

A

ccKir2.1 MGSVTANRYSIVSSEEDGMKLATAAVANGFGNGKSKVHTRQOCRSRFVKKDGHNCVQFIN 60
 omKir2.1a MGSVTRNRYISIVSSEEDGMKLATAAVANGFGNGKSKVHTRQOCRSRFVKKDGHNCVQFIN 58
 hKir2.1 MGSVTRNRYISIVSSEEDGMKLATAVANGFGNGKSKVHTRQOCRSRFVKKDGHNCVQFIN 60
 gpKir2.1 MGSVTRNRYISIVSSEEDGMKLATAVANGFGNGKSKVHTRQOCRSRFVKKDGHNCVQFIN 60
 rKir2.1 MGSVTRNRYISIVSSEEDGMKLATAVANGFGNGKSKVHTRQOCRSRFVKKDGHNCVQFIN 60
 mKir2.1 MGSVTRNRYISIVSSEEDGMKLATAVANGFGNGKSKVHTRQOCRSRFVKKDGHNCVQFIN 60

ccKir2.1 VSEKSGORYLADIFTTCVDIRWRWMLVFICLAFVLSWLFPGCVFVWLAIALPHGDLN--G 118
 omKir2.1a VSEKSGORYLADIFTTCVDIRWRWMLVFICLAFVLSWLFPGCVFVWLAIALPHGDLN--DAQ 116
 hKir2.1 VGEKGORYLADIFTTCVDIRWRWMLVFICLAFVLSWLFPGCVFVWLAIALPHGLDLDASKE 120
 gpKir2.1 VGEKQORYLADIFTTCVDIRWRWMLVFICLAFVLSWLFPGCVFVWLAIALPHGLDLDASKE 120
 rKir2.1 VGEKGORYLADIFTTCVDIRWRWMLVFICLAFVLSWLFPGCVFVWLAIALPHGLDLDASKE 120
 mKir2.1 VGEKGORYLADIFTTCVDIRWRWMLVFICLAFVLSWLFPGCVFVWLAIALPHGLDLDASK 120

ccKir2.1 KCVSEVNSFTAAPLFSIETOTTIGYGRCVTDECPAVFVWFQSI VGCIDAFIIGAVM 178
 omKir2.1a KCVSEVNSFTAAPLFSIETOTTIGYGRVYTDDECPAVFVWFQSI VGCIDAFIIGAVM 176
 hKir2.1 ACVSEVNSFTAAPLFSIETOTTIGYGRCVTDECPAVFVWFQSI VGCIDAFIIGAVM 180
 gpKir2.1 ACVSEVNSFTAAPLFSIETOTTIGYGRCVTDECPAVFVWFQSI VGCIDAFIIGAVM 180
 rKir2.1 ACVSEVNSFTAAPLFSIETOTTIGYGRCVTDECPAVFVWFQSI VGCIDAFIIGAVM 180
 mKir2.1 ACVSEVNSFTAAPLFSIETOTTIGYGRCVTDECPAVFVWFQSI VGCIDAFIIGAVM 180

ccKir2.1 AKMAKPKKRNETLVFSHNAVIA MRDVKLCMLWRVGNLRKSHLVEAHVRAQLLSRITSE 238
 omKir2.1a AKMAKPKKRNETLVFSHNAVIA MRDVKLCMLWRVGNLRKSHLVEAHVRAQLLSRITSE 236
 hKir2.1 AKMAKPKKRNETLVFSHNAVIA MRDVKLCMLWRVGNLRKSHLVEAHVRAQLLSRITSE 240
 gpKir2.1 AKMAKPKKRNETLVFSHNAVIA MRDVKLCMLWRVGNLRKSHLVEAHVRAQLLSRITSE 240
 rKir2.1 AKMAKPKKRNETLVFSHNAVIA MRDVKLCMLWRVGNLRKSHLVEAHVRAQLLSRITSE 240
 mKir2.1 AKMAKPKKRNETLVFSHNAVIA MRDVKLCMLWRVGNLRKSHLVEAHVRAQLLSRITSE 240

ccKir2.1 EYIPLDQIDIDVGFDSGIDRIPLVSPITIVHEIDEDSPYLDSKQIDINADFEIVVILEG 298
 omKir2.1a EYIPLDQIDIDVGFDSGIDRIPLVSPITIVHEIDEDSPYLDSKQIDINADFEIVVILEG 296
 hKir2.1 EYIPLDQIDIDVGFDSGIDRIPLVSPITIVHEIDEDSPYLDSKQIDINADFEIVVILEG 300
 gpKir2.1 EYIPLDQIDIDVGFDSGIDRIPLVSPITIVHEIDEDSPYLDSKQIDINADFEIVVILEG 300
 rKir2.1 EYIPLDQIDIDVGFDSGIDRIPLVSPITIVHEIDEDSPYLDSKQIDINADFEIVVILEG 300
 mKir2.1 EYIPLDQIDIDVGFDSGIDRIPLVSPITIVHEIDEDSPYLDSKQIDINADFEIVVILEG 300

