

Signal peptide | Leucine zipper | LRR1 | LRR2 |

AtSERK1 : -----MESS---YVVFILLSLILPNHSLWLAS-----ANLEGDALHTHTVRVTVDP---NNVLQSWDPITLVNPTCFWHVTCNNNSVIRVDLGNABLSGHVLVPELGVLKNLOYLELYSNNTITGPIPSNLTGLNLNLVSLDMLN : 127

AtSERK2 : -----MGRKKFEAFGFVCLISLLLFNSLWLAS-----SNMEGDALHSLIRANVTVDP---NNVLQSWDPITLVNPTCFWHVTCNNNSVIRVDLGNADLSGQLVQVLQGLQKNLOYLELYSNNTITGVPVSDLTGLNLNLVSLDMLN : 130

MtSERK1 : -----MEETKFCALAFICAFFLLILH-PLWLVS-----ANMEGDALHNLIRTNLODP---NNVLQSWDPITLVNPTCFWHVTCNNNDNSVIRVDLGNALSGHVLVQVLQGLQKNLOYLELYSNNTITGPIPSDLTGLNLNLVSLDMLN : 129

AtSERK3 : -----MERRLMIP-----CFFWLLILVLDLVRVS-----GNABGDALSALKNSLAD---PNKVLQSWDATLVPTCTCFWHVTCNSDNSVIRVDLGNANLSGQLVQVLQGLPNLOYLELYSNNTITGPIEQGLTGLNLNLVSLDMLN : 126

AtSERK4 : --MTSSKMEQRSL--CFLYLLLFNFTLRVA-----GNABGDALTQIKNSLSSGDPANNVLQSWDATLVPTCTCFWHVTCNPENKVIRVDLGNAKLSGKLVPVPELQGLNLLOYLELYSNNTITGPIPEELGLDLVLVSLDMLN : 133

AtSERK5 : -----MEHGSSR-----GFIWLLILFLDFVSRVT-----GKTCVDALIAIRSSLSGGDHTNNILQSWNATHVTPCSWFHVTCONTENSVIRLDLGSANLSGELVQVLQGLPNLOYLELYNNNTITGPIPEELGLDLMLVLVSLDMLN : 128

MtSERK2 : ---MEQVTSSSSS---KTLLFLFWAILVFDLVLKAS-----SNVBDGDAINALKSNLNDP---NNVLQSWDATLVNPTCFWHVTCNGDNSVIRVDLGNABLSGHVLVQVLQGLDLNLLOYLELYSNNTITGPIPEELGLNLNLVSLDMLN : 131

MtSERK3 : ---MITVSYDEVVTGEPPTLASLVIYHDIVNVDY-----IKHGSDTLIALKSNLNDP---NSVFQSWNATNVNCEWFHVTCONDDKSVILIDLENANLSGTLISKFDLSNLLOYLELYSNNTITGPIPEELGLNLNLVSLDMLN : 135

MtSERK4 : -----MNINME-----QASFLFWAILVHLLLKAS-----SNEBESDAINALKSNLNDP---NNVFDNWDTLLVNPTCFWHVTCNDKDKVISVDLGNANLSGTLVSQLGLDLNLHKLLELYNNNTITGPIPEELGLTLNLVSLDMLN : 128

MtSERK5 : MNINMEQVASSS---TVSFLFWAILVHLLLKAS-----SNEBESDALFAFRNNDP---NNALQSWDATLVNPTCFWHITCSGGR-VIRVDLGNANLSGTLVSNLGVLSNLBYLELYNNNTITGPIPEELGLNLNLVSLDMLN : 132

MtSERK6 : ---MERVTPSSN---KASFLLSSTTVLHLLLQAS-----SNEBESDMLIAFKSNLNDP---NNALESWBSTLLNPTCFWHVTCSGDR-VIRVDLGNANLSGTLVSSLGGLSNLOYLELYNNNTITGPIPEELGLNLNLVSLDMLN : 129

MtSERKL1 : -----MPLNFLLLLLFLFHSHPFSSASE-----PRNPEVVAIMSTKEALNDP---HNVLSNWDEFSVDPCSWAMITCSSDSFVIGLGAPSQLSGTLSSSLANLNLKQVILQNNNTISGKIPPELGLNLPLQLQLDLSNN : 127

