```
1g12620        1 VARTKQYDLVLDLCKQMELKGIAHNLYTLSIMINCCCRCRKLSLAFSAMGKIIKLGYEPDTVTFSTLINGLCLEGRVSEA
1g12770        1 IAKTKQYELVLALCKQMESKGIAHSIYTLSIMINCFCRCRKLSYAFSTMGKIMKLGYEPDTVIFNTLLNGLCLECRVSEA
1g12700        1 IARTKQFNLVLDFCKQLELNGIAHNIYTLNIMINCFCRCCKTCFAYSVLGKVMKLGYEPDTTTFNTLIKGLFLEG-----
1g63070        1 IAKMNKFDLVISLGEQMQNLGISHNLYTYSIFINYFCRRSQLSLALAILGKMMKLGYGPSIVTLNSLLNGFCHGNRISEA
1g63080        1 IAKMKKFDLVISFGEKMEILGVSHNLYTYNIMINCLCRRSQLSFALAILGKMMKLGYGPSIVTLNSLLNGFCHGNRISEA
1g63130        1 IAKMNKFDLVISLGEQMQNLGISHNLYTYSILINCFCRRSQLSLALAVLAKMMKLGYEPDIVTLNSLLNGFCHGNRISDA
1g63150        1 VAKMNKFELVISLGEQMQTLGISHDLYTYSIFINCFCRRSQLSLALAVLAKMMKLGYEPDIVTLSSLLNGYCHSKRISDA
Rfo            1 VVRMERPDLVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEA
Rf-1petunia    1 LVHMKHYSSVVSIFREIHKLRIPVDAFALSTVVNSCCLMHRTDLGFSVLAIHFKKGIPYNEVTFTTLIRGLFAEN-----
Rf-1rice       1 LCKAQAMDKAMEVLNTMVKNGVMPDCMTYNSILHGYCSSGQPKEAIGFLKKMRSDGVEPDVVTYSLLMDYLCKNGRCMEA
consensus      1 iakmkkfdlvisl  qme lgi hnlytysimincfCr sqlslalsvlgkmmklGyepdivtfntLlnglche rvsea

1g12620       81 LELVDRMVEMGHKPTLITLNALVNGLCLNGKVSDAVLLIDRMVET-GFQPNEVTYGPVLKVMCKSGQTALAMELLRKMEE
1g12770       81 LELVDRMVEMGHKPTLITLNTLVNGLCLNGKVSDAVVLIDRMVET-GFQPNEVTYGPVLNVMCKSGQTALAMELLRKMEE
1g12700       76 ------------------------------KVSEAVVLVDRMVEN-GCQPDVVTYNSIVNGICRSGDTSLALDLLRKMEE
1g63070       81 VALVDQMVEMGYQPDTVTFTTLVHGLFQHNKASEAVALVERMVVK-GCQPDLVTYGAVINGLCKRGEPDLALNLLNKMEK
1g63080       81 VALVDQMVEMGYQPDTVTFTTLVHGLFQHNKASEAVALVERMVVK-GCQPDLVTYGAVINGLCKRGEPDLALNLLNKMEK
1g63130       81 VSLVGQMVEMGYQPDSFTFNTLIHGLFRHNRASEAVALVDRMVVK-GCQPDLVTYGIVVNGLCKRGDIDLALSLLKKMEQ
1g63150       81 VALVDQMVEMGYKPDTFTFTTLIHGLFLHNKASEAVALVDQMVQR-GCQPDLVTYGTVVNGLCKRGDIDLALNLLNKMEA
Rfo           81 LDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMED-GLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEE
Rf-1petunia   76 ------------------------------KVKDAVHLFKKLVRENICEPDEVMYGTVMDGLCKKGHTQKAFDLLRLMEQ
Rf-1rice      81 RKIFDSMTKRGLKPEITTYGTLLQGYATKGALVEMHGLLDLMVRN-GIHPDHYVFSILICAYAKQGKVDQAMLVFSKMRQ
consensus     81 l lvdqmvemg kpd itf tlv gl  h kvseavaLvdrmv   gcqPdvvtyg vlnglckrGdtdlAl llrkMe

1g12620      160 R-KIKLDAVKYSIIIDGLCKDGSLDNAFNLFNEMEIKGFKADIIIYTTLIRGFCYAGRWDDGAKLLRDMIKRKITPDVVA
1g12770      160 R-NIKLDAVKYSIIIDGLCKDGSLDNAFNLFNEMEIKGFKADIITYNTLIGGFCNAGRWDDGAKLLRDMIKRKISPNVVT
1g12700      125 R-NVKADVFTYSTIIDSLCRDGCIDAAISLFKEMETKGIKSSVVTYNSLVRGLCKAGKWNDGALLLKDMVSREIVPNVIT