ccKir2.1 MVEATAMTQCRSSYLANEILMGHRYEPLVFEKHYKVDYSRPHKTYEVNTPCLSARD 358
 omKir2.1a MVEATAMTQCRSSYLANEILMGHRYEPLVFEKHYKVDYSRPHKTYEVNTPCLSARD 356
 hKir2.1 MVEATAMTQCRSSYLANEILMGHRYEPLVFEKHYKVDYSRPHKTYEVNTPCLSARD 360
 gpKir2.1 MVEATAMTQCRSSYLANEILMGHRYEPLVFEKHYKVDYSRPHKTYEVNTPCLSARD 360
 rKir2.1 MVEATAMTQCRSSYLANEILMGHRYEPLVFEKHYKVDYSRPHKTYEVNTPCLSARD 360
 mKir2.1 MVEATAMTQCRSSYLANEILMGHRYEPLVFEKHYKVDYSRPHKTYEVNTPCLSARD 360

ccKir2.1 LAEKKYILSNANSFCYENEVALTSKEEEDSENG--VPESTSTDPDIDLHNOQASVPLE 417
 omKir2.1a LAEKKYILSSANSFCYENEVALTSKEEEDSENG--VPESTSTDPDIDLHNOQASVPLE 415
 hKir2.1 LAEKKYILSNANSFCYENEVALTSKEEEDSENG--VPESTSTDPDIDLHNOQASVPLE 417
 gpKir2.1 LAEKKYILSNANSFCYENEVALTSKEEEDSENG--VPESTSTDPDIDLHNOQASVPLE 417
 rKir2.1 LAEKKYILSNANSFCYENEVALTSKEEEDSENG--VPESTSTDPDIDLHNOQASVPLE 417
 mKir2.1 LAEKKYILSNANSFCYENEVALTSKEEEDSENG--VPESTSTDPDIDLHNOQASVPLE 418

ccKir2.1 PRPLRRESEI 427
 omKir2.1a PRPLRRESEI 425
 hKir2.1 PRPLRRESEI 427
 gpKir2.1 PRPLRRESEI 427
 rKir2.1 PRPLRRESEI 427
 mKir2.1 PRPLRRESEI 428

B

ccKir2.2 -MSVGRNINRYSIVSSEEDGLRLTTHMGGKSKVHTRQOCRSRFVKKDGHNCVQFIN 56
 omKir2.2a -MSVGRNINRYSIVSSEEDGLRLTTHMGGKSKVHTRQOCRSRFVKKDGHNCVQFIN 59
 rKir2.2 MTAASRANPYSIVSSEEDGLHLVMTSGA-----NGFGNGKVHTRRRCRMRFVKKNQCNI 55
 mKir2.2 MTAASRANPYSIVSSEEDGLHLVMTSGA-----NGFGNGKVHTRRRCRMRFVKKNQCNI 55
 gpKir2.2 MTAASRANPYSIVSSEEDGLHLVMTSGA-----NGFGNGKVHTRRRCRMRFVKKNQCNI 55
 hKir2.2 MTAASRANPYSIVSSEEDGLHLVMTSGA-----NGFGNGKVHTRRRCRMRFVKKNQCNI 55

ccKir2.2 QFINNNEKSRYLADIFTTCVDIRWRYMLVFTVVFVLSWLAFAFVWVIALPHGDLN 116
 omKir2.2a QFANMDEKRSRYLADMFTTCVDIRWRYMLVFTVVFVLSWLAFAFVWVIALPHGDLN 119
 rKir2.2 EFANMDEKSORYLADMFTTCVDIRWRYMLVFTVVFVLSWLAFAFVWVIAHAGDLE-P 114
 mKir2.2 EFANMDEKSORYLADMFTTCVDIRWRYMLVFTVVFVLSWLAFAFVWVIAHAGDLE-P 114
 gpKir2.2 EFANMDEKSORYLADMFTTCVDIRWRYMLVFTVVFVLSWLAFAFVWVIAHAGDLE-P 114
 hKir2.2 EFANMDEKSORYLADMFTTCVDIRWRYMLVFTVVFVLSWLAFAFVWVIAHAGDLE-P 114

ccKir2.2 AGDDNFTPCVLQVNSFTAAPLFSIETOTTIGYGRCVTEECPAVFVWFQSI VGCIDC 176
 omKir2.2a AGDDNFTPCVLQVNSFTAAPLFSIETOTTIGYGRCVTEECPAVFVWFQSI VGCIDC 179
 rKir2.2 AEGRRGTPCVLQVHGFMAAFPLFSIETOTTIGYGLRCVTEECPAVFVWFQSI VGCIDS 174
 mKir2.2 AEGRRGTPCVLQVHGFMAAFPLFSIETOTTIGYGLRCVTEECPAVFVWFQSI VGCIDS 174
 gpKir2.2 AEGRRGTPCVLQVHGFMAAFPLFSIETOTTIGYGLRCVTEECPAVFVWFQSI VGCIDS 174
 hKir2.2 AEGRRGTPCVLQVHGFMAAFPLFSIETOTTIGYGLRCVTEECPAVFVWFQSI VGCIDS 174

