Science Letters ISSN 2345-5463

DOI: https://doi.org/10.47262/SL/10.1.132022040

# Supplementary Material

# Genomic Identification of HKT, AKT and KEA Gene Families Involved in Potassium Transport

Hira Tahir[1], Humaira Saleem[2], Sadia Saleem[2], Noor Fatima[2], Aleena Khaleel[2], Adeela Shaukat[3]*

[1]Department of Botany, GC Women University, Faisalabad, Pakistan

[2]Department of Bioinformatics and Biotechnology, Government College University, Faisalabad, Pakistan

[3]Department of Biotechnology, University of Central Punjab, Lahore, Pakistan

## Gene Alignments

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TaAKT3.1      ------------------------------------------------------------  0
TaKAT2.1      ------------------------------------------------------------  0
TaTPK1.1      ------------------------------------------------------------  0
TaAKT2.1      ------------------------------------------------------------  0
TaAKT1.1      ------------------------------------------------------------  0
TaKAT1.1      ------------------------------------------------------------  0
TaKEA5.1      ------------------------------------------------------------  0
TaTPK2.1      ------------------------------------------------------------  0
TaHKT2.1      ------------------------------------------------------------  0
TaHKT1.4      ------------------------------------------------------------  0
TaHKT1.3      ------------------------------------------------------------  0
TaHKT1.7      ------------------------------------------------------------  0
TaKAT5.1      ------------------------------------------------------------  0
TaHKT1.8      ------------------------------------------------------------  0
TaKAT1.8      ------------------------------------------------------------  0
TaHKT1.5      ------------------------------------------------------------  0
TaKAT4        ------------------------------------------------------------  0
TaHKT1.1      ------------------------------------------------------------  0
TaHKT1.2      ------------------------------------------------------------  0
TaKAT6.1      ------------------------------------------------------------  0
TaKEA3.1      ------------------------------------------------------------  0
TaKEA4.1      ------------------------------------------------------------  0
TaHKT2.2      ------------------------------------------------------------  0
TaHKT2.3      MLMRRRRQRPVLPRLLLATLLIASAVAFLPRAAGDAAEAGDEGRVGEAVAAVERADAAAA 60
TaKEA2.1      ---------------------------MAPAAAAG---TPRGRRFTAAVLAVAVALALAP 30

TaAKT3.1      ------------------------------------------------MAMAGVGSQ---  9
TaKAT2.1      ------------------------------------------------------------  0
TaTPK1.1      ------------------------------------------------------------  0
TaAKT2.1      ------------------------------------------------------------  0
TaAKT1.1      ----------------------------------MTQAHSK---SHFHQFWDG------- 16
TaKAT1.1      -------------------------------MARSSRARTGSRVTRCFPCYDG------- 22
TaKEA5.1      -------------------------------------RSGAARMRACGPWGEGGSGV--- 20
TaTPK2.1      -----------------------------------TDRRKMPSGPGCAPWGRGGGVQ--- 22
TaHKT2.1      ------------------------------------------------------------  0
TaHKT1.4      ------------------------------------------------------------  0
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TaHKT1.3        ------------------------------------------------------------  0
TaHKT1.7        ------------------------------------------------------------  0
TaKAT5.1        ------------------------------------------------------------  0
TaHKT1.8        ------------------------------------------------------------  0
TaKAT1.8        ------------------------------------------------------------  0
TaHKT1.5        ------------------------------------------------------------  0
TaKAT4          ------------------------------------------------------------  0
TaHKT1.1        ------------------------------------------------------------  0
TaHKT1.2        ------------------------------------------------------------  0
TaKAT6.1        ------------------------------------------------------------  0
TaKEA3.1        ------------------------------------------------------------  0
TaKEA4.1        ------------------------------------------------------------  0
TaHKT2.2        ------------------------------------------------------------  0
TaHKT2.3        ALGAAE-------AGG--EAAQGNATTKEHSLADMIDRALEKEFPDS-EGDQGGGETDPG110
TaKEA2.1        AAGRPDKETREKFYGSLVANGTHNATAGDNSIADMFGRVLDKEFSDS-DASE---VPDKN 86


TaAKT3.1        ---------RGSSSS--R-ML-L------------PRNISLSTGHLPEALG-----GAPP 39
TaKAT2.1        ---------------------------------------------LPEALG-----GAPP 10
TaTPK1.1        -----------------------------------FNLRNLSKLMLPP-LGSSLS-QSTS 23
TaAKT2.1        ---------------------MD------------NISNIFHNDLLPS-LGARA—NQSI  24
TaAKT1.1        -------------------LHIN------------GSSDSFAIELLPS-LGATI—NHSN  42
TaKAT1.1        -------------------DR-T------------GDFSGCPNDLLPS-LGATA—AAQP  47
TaKEA5.1        ---------VGDAHALEREMSRD------------GSHYSLSSGILPS-LGARS—NRRV  56
TaTPK2.1        ---------S---------SVER------------GGRFSVFTAVLPS-LGEHSHSFRRR 51
TaHKT2.1        ------------------------------------------------------------  0
TaHKT1.4        --------------------------------MHPNTSTHTYSDSSTSN----------- 17
TaHKT1.3        ------------------------------------------------------------  0
TaHKT1.7        ------------------------------------------------------------  0
TaKAT5.1        -------------------MH-----------AHPDASTQYRVDITTSN----------- 19
TaHKT1.8        ------------------------------------------------------------  0
TaKAT1.8        ------------------------------------------------------------  0
TaHKT1.5        ------------------------------------------------------------  0
TaKAT4          ------------------------------------------------------------  0
TaHKT1.1        -------------------MH-------------RFSSALVFLQNLPSHTAMKL------ 22
TaHKT1.2        ------------------------------------------------------------  0
TaKAT6.1        ------------------------------------------------------------  0
TaKEA3.1        ------------------------------------------------------------  0
TaKEA4.1        ------------------------------------------------------------  0
TaHKT2.2        -------------------------------------------------AGVGV----EI  7
TaHKT2.3        SFNNTVAEKQGVLETVARRVTKKN-ET-KDNNS--FPFKEVFLDR-SEQEDVPT—LIDR 163
TaKEA2.1        SFNNSISDHQAVLETVAVITHDKKNDTQQANSSRPFQIGDMFGSQNENSDDTET—VIDK 144