MtSERKL2 : -----MEFCSLVWLLGLLHV-LMKVSSAAL---SPSGINYEVALMAIKNNDP---HNVLNWDINVYDPCSWRMITCTPDGSVSAIGFPSQNLSGTLSPKLTGNLTNLQSVILQNNATISGHPALGLTGLNLNLVSLDMLN : 132

MtSERKL3 : ---MFVEMN---LLFLLLLVLCVCSFALP-----QLDICEDALYALKSLNAS---PNCNTNWNKNOVNPTCSWNYCDONSNVQVSLAFMGFAGSLTPRIGALKSLTTLSQLGNNITGPIPEFGLTLNLVSLDMLN : 127

AtN1K1 : -----MESTIVMMMI TRSFFCFGLFCLLCSVHGHLSPKGVNFVQAIDGIRKASLHDP---HGVLDNWRDAVDPCSWMTICSSENFVIGLGTPSNLSGTLSPSHTNLNLRIVILQNNNTIKGKIPPELGLTLNLVSLDMLN : 139

AtN1K2 : ---MLQGRREAKKSYALFSSSTFFFFF---ICFLSSSS-AELTDKGVNFVVAIMGIRKSSLTDP---HGVLMNWDITAVDPCSWNMTICSS-DGFWIRLEAPSQLSGTLSSSLGNLTNLQTVILQNNNTIGKIPPELGLTLNLVSLDMLN : 139

AtN1K3 : -----MEGVRVFWRLGFLVFWFDFISSATL---SPTGVNVEVTAIVAKNNDP---YKVLNWDVNSVDPCSWRMVCCT-DGVYSSLDLPSQSLSGTLSPRIGNLTYLOSVILQNNATISGPIPETGLRLEKLSLGLDLSNN : 132

LRR3 | LRR4 | LRR5 | SPP domain | Transmembrane domain

AtSERK1 : SFSCHIEESLCKLSKIRFLR-LNNNSLTGSPISLNNITTLQVLDLSNNRLSGVPDNGSFSFLTPISFANNLDCGPVTSHPCCPGSPPFSPPPFFIQQPPVSTPSGYGITGAIAGGVAAGAALLFAAPAIATAWRRRKP-LDIEFFDV : 274

AtSERK2 : SFTCHIEDSLCKLKKIRFLR-LNNNSLTGPIPSLNNITTLQVLDLSNNRLSGVPDNGSFSFLTPISFANNLDCGPVTSRRCPCGSPPFSPPPFFIQQPIVPTPGGYSATGAIAGGVAAGAALLFAAPALATAWRRRKP-QEIEFFDV : 277

MtSERK1 : RFNCHIEDSLCKLSKIRFLR-LNNNSLMGPIPSLNNISALQVLDLSNNQLSGVPDNGSFSFLTPISFANNLDCGPVTHGPCPGSPPFSPPPFFVPPPPISAPGSGGATGAIAGGVAAGAALLFAAPAIATAWRRRKP-QEIEFFDV : 276

AtSERK3 : NLSCHIEESLCKLKKIRFLR-LNNNSLTGPIPSLAVTLQVLDLSNNPLGDPVNGSFSFLTPISFANTKLTP-----LPA-SPPPP--ISPTPPSPA GSNRITGAIAGGVAAGAALLFAVPAIALAWRRRKP-QDHFFDV : 261

AtSERK4 : SISCHIEESLCKLKKIRFLR-LNNNSLTGPIPTLTSVQ-LQVLDLSNNRLSGDIPVNGSFSFLTPISFANNSLTD-----LPEPPPTS--TSPTPPPPS GG-QMTAIIAGGVAAGAALLFAVPAIAFAWRRRKP-QDHFFDV : 266

AtSERK5 : NISCHIEESLCKLKKIRFLR-LNNNSLTGPIPSLALP-LDVLDLSNNRLSGDIPVNGSFSOFTSMSFANNKLR-----PRPAS--PSPS---PS G---TSAIIIVGVAAGAALLFAL-----AWILRKKL-QGHFLDV : 247

MtSERK2 : HLSCHIEETLCKLKKIRFLR-LNNNLTCGPIPSLNVSSLQVLDLSNNLDLCTIPVNGSFSFLTPISYQNNRRLI-----QPKNAPAP--LSPAPTSS GG-SNTGAIAGGVAAGAALLFAAPAIALAYRRRKP-QDHFFDV : 265

