK	VY	FE	VWEI	YEDNHP	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	CT	Q	PH	CR	SS	SR	V	A	M	TG	----	DVEA	I	:	957												
TapERK7	ET	TY	FE	KV	WVD	Y	EN	GN	P	----	LDF	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	CT	Q	PH	CR	SS	SR	V	A	M	TG	----	DA	DF	:	981								
TapERK8	NK	VY	FE	VWEI	YENNH	P	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	CT	Q	PH	CR	SS	SR	V	A	M	TG	----	DVEA	I	:	958											
TapERK9	NK	VY	FE	VWEI	YEDNRA	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	CT	Q	PH	CR	SS	SR	V	A	M	TG	----	DVEA	I	:	959												
TapERK10	NK	VY	FE	VWEI	YENNH	P	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	CT	Q	PH	CR	SS	SR	V	A	M	TG	----	DVEA	I	:	960											
TapERK11	NK	VY	FE	VWEI	YEDNRP	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	CT	Q	PH	CR	SS	SR	V	A	M	TG	----	DVEA	I	:	868												
TapERK12	ET	TY	FE	KV	WVD	Y	EN	GN	P	----	LDF	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	CT	Q	PH	CR	SS	SR	V	A	M	TG	----	DA	DF	:	980								
TapERK13	DE	LD	WARFL	TQALETGN	----	AGE	LD	PE	LD	N	N	NE	VE	F	FM	EA	AA	AC	I	H	Y	A	R	R	SM	SCV	VRA	D	---	SLT	--	DVD	M	:	623									
TapERK14	DD	LD	WARFL	TQALEDGN	----	HDA	VD	PH	L	G	I	D	F	N	D	N	E	A	AM	AC	AS	AC	V	H	E	A	R	R	SM	SCV	VRA	EG	---	DVSL	DD	:	536							
TapERK15	EE	LD	WARFL	VDALETDD	----	FRE	AD	PE	LE	C	R	Y	S	K	I	E	R	FM	EA	AA	AC	I	H	V	T	R	R	SM	SCV	VRA	D	---	VDG	--	GST	M	:	639						
TapERK16	DE	LD	WARFL	SQAIEHRD	----	FGD	PD	PE	M	N	K	F	E	E	N	Y	H	M	GA	AA	AC	I	H	A	V	M	R	R	SM	SCV	VRA	D	---	SLA	--	DS	--	HN	M	:	628			
TapERK17	PE	LD	WARFL	TKALEEEN	----	YEE	LD	PE	L	G	T	N	Y	D	A	I	D	A	L	I	AC	AA	AV	Q	A	R	S	R	R	SM	SCV	VRA	EG	---	ELSA	ED	:	612						
TapERK18	DE	LD	WARFL	TQALETGN	----	AGE	LD	PE	LD	N	N	NE	VE	F	FM	EA	AA	AC	I	H	A	P	R	R	SM	SCV	VRA	D	---	SLA	--	DGD	M	:	623									
TapERK19	DD	LD	WARFL	TQALEDGN	----	HDA	VD	PH	L	G	I	D	F	N	D	N	E	A	AM	AC	AS	AC	V	H	E	A	R	R	SM	SCV	VRA	EG	---	DVSL	DD	:	540							
TapERK20	EE	LD	WARFL	VDALETDD	----	FRE	AD	PE	LE	C	R	Y	S	K	I	E	R	FM	EA	AA	AC	I	H	V	T	R	R	SM	SCV	VRA	D	---	VDG	--	GST	M	:	639						
TapERK21	DE	LD	WARFL	SQAIEHRD	----	FGD	PD	PE	M	N	K	F	E	E	N	Y	H	M	GA	AA	AC	I	H	A	V	M	R	R	SM	SCV	VRA	D	---	SLA	--	DS	--	HN	M	:	630			
TapERK22	PE	LD	WARFL	TKALEEEN	----	YEE	LD	PE	L	G	T	N	Y	D	A	I	D	A	L	I	AC	AA	AV	Q	A	R	S	R	R	SM	SCV	VRA	EG	---	ELSA	ED	:	696						
TapERK23	DE	LD	WARFL	TQALETGN	----	VGE	LD	PE	LD	N	N	NE	VE	F	FM	EA	AA	AC	I	H	A	P	R	R	SM	SCV	VRA	D	---	SLT	--	DVD	M	:	337									
TapERK24	DD	LD	WARFL	TQALEDGN	----	HDA	VD	PH	L	G	I	D	F	N	D	N	E	A	AM	AC	AS	AC	V	H	E	A	R	R	SM	SCV	VRA	EG	---	DVSL	DD	:	541							
TapERK25	DE	LD	WARFL	SQAIEHRD	----	FGD	PD	PE	M	N	K	F	E	E	N	Y	H	M	GA	AA	AC	I	H	A	V	M	R	R	SM	SCV	VRA	D	---	SLA	--	DS	--	HN	M	:	629			
TapERK26	PE	LD	WARFL	TKALEEEN	----	YEE	LD	PE	L	G	T	N	Y	D	A	I	D	A	L	I	AC	AA	AV	Q	A	R	S	R	R	SM	SCV	VRA	EG	---	ELSA	ED	:	323						
TapERK27	ED	LD	WARFL	ARAL	SEGG	S	----	FDE	VD	Q	L	E	N	K	Y	D	R	Q	E	M	A	A	S	A	A	V	H	A	K	R	R	SM	SCV	VRA	EG	---	DAS	LD	:	566				
TapERK28	NK	VY	FE	VWEI	YEDGQP	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	V	CT	Q	PH	CR	SS	SR	V	A	M	AG	----	DVEA	I	:	820											
TapERK29	ED	LD	WARFL	ARAL	SEGN	S	----	FDE	VD	Q	L	E	N	K	Y	D	R	Q	E	M	A	A	S	A	A	V	H	A	K	R	R	SM	SCV	VRA	EG	---	DAS	LD	:	563				
TapERK30	ED	LD	WARFL	ARAL	ADG	S	----	DY	DA	AD	PE	L	Q	S	S	E	P	V	E	M	A	V	A	S	A	AC	V	H	A	K	R	R	SM	SCV	VRA	EG	---	DMS	LD	:	508			
TapERK31	ED	LD	WARFL	ARAL	ADG	S	----	DY	DA	AD	PE	L	Q	S	S	E	P	V	E	M	A	V	A	S	A	AC	V	H	A	K	R	R	SM	SCV	VRA	EG	---	DMS	LD	:	548			
TapERK32	SK	VY	FE	VWEI	YEDGQP	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	V	CT	Q	PH	CR	SS	SR	V	A	M	AG	----	DVEA	I	:	962											
TapERK33	DE	LD	WARFL	NRA	IDEQE	----	FEE	VD	PE	L	D	G	N	Y	D	D	V	E	F	V	EA	AA	AC	I	H	A	A	R	R	SM	SCV	VRA	D	---	SIT	LD	:	678						
TapERK34	DE	LD	WARFL	NRA	IDEQE	----	FEE	VD	PE	L	D	G	N	Y	D	D	V	E	F	V	EA	AA	AC	I	H	A	A	R	R	SM	SCV	VRA	D	---	SIT	LD	:	685						
TapERK35	SK	VY	FE	VWEI	YEDGQP	----	LD	VD	PE	LE	E	FD	SE	LA	LA	KV	LL	V	CT	Q	PH	CR	SS	SR	V	A	M	AG	----	DVEA	I	:	959											
TapERK36	EE	LD	WARFL	ADA	IETGN	----	HDE	AD	PE	L	E	G	R	N	K	A	E	V	M	EA	AA	AC	I	H	A	P	R	R	SM	SCV	VRA	D	---	DVD	V	D	E	G	S	M	:	696		
TapERK37	DE	LD	WARFL	NRA	IDEQE	----	FEE	VD	PE	L	D	G	N	Y	D	D	V	E	F	V	EA	AA	AC	I	H	A	A	R	R	SM	SCV	VRA	D	---	SIT	LD	:	684						
AtPERK1	DD	LD	WARFL	NRA	SEEGD	----	FE	G	A	S	M	G	N	E	Y	D	R	E	N	E	A	AM	AC	AS	AC	V	H	E	A	R	R	SM	SCV	VRA	EG	---	NVSL	DD	:	563				
AtPERK2	DN	LD	WARFL	NQV	SELGN	----	FE	V	I	K	L	I	N	E	Y	D	R	E	N	E	A	AM	AC	AS	AC	V	H	S	A	P	R	R	SM	SCV	VRA	EG	---	NISP	SD	:	637			
AtPERK3	DD	LD	WARFL	VQALEESN	----	FE	G	A	S	M	G	N	E	Y	D	R	E	N	E	A	AM	AC	AS	AC	V	H	E	A	R	R	SM	SCV	VRA	EG	---	NISP	SD	:	466					
AtPERK4	DD	LD	WARFL	ARAL	DGN	S	----	FNE	AD	PE	L	E	G	N	Y	D	R	E	N	E	A	AM	TC	AS	AS	I	H	G	R	R	SM	SCV	VRA	EG	---	EVS	LD	:	566					
AtPERK5	ED	LD	WARFL	CLK	AQ	D	G	D	----	Y	N	Q	AD	PE	L	E	L	N	Y	S	H	Q	E	V	C	A	S	A	A	I	H	E	A	R	R	SM	SCV	VRA	EG	---	DMS	M	:	594
AtPERK6	ED	LD	WARFL	CLN	AQ	D	G	D	----	Y	S	E	VD	PE	L	E	N	Q	Y	E	P	H	E	A	Q	V	AC	AA	V	H	A	R	R	SM	SCV	VRA	EG	---	DAT	LD	:	619		
AtPERK7	ED	LD	WARFL	CMR	VQA	D	G	E	----	Y	G	E	VD	PE	L	E	H	Q	Y	E	P	H	E	A	Q	V	AC	AA	V	H	A	R	R	SM	SCV	VRA	EG	---	SEG	--	DM	G	:	619
AtPERK8	DE	LD	WARFL	GQA	IENEE	----	FDE	VD	PE	L	I	G	N	F	I	P	G	E	N	F	M	EA	AA	AC	V	H	E	A	R	R	SM	SCV	VRA	D	---	TLE	--	EAT	M	:	624			
AtPERK9	DE	LD	WARFL	SHA	IETEE	----	FDS	AD	PE	L	G	G	N	Y	D	V	E	S	E	F	M	EA	AA	AC	V	H	L	A	T	R	R	SM	SCV	VRA	D	---	SLA	--	AE	--	DT	M	:	658
AtPERK10	DE	LD	WARFL	SNA	IETEE	----	FTA	AD	PE	L	E	G	N	Y	D	R	E	N	E	A	AM	EA	AA	AC	I	H	E	A	T	R	R	SM	SCV	VRA	D	---	SLA	--	EE	--	DT	M	:	712
AtPERK11	EE	LD	WARFL	IEA	EKGD	----	ISE	VD	PE	L	E	N	D	Y	V	E	S	F	Y	M	E	T	A	SC	V	H	A	L	R	R	SM	SCV	VRA	D	---	TRD	--	DLS	DT	:	653			
AtPERK12	EE	LD	WARFL	LKA	IETGD	----	LSE	LD	PE	L	E	K	R	Y	V	E	H	E	F	M	E	T	A	AC	V	H	G	P	R	R	SM	SCV	VRA	D	---	CDG	--	DSG	M	:	654			
AtPERK13	EE	LD	WARFL	HKA	IETGD	----	FSE	VD	PE	L	E	K	R	Y	V	E	H	E	F	M	E	T	A	AC	V	H	G	P	R	R	SM	SCV	VRA	D	---	SEG	--	DM	G	:	636			
AtPERK14	NQ	LD	WARFL	TKA	ISGES	----	FDF	VD	PE	L	E	K	N	Y	D	T	T	C	A	N	A	AC	AS	AC	I	H	Q	A	W	L	R	R	SM	SCV	VRA	EG	---	EVAL	R	--	KV	M	:	674
AtPERK15	DDD	LD	WARFL	IQA	INDGN	----	FDG	VD	PE	L	E	N	D	F	I	N	E	T	M	V	AC	AA	AS	V	H	A	K	R	R	SM	SCV	VRA	EG	---	NIS	LD	:	427						
OsPERK1	DD	LD	WARFL	MRA	SDDGN	----	YDA	VD	PE	L	I	G	Q	E	Y	N	G	E	N	E	A	AM	AC	AS	AC	V	H	E	A	R	R	SM	SCV	VRA	EG	---	DVSL	DD	:	506				
OsPERK2	DS	LD	WARFL	SEA	TEEGN	----	FDI	VD	PE	L	I	G	D	D	Y	D	E	N	I	M	M	E	C	AA</																				