TaAKT3.1        PLRPNVINPYGRPY---------------------------------------------- 53
TaKAT2.1        PLRPNVINPYGRPYRCARLDRLRHA----------------------------------- 35
TaTPK1.1        DSDKRVVSPLDS------------------------------------------------ 35
TaAKT2.1        KLRKFIISPYDS------------------------------------------------ 36
TaAKT1.1        KLKKFIVSPYDP------------------------------------------------ 54
TaKAT1.1        TSGKYLVSPYGR------------------------------------------------ 59
TaKEA5.1        KLRRFIISPYDR------------------------------------------------ 68
TaTPK2.1        SVRRCVVSPYDP------------------------------------------------ 63
TaHKT2.1        ------MGRVK-------RFYQDFI----HI---KLHSF------CRISR--YVVDSIA- 31
TaHKT1.4        ------MAGAHRKVRELLEHTRRRSTAALNNVMSLMRSL--SGSYAQH-HVKERVARWRR 68
TaHKT1.3        ------MAGARHKVAELLRHARRLSTAALDKALSLLSSP-SSWSYVQHHVVKEPVARLRR 53
TaHKT1.7        ------MAGARHKVGELLRHARRRSTAALDKALSLLSSP—SWSYVQHHVVKERVARWRR  52
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TaKAT5.1      ------MAGARHKVGELLRHARRRSTAALDKALSLLSSH—SWSYVQHHVVKERVKRWRH  71
TaHKT1.8      -----------------------------------MGSLHVSCSTTQHSK-------LQR 18
TaKAT1.8      --------------------------------------------MSQHSK-------LHR  9
TaHKT1.5      -----------------------------------MGSLHVSSSATQHSK-------LER 18
TaKAT4        -----------------------------------MGSLHVSSSATQHSK-------LER 18
TaHKT1.1      ---PLFSLEALRITKEMVKHFHEFV----ST---RLGSL----SKCTADL-------FRR 61
TaHKT1.2      ------MNNSLVVYLKSLRTFCAFA----PT---KLSSF----AKSAWQS-------MKY 36
TaKAT6.1      ------MNNSLVVYLKSLQTFCAFA----ST---KFSSF----AKSAWQS-------MKY 36
TaKEA3.1      ------------------------------------------------------------  0
TaKEA4.1      ------------------------------------------------------------  0
TaHKT2.2      ASAVEVI-------NDLGFDTLTFL---------------------------GVTVLV-- 31
TaHKT2.3      KDNVFIISNRKSKYPVLQLDLTLIS---------------------------DLVVVIVS196
TaKEA2.1      EDNVFVMSNRKTKYPTLQLDLRLIK---------------------------DLVVIIVS177


TaAKT3.1      --------RYWQMFLI-VLVAYSAWASPFELALEKA-VSRAHLVVDLVVDVFFCADIVVS103
TaKAT2.1      CTALDLDRRYWQMFLI-VLVAYSAWASPFELALEKA-ASRAHLVVDLVVDVFFCADIVVS 93
TaTPK1.1      ------RYRCWETFMV-ILVAYSAWVYPFEVAFMEARPKGGLEVADMVVDIFFAVDIVLT 88
TaAKT2.1      ------RYRIWETFLL-VLVVYSAWIYPFELAFLRH-LSWKLFLVENIVNSFFAIDIVLT 88
TaAKT1.1      ------RYRFWELFLI-VLVVYSAWVCPFELAFLRN-LPSKLVLVENIVNGFFAIDIVMT106
TaKAT1.1      ------RYRVWETFLI-LLVVYSAWICPLEFAFLRH-LPRAPFVVDDVVNGFFAVDILLT111
TaKEA5.1      ------RYRLWETFLI-VLVVYSAWVSPFEFGFIRI-PTGGLAATDNAVNAIFAVDIILT120
TaTPK2.1      ------RYRLWDNYIV-CLVLYSAWVSPFEFGFLQN-PHGALAIADNIVNAFFAMDIVLT115
TaHKT2.1      FVYRFVALHVHPFWIQLSYFLAIAILGSVLLMSLKPSN---PDFSPPYIDMLFLSTSALT 88
TaHKT1.4      ALAGRLSPRLGSLLVHVAYFLAVSWLGYLVLAQLRFRAGGEGTRRPGAIDLFFTAVSAAT128
TaHKT1.3      ALAGRFWRRLGSLLVHVAYFLAVSWLGYLLLAQLRFRAGGDGTRRPRGIDLFFTAVSAAT113
TaHKT1.7      ALAGRFWRRLGSLLVHVAYFLAVSWLGYLLLAQLRFRAGSDGTRRPRGMDLFFTAVSAAT112
TaKAT5.1      ALAGRFWRRLGSLLVHVAYFLAVSWLGYLLLAQLRFRAGGDGTRRPRGIDLFFTAVSAAT131
TaHKT1.8      V-YQLLFFHVHPFWLHFLYFVTISFLGFVILKALPMKT—SMVSRPIDLDLIFTSVSATT  75
TaKAT1.8      A-YQLLFFHVHPFWLQLLYFVSISFFGFVILKALPMKT--G---MPMDLDLIFTSVSATT 63
TaHKT1.5      A-YQLLVFHVHPFWLQLLYFVSISFFGLVILKALPMKT—STVPRPMDLDLIFTSVSATT  75
TaKAT4        A-YQLLVFHVHPFWLQLLYFVSISFFGLVILKALPMKT—STVPRPMDLDLIFTSVSATT  75
TaHKT1.1      S-YLFLVFKSNPLVVQLIYLMSISFAGFLALKNLAPLN---KP-SPRNLDLIFTSVSTVT116
TaHKT1.2      S-C-QFICQTNPLFIQVTYFTLISFAGYEALKVLNSQD---KSNTLKDLDVLFTSVSAST 91
TaKAT6.1      S-C-RFICQTNPLFIQVTYFTLISFAGYEALKVLNSQD---KSNTLKNLDVLFTSVSAST 91
TaKEA3.1      ------------------------------------------------------------  0
TaKEA4.1      ------------------------------------------------------------  0
TaHKT2.2      ----VPAFRVVKASPILGFFCAGVVLN--QFGLIRNLTDVKLLSEWGILFLLFEMG---- 81
TaHKT2.3      ATCGGIAFACLGQPVITGYLLAGSIIGPGGFSFVNELVQVETVAQFGVIFLLFALG----252
TaKEA2.1      ATAGGIIFSCLGQPVIVGYLLAGSLIGPGGLNLINEMVQVETFAQFGVVFLLFALG----233


TaAKT3.1      -----------F---------FVAYRDRSTDLL----------VDDRGKIA---------124
TaKAT2.1      -----------F---------FVAYRDRSTDLL----------VDDRSKIA---------114
TaTPK1.1      -----------F---------FVAYIDSRTQLL----------VRDRRRIT---------109
TaAKT2.1      -----------F---------FLAYLDHKSYLL----------VDNPKRIA---------109
TaAKT1.1      -----------F---------FVAYVDSKTHLL----------VDDRKRVA---------127
TaKAT1.1      -----------F---------FVPYVDNRSYLV----------VDDPKKIA---------132
TaKEA5.1      -----------F---------FVAYLDRLTYLL----------EDDPKRIA---------141
TaTPK2.1      -----------F---------FVAYTDKRTYLL----------VDDPAKIA---------136
TaHKT2.1      VSGLSAITMEDLSSSQIVVLTLLMLAGGEIF-----------------------------119
TaHKT1.4      VSSMSTVEMEAFSNGQLLVLTVLMFVGGEVF-----------------------------159
TaHKT1.3      VSSMSTVEMEVFSNGQLLVLTVLMFVGGEVF-----------------------------144
TaHKT1.7      VSSMSTVEMEVFSNGQLVVLTTLMFVGGEVF-----------------------------143
TaKAT5.1      VSSMSTVEMEVFSNGQLLVLTVLMFVGGEVF-----------------------------162
TaHKT1.8      VSSMVAVEMESFSNPQLLLLTILMLLGGEVF-----------------------------106
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TaKAT1.8        VSSMVAVEMESFSNPQLLLLTLLMLLGGEVF----------------------------- 94
TaHKT1.5        VSSMVAVEMESFSNPQLLLLTLLMLLGGEVF-----------------------------106
TaKAT4          VSSMVAVEMESFSNPQLLLLTLLMLLGGEVF-----------------------------106
TaHKT1.1        VSSMATIEMEDFSGQQLWVFIILMILGGEVF-----------------------------147
TaHKT1.2        VSSMATVEMEEFSSKQLWVLAILMLIGSEVF-----------------------------122
TaKAT6.1        VSSMATVEMEEFSSKQLWVLAILMLIGSEVF-----------------------------122
TaKEA3.1        ------------------------------------------------------------  0
TaKEA4.1        ------------------------------------------------------------  0
TaHKT2.2        ---------LELSLSRLKALAKFAFGIGLPQVLLSTLAFAAFELPPNGAIGTRILQFLFN132
TaHKT2.3        ---------LEFSTAKLRAVRAVAVLGGLLQIILF--------------------MFLCG283
TaKEA2.1        ---------LEFSLPKLRVVGPVAVLGGVLQIALF--------------------MFLCG264