ccKir2.2 FMIGAIMAKMARPKRAQTLLFSHNAVIALRDGKLCMLWRVGNLRKSHIVEAHVRAQLIK 236
 omKir2.2a FMIGAIMAKMARPKRAQTLLFSHNAVIALSRDKSCLCLMWRVGNLRKSHIVEAHVRAQLIK 239
 rKir2.2 FMIGAIMAKMARPKRAQTLLFSHNAVIALRDGKLCMLWRVGNLRKSHIVEAHVRAQLIK 234
 mKir2.2 FMIGAIMAKMARPKRAQTLLFSHNAVIALRDGKLCMLWRVGNLRKSHIVEAHVRAQLIK 234
 gpKir2.2 FMIGAIMAKMARPKRAQTLLFSHNAVIALRDGKLCMLWRVGNLRKSHIVEAHVRAQLIK 234
 hKir2.2 FMIGAIMAKMARPKRAQTLLFSHNAVIALRDGKLCMLWRVGNLRKSHIVEAHVRAQLIK 234

ccKir2.2 PRVTEEGEYIPLDQIDIDVGFDPKGLDRIPLVSPITIVHEIDEDSPFLGISRDLETAADF 296
 omKir2.2a PRVTEEGEYIPLDQIDIDVGFDPKGLDRIPLVSPITIVHEIDEDSPFLGISRDLETAADF 299
 rKir2.2 PRVTEEGEYIPLDQIDIDVGFDPKGLDRIPLVSPITIVHEIDEDSPFLGISRDLETDFFE 294
 mKir2.2 PRVTEEGEYIPLDQIDIDVGFDPKGLDRIPLVSPITIVHEIDEDSPFLGISRDLETDFFE 294
 gpKir2.2 PRVTEEGEYIPLDQIDIDVGFDPKGLDRIPLVSPITIVHEIDEDSPFLGISRDLETDFFE 294
 hKir2.2 PRVTEEGEYIPLDQIDIDVGFDPKGLDRIPLVSPITIVHEIDEDSPFLGISRDLETDFFE 294

ccKir2.2 IVVILEGMVEATAMTQARRSSYLANEILMGHRYEPLVFEKNOYKIDYSHFHKTYEVPST 356
 omKir2.2a IVVILEGMVEATAMTQARRSSYLANEILMGHRYEPLVFEKNOYKIDYSHFHKTYEVPST 359
 rKir2.2 IVVILEGMVEATAMTQARRSSYLANEILMGHRYEPLVFEKNOYKIDYSHFHKTYEVPST 354
 mKir2.2 IVVILEGMVEATAMTQARRSSYLANEILMGHRYEPLVFEKNOYKIDYSHFHKTYEVPST 354
 gpKir2.2 IVVILEGMVEATAMTQARRSSYLANEILMGHRYEPLVFEKNOYKIDYSHFHKTYEVPST 354
 hKir2.2 IVVILEGMVEATAMTQARRSSYLANEILMGHRYEPLVFEKNOYKIDYSHFHKTYEVPST 354

ccKir2.2 PRCSAKDLMVENKFLVPSANFCYENLAFLSRDEDE-----VPEGKPE--RAMS--LSP 409
 omKir2.2a PRCSAKDLMVENKFLVPSANSFCYENLAFLSRDEDEDEE--E--VVMGMSGSFRALANLNSP 418
 rKir2.2 PRCSAKDLVFNKFLVPSANSFCYENLAFLSRDEDE-----VADL-----RDGRSP 401
 mKir2.2 PRCSAKDLVFNKFLVPSANSFCYENLAFLSRDEDE-----VADL-----RDGRSP 401
 gpKir2.2 PRCSAKDLVFNKFLVPSANSFCYENLAFLSRDEDE-----VPEGQDGRSRODGLSP 406
 hKir2.2 PRCSAKDLVFNKFLVPSANSFCYENLAFLSRDEDE-----VADLQDGRSRODGLSP 406

ccKir2.2 ERTPRHFDFRLQNP-RCTEQRYSRRESEI 437
 omKir2.2a DRNNRHDFRLQNT-RELDORYSRRESEI 446
 rKir2.2 C--PRHDFDRLOA--SEALR-PYRRESEI 427
 mKir2.2 C--PRHDFDRLOA--SEALR-PYRRESEI 427
 gpKir2.2 C--PRHDFDRLOA--SEALR-PYRRESEI 433
 hKir2.2 C--PRHDFDRLOA--SEALR-PYRRESEI 433