MtSERK3 : HLSCHIEETLCKLKKIRFLR-LNNNSLTGPIPSLNVATLQVLDLSNNNLGDPVNGSFSFLTSSSYQNNRLK-----QPKIIHAP--LSPASSASS GN-SNTGAIAGGVAAGAALLFAAPAIALAYRRRKP-QDHFFDV : 269

MtSERK4 : NLSCHIEETLCKLKKIRFLR-LNNNSLTGPIPSLAKVTTLQVLDLSNNNLGDPVNGSFSFLTPISYLHT-KLN-----TSLIIPAP--LSPSPASS AS-SDTGAIAGGVAAGAALLFAAPAIALVRRRKP-QDHFFDV : 261

MtSERK5 : NISCHIEETLCKLKKIRFLR-LNNNSLTGPIPSLNVTTLQVLDVSNNLGDPVNGSFSFLTPISYHNNPRIK-----QPKNIYPV--LSPSPASS GS-SNTGAIAGGVAAGAALLFAAPAIALAYRRRKP-QDHFFDV : 266

MtSERK6 : NLTCHIEETLCKLKKIRFLR-LNNNSLTGPIPSLNVTTLQVLDVSNNLGDPVNGSFSFLTPISYHNNPRMK-----QOKIITVP--LSPSPASS GS-INTGAIAGGVAAGAALLFAAPAIALAYRRRKP-QDHFFDV : 263

MtSERKL1 : RFSCHIEESSNLQSLQVLR-LNNNSLTGPIPSLNNITQLAFLDLSNNNLGDLPLKFPARS---FIVGNPLICVSTIEGSGSVTLMVPVFSQA---ILQGHKHS-KKLIIVLVSVFSCSVILVFLGLFWRRKQOH--GAILYI : 266

MtSERKL2 : EFSCHIEESLCKLKNLYLR-LNNNSLTGCPISLNNIESITLVDLSYNNNLGDLPLRIQARLI---KIIVGNPLICGP-KENNCSTVLPEPSLPDPDALKAKPDSGKKGHVLAFAESFGAAFFVVIIVGLLVWRYRRHN-QQIEFFDI : 274

MtSERKL3 : KLTCHIEESSNLCKLKKIRFLR-LSCNNNLGTPISLNLNLIINILHDSNEHNGQIP---EQLFNVPKFNETGNKLNCG---ASYQHLCSTDNANGSSSHKPKVGLIVGTIVGSLILILGLS---LLFFVCKGHR-RDVHFDV : 258

AtN1K1 : FFHCHIEFSVCLQSLQVLR-LNNNSLTGVPPISLNNITQLAFLDLSYNNNLGDLPLRFAAKKFS---IVGNPLICPTGTEPCDCNGTTPKLSMMLNQTFVPLVYAGGSRN-HKMLIVLVSVGVTSIFIIVGLFWRRKQHN-ONTFFDV : 283

AtN1K2 : NFTCHIEFTGLSKNLQVLR-LNNNSLTGPIPSLNNITQLTFVDLSYNNNLGDLPLRSLAKFN---VMGNSQICPTGTEKDCNGTTPKLSMTLNSQNKSSDGGTKN-RKIIIVVSVSLTCTVCLIIIGFGLLWRRRHNKQVLEFFDI : 285

AtN1K3 : SFTCHIEESLCKLKNLYLR-LNNNSLTGCPISLNLKIEGLTLVDLSYNNNLGDLPLKVSARLFFK---VIGNALICGP---KAVNSCSAVPEPLTLPDQDGPDE-SGTRTNGHVALFAASFSAAFFVFTTSGMFLWRYRRN-KQIEFFDV : 273

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AtSERK1 : PA-BEDPEVHLGOLKRFSLRELQVADSFNSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERTPGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERPPSQFLDWPTKRRIALGSARGLSYLH : 418

AtSERK2 : PA-BEDPEVHLGOLKRFSLRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERTPGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERPPSQFLDLAHSIRQRIALGSARGLSYLH : 421

MtSERK1 : PA-BEDPEVHLGOLKRFSLRELQVATDSFSKNILGRGGFGKVKYKRIADGSIVAVKRLKEERTPGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERPPHQFLDWPTKRRIALGSARGLSYLH : 420