TaAKT3.1        -------VRYLTRPWFVLDVASTIPLQIVYQLVRG--KK----NGPCGFLILLRLWRLRR171
TaKAT2.1        -------VRYLTRPWFVLDVASTIPLQIVYQLVRG--KR----NGPCGFLILLRLWRLRR161
TaTPK1.1        -------FRYLS-TFFIMDVASTIPYQGIAYLVNG--EVR--EGMVYSLLGLLRLWRLRK157
TaAKT2.1        -------ARYLS-SWFILDVCSTIPYQPFGLLFNK--H-G--NGLAYRTLNMLRLWRLRR156
TaAKT1.1        -------VRYLS-TWFIFDVCSTAPFQPIILLFTH--K-G--NDLSFKVLNLLRLWRLNR174
TaKAT1.1        -------LRYLS-TWFIFDVCSTVPFRSITRLFTR--H-E--HSLGLKFLNVLRLWRLRR179
TaKEA5.1        -------WRYAT-SWLVLDVASTIPSEIARRMLPS--K-L----RSYGFFNMLRLWRLRR186
TaTPK2.1        -------WRYAS-TWLVLDVASTVPTELSRRILPP--D-L----RTYGVFGMLRLWRLRR181
TaHKT2.1        --------------------VSLLGLMLRVNHQDM--PDL--PSMKISSVPVE-L-----149
TaHKT1.4        --------------------LSLLGLASKWSKLRK--QAVRK-SRRVEIHDVAELEM---193
TaHKT1.3        --------------------LSLLGLASKWSKLRK--Q-IHKSSRRVEIHHVAELEM---178
TaHKT1.7        --------------------LSLLGLASKWSKLRK--QTVHKSSRRVDNHDVPELEM---178
TaKAT5.1        --------------------LSLLGLASKWSKLRK--QAVHKSSRRVDNHDVPELEM---197
TaHKT1.8        --------------------TSMLGLYFTYIKSKK--KEA--PHDHGDGGGKV---E---136
TaKAT1.8        --------------------TSMLGLHFTYLKSKT--KEAQAPHEHDHADKGK---P---126
TaHKT1.5        --------------------TSMLGLHFTYVKSKK--KEAQAPHDHDDGDKGK---P---138
TaKAT4          --------------------TSMLGLHFTYVKSKK--KEAQAPHDHDDGDKGK---P---138
TaHKT1.1        --------------------TSMVGLHFKNARANT--EGALQTRLAFISRDIE---S---179
TaHKT1.2        --------------------TSILGLHFMRAKFNT--ENSLNTRDHISHVDIE---S---154
TaKAT6.1        --------------------TSVLGLHFMRAKFNK--ENSLNTRDHISHIDIE---S---154
TaKEA3.1        ----------------------MSDNSIQRALLPE--NPDANVLQRKPSQGAKRFRR-CR 35
TaKEA4.1        ----------------------MVAGGVQQPLLSGGDGNAAGAIRQKPPDGVKRFRR-CR 37
TaHKT2.2        SRPDLVNIRSVDEAIVIGAALSLSSSAFVLQLLAE--KGELATRFGSATLGILLLQD-IA189
TaHKT2.3        ISAT-LCGGKTKEGVFVGVLLSMSSTAVVLKFLME--KNSINALHGQVTVGILVLQD-CA339
TaKEA2.1        LTAA-LCGAKLSEGVFVGTFLSMSSTAVVSKFLVE--KGSTNALHGQVTIGTLILQD-CA320


TaAKT3.1        ASKLFARLEKD---------------------TRLSYFWTR-----FIKLFCVA----LF201
TaKAT2.1        ASKLFTRLEKD---------------------TRLSYFWTR-----FIKLVCVA----LF191
TaTPK1.1        VKQFFTRLEKD---------------------IRFSYFWVR-----CARLIAVT----LF187
TaAKT2.1        LSALFARLEKD---------------------IRLNYYWIR-----CTKLISVT----LF186
TaAKT1.1        VSTLFARLEKD---------------------IRFNYFWTR-----CSKLISVT----LF204
TaKAT1.1        VSSLFARLEKD---------------------IRFNYAVIR-----CTKLISVT----LF209
TaKEA5.1        VSSLFARLEKD---------------------RHFNYFWVR-----CAKLICVT----LF216
TaTPK2.1        VGALLSRMEKD---------------------RKFSYFWVR-----CSKLVAVT----LF211
TaHKT2.1        -----QEIDLANSVALCDESQLEEA----AHAIPPKKCTELK-RSRPVKCLGYVVFGYFA199
TaHKT1.4        -PPVAAAGEFDNPTSITS-----TADDEMSKPLD-RFDDTRL-RRDAVLSLFFVVLAILL245
TaHKT1.3        -PPVDAATEFDNPTSMTS-----TADDEISKPLG-HSHDTRL-RRDAVLSLFFVVLAILL230
TaHKT1.7        -PPVDAATELDNPTSMTS-----TVDDEMSKPLD-HFDDTRL-RRDAVLSLFFVVLAILL230
TaKAT5.1        -PPVDAATELANPTSMTS-----TVDDEMSKPLD-HFDDTRL-RRDAVLSLFFVVLAILL249
TaHKT1.8        -PA-PSSLELPATTFMDDS--T--AQNQMEQGFN-KEQPRYG-RAFLTRLLLFIVLGYHV188
TaKAT1.8        -AP-SSSLQLTANTCMDDV--D-----RVEQGF--KDQPRYD-RAFLTRLLLFIVLGYHV174
TaHKT1.5        -AP-SSSLELAVTTGMDDV--D-----RVEQGF--KDQPRYD-RAFLTRLLLFIVLGYHV186
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TaKAT4        -AP-SSSLELAVTTGMDDV--D-----RVEQGF--KDQPRYD-RAFLTRLLLFIVLGYHV186
TaHKT1.1      -SDDFNNSSQNYMEGIQPEETMPHNQVQESKGMN-H---------KSRNILAHVVAGYFI228
TaHKT1.2      -INVTN-FDPNTSHGTKDEVSFSELHLANKQHVD-P---------KTTVLLGAAVTVYLL202
TaKAT6.1      -INVAN-FDPNTSHGTKDAVSFSEIRLANKQHVD-P---------KTTVLLGTAVTVYLL202
TaKEA3.1      SAPRSETDEKP---------------QENGSSLPAKELFSVVR—PSFRLVGFLLFLYLL  78
TaKEA4.1      TAPSADPAALEEPRPLTPPG---NASRTESAASPAKEVLESGRPSSSFRLVGLLLFAYVV 94
TaHKT2.2      VVPLLVIL------PV-----------LESQNVVEQSVWPML-LAESLKALGGLGILSL 231
TaHKT2.3      VGLLFALL------PI-----------LSGASGLLHGVASMT-KSLVL-LISFLGILSIL380
TaKEA2.1      VGLLFALI------PV-----------LGGSSGIFGGMMSMG-RLLLV-LSIFITVAYMM361