1g63070      160 G-KIEADVVIYNTIIDGLCKYKHMDDAFDLFNKMETKGIKPDVFTYNPLISCLCNYGRWSDASRLLSDMLEKNINPDLVF
1g63080      160 G-KIEADVVIYSTVIDSLCKYRHVDDALNLFTEMDNKGIRPDVFTYSSLISCLCNYGRWSDASRLLSDMLERKINPNVVT
1g63130      160 G-KIEPGVVIYNTIIDALCNYKNVNDALNLFTEMDNKGIRPNVVTYNSLIRCLCNYGRWSDASRLLSDMIERKINPNVVT
1g63150      160 A-RIKANVVIFNTIIDSLCKYRHVEVAVDLFTEMETKGIRPNVVTYNSLINCLCNYGRWSDASRLLSNMLEKKINPNVVT
Rfo          160 VSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVT
Rf-1petunia  126 G-ITKPDTCIYNIVIDAFCKDGMLDGATSLLNEMKQKNIPPDIITYTSLIDGLGKLSQWEKVRTLFLEMIHLNIYPDVCT
Rf-1rice     160 Q-GLNPNAVTYGAVIGILCKSGRVEDAMLYFEQMIDEGLSPGNIVYNSLIHGLCTCNKWERAEELILEMLDRGICLNTIF
consensus    161 g kik dvviystiIdglCkdghlddAinlf eMe kgikpdvitYnsli glcn grWsda kLl dMlerkI pnvvt

1g12620      239 FSALIDCFVKEGKLREAEELHKEMIQRGISPDTVTYTSLIDGFCKENQLDKANHMLDLMVSKGCGPNIRTFNILINGYCK
1g12770      239 FSVLIDSFVKEGKLREADQLLKEMMQRGIAPNTITYNSLIDGFCKENRLEEAIQMVDLMISKGCDPDIMTFNILINGYCK
1g12700      204 FNVLLDVFVKEGKLQEANELYKEMITRGISPNIITYNTLMDGYCMQNRLSEANNMLDLMVRNKCSPDIVTFTSLIKGYCM
1g63070      239 FNALIDAFVKEGKLVEAEKLYDEMVK----------------------------------SKHCFPDVVAYNTLIKGFCK
1g63080      239 FNSLIDAFAKEGKLIEAEKLFDEMIQRSIDPNIVTYNSLINGFCMHDRLDEAQQIFTLMVSKDCLPDVVTYNTLINGFCK
1g63130      239 FSALIDAFVKEGKLVEAEKLYDEMIKRSIDPDIFTYSSLINGFCMHDRLDEAKHMFELMISKDCFPNVVTYNTLIKGFCK
1g63150      239 FNALIDAFFKEGKLVEAEKLHEEMIQRSIDPDTITYNLLINGFCMHNRLDEAKQMFKFMVSKDCLPNIQTYNTLINGFCK
Rfo          240 YNALINAFVKEGKFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCG
Rf-1petunia  205 FNSVIDGLCKEGKVEDAEEIMTYMIEKGVEPNEITYNVVMDGYCLRGQMGRARRIFDSMIDKGIEPDIISYTALINGYVE
Rf-1rice     239 FNSIIDSHCKEGRVIESEKLFELMVRIGVKPNVITYNTLINGYCLAGKMDEAMKLLSGMVSVGLKPNTVTYSTLINGYCK
consensus    241 fnalidafvKEGklveaeklydeMi rgi pn itynslidgfcm nrldea hmfdlmvskgc P ivtyntLInGyck

1g12620      319 ANLIDDGLELFRKMSLRGVVADTVTYNTLIQGFCELGKLEVAKELFQEMVSRRVRPDIVSYKILLDGLCDNGEPEKALEI
1g12770      319 ANRIDDGLELFREMSLRGVIANTVTYNTLVQGFCQSGKLEVAKKLFQEMVSRRVRPDIVSYKILLDGLCDNGELEKALEI
1g12700      284 VKRVDDGMKVFRNISKRGLVANAVTYSILVQGFCQSGKIKLAEELFQEMVSHGVLPDVMTYGILLDGLCDNGKLEKALEI
1g63070      285 YKRVEEGMEVFREMSQRGLVGNTVTYTTLIHGFFQARDCDNAQMVFKQMVSDGVHPDIMTYNILLDGLCNNGNVETALVV
1g63080      319 AKKVVDGMELFRDMSRRGLVGNTVTYTTLIHGFFQASDCDNAQMVFKQMVSDGVHPNIMTYNTLLDGLCKNGKLEKAMVV
1g63130      319 AKRVDEGMELFREMSQRGLVGNTVTYTTLIHGFFQARECDNAQIVFKQMVSDGVLPDIMTYSILLDGLCNNGKVETALVV