AtSERK3 : PA-BEDPEVHLGOLKRFSLRELQVADSFNSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERTQGGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERPPSQFLDWPKRRIALGSARGLSYLH : 405

AtSERK4 : PA-BEDPEVHLGOLKRFSLRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERTQGGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERPPGQFLDWPKRRIALGSARGLSYLH : 410

AtSERK5 : PA-BEDPEVHLGOLKRFSLRELQVATEKFSKRNVLGRGGFGKVKYKRIADGTIVAVKRLKEERTKGGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERPPGQFLDWPKRRIALGSARGLSYLH : 391

MtSERK2 : PA-BEDPEVHLGOLKRFSLRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERTQGGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERNEVDQFLDWPKRRIALGSARGLSYLH : 409

MtSERK3 : PA-BED-LEHLVQITRSLRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERTQGGGL---LOFOTEVELISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERNGSQFLDWPKRRIALGSARGLSYLH : 411

MtSERK4 : PA-BEDPEVHLGOLKRFSLRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERAQGGGL---LOFOTEVEIISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERNDSQFLDWPKRRIALGSARGLSYLH : 405

MtSERK5 : PA-BEDPEVHLGOLKRFSLRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERSKGGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERNDSQFLDWPKRRIALGSARGLSYLH : 410

MtSERK6 : PA-BEDPEVHLGOLKRFSLRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKEERTQGGGLQGGGL---LOFOTEVEMISMVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERNDSQFLDWPKRRIALGSARGLSYLH : 411

MtSERKL1 : G-DYKEEAVVSLGNLHFGFRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKDVGNSAGGL---LOFOTELEMISSLAVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERNDQFLDWPKRRIALGSARGLSYLH : 407

MtSERKL2 : S-E-HYDPEVRLGHUKRYRFEELRAATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKDYNAAAGGL---LOFOTEVETISLAVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERDHIHGRALDWTRKRRIALGSARGLSYLH : 418

MtSERKL3 : A-G-EVRRITLGLKFSRRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLTDVESPAGGL---QAFOREVEMISSLAVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERLKPGEISILNADTRKRRIALGSARGLSYLH : 402

AtN1K1 : K-DGNHHEVSLGNLHFGFRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKDGGALAGGL---LOFOTEVEMISLAVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERAKVFLDWGTRKRRIALGSARGLSYLH : 424

AtN1K2 : N-E-QNKEEMCLGNLRRFNFRELQVATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKDINNAGGL---VOFOTELEMISSLAVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERAKVFLDWGTRKRRIALGSARGLSYLH : 425

AtN1K3 : N-E-QYDPEVSLGHUKRYRFEELRSATDSFSKNILGRGGFGKVKYKRIADGTIVAVKRLKDGNIAAGGL---VOFOTEVETISLAVHNRNLLRLRGFCMPTERLLVYPMMANGSVASOLRERDNIHGRALDWTRKRRIALGSARGLSYLH : 417

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AtSERK1 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKEKKLMLVDPDLQSNY-----EREVEQLIOVALLCTQG : 561

AtSERK2 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKEKKLMLVDPDLQSNY-----EAEVEQLIOVALLCTQG : 564

MtSERK1 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKEKKLMLVDPDLQSNY-----EAEVEQLIOVALLCTQG : 563

AtSERK3 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKEKKLMLVDPDLQSNY-----DEVEQLIOVALLCTQG : 548

AtSERK4 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKEKKLMLVDPDLQSNY-----EAEVEQLIOVALLCTQG : 553

AtSERK5 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKEKKLMLVDPDLQSNY-----EAEVEQLIOVALLCTQG : 534

MtSERK2 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKDKLMLVDPDLQSNY-----DEVEQLIOVALLCTQG : 552

MtSERK3 : YSCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKEKKLMLVDPDLQSNY-----DEVEQLIOVALLCTQG : 553

MtSERK4 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKDKLMLVDPDLQSNY-----DEVEQLIOVALLCTQG : 548

MtSERK5 : DHCDEKIIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIQDKLMLVDPDLQSNY-----DEVEQLIOVALLCTQG : 553

MtSERK6 : DHCDEKVIHRDVKAANILLDEEFBAVVGDFGLAKLMYKQKHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKGLIKDKLMLVDPDLQSNY-----DEVEQLIOVALLCTQG : 560