TaAKT3.1      ALHCASCVYLWLAFHYRDKEQTWIG-SLRGDFKERSVWFAYTYAVYWSMTT-MATVGYG-258
TaKAT2.1      ALHCASCVYLWLAFHYRDKEQTWIG-SLRGDFKERSVWFAYTYAVYWSMTT-MATVGYG-248
TaTPK1.1      LVHCAGCLYYLLADRYPDRDKTWIG-AVIPNFRQESLWIRYISSIYWSITT-MTTVGYG-244
TaAKT2.1      AIHCSGCFIYLIADTYPDPSRTWIG-AAIPNYRSESLWIRYVTAIYWSITT-LTTTGYG-243
TaAKT1.1      AVHCAGCFNYMLADRYPYPENTWIG-AVMPTFRSESLWTRYVTALYWSITT-LTTTGYG-261
TaKAT1.1      AVHCAGCINYLIADRYPDPARTWIG-AAHPDFREDGLWVRYVTCLYWSITT-MTTTGYG-266
TaKEA5.1      AVHCAACFYYLLADRYPDPKETWIG-NTMPDFHSKGLWIRYVTSVYWSITT-LTTVGYG-273
TaTPK2.1      AVHCSGCFYYLLADRYPNPAETWIS-ISMPQFHNESIWNRYVASMYWSITT-LTTVGYG-268
TaHKT2.1      VIHVLGFLL------------VFLY-ITHVPTASAPLNKKGINIVLFSLSVTVASCANA-245
TaHKT1.4      TVHVVGAVA------------VAAYILHASPAARRTLREKALNEWTFAVFTTVSTFSSC-292
TaHKT1.3      AVHVLGAGA------------IAAYILHASPAARRTLRGKALNVWTFAVFTTVSTFSSC-277
TaHKT1.7      AVHVLGAGA------------IVAYIVHASPAARRTLRDKALNVWTFAVFTTVSTFSSC-277
TaKAT5.1      AVHVLGSGA------------IVAYVLHASPAARRTLRDKALNMWTFAVFTTVSTFSSC-296
TaHKT1.8      VVHLAGYSL------------MLLY-LSVVSGARAVLAGKGISLHTFSVFTVVSTFANG-234
TaKAT1.8      VVHLAGYSL------------MLVY-LSVVSGARAVLAGKGISLHTLSVFTVVSTFANG-220
TaHKT1.5      VVHLAGYSL------------MLVY-LSVVSGARAVLTGKGISLHTFSVFTVVSTFANC-232
TaKAT4        VVHLAGYSL------------MLVY-LSVVSGARAVLTGKGISLHTFSVFTVVSTFANC-232
TaHKT1.1      AAIVCSSVV------------ITIF-LWIDSDARHLLKSKHIKMWTFSIFTAVSSFANC-274
TaHKT1.2      ITNLGSSLV------------IYLY-LKLVPDAQEVLKRKGIGLFLFSVFTAISSVANC-248
TaKAT6.1      ITNLGSSLL------------IYLY-LKLVPDAQEVLKRKGVGLFLFSVFTAISSVANC-248
TaKEA3.1      V----G--V------------VVFY-LVMDQLSGKRT-NRVLDALYFCIVT-MTSVGYG-116
TaKEA4.1      A----G--T------------TAFY-LAMDHMSGHRSGSRVIDAVYFCVVT-MTTVGYG-133
TaHKT2.2      G----KYLI------------RRIF-EFVA--ESRS----SEAFVALCLLT-VSGTSLLT267
TaHKT2.3      S----RTCV------------PWFL-KLMISLSSQTNELYQLAAVAFCLLF-----AWCS418
TaKEA2.1      T----WSFI------------PRFL-KLMIQLSSQTNELYQLAAVAFCLLL-----AWCS399
                                                             .:       .

TaAKT3.1      DLHAANTGEKLFSILFMLCNMGVACYVIGNMTNLVVH--------------------GAT298
TaKAT2.1      DLHAANTGEKLFSILFMLCNMGVACYVIGNMTNLVVH--------------------GAT288
TaTPK1.1      DLHAQNNLEMIFNIFYMLFNLGLTAYLIGNMTNLVVE--------------------GTR284
TaAKT2.1      DLHAENPREMSFCICFMLFNLGLTAYLIGNMTNLVVQ--------------------GSC283
TaAKT1.1      DLHAENPREMLFDIFYMLFNLGLTAYLIGNMTNLVVH--------------------GTS301
TaKAT1.1      DLHAQNAREMLFGISYMLFNLWLTAYLIGNMTNLVVH--------------------STS306
TaKEA5.1      DYHAENIREMIFNIFYMFFNLGLTAYLIGNMTNLVVH--------------------GTS313
TaTPK2.1      DMHAVNSREMLFTTFYMLFNLGLTAYLIGNMTNLVVH--------------------GTS308
TaHKT2.1      GLVPTNENMVIFSKNSGLLLLLSGQILAGNTL-FPLFLRL-----------LVWFLGRLT293
TaHKT1.4      GYMPTNENMAVFKRDTGLQLLLVPQALVGNTL-FPPLLAA-----------CVRAAAAAT340
TaHKT1.3      GYMPTNENMIVFKRDTGLQLLLVPQALVGNTL-FPPLLAA-----------CVRFAAAAT325
TaHKT1.7      GYMPTNENMIVFKRDTGLQLLLVTQALVGNTL-FPPLLAA-----------CVRVAAAAT325
TaKAT5.1      GYMPTNENMIVFKRDTGLQLLLVPQALVGNTL-FPPLLAA-----------CVRVAAAAT344
TaHKT1.8      GFVPNNEGMVVFRSFPGLLLLVMPHVLLGNTL-FPVFLRL-----------AIWALRRVT282
TaKAT1.8      GFMPNNEGMVAFRSFPGLLLLVMPHVLLGNTL-FPVFLRL-----------AIWALRRVT268
TaHKT1.5      GFVPNNEGMIAFRSFPGLLLLVMPHVLLGNTL-FPVFLRL-----------AIWALRRVT280
TaKAT4        GFVPNNEGMIAFRSFPGLLLLVMPHVLLGNTL-FPVFLRL-----------AIWALRRVT280
TaHKT1.1      GFTPLNDSMAIFKNNPTFLLLVTPQILVGNTL-FAPLLRL-----------SIWTLGKLS322
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TaHKT1.2        GFTPVNENMIIFQKNSGLLLLIIPQMLVGNTL-FAPCLRF-----------MVWSLQKIT296
TaKAT6.1        GFTPVNENMVIFQKNSGLLLLIIPQMLVGNTL-FAPCLRF-----------MVWSLQKIT296
TaKEA3.1        DLVP-NSDTTKLLACV----FVFTGMAIIALF-VSKSADYLVEKQEVLFFKALHMNMKCG170
TaKEA4.1        DLVP-SSDTGKLLASA----FAFGGVAVVGTS-LSKSADYLVEKQESLVFRAVHANGKH-186
TaHKT2.2        QWLGFSDTLGAFLAGA----------LLAETN-FRTQ-----------------------293
TaHKT2.3        DKLGLSLELGSFAAGV----------MISTTD-LAQH-----------------------444
TaKEA2.1        DYLGLSLELGSFLAGV----------MISTTD-FAHH-----------------------425
                     .     :                     .

