

SAV4029 -----MVE--TDWKNDLRQGYRLTPQRQLVLEAVD-KL-EHATP 36  
SCO4180 -----MVE--TDWKSDLRQGYRLTPQRQLVLEAVD-EL-EHATP 36  
Franean1DRAFT 3571 -----MAKVDDWETRLRLRARGYRLTPQRQLVLEAVA-RL-GHATP 38  
Acel 0061 -----MPKQSSDRPSRSAQWQRLRSKGYRLTPQRRLVLEAVA-AL-RHATP 46  
Noca 4251 -----MT--EELARLRQGYRLTPQRQLVLAQAVE-KL-GHATP 35  
Acel 2095 -----MRSFVDRRAAGMRVTPARLAVLQELP-VG-VHRSV 34  
Noca 0839 -----MAPAEEDLRAAGLRVTRPRVAVLAEVS-EH-PHADV 34  
Mkms 4974 -----  
Mmcs 4885 -----  
Mjls 5253 -----MTFARETTPEARLRASGLRVTPARLAVLSALE-QA-PHSTA 39  
MSMEG 6253 -----MTLVHDHDPKALLRASGLRVTPARVAVLEVLA-EQ-PHSTA 39  
FRAAL3168 -----MATDRATTLRGAGLRVTGPRLAVLDVLA-EH-PHATA 35  
nfa3250 -----MHETAEPRDRLRAGLRVTAPRLAVLKAVS-AH-PHADA 38  
RHA1\_ro04308 -----MRHDT-DEKAQLREVGLRVTPARVAVLNAVA-VR-PHSDV 37  
Tfu 0145 -----MDDAASLRAGLRVTAARLAILDAVR-QG-NHLDA 33  
MAV 2752 -----MADLRVTRPRVAVLEVVD-AN-PHADT 25  
MAP1669c -----MESTADYADRLRMADLRVTRPRVAVLEVVD-AN-PHADT 37  
MUL 2189 -----MADLRVTRPRVAVLEAVG-DH-PHADT 25  
Mjls 2712 -----MAVVSSSEYVDQLRGADLRVTRPRVAVLEAVH-AH-PHADT 40  
Mmcs 2681 MITPLGLKSRICLARRPIGVSAQNARDELLTYSKKAQDMAVVSSSEYVDQLRGADLRVTRPRVAVLEAVH-AH-PHADT 78  
Mkms 2726 -----MAVVSSSEYVDQLRGADLRVTRPRVAVLEAVH-AH-PHADT 40  
MSMEG 3460 -----MPSRAEFEAQLRMDDLVRTRPRIAVMEAVH-AN-PHADT 37  
Mb1944c -----MSSVSSIPDYAEQLRTADLRVTRPRVAVLEAVN-AH-PHADT 40  
MT1960 -----MSSVSSIPDYAEQLRTADLRVTRPRVAVLEAVN-AH-PHADT 40  
Rv1909c -----MSSVSSIPDYAEQLRTADLRVTRPRVAVLEAVN-AH-PHADT 40  
BCG 1948c -----MSSVSSIPDYAEQLRTADLRVTRPRVAVLEAVN-AH-PHADT 40  
RHA1\_ro05274 -----MPDYAALLRGAELRVTRPRVAVLEAVH-AR-PHADT 34  
Mvan 2983 -----MTSDYAEALLRGAELRVTRPRIAVLEAVE-AH-PHADT 35  
Franean1DRAFT 1681 -----MVAVLLSGFLDWFQKMGDHFVVVATAEDFRMLRGAALRVTRPRVAVLTAVY-AH-PHADT 58  
Noca 0874 -----MATTTDRTRDFPELLRGAALRVTRPRLAVLCAVH-AL-PHADT 41  
MSMEG 6383 -----MHHTDFEQLLRSAGMRVTRPRIAVLRSVY-AH-PHADT 37  
Mvan 3209 -----MEPMTEEPDYSAVLSAALRVTRPRMAVLHAVG-RH-PHADT 40  
nfa29490 -----MSKVPDFEQLLRGAELRVTRPRLAVLSVH-EH-PHSDT 37  
SCO0561 -----MTASRNRKPAFADELRRAGLRVTAARVALLETVR-AG-DHLDA 42  
AAur 3058 -----MDHTTEQAEWAALHAGRRVTKORLAVLAAVQ-HH-PHSPA 41  
Arth 3077 -----MIVHEAGQDAWAALRAHGRVTKORLAVLTAVE-RH-PHSPA 41  
Lxx02790 -----MDTAQLEDTLRSAGLRVTRGRLAVLSALS-DR-PHSDA 36  
SAV3053 -----MSDLLERLRGRGWRMTAQRVVVAEVLDDGH-VHLTA 35  
SCO5206 -----MSDLLERLRGRGWRMTAQRVVVAEVLDDGEH-VHLTA 35  