		*	1040	*	1060	*	1080	*	1100							
TaPERK1	:	-EGRP	---GHSRFFGSYS	---	SSDYDSGQYNEDMKKFKK	---	MAFTTNDY	---	T	SQYSAPTS	---	EYQGIPS	:	625		
TaPERK2	:	-EGRP	---GHSRFFGSYS	---	SSDYDSGQYNEDMKKFKK	---	MAFTTNDY	---	T	SQYSAPTS	---	EYQGIPS	:	443		
TaPERK3	:	-NGQP	---GQSELEN	---	VANTAEIRMEQRMVQGNQDD	---		---		SAFSQYS	---	WISRSRAD	:	645		
TaPERK4	:	-EGRP	---GHSRFFGSYS	---	SSDYDSGQYNEDMKKFKK	---	MAFTTNDY	---	T	SQYSAPTS	---	EYQGIPS	:	620		
TaPERK5	:	-DVTK	---GHSRFFGSYS	---	PSYITEWQITGG-NTTYMST	---		---	DV	GQPSAPRPNSSPSSRTSSP	---		:	1005		
TaPERK6	:	-DVTK	---GHSRFFGSYS	---	PSYITEWQIKGG-NTTYMST	---		---	DV	GQSSAPRPHSSTSTQSSP	---		:	1003		
TaPERK7	:	GEEIK	---		PSYITEWQVKAGSSSYTGTSSQAGLSSSSTTQQS	---		---		GGGHAAGGDATPATGNPSP	---		:	1042		
TaPERK8	:	-DVTK	---		PSYITEWQITGG-NTTYMST	---		---	DV	GQPSAPRPNSSPSSRTSSP	---		:	1004		
TaPERK9	:	-DVTK	---		PSYITEWQIKGG-NTTYMST	---		---	DV	GQSSAPRPHSSTSTQSSP	---		:	1005		
TaPERK10	:	-DVTK	---		PSYITEWQITGG-NTTYMST	---		---	DV	GQPSAPRPNSSPSSRTSSP	---		:	1006		
TaPERK11	:	-DVTK	---		PSYITEWQIKGG-NTTYMST	---		---	DV	GQSSAPRPNSSPSSRTSSP	---		:	914		
TaPERK12	:	GEEIK	---		PSYITEWQVKAGSSSYTGTSSQAGLSSSSTTQQS	---		---		GGGHAAGGDATPATGNPSP	---		:	1041		
TaPERK13	:	-NGQP	---GMSEMEN	---	APNTAEIRLEQRMAFGSQDF	---		---		TDFIQSSS	---	WNSSRQGG	:	672		
TaPERK14	:	-EGRP	---GHSRFFMGSHA	---	SSEYDTSQYNEDMKKFKK	---	MALGTSSF	---	Q	SQLEPSSGEHEQHQNPS	---		:	597		
TaPERK15	:	-NGKL	---GHSTAYDS	---	GQYSADTELFRMGFEADLDT	---		---		AEYGLSDGGVLPVGNSSGQQLD	---		:	694		
TaPERK16	:	-NGQP	---GRSEVEL	---	EPRTTEIRLEQLREFGSRE-C	---		---		DELSQAS	---	WRSRDL	:	675		
TaPERK17	:	-GQAP	---GQSAMHRSGGG	---	NTDEVRRLLRRMAFGPGTG	---	TAGGTISEY	---	A	SEMSAPTS	---	EYGLNPS	:	672		
TaPERK18	:	-NGQP	---GMSEMEN	---	APNTAEIRLEQRMAFGSQDF	---		---		TDFIQSSS	---	WNSSRQGG	:	672		
TaPERK19	:	-EGRP	---GHSRFFMGSHA	---	SSEYDTSQYNEDMKKFKK	---	MALGTSSF	---	Q	SQLEPSSD	---	EHERQDPS	:	599		
TaPERK20	:	-NGKL	---GHSTAYDS	---	GQYSADTELFRMGFEADLDT	---		---		AEYGLSDQDELPPGSGRQR	---		:	693		
TaPERK21	:	-NGQP	---GRSEVEL	---	EPRTTEIRLEQLREFGSRE-C	---		---		DELSQAS	---	WRSRDL	:	677		
TaPERK22	:	-GQAP	---GQSAMHRSGGG	---	NTDEVRRLLRRMAFGPGTG	---	TAGGTISEY	---	A	SEMSAPTS	---	EYGLNPS	:	756		
TaPERK23	:	-NGQP	---GMSEMEN	---	APNTAEIRLEQRMAFGSQDF	---		---		TDFIQSSS	---	WNSSRQGG	:	386		
TaPERK24	:	-EGRP	---GHSRFFMGSHA	---	SSEYDTSQYNEDMKKFKK	---	MALGTSSF	---	Q	SQLEPSSG	---	EHEHQEPS	:	600		
TaPERK25	:	-NGQP	---GRSEVEL	---	EPRTTEIRLEQLREFGSRE-C	---		---		DELSQAS	---	WRSRDL	:	676		
TaPERK26	:	-GQAP	---GQSAMHRSGGG	---	NTDEVRRLLRRMAFGPGTG	---	TAGGTISEY	---	A	SEMSARTS	---	EYGLNPS	:	383		
TaPERK27	:	-EGRP	---GQSMIYS	---	SDESGSYAANIRLRQVAFESS-GEY	---		---		NEYS	---	GTGESG	:	614		
TaPERK28	:	-DWPK	---		PSYITEWHIKGGDTSYMS	---		---		EVNGQSSVP	---	AP	:	857		
TaPERK29	:	-EGRP	---GQSMIYS	---	SDESGSYAANIRLRQVAFESS-EEY	---		---		NEYS	---	GTGESG	:	611		
TaPERK30	:	-DGRP	---GQSRLEF	---	EGAGSCSSDNRTKVVVV	---	ASPEY	---		GRFGRPSFV	---	SSDRPISD	:	561		
TaPERK31	:	-DGRP	---GQSRLEF	---	EEAGYSDDNRAKEVAV	---	ASPEY	---		GRSRRPSFV	---	SSDRPISD	:	601		
TaPERK32	:	-DWPK	---		PSYITEWQIKGGDTSYMS	---		---		EVNGQSSSEP	---	AP	:	999		
TaPERK33	:	-NGQP	---GKSQMEN	---	AANTADIRLEQRMAFGSQDFS	---		---		SEYIQSKA	---	SLSGRDDL	:	728		
TaPERK34	:	-NGQP	---GKSQMEN	---	AANTADIRLEQRMAFGSQEFT	---		---		SEYIQSKA	---	SLSGRDDL	:	735		
TaPERK35	:	-DWPK	---		PSYITEWQIKGGDTSYMS	---		---		EVNGQSSSEP	---	AP	:	996		
TaPERK36	:	-NGKV	---GQSQVFN	---	SQEAALRQLRTPSPFRSSRGS	---		---		SSRPGSSS	---	RPGSTVP	:	747		
TaPERK37	:	-NGQP	---GKSQMEN	---	AANTADIRLEQRMAFGSQDFS	---		---		SEYIQSKA	---	SLSGRDDL	:	734		
AtPERK1	:	-EGRP	---GHSNVYSSYGG	---	STDYDTSQYNDDMKKFKK	---	MALGTQYEG	---	T	GEYSNPTS	---	DYGLYPS	:	623		
AtPERK2	:	-GQTP	---GHSNVYSSYGG	---	STDYDSSQYDNEGNKFKK	---	VGL	---	E	TQDLYSNPIS	---	EYDLYPS	:	692		
AtPERK3	:	-GQTP	---GHSNVYSSXRG	---	STYDTRMXTYTRKERI	---	KMG	---	H	GXGEYSNPTS	---	DYRLYPSG	:	522		
AtPERK4	:	-EGRP	---GHSNVYVSL	---	GASSDYSQTSYNADMKKFKK	---	RQIALS	---		QEFVSDCE	---	GLTSSNDSR	:	622		
AtPERK5	:	-EGRP	---GQSTYLSPG	---	SVSSEYDASSYADMKKFKK	---	LALENKEY-Q	---		SEYGGTSEYGLNPSASSSE	---		:	657		
AtPERK6	:	-EGGA	---GQSSFLGRG	---	SSS-DYDSSYADMKKFKK	---	RVALDSHEYGA	---		SEYNTSEYGLDPSSSSSE	---		:	682		
AtPERK7	:	-DGRP	---GQSSSGGEG	---	SS-DYEMGTGAEWRKFKVTLERDYG	---		---		SEYGATSEYGLDPSSSSSE	---		:	681		
AtPERK8	:	-NGRP	---GQSQVEDS	---	RQQAQIRMEQRMAFGSQDYS	---		---		DFDPRSQSHSSWGRDQ	---		:	676		
AtPERK9	:	-NGRL	---GESEVENS	---	AQQAELRLERRMAFGSQNYS	---		---		DFFSHSS	---	YNSRDANV	:	708		
AtPERK10	:	-NGRL	---GESEVENS	---	AQQAELRLERRMAFGSQNYS	---		---		DSLFRNS	---	YISKDENL	:	762		
AtPERK11	:	-NGKV	---GQSRVYDS	---	GQYSADTELFRMGFEADLDT	---		---	TN	GYYPSP	---	DYATS	:	701		
AtPERK12	:	-NGKI	---GQSTTYDS	---	GQYNEDIRMEQRMAFGSQDYS	---		---	LY	GNYSK	---	SSDF	:	705		
AtPERK13	:	-NGNKV	---GQSSAYDS	---	GQYNNDIMKFKMAFGDSSDSSG	---		---	MY	GDYVQDSRKGNGASSEF	---		:	695		
AtPERK14	:	-EETGN	---S-VTYSSE	---	NFNDITP	---	RYGNKRRFDT	---	S	DGY	---	TS	---	EYGNPS	:	720
AtPERK15	:	-EGAP	---GQSTYSLDG	---	SSDYDTSQYNEDMKKFKK	---	MAFESKTF	---	G	SECGLTS	---	DNGQNPS	:	485		
OsPERK1	:	-EGRP	---GHSRFLGSYN	---	SNEYDTGHYNEDMKKFKK	---	MAFGSGLN	---	E	SQQQPTPE	---	FVFNRS	:	563		
OsPERK2	:		---	SIFR	---	ITYAEDTYSSIMESGESIGPRSR	---			APRSQRNTSSDYSSQALTDKA	---		:	560		
OsPERK3	:		---	SIFR	---	ITYAEDTYSSIMESG	---			LPRS	---	DLF	:	512		
OsPERK4	:	-EGRP	---GQSMVFGTAETGGSISEASGSYTFMDRIQEAT	---	AARLE	---		---		GR	---	RDDVSFSG	:	540		
OsPERK5	:	-NGQP	---GQSELEN	---	VANTAEIRMEQRMAFGSNHDD	---		---		SDMSQYG	---	WSSSRQ	:	396		
OsPERK6	:	-NGKV	---GQSQVETG	---	GSDAADTQQLRRIAFASEEFTGEF	---		---		EQRTTNSSES	---	RPMNRIP	:	747		
OsPERK7	:	-DGRP	---GQSAMSSSS	---	GDSSSGSGSYTAQMERVRRTAASPASPEY	---		---		SEYQYGCP	---	SPASSAGD	:	501		
OsPERK8	:		---	SLDHH	---	HDDDFSASSEIRHRQVAFDS	---	GDY	---	DDYS	---	TTSTST	:	559		
GmPERK1	:	-NGRL	---GESEVED	---	AQQAELRLERRMAFGNQDYS	---		---		DPHSCA	---		:	720		
GmPERK2	:	-DGRP	---GQNVAYNSS	---	SSSDQYDTMQYNADMKKFKK	---	KAVERN	---		EEFG	---	TSSGSSG	:	625		
GmPERK3	:	-DGRP	---GQNVAYNSS	---	SSSDQYDTMQYNADMKKFKK	---	KAVERN	---		QEFN	---	DSS	:	598		
GmPERK4	:	-NGRL	---GESEVEDS	---	AQQAELRLERRMAFGSQNYS	---		---		DFFSRAS	---	LN	:	740		
GmPERK5	:	HEGKP	---GQSSMESSA	---	SR-EYGAEYADMRERKALDSSGVG	---		---		SEYGGTSEYGLNPSSSSSE	---		:	626		
GmPERK6	:	-GDTT	---	G	---	ITTDTV	---				---		:	552		
GmPERK7	:	-GDTT	---	G	---	ITTDTV	---				---		:	552		
GmPERK8	:	-EGRP	---GHSTMYSSHE	---	SSDYDTAQYKEDMKKFKK	---	MALGTQYEG	---	A	SEYSAATS	---	EYGLNPS	:	641		
GmPERK9	:	-NGKP	---GQSSVEDS	---	AQQAELRLERRMAFGSQD-S	---		---		SFFNESQ	---	SSWRSRDHNS	:	710		
GmPERK10	:	-NGKY	---GHSTVYDS	---	GQYDKAIMLEFRMLANGTFVDSDFE	---		---	IY	REYLSRDTSMTRSGSHQE	---		:	691		
GmPERK11	:	-EGRP	---GHSTMYSSHE	---	SSDYDTAQYKEDMKKFKK	---	MALGTQYEG	---	A	SEYSAATS	---	EYGLNPS	:	634		
GmPERK12	:	-DGRP	---GQNVAYNSS	---	PSSNQYDTMQYNADMKKFKK	---	KAVERN	---		DFEG	---	TSSGSSG	:	623		
GmPERK13	:	-NGRI	---GDS	---	ALQSAELRLERRMAFGIQDYN	---		---		DFLPRE	---		:	532		
GmPERK14	:	-DGRP	---GQNVAYNSS	---	PSSNQYDTMQYNADMKKFKK	---	KAVERN	---		QEFN	---	DSS	:	589		
GmPERK15	:	-NGKY	---GHSTVYDS	---	GQYDKAIMLEFRMLANGTFVDSDFE	---		---	MV	REYLSRDTSMTRSGSQQE	---		:	599		
GmPERK16	:	-NGKP	---GQSSVEDS	---	AQQAELRLERRMAFGSQD-S	---		---		GFFNESQ	---	SSWRSRDHDP	:	742		