TaAKT3.1        TTFRMRDMVD-QVARYGKANRLPA---------------WMREQMVESV----------Q332
TaKAT2.1        TTFRMRDMVD-QVARYGKANRLPV---------------WMREQMVESV----------Q322
TaTPK1.1        RTMEFRNSIR-AASNFVCRNHLPP---------------RLQQQILAYM----------C318
TaAKT2.1        RTRNFRDTIH-AASRFAARNQLPE---------------QIRDEMLAHI----------C317
TaAKT1.1        RTQKFRDSIY-AASEFAARNQLPV---------------SIKEQMLSHF----------C335
TaKAT1.1        RTRDFRDMVQ-AATEFAARNQLPR---------------QIEEQMLNHI----------C340
TaKEA5.1        RTRKYRDTIQ-AATSFALRNQLPP---------------RLQDQMISHL----------S347
TaTPK2.1        RTRKYRDKIQ-AATSFAQRHELPE---------------RLQDQMISHL----------S342
TaHKT2.1        KVKELRHMIK-NPEEVHFANLLP----------------RLPTAFLSSTVVGLVAAGVTM336
TaHKT1.4        RRVELKETAKEGGELTGYYHLLP----------------ARRCAMLAATVAGFVAVQAAM384
TaHKT1.3        RRVELKETAKKGRELTGYYHLLP----------------ARRCAMLAATVVGFLTVQVAM369
TaHKT1.7        RRVELKETAKKGRELTGYYHLLP----------------ARRCAMLAATVVGFLAVQVAM369
TaKAT5.1        RRVELKETAKKGRELTGYYHLLP----------------ARRCAMLAATVVGFLAVQVAM388
TaHKT1.8        RRPELG-----QLQSIGYGHLLT----------------SRHTCFLAFTVATFVLAQLSL321
TaKAT1.8        RRPELG-----ELQSIGYDHLLT----------------SRHTCFLAFTVAMFVLAQLLL307
TaHKT1.5        RRPELG-----ELRSIGYDHLLT----------------SRHTWFLAFTVAAFVLAQLSL319
TaKAT4          RRPELG-----ELRSIGYDHLLT----------------SRHTWFLAFTVAAFVLAQLSL319
TaHKT1.1        SREEYAYILQ-HPKEIGYRHLQP----------------HKNSVQLVLTGVMLILLQAML365
TaHKT1.2        GKQEWSFILE-HPKATRYRHLMS----------------TRKSAYLVLTVVGFIILQTIL339
TaKAT6.1        GKQEWCYILE-HANAIGYRHLMS----------------TRKCACLILTVVGFIILQTIL339
TaKEA3.1        EARMLRQIET----NKTKYKFYTAALLLVTAIVVGTVFLWKVEKLSLVD-------SFYC219
TaKEA4.1        PARELRAMEM----NKTWYKLYAAGALLAASVASGTLVLWKGEGMRPVD-------ALYC235
TaHKT2.2        ---IEADIR-------PFRGLLLGLFFVTTGTSIDMQLLIREWPNVLSLLAGLIAIKTLI343
TaHKT2.3        ---TLEQIE-------PIRNLFAALFLASIGMLINVHFLWNHVDILLAAVILVITIKTFI494
TaKEA2.1        ---TLEQVE-------AIRNLFAALFLASIGMLIHFKFLWNHVDILLAAVILVIIVKSIV475


TaAKT3.1        LRFQMA-ELLLPDE-VLSELPKAA-------RSAVAQHLYKATVEDCY---LFRGASDNL380
TaKAT2.1        LRFQMA-ELLLPDE-VLSELPKAA-------RSAVAQHLYKATVEDSY---LFRGASDNL370
TaTPK1.1        LKFRA--ESLNQQQ-LMDQLPKSI-------CKSICEHLFLPVVKEVY---LFKGISREA365
TaAKT2.1        LRYKT--EGLKQKE-TLDSLPKAI-------RSSIACHLYLPVLEKIY---LFHGVSFTC364
TaAKT1.1        LQFKT--EGYNQKT-MLNGLPKGI-------RSSIAYSLFFPILRRAY---LFHGVSNSF382
TaKAT1.1        LRFKA--EGLKQQD-TLDILPKAM-------RSSISLYLFFPVVQGAY---LFRGVSPSF387
TaKEA5.1        LKFRTDSEGLQQQE-TLDALPKAI-------RSSISQYLFLNLVQNIY---LFQGVSNDL396
TaTPK2.1        LKFRTHSEGLQQQE-TLDALPKAL-------RSSISHHLFFGLVQNVY---LFQGVSNDL391
TaHKT2.1        FCAV------DWNSSVFDGLSSYQKTVNAFFMVVNARHS----GENSID---CSLMSPVI383
TaHKT1.4        LCGM------EWGG-ALSGMSAWEKVSNAVFLAVNSRHT----GETTLD---LSTLAPAI430
TaHKT1.3        LCGM------EWGG-ALRGMSPWEKVCSAVFLAVNSRHT----GESTLD---ISTLAPAI415
TaHKT1.7        LCGM------EWGG-ALRGMSPWEKVSNAVFLAVNSRHT----GESTLD---LCTLAPAV415
TaKAT5.1        LCGM------EWGG-ALRGMSAWEKVSNAVFLAVNSRHT----GESTLD---LFTLAPAI434
TaHKT1.8        FCAM------EWGSNGLHGLTAAQKLVAALFMSVNSRHT----GEMVVD---LSTMSSAV368
TaKAT1.8        FCAM------EWGSDGLHGLTAAQKLVTALFMSVNSRHT----GEMVVD---HSTVSSAV354
TaHKT1.5        FCAM------EWGSNGLRGLTAVQKLVAGLFMSVNSRHT----GEMVVD---LSTVSSAL366
TaKAT4          FCAM------EWGSNGLRGLTAVQKLVAGLFMSVNSRHT----GEMVVD---LSTVSSAL366
TaHKT1.1        ICYF------EWDSKSLEGMGWFQKLIGSLFQSANSRHA----GETVID---ISTLSPPI412
TaHKT1.2        FCSL------EWSSEAIQEMSSYQKIVGALFQSTNARHA----GETIVD---LSSISSAI386
TaKAT6.1        FCAL------EWSSEALQEMSSYQKIVGALFQSTNARHA----GETIVD---LSSISSAI386
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TaKEA3.1        VCATITTLGYGDKSF-----SSQLGRTFAVFWI------------------ITSTIILAL256
TaKEA4.1        VCATVTTLGYGDRSF-----TSSAGRAFAAVWV------------------TVSTVVVAL272
TaHKT2.2        TTALATRVGLTFQESVRIGLLLSQGGEFGFVVFSLANRLGVLPLELNKLLIIVVVLSMAL403
TaHKT2.3        VSIVVKGFGYNNKTSLLVGMSLAQIGEFAFVLLSRASSIHLIEGKLYLLLLGTTALSLVT554
TaKEA2.1        ITAVIKSFGYSIRTAFIVGLSLAQIGEFAFVLLSRASHHHLIGGKMYLLLLGTTALSLVT535