FRAAL2798 -----MEDRRFPVGAATAAAGHDAIPGRRDDLAAAGIAELRALGERVTPARRAVLRVLAGTS-EHLSV 63  
Franci3 2661 -----MKDITWIVKDSQTRDR-----GRRGDPSAAGIAALRARGERVTPARRAVLQVLAGTS-EHLSV 56  
Rxy1 1144 -----MSFRRTTRQREAILAALRDAP-GPLSA 26  
FRAAL0074 -----MRATRQGDVCAALTEID-AFTSA 23  
Franci3 0061 -----MERRPAPSRGT--AVRATRQGDVSAALAEID-AFTSA 35  
Franean1DRAFT 4289 --MDVVASVEGERVSSPRGMSAASDRAAGGAGSGDRPNGAVSRPGRGRGT--SVRATRQGDVSSALAEID-AFTSA 74  
Tfu 0856 -----MSSRR--EAVRQALHKSNGPFRSA 21  
MAV 2036 -----MTPSGDG--AGVSVRSTRQRAAISTLLETVD-DFRSA 34  
MAP2139 -----MTPSGDG--AGVSVRSTRQRAAISTLLETLD-DFRSA 34  
Mb2380 -----MSAAG-----VRSTRQRAAISTLLETLD-DFRSA 28  
BCG 2373 -----MSAAG-----VRSTRQRAAISTLLETLD-DFRSA 28  
MT2428 -----MSAAG-----VRSTRQRAAISTLLETLD-DFRSA 28  
Rv2359 -----MSAAG-----VRSTRQRAAISTLLETLD-DFRSA 28  
ML0824 -----MMTGAS-----VRSTRQRAAISTLLETVD-DFRSA 29  
MUL 3612 -----MTGTS-----VRSTRQRAAISTLLETVD-DFRSA 28  
MSMEG 4487 -----MNGAV-----RSTRQRAAIDLLNEIE-GFRSA 27  
Mvan 3820 -----MNGAV-----RSTRQRAAISALLENIE-DFRSA 27  
Mjls 3458 -----MSPAP-----VRATRQRAAIDLLDGLD-EFRSA 28  
Mkms 3510 -----MSPAP-----VRATRQRAAIDLLDGLD-EFRSA 28  
Mmcs 3447 -----MSPAP-----VRATRQRAAIDLLDGLD-EFRSA 28  
nfa14570 -----MQDKTSAPQKP--VGIRSTRQSAIAALLGDID-EFRSA 36  
RHA1\_ro01222 -----MTQNTGQ-RKPVVVGVRATKORSAISALLDDIE-EFRSA 37  
SAV5631 -----MTAGSF-----VGRSTRQRAAVAAALDEV-EFRSA 32  
SCO2508 -----MTAGFP-----VKGRATRQRAAVSAALQVE-EFRSA 32  
Noca 1934 -----MSTEAETP-----RLRPTQRRAVTEALDSFS-DFRSA 34  
Acel 2085 -----MSGSEGE-----RQSRSTRQKRALAQVMAESR-QFRSA 32  
BAD 0517 -----MSEHI-----VRQTRQKDAIRDALNGCD-EFISA 28  
BL1128 -----MLPMEVHEI-----ERQTKQKDAIRAALADCE-EFISA 32  
Lxx25010 -----MV-----KRNTWQREAVREALSSE-EFISA 25  
AAur 2630 -----MGFASIPREVSLSMPQGTSSATGNEAPATSGVKEQRVTKORLAVSAALDELD-DFVST 58  
Arth 2638 -----MAHGAKAEGTKLSAPASAGGREQVTKORLAVSAALDELD-DFVST 45  
PPA0948 -----MENRR-----RTTKORLAIKRALFDDEF-FFLTA 27  
CE2180 -----MLKKPSRPLRSRIRGNHCFEFDSEQEGMGLNRHGEK--STPKLGVSTRQKAVVDILEEID-NFASA 65  
NCg12200 -----MGINRISQG--SAPKLGVRSTRQKAVVDILEEID-NFASA 38  
DIP1710 -----MNRTIDR--SVPKLGVRSTRQKAVVGLKDL-DYFASA 36  
jk0612 -----MNPATN--KLPKIGQNRTRQRAVAELLEGLT-TFSSA 36  
FRAAL5117 -----MAVLEVLRAAD-DHPTA 16  
Franci3 3112 -----MNDQNT-----DLRLTPQRMAVLAVALAAAR-DHPTA 29  
Franean1DRAFT 4643 -----MPERT-----ELRLTPQRTRVLEVLKAAE-DHPTA 29  