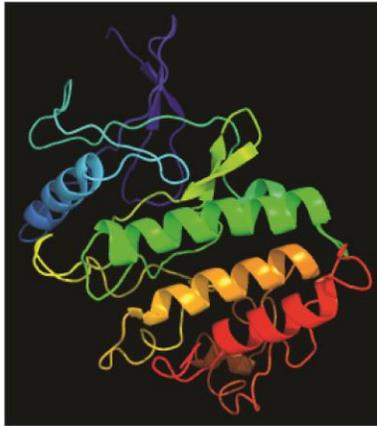
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TaPERK2	:	-ASSSEG--QQTQ-EIETGTMKKGHSG--YSSGYSGPS-----	:	476			
TaPERK3	:	AEATSSNSRIL-----	:	656			
TaPERK4	:	-ASSSEG--QQTQ-EIETGTMKKGHSG--YSSGYSGPS-----	:	653			
TaPERK5	:	FLSSVIDEGR-----	:	1015			
TaPERK6	:	FLSSVIDEGR-----	:	1013			
TaPERK7	:	MFTSIIDEGR-----	:	1052			
TaPERK8	:	FLSSVMDEGR-----	:	1014			
TaPERK9	:	FLSSVIDEGR-----	:	1015			
TaPERK10	:	FLSSVIDEGR-----	:	1016			
TaPERK11	:	FLSSVIDEGR-----	:	924			
TaPERK12	:	IFTSIIDEGR-----	:	1051			
TaPERK13	:	-DADASGGFMHSQLQP-----	:	687			
TaPERK14	:	-VPSSDGH-QQTQ-EVELGTSTKRDDGD--VESQASMR-----	:	630			
TaPERK15	:	GEAHQINQLGSPAGRLNPPATLHRT-----	:	720			
TaPERK16	:	-----	:	-			
TaPERK17	:	-SEYTASSAADTEDMTDFPHRAGAGRGS AEGGSGEAGRGTTTEGFSRRTTVRRTGRG	:	727			
TaPERK18	:	GDVDASGGPRQSQP-----	:	686			
TaPERK19	:	-VQSSDGH-RQTQ-EVELGTT-KRDDGD--VESQTSMR-----	:	631			
TaPERK20	:	-----TAAGR-----	:	698			
TaPERK21	:	-----	:	-			
TaPERK22	:	-SEYTASSAADTEDMTDFPHRAGTGRGA AEGASGEAGRGTTTEGFSRRTTGRRTSRG	:	811			
TaPERK23	:	-DVDASGGPRHPQSQP-----	:	401			
TaPERK24	:	-VPSSDGH-QQTQ-EVELGTR-KRDDGD--VESQASMR-----	:	632			
TaPERK25	:	-----	:	-			
TaPERK26	:	-SEYTASSAADTEDMTDFPHRAGTGRGA AEGVSGEAGRGTTTEGFSRRTTVRRTGRG	:	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	:	-GSSSEGQ-ATREM--EMGKIKKTGGY---SGPSL-----	:	652			
AtPERK2	:	-WSSDGGQ-TTQK--ATGNIKRPGQY---G-----	:	717			
AtPERK3	:	GRSSEGQ-ATRGNGFEMGKIKRTAQR---GGDSL-----	:	554			
AtPERK4	:	DMGTKSPTPPK-----	:	633			
AtPERK5	:	EMNRGSMKRNPNL-----	:	670			
AtPERK6	:	EIRRGANNKTTPSRDH-----	:	700			
AtPERK7	:	EMHIGGSTSKTTTTNRGI-----	:	699			
AtPERK8	:	-SREVP-----	:	681			
AtPERK9	:	-----	:	-			
AtPERK10	:	-----	:	-			
AtPERK11	:	HEYESERAFNTSHRNH-----	:	718			
AtPERK12	:	SGNESETRPFNNRRF-----	:	720			
AtPERK13	:	TRNETENRNFNRRY-----	:	710			
AtPERK14	:	-QSSSEHQVNT-----	:	731			
AtPERK15	:	-GSSSITEGQRTTQEIPEKNTKDT-----	:	509			
OsPERK1	:	-VSMGDAR-QIPETEMEMGSLKKGDSNGTRDSQAS-----	:	597			
OsPERK2	:	NRSPAKGR-----	:	568			
OsPERK3	:	TKQFNRY-----	:	520			
OsPERK4	:	EMSAEWKQPPHRVSR-----	:	555			
OsPERK5	:	-----	:	-			
OsPERK6	:	E-----	:	748			
OsPERK7	:	NASSGEHDNQWRKAHR-----	:	517			
OsPERK8	:	HSSRLPPKR-----	:	568			
GmPERK1	:	-----	:	-			
GmPERK2	:	EVSQKQRL-----	:	634			
GmPERK3	:	ELSSKEMGYH-----	:	608			
GmPERK4	:	-----	:	-			
GmPERK5	:	QSSAEYARRTTGGGRMHTP-----	:	645			
GmPERK6	:	-----	:	-			
GmPERK7	:	-GSSSEAQQSFRDIV-----	:	673			
GmPERK8	:	-GSSSEAQSRQTTREMEMRKMKNQGF-----GSS-----	:	671			
GmPERK9	:	NMFSSQNKTPWNV-----	:	724			
GmPERK10	:	LIRHSSGSLNLELSTCIGVVLNENRD-----	:	718			
GmPERK11	:	-GSSSEAQSRQTTREMEMRKMKNQGF-----GSS-----	:	664			
GmPERK12	:	EVSQKQRL-----	:	632			
GmPERK13	:	-----	:	-			
GmPERK14	:	ELSSKEMSYH-----	:	599			
GmPERK15	:	LIQHSSSGEFDSRDINMHRSSIE-----	:	622			
GmPERK16	:	TTVFSQNKTGHN-----	:	756			