TaAKT3.1        VVQLVSE--------MKAEFFPPKMDIVLENENPTD------------CYIIASGQVDVL420
TaKAT2.1        VVQLVSE--------MKAEFFPPKMDIVLENEIPTD------------CYIIASGQV---407
TaTPK1.1        QLLLVTK--------TKPEYIPPKEDVIVQNEAADD------------VYIVVSGEVEIV405
TaAKT2.1        RLQLVTT--------MEAEYYPPRETVILQNETPTD------------VYILVSGAVEER404
TaAKT1.1        IAELVME--------VQPEYFPPKEDIILQNEGAAD------------IYLIVSGAVNMI422
TaKAT1.1        IQQLVTE--------MVAEYYAPKEDIILQNEYPSD------------LHLLVTGEVDIV427
TaKEA5.1        IFQLVSE--------MKAEYFPPREDVILQNEAPTD------------FYILVSGSVELV436
TaTPK2.1        IFQLVSE--------MSAEYFAPREDVILQNEAPSD------------FYIIVTGSVELL431
TaHKT2.1        IVLFIVMMYLP----SSATFATPNGDTKTTNENTK-GKAKRGSLVQNLAFSPLGCNIIFV438
TaHKT1.4        LVLFVLMMYLP----PYTTWFPFGESSSV--KDHPTEETQGVRLLKSTLLSQLSYLAIFV484
TaHKT1.3        LVLFVLMMYLP----PYTTWFPFEERSGV--KDHPTEETQGVRLLKSTLLSQFSYLAIFV469
TaHKT1.7        LVLFVLMMYLP----PYTTWFPFEESSGV--KDHPTEETQGARLLKSTLLSQLSYLVIFV469
TaKAT5.1        LVLFVLMMYLP----PYTTWFPFEESSGV--KDQPREETQGVRLLKSTLLSQLSYLAIFV488
TaHKT1.8        VVLYVVMMYLP----PYTTFLPVEDDSDQQVGADQHHQKRVTSIWRKLLMSPLSFLAIFI424
TaKAT1.8        VVLYVVMMYLP----PYTTFLPVEDDSDQQVGADQHHQKRVTSIWRKLLMSPLSCLAIFI410
TaHKT1.5        VVLYVVMMYLP----PYTTFLPVEDDSDQQVGADQRDQKRITSMWRKLLMSPLSCLAIFI422
TaKAT4          VVLYVVMMYLP----PYTTFLPVEDDSDQQVG----------------------------394
TaHKT1.1        MVIFALVMYLP----SGTSILATCGDNRS--LADKKENPNGRATWKKFAMTKRTCLVIIT466
TaHKT1.2        IVLYTVMMYLP----GYTSLLPNYDDRYS--KAEKRYSRKG--LLEDWIFSQLTYLAIFV438
TaKAT6.1        IFLYIVMMYLP----GYTSFFTNYDDRYS--KDEKRYNRKG--LLEDWILSQLSYLAIFV438
TaKEA3.1        FFMYLAEIYTERRQKMLAKWVLTRRVTTMDLEAADL------------DNDRKVGAAEF-303
TaKEA4.1        FFLYVAELYAERRQRALARWVLTRRTTNTDLEAADL------------DGDRRVGAAEF-319
TaHKT2.2        TPLLNDL-------GRKAAGIIDERSETKEKPAEEA----------------NYGATEPI440
TaHKT2.3        TPLLFKMIPAVVHLGVLLRWFSVDSNQV-ELGLKGE------------VLRIDSGKRINL601
TaKEA2.1        TPLIFKLIPVVTQLGILMRWFPSESGVQNELPLQEK------------ATMLDVYNRTL-582


TaAKT3.1        RTAK--DDGLEKFVMRIGPHGMAGEIGVMLNIPQPFTIRSRTLTQVIRISRSHLQNTVRP478
TaKAT2.1        ------------FIMRIGPHGMAGEIGVMLNIPQPFTIRSRTLTQVIRISRSHLQSTIWP455
TaTPK1.1        YFNG----EREEVMGKLGTMDIFGEVSALSDRPQTFTFRTRTLSQLLRLKQATLREVMQS461
TaAKT2.1        IMID----GREKVEKLLSGGDIFGEIGVLCNIPQPFTFRTSRISQLLRLNTTVLKNIIQE460
TaAKT1.1        TTIN----GNEQVYAKVTNGDMFGEVGALCNITQPFTFRTAELSQLLRISRTRLREAIQN478
TaKAT1.1        AFLD----GTEQVYGKATEGGLLGEIGVLCNKPQPFTFRTAKLSQVLRISRPKLMDIIQE483
TaKEA5.1        EVPNGAEHGAEQVVGVAKSGEVIGEIGVLCYRPQLFTVRTRSLCQLLRMNRTAFLSIVQS496
TaTPK2.1        EIQN---NGAEQLASTAKSGQVIGEIGVLCYRPQLFTARTKSLCQLLRLDRADFLKVVQS488
TaHKT2.1        IVAC------------------ITERRRLRNDPLNFSTL---------------------459
TaHKT1.4        IAIC------------------VTEREKLKEDPLNFNLL---------------------505
TaHKT1.3        IAVC------------------ITEREKLKEDPLNFNLL---------------------490
TaHKT1.7        IAIC------------------ITEREKLKEDPLNFNLL---------------------490
TaKAT5.1        IAIC------------------ITEREKLKEDPLNFNLL---------------------509
TaHKT1.8        AVVC------------------ITERRQISDDPLNFNVL---------------------445
TaKAT1.8        AVVC------------------ITERRQISDDPLNFNIL---------------------431
TaHKT1.5        AVVC------------------ITERRQISDDPLNFNVL---------------------443
TaKAT4          ------------------------------------------------------------394
TaHKT1.1        ILAC------------------ITERKSMTADPLNFSIF---------------------487
TaHKT1.2        MLIC------------------ITEREALTTDPLNFNVF---------------------459
TaKAT6.1        MLIC------------------ITEREALTTDPLNFNVF---------------------459
TaKEA3.1        VVYK------------------LKELGKISQEDIS-------------------------320
TaKEA4.1        VLYK------------------LKELGKISQEEIS-------------------------336
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TaHKT2.2      VILG------------------FGEMGQVLA-----------------------------453
TaHKT2.3      IIQG------------------PHDS----------------------------------609
TaKEA2.1      ------------------------------------------------------------582


