AmqKirA AmqKirB
Nv1
Nv2
Nv3
Nv4
rKir1.1
mKir2.1
hKir2. 2
hKir3.1
hKir3. 4
hKir4.1
hKir5.1
hKir6. 2
hKir7.1

-     -         - MEPAHKNVNYELVSNSN - - - - ENIHRDDVPITFRG- - TREARRR-ERIVKRSNGR 48 - - - MSVQFSNS - YEKISETEGTVREEATDAAPTIVSFQP - - - TVPTRLRPERTVKRSTAR 53
49
-- - MGSVRTNRYSIVSSEEDGMKLATMA - -VANGFGNGKSKV ..... 4
-     - MTAASRANPYSIVSSEEDGLHLVTMS - -GANGFGNG--KVHTRRRCRNRFVKRNGQC 53
-MSALRRKFGDDYQVVTTSSSGSGLQPQG- - - PGQDPQQQLV ..... 53
MAGDSRNAMNQDMEIGVTPWDPKKIPKQARDYVPIATDRTRLIAEGKKPRQRYMEKSGKC 60


M1

AmqKirA AmqKirB Nv1
Nv2
Nv3
Nv4
rKir1.1 mKir2.1 hKir2. 2 hKir3.1 hKir3.4 hKir4.1 hKir5.1 hKir6. 2 hKir7.1

AmqKirA AmqKirB
Nv1
Nv2
Nv3
Nv4
rKir1.1
mKir2.1
hKir2. 2
hKir3.1
hKir3. 4
hKir4.1
hKir5.1
hKir6.2
hKir7.1

AmqKirA AmqKirB Nv1
Nv2
Nv3
Nv4
rKirl.1
mKir2.1
hKir2.2
hKir3.1
hKir3. 4
hKir4.1
hKir5.1
hKir6.2
hKir7.1



AmqKirA AmqKirB
Nv1
Nv2
Nv3
Nv4
rKir1.1
mKir2.1
hKir2.2
hKir3.1
hKir3. 4
hKir4.1
hKir5.1
hKir6.2
hKir7.1

AmqKirA AmqKirB Nv1
Nv2
Nv3
Nv4
rKir1.1 mKir2.1 hKir2.2 hKir3.1 hKir3. 4 hKir4.1 hKir5.1 hKir6.2 hKir7.1



AmqKirA
AmqKirB
Nv1
Nv2
Nv3
Nv4
rKir1.1
mKir2.1
hKir2. 2
hKir3.1
hKir3.4
hKir4.1
hKir5.1
hKir6. 2
hKir7.1



KAADTPDRLEID SLFDHTYASS-TPTCSAR--E------------------------------ 317

QSPFDVQYYASDYSKFDDMKKVAMPDLSPFEYYQQHPLRDENDTSLPNLYI-------- 307

E--EKHYYKVDYSREHKTYEVPNTPLCSAR--DLAEKKYILSNANSFCYENEV----- 380
E---EKNQYKIDYSEFHKTYEVPSTPRCSAK--DLVENKFLLPSANSFCYENEL------ 381
L---EEGFEKVDYSQEHATFEVP-TPPYSVK--EQEEMLLMSSPLIAPAITNSKERHNSV 386
L---EKGFYEVDYNTFHDTYETN-TPSCCAK--ELAEMKRE---------------------3 373

V---KRKYYKVNCLQFEGSVEVY-APFCSAKZLDWKDQQLHIEKAPPVRESCTS------ 365
E---EDGRYSVDYSKFGNTVKVP-TPLCMAR--QLDEDHSLLEALT---LASAR------ 365
RG--SKGEYQIKMENEDKTVPEFPTPLVSKS333