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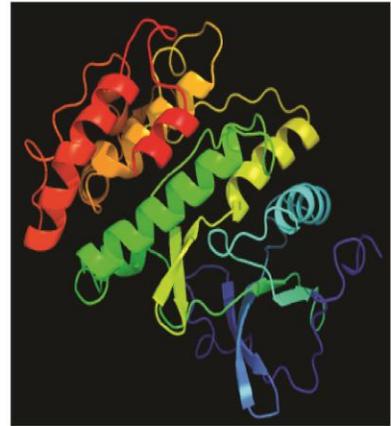
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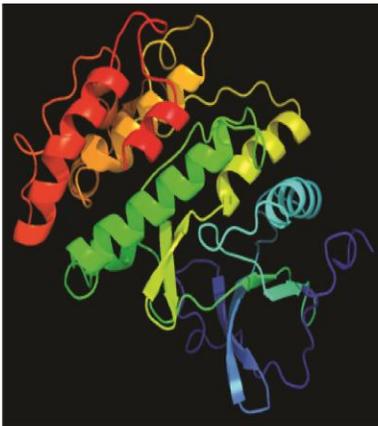
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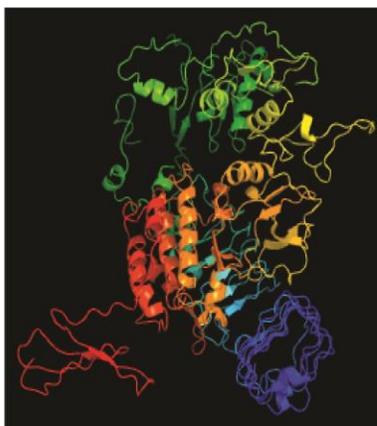
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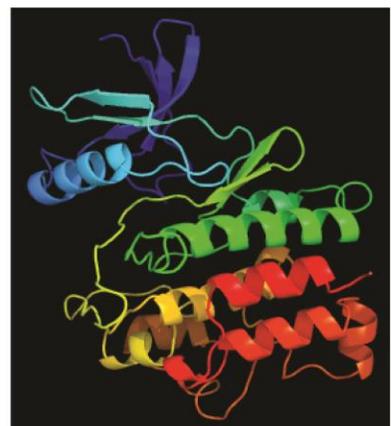
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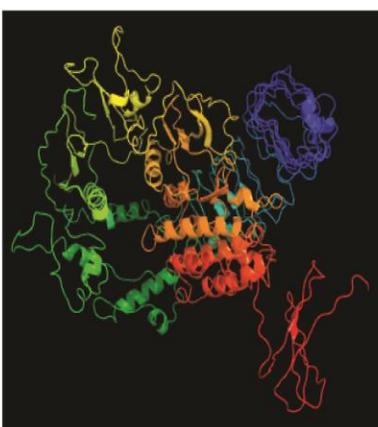
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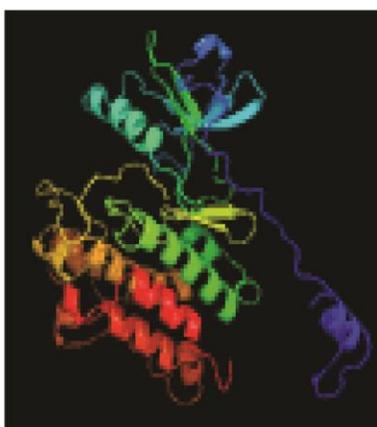
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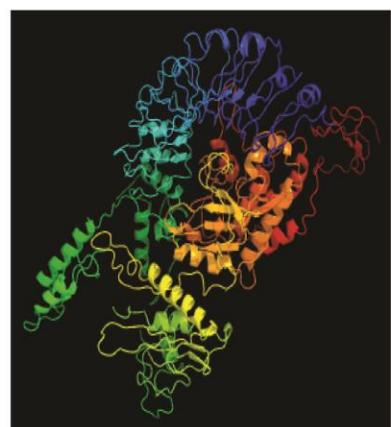
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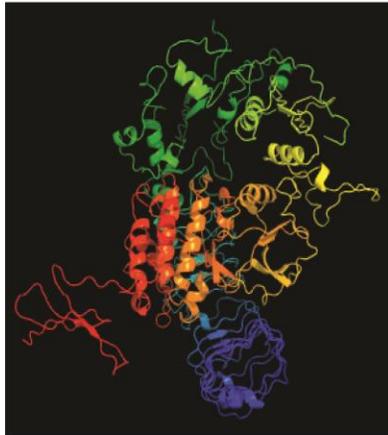
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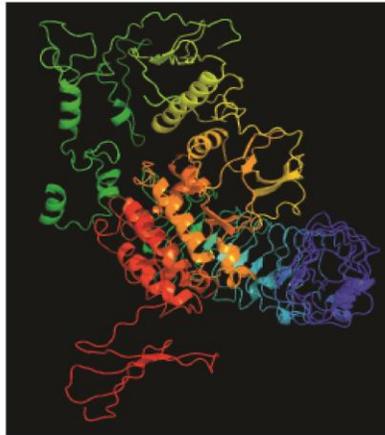
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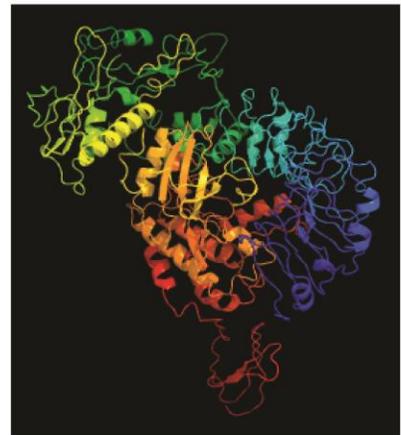
TaPERK10