TaAKT3.1      ATADGDTIFSNFVQYLESLKVRHG---EE--------------------LTFARDVGHDT515
TaKAT2.1      ATADGDTIFSNFVQYLESLKVRHG---EE--------------------LTFARELGHDT492
TaTPK1.1      KPDDSALIVRNFLKHQIEVHDMKDLLGESTGA----GGCG---NIVPCNLLTVAATGNAG514
TaAKT2.1      NKHDKEIIMNNLYQKMNSDQRFST---DTME------------------VC------E--491
TaAKT1.1      HREDNDILMNNLFQKLKLPENLPE---VNQPDRR-FLS--------KYDLFH-IPREERM525
TaKAT1.1      NAEDGEIIRINLEQVNV-------------------------------------------500
TaKEA5.1      NVGDGTIIMNNLIQLLKEQ-TDGVMVGVLKEIES-MLARGR--LDLPITLCFAVTRGDDH552
TaTPK2.1      NVGDATIIMNNLIQYLKEHKGDGVISGIAKDIER-MLATGQ--LDLPITLCFAASRGDDF545
TaHKT2.1      -------------NMIFEVISAYGNVGL---STG--YSCSRLHQLHPEIICQDKPYSFSG501
TaHKT1.4      -------------SIVVEVVSAYGNVGF---SMG--YSCSR--QISPDGMCTDRWTGFAG545
TaHKT1.3      -------------SIVVEVVSAYGNVGF---SMG--YSCSR--QISPDRLCTDRWTGFAG530
TaHKT1.7      -------------SIVVEVVSAYGNVGF---SMG--YSCSR--QISPDGMCTDRWTGFAG530
TaKAT5.1      -------------SIVVEVVSAYGNVGF---SMG--YSCSR--QISPDGMCTDRWTGFAG549
TaHKT1.8      -------------NITVEVISAYGNVGF---STG--YSCAR--QVTADGGCRDTWVGFSG485
TaKAT1.8      -------------NITVEVISAYGNVGF---STG--YSCGR--QVTPDGGCRDTWVGFSG471
TaHKT1.5      -------------NITVEVISAYGNVGF---STG--YSCGR--QVTPDGGCRDTWVGFSG483
TaKAT4        ------------------------------------------------------------394
TaHKT1.1      -------------SVIFEVMSAYGNVGY---SLG--YSCDK--LLRPDSACRDASYGFVG527
TaHKT1.2      -------------SILFEVVSAYGNVGF---SMG--YSCKR--LLKQDVHCKDASFGFVG499
TaKAT6.1      -------------SLLFEIVSAYGNVGF---SMG--YSCKR--LLKQDLHCKDASYGFVG499
TaKEA3.1      -----------------SFLEEFDKLD--VDQSG-TLSTYD---LTQAQSGQ--------349
TaKEA4.1      -----------------EFMEEFDMLD--ADHNG-TLSPSD---LAVAQPTTA-------366
TaHKT2.2      -----------------KFLAAPLSFGLERDTEGWPYVAFD---LNPAVVKSARKSGFPV493
TaHKT2.3      ------------------------------------------------------------609
TaKEA2.1      ------------------------------------------------------------582


TaAKT3.1      L--------------------------------------P--------------------517
TaKAT2.1      L--------------------------------------P--------------------494
TaTPK1.1      FLEDLLKVGMDPDVGDSKGRTALHIAASKGYEGCVQ-ALLMHGCNI------NIKDAQGN567
TaAKT2.1      ---ETLD---------------QHFGEYNGCFASNQ--VNINNESK--------------517
TaAKT1.1      L--QWPH---------------QHYTEQKSIDLGSK--VPISGDGP------HSTKLFGQ560
TaKAT1.1      ------------------------------------------------------------500
TaKEA5.1      LLHQLLKRNLDPNESDQDGRTALHIAASKGNEQCVK-LLLEYGADP------NARDSEGK605
TaTPK2.1      LMHQLLKRGLDPNETDNCGRTALHIAASNGSEQCVR-RLLENGADA------NARDPEGK598
TaHKT2.1      WWSD-------------GGKFLL-------------VLVMLYGRLKVFAVST--GKSWRV533
TaHKT1.4      RWSD-------------SGKLIL-------------ILVMLFGRLKKFSMNA--GKAWKL577
TaHKT1.3      RWSD-------------SGKLIL-------------ILVMLFGRMKKFSMKA--GKAWKL562
TaHKT1.7      RWSD-------------SGKLIL-------------ILVMLFGRLKKFSMYT--GKAWKL562
TaKAT5.1      RWSD-------------SGKLIL-------------ILVMLFGRMKKFSMKA--GKAWKL581
TaHKT1.8      KWSW-------------QGKLVL-------------IAVMFYGRLKKFGMHG--GEAWRI517
TaKAT1.8      KWSW-------------QGKLVL-------------IAVMFYGRLKKFSMHG--GEAWMI503
TaHKT1.5      KWSW-------------QGKLAL-------------IAVMFYGRLKKFSMHG--GEAWRI515
TaKAT4        ------------------------------------------------------------394
TaHKT1.1      RWSD-------------KGRLII-------------ILVMFLGRFKAYTLR---------552
TaHKT1.2      KWSD-------------KGKMIL-------------IIVMVFGRLKAYNLKG--GKAWKL531
TaKAT6.1      KWSD-------------EGKMIL-------------IIVMVFGRLKGYNLKG--GKAWKL531
TaKEA3.1      ------------------------------------------------------------349
TaKEA4.1      ------------------------------------------------------------366
TaHKT2.2      LYGD-------------GSRPAVMQS--AGISSPKAVMIMYTGKEETVESVDRLRQAFPA538
TaHKT2.3      ------------------------------------------------------------609
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TaKEA2.1      ------------------------------------------------------------582


TaAKT3.1      ------------------------------------------------------------517
TaKAT2.1      ------------------------------------------------------------494
TaTPK1.1      TALWQAIAARHHK-------VFSNLYHVARVSNPRAAGDLLCLAARRGDVDTLRELLKHG620
TaAKT2.1      ----------------------------------------------------------AG519
TaAKT1.1      VPQQEDIHNKSNC-------K----------YRLSDGMMDKE---------------EDL588
TaKAT1.1      ------------------------------------------------------------500
TaKEA5.1      VPLWEAVYAKHDT-------VVQLLVKGGAELSSGDTSLYACTAVEQNNIELLKQILKHV658
TaTPK2.1      VPLWEALCRRHQT-------VVQVLVEAGADLSAGDGGMYARVAVEEDDAVLLGEIARCG651
TaHKT2.1      ------------------------------------------------------------533
TaHKT1.4      S-----------------------------------------------------------578
TaHKT1.3      S-----------------------------------------------------------563
TaHKT1.7      S-----------------------------------------------------------563
TaKAT5.1      S-----------------------------------------------------------582
TaHKT1.8      V-----------------------------------------------------------518
TaKAT1.8      I-----------------------------------------------------------504
TaHKT1.5      V-----------------------------------------------------------516
TaKAT4        ------------------------------------------------------------394
TaHKT1.1      ------------------------------------------------------------552
TaHKT1.2      R-----------------------------------------------------------532
TaKAT6.1      R-----------------------------------------------------------532
TaKEA3.1      ------------------------------------------------------------349
TaKEA4.1      ------------------------------------------------------------366
TaHKT2.2      VPVYVRAQDMSHLLDLRKAGATDVVLENAETSLQLGSMLMKGLGVMSDDVSFLSKLVRDS598
TaHKT2.3      ------------------------------------------------------------609
TaKEA2.1      ------------------------------------------------------------582