MtSERKL1 : EQCDEKIIHRDVKAANILLDDYBAVVGDFGLAKLLDHAESHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKKIQDKLMLVDPDLQSNY-----DRIEVEQLIOVALLCTQG : 549

MtSERKL2 : EQCDEKIIHRDVKAANILLDDYBAVVGDFGLAKLLDHRKSHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKKIQDKLMLVDPDLQSNY-----DRIEVEQLIOVALLCTQG : 560

MtSERKL3 : EQCDEKIIHRDVKAANILLDDYBAVVGDFGLAKLLDHRKSHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKKIQDKLMLVDPDLQSNY-----DRIEVEQLIOVALLCTQG : 545

AtN1K1 : EQCDEKIIHRDVKAANILLDDYBAVVGDFGLAKLLDHAESHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKKIQDKLMLVDPDLQSNY-----DRIEVEQLIOVALLCTQG : 568

AtN1K2 : EQCDEKIIHRDVKAANILLDDYBAVVGDFGLAKLLDHRKSHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKKIQDKLMLVDPDLQSNY-----DRIEVEQLIOVALLCTQG : 567

AtN1K3 : EQCDEKIIHRDVKAANILLDDYBAVVGDFGLAKLLDHRKSHVTAVRGITGHIAPERYLSTGKSEKTDVFGYGYMLLELITGQAFDLARLANDDD-VMLLDWVKKIQDKLMLVDPDLQSNY-----DRIEVEQLIOVALLCTQG : 559

XI C-terminal domain

AtSERK1 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----VEVLRREEIDLS--PNPNSDYILD-----STYNLHAVELSGPR : 625

AtSERK2 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----VEVLRQEEVLS--SHPSTDYILD-----STDNLHAMELSGPR : 628

MtSERK1 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----GEVLRQEEVLS--PHPNSDYILD-----STYNLHAVELSGPR : 627

AtSERK3 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----EEMFRQDFNYPTHHPAVSGDIIG-----DSTQENNEYPSGPR : 615

AtSERK4 : SAMBRPKMSEVVRMLEGGLAEKMEQWOK-----EEMPIHDFNYQAYPHAQTDYLIP-----YNSNLIENDYPSGPR : 620

AtSERK5 : SAMBRPKMSEVVRMLEGGLAEKMEQWOK-----EEMPIHDFNYQAYPHAQTDYLIP-----YNSNLIENDYPSGPR : 601

MtSERK2 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----EETVRQDFNNNHMHNNANIV-----VDSTSHIQPDELSGPR : 619

MtSERK3 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----EETVRQDFNNNHMHNNANIV-----VDSTSHIQPDELSGPR : 586

MtSERK4 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----EETVRQDFNNNHMHNNANIV-----VDSTSHIQPDELSGPR : 615

MtSERK5 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----EETNRDFNNNHMHNNANIV-----VDSTSHIQPDELSGPR : 620

MtSERK6 : SEMBRPKMSEVVRMLEGGLAEKMEQWOK-----EETVRQDFNNNHMHNNANIVDSTSHIQPDELSGPR : 642

MtSERKL1 : MTSBRPKMSEVVRMLEGGLAEKMEQWOK-----EETNRDFNNNHMHNNANIVDSTSHIQPDELSGPR : 640

MtSERKL2 : MTSBRPKMSEVVRMLEGGLAEKMEQWOK-----EETNRDFNNNHMHNNANIVDSTSHIQPDELSGPR : 625

MtSERKL3 : MTSBRPKMSEVVRMLEGGLAEKMEQWOK-----EETNRDFNNNHMHNNANIVDSTSHIQPDELSGPR : 609

AtN1K1 : LPSBRPKMSEVVRMLEGGLAEKMEQWOK-----RQSDVSKSNRNIELMSSSDRSLDST-----DDSSLLVQAMELSGPR : 638

AtN1K2 : LPSBRPKMSEVVRMLEGGLAEKMEQWOK-----RQSDVSKSNRNIELMSSSDRSLDST-----DDSSLLVQAMELSGPR : 636

AtN1K3 : NPSBRPKMSEVVRMLEGGLAEKMEQWOK-----RQSDVSKSNRNIELMSSSDRSLDST-----DDSSLLVQAMELSGPR : 632