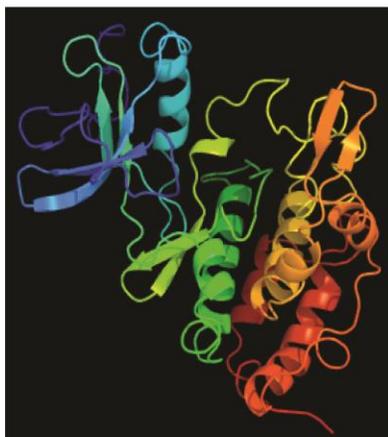
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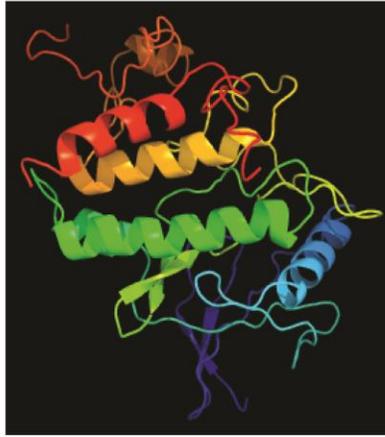
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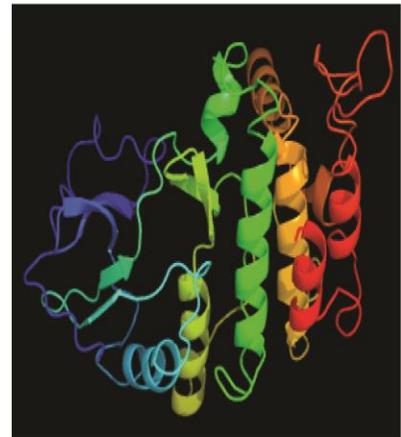
TaPERK13