TaAKT3.1      ------------------------------------------------------------517
TaKAT2.1      ------------------------------------------------------------494
TaTPK1.1      LDVD-TEDHDGSTALRVALSEGQADAARFLVMNGASVDKADLDGDGSAPRQTTVPAAELR679
TaAKT2.1      ETIRLACSEER-------------------------------------------------530
TaAKT1.1      NEVRINCETKT-------------SA------------------------------EE--603
TaKAT1.1      ------------------------------------------------------------500
TaKEA5.1      IDVN-RPSKDGNIPLHRAVCDGNVEMVELLLRHGADIDKQDSNGWTPRALAEQQGHEEIQ717
TaTPK2.1      GDVAAACSSDGTTPLHRAVLDGNARMVRVLLEHGADPDREDARGLTPTALADRHAHADIQ711
TaHKT2.1      ------------------------------------------------------------533
TaHKT1.4      ------------------------------------------------------------578
TaHKT1.3      ------------------------------------------------------------563
TaHKT1.7      ------------------------------------------------------------563
TaKAT5.1      ------------------------------------------------------------582
TaHKT1.8      ------------------------------------------------------------518
TaKAT1.8      ------------------------------------------------------------504
TaHKT1.5      ------------------------------------------------------------516
TaKAT4        ------------------------------------------------------------394
TaHKT1.1      ------------------------------------------------------------552
TaHKT1.2      ------------------------------------------------------------532
TaKAT6.1      ------------------------------------------------------------532
TaKEA3.1      ------------------------------------------------------------349
TaKEA4.1      ------------------------------------------------------------366
TaHKT2.2      MELQAQEALNNV-------EDRETTTMESLQVRVSDLVESNGNGSGMIPREQSLGLSSRP651
TaHKT2.3      ------------------------------------------------------------609
TaKEA2.1      ------------------------------------------------------------582
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TaAKT3.1       ---------FQNG----------------DPIRVV----------I--------------528
TaKAT2.1       ---------FQNG----------------DPIRVV----------I--------------505
TaTPK1.1       ELV----KRREVGH----------------PI-TIYD--------SPASTVTAASSS---707
TaAKT2.1       ------------------------------------------------------------530
TaAKT1.1       --FCIKIKSEDKTAA-SSQQTILAKMQPGSPQRT--------------------------634
TaKAT1.1       ------------------------------------------------------------500
TaKEA5.1       NLFRSVIAPRKYTSN--------GRVTP--MLLGRFSSDPSMQKVIHED-----------756
TaTPK2.1       QLFASHRHRDQQGAPKPSSTEEVAAVAPAAPQVTRFRSAPSARVLPPSGTVGSSSSSPSP771
TaHKT2.1       ------------------------------------------------------------533
TaHKT1.4       ------------------------------------------------------------578
TaHKT1.3       ------------------------------------------------------------563
TaHKT1.7       ------------------------------------------------------------563
TaKAT5.1       ------------------------------------------------------------582
TaHKT1.8       ------------------------------------------------------------518
TaKAT1.8       ------------------------------------------------------------504
TaHKT1.5       ------------------------------------------------------------516
TaKAT4         ------------------------------------------------------------394
TaHKT1.1       ------------------------------------------------------------552
TaHKT1.2       ------------------------------------------------------------532
TaKAT6.1       ------------------------------------------------------------532
TaKEA3.1       ------------------------------------------------------------349
TaKEA4.1       ------------------------------------------------------------366
TaHKT2.2       EVRVIKTTPEN-SMP---------------NLNTKNESEDGVKYCLLET-----------684
TaHKT2.3       ------------------------------------------------------------609
TaKEA2.1       ------------------------------------------------------------582


TaAKT3.1       --------------------------HGQIP-----------------------------533
TaKAT2.1       --------------------------HGQIP-----------------------------510
TaTPK1.1       ----------SGELRQGRFQGSTRS-----DSAHWPRV--SI-------YKGHPF-----738
TaAKT2.1       ------------------------------------------------------------530
TaAKT1.1       ----------SENISRSRYQDY----SG-IKAAN-KRVTIHIYS----------------662
TaKAT1.1       ------------------------------------------------------------500
TaKEA5.1       -----VEQQPSKVLPQRRKVSFHNSLFGVISSAHPRRETDHLLSRGLAATGGPTYPQAH-810
TaTPK2.1       NRAGRQSNSSSARSTPQRMASFRNSLFGVISSSFHGNRHD--------GGGGTSFHHRHE823
TaHKT2.1       ------------------------------------------------------------533
TaHKT1.4       ------------------------------------------------------------578
TaHKT1.3       ------------------------------------------------------------563
TaHKT1.7       ------------------------------------------------------------563
TaKAT5.1       ------------------------------------------------------------582
TaHKT1.8       ------------------------------------------------------------518
TaKAT1.8       ------------------------------------------------------------504
TaHKT1.5       ------------------------------------------------------------516
TaKAT4         ------------------------------------------------------------394
TaHKT1.1       ------------------------------------------------------------552
TaHKT1.2       ------------------------------------------------------------532
TaKAT6.1       ------------------------------------------------------------532
TaKEA3.1       ------------------------------------------------------------349
TaKEA4.1       ------------------------------------------------------------366
TaHKT2.2       -ADGEETVEPPAEARR--------------------------------------------699
TaHKT2.3       ------------------------------------------------------------609
TaKEA2.1       ------------------------------------------------------------582


TaAKT3.1       -----------HGSGMAGNRAAGKLVCLPGSLEELMKLGEDKF--GMAARHVLTADGAEV580
TaKAT2.1       -----------HGSGMAGNRAAGKLVCLPGSLEELLKLGEDKF--GMAARHVLTADGAEV557
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TaTPK1.1        --------------VRNHSSEAGKLINLPATMEEFKTIIGEKLKVDTEKALILNGEGAEI784
TaAKT2.1        ------------------------------------------------------------530
TaAKT1.1        HN------------AIGSTVQNGKLISLPDSLEELIKIGRQKF-PDFHPTKVVSRDYAEI709
TaKAT1.1        ------------------------------------------------------------500
TaKEA5.1        ---HNPLIRVTISCPEMGNTAGKL-VILPGSIKELLQLGAKKF--DMMPTKVLTIEGAEV864
TaTPK2.1        RNPISSHVRVTISCPEQGRSQRRLLVFVPETMLQLLELGGNRF--GFTATRVITSDGAEI881
TaHKT2.1        ------------------------------------------------------------533
TaHKT1.4        ------------------------------------------------------------578
TaHKT1.3        ------------------------------------------------------------563
TaHKT1.7        ------------------------------------------------------------563
TaKAT5.1        ------------------------------------------------------------582
TaHKT1.8        ------------------------------------------------------------518
TaKAT1.8        ------------------------------------------------------------504
TaHKT1.5        ------------------------------------------------------------516
TaKAT4          ------------------------------------------------------------394
TaHKT1.1        ------------------------------------------------------------552
TaHKT1.2        ------------------------------------------------------------532
TaKAT6.1        ------------------------------------------------------------532
TaKEA3.1        ------------------------------------------------------------349
TaKEA4.1        ------------------------------------------------------------366
TaHKT2.2        ------------------------------------------------------------699
TaHKT2.3        ------------------------------------------------------------609
TaKEA2.1        ------------------------------------------------------------582

TaAKT3.1        DDVRALRDGDHLFLS---------------  595
TaKAT2.1        DDVRALRDGDHLFLS---------------  572
TaTPK1.1        DSLDVIRDNDKLFIVTEEHMRMLASMDS--  812
TaAKT2.1        ------------------------------  530
TaAKT1.1        DDISVIRDGDHIFFLQI-------------  726
TaKAT1.1        ------------------------------  500
TaKEA5.1        DEVELIRDGDHLVLASDDWVPDDTQIRGKN  894
TaTPK2.1        DDVRLVRDGDHLLLVSDQWAPDTTSAHRNQ  911
TaHKT2.1        ------------------------------  533
TaHKT1.4        ------------------------------  578
TaHKT1.3        ------------------------------  563
TaHKT1.7        ------------------------------  563
TaKAT5.1        ------------------------------  582
TaHKT1.8        ------------------------------  518
TaKAT1.8        ------------------------------  504
TaHKT1.5        ------------------------------  516
TaKAT4          ------------------------------  394
TaHKT1.1        ------------------------------  552
TaHKT1.2        ------------------------------  532
TaKAT6.1        ------------------------------  532
TaKEA3.1        ------------------------------  349
TaKEA4.1        ------------------------------  366
TaHKT2.2        ------------------------------  699
TaHKT2.3        ------------------------------  609
TaKEA2.1        ------------------------------  582
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