1g63150      319 CKRVEDGVELFREMSQRGLVGNTVTYTTIIQGFFQAGDCDSAQMVFKQMVSNRVPTDIMTYSILLHGLCSYGKLDTALVI
Rfo          320 AKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGKLKDALEM
Rf-1petunia  285 KKKMDKAMQLFREISQNGLKPSIVTCSVLLRGLFEVGRTECAKIFFDEMQAAGHIPNLYTHCTLLGGYFKNGLVEEAMSH
Rf-1rice     319 ISRMEDALVLFKEMESSGVSPDIITYNIILQGLFQTRRTAAAKELYVRITESGTQIELSTYNIILHGLCKNKLTDDALQM
consensus    321 akrvddgmelfrems rGlvantvTystliqGffq g  e A mlf emvs gv pdimty ilLdGlc ngkle Al i

1g12620      399 FEKIEKSK-----------MELDIGIYNIIIHGMCNASKVDDAWDLFCSLPLKGVKPDVKTYNIMIGGLCKKGSLSEADL
1g12770      399 FGKIEKSK-----------MELDIGIYMIIIHGMCNASKVDDAWDLFCSLPLKGVKLDARAYNIMISELCRKDSLSKADI
1g12700      364 FEDLQKSK-----------MDLGIVMYTTIIEGMCKGGKVEDAWNLFCSLPCKGVKPNVMTYTVMISGLCKKGSLSEANI
1g63070      365 FEYMQKRD-----------MKLDIVTYTTMIEALCKAGKVEDGWDLFCSLSLKGVKPNVVTYTTMMSGFCRKGLKEEADA
1g63080      399 FEYLQKSK-----------MEPDIYTYNIMSEGMCKAGKVEDGWDLFCSLSLKGVKPDVIAYNTMISGFCKKGLKEEAYT
1g63130      399 FEYLQRSK-----------MEPDIYTYNIMIEGMCKAGKVEDGWDLFCSLSLKGVKPNVVTYTTMMSGFCRKGLKEEADA
1g63150      399 FKYLQKSE-----------MELNIFIYNTMIEGMCKAGKVGEAWDLFCSLSIK---PDVVTYNTMISGLCSKRLLQEADD
Rfo          400 FKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQ
Rf-1petunia  365 FHKLERRR-----------EDTNIQIYTAVINGLCKNGKLDKAHATFEKLPLIGLHPDVITYTAMISGYCQEGLLDEAKD
Rf-1rice     399 FQNLCLMD-----------LKLEARTFNIMIDALLKVGRNDEAKDLFVAFSSNGLVPNYWTYRLMAENIIGQGLLEELDQ
consensus    401 Fe lqksk           meldi tynimiegmckagkvddawdlfcsl lkgvkpdvmtYttMisglckkglleead

1g12620      468 LFRKMEEDGHSPNGCTYNILIRAHLGEGDATKSAKLIEEIKRCGFSVDAST-VKMVVDML
1g12770      468 LFRKMTEEGHAPDELTYNILIRAHLGDDDATTAAELIEEMKSSGFPADVST-VKMVINML
1g12700      433 LLRKMEEDGNAPNDCTYNTLIRAHLRDGDLTASAKLIEEMKSCGFSADASS-IKMVIDML
1g63070      434 LFVEMKEDGPLPNSGTYNTLIRARLRDGDEAASAELIKEMRSCGFAGDAST-FGLVTNML
1g63080      468 LFIKMKEDGPLPDSGTYNTLIRAHLRDGDKAASAELIKEMRSCRFAGDAST-YGLVTDML
1g63130      468 LFREMKEEGPLPDSGTYNTLIRAHLRDGDKAASAELIREMRSCRFVGDAST-IGLVTNML
1g63150      465 LFRKMKEDGTLPNSGTYNTLIRANLRDCDRAASAELIKEMRSSGFVGDAST-ISLVTNML
Rfo          480 MFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDGLELFCEMGRRGIVANAITYITLICGFR
Rf-1petunia  434 MLRKMEDNGCLPDNRTYNVIVRGFFRSSKVSEMKAFLKEIAGKSFSFEAAT-VELLMDII
Rf-1rice     468 LFLSMEDNGCTVDSGMLNFIVRELLQRGEITRAGTYLSMIDEKHFSLEAST-ASLFIDLL
consensus    481 lfrkM edg lp sgtyntlirahlrdgd tasaelikemkscgf adast v lvvdml
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