TaPERK14



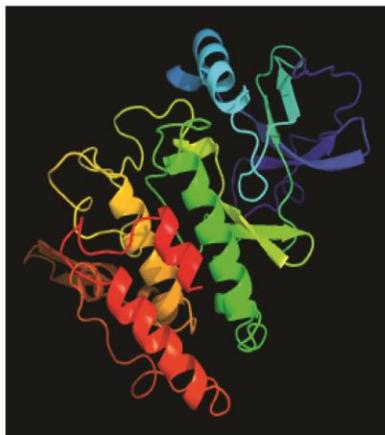
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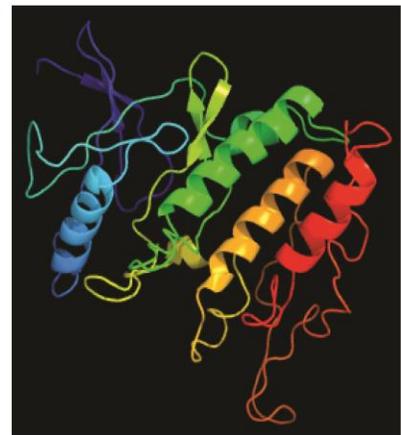
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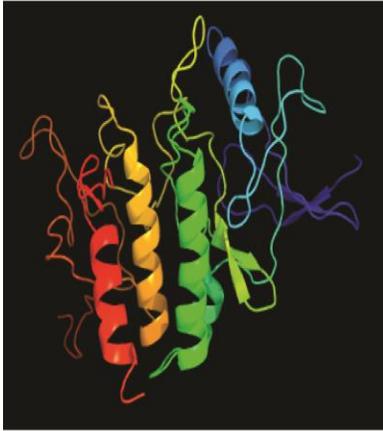
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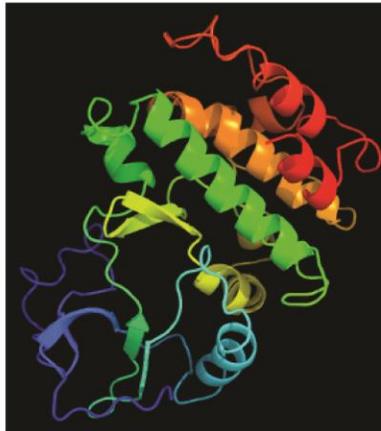
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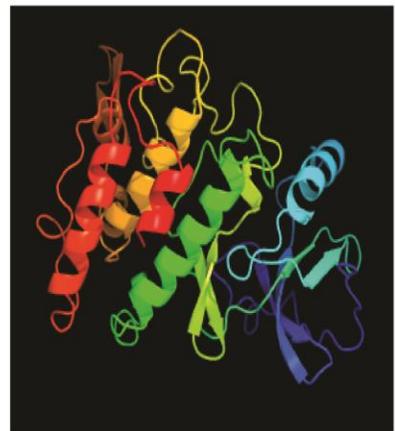
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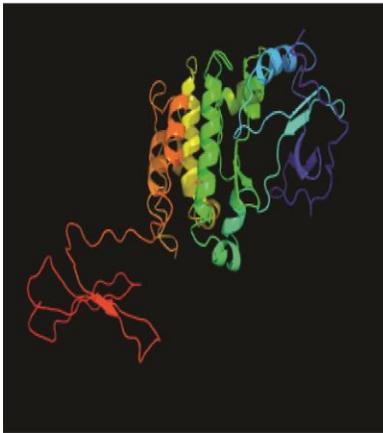
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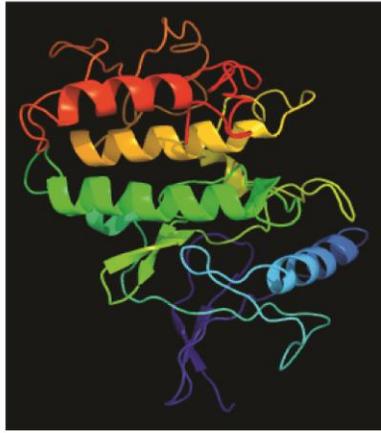
TaPERK21



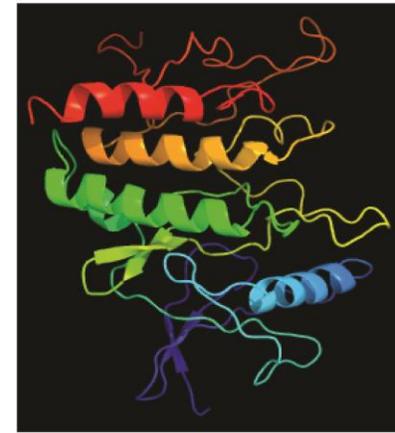
TaPERK22



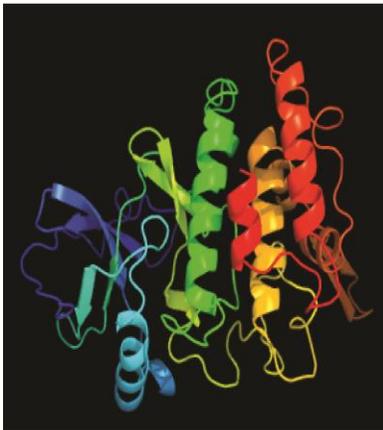
TaPERK23



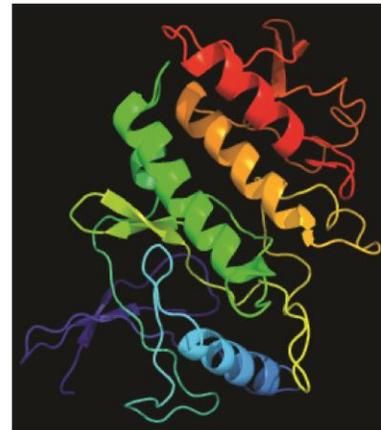
TaPERK24



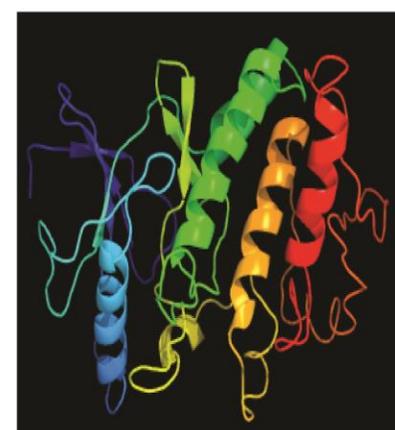
TaPERK25



TaPERK26



TaPERK27



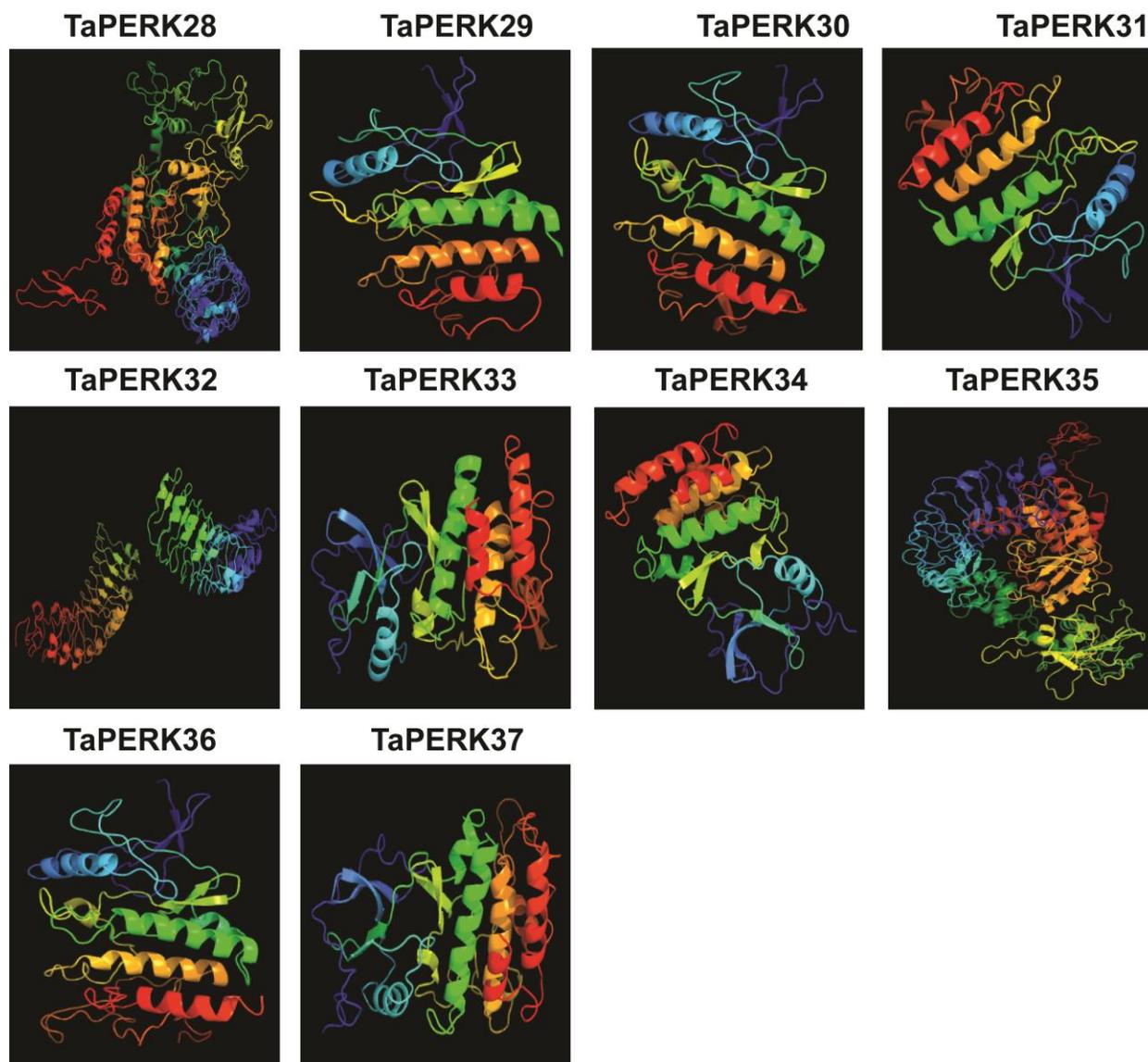


Figure S6. Alignment and 3-dimensional structure of the TaPERK protein sequences. **A.** The conserved protein tyrosine kinase domain is boxed with red color. Colored and shaded amino acids are chemically similar residues. Dashes indicate gaps introduced to maximize the alignment of the homologous region.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

C

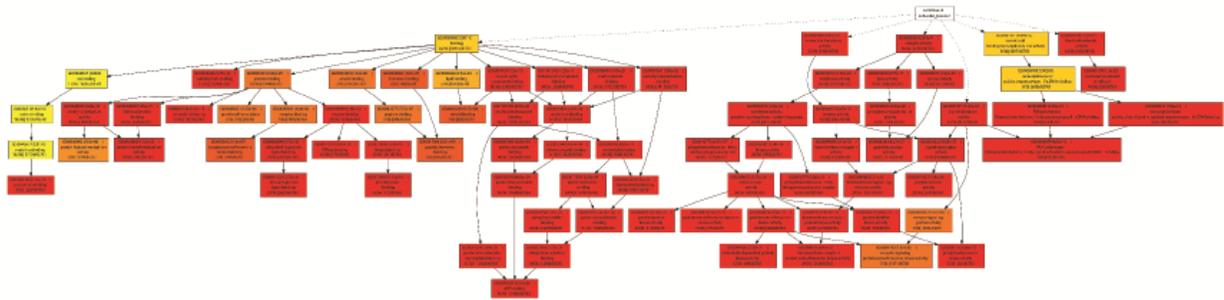


Figure S7. Gene ontology term distribution TaPERK gene family predicted using AgriGO **A.** Biological Process. **B.** Cellular component. **C.** Molecular function.

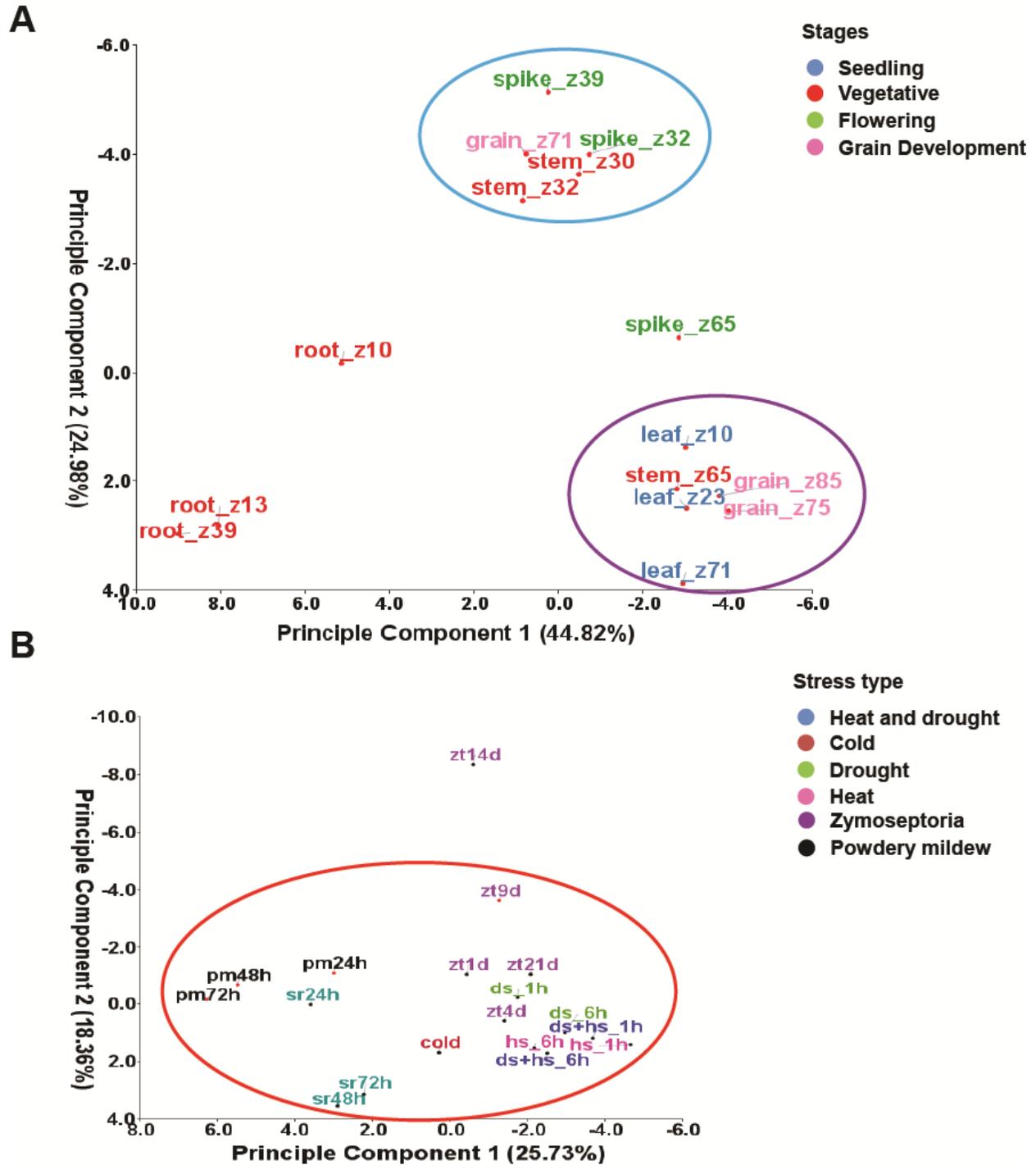


Figure S8. PCA plots displaying grouping of different (A) Developmental stages (B) Biotic and abiotic stress conditions based on the TaPERK expression pattern. DS: Drought stress, HS: Heat stress, Zt: *Zymoseptoria tritici*, PM: Powdery mildew; SR: Stripe rust, h: hour and d: days.

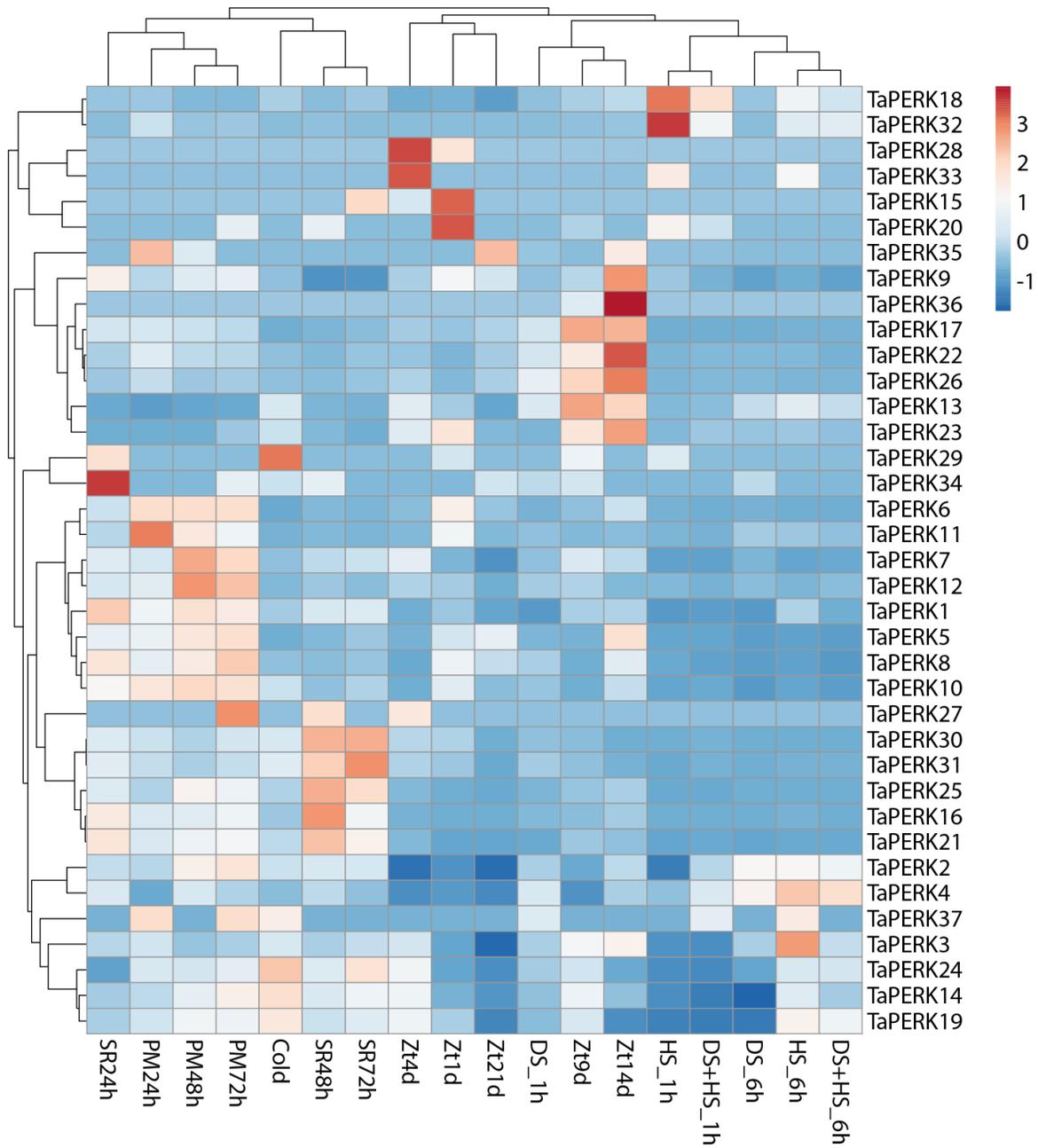


Figure S9. Heatmaps representing the expression pattern of TaPERK genes in different stress conditions. TPM values were directly used to construct the heatmaps. DS: Drought stress, HS: Heat stress, Zt: *Zymoseptoria tritici*, PM: Powdery mildew; SR: Stripe rust, h: hour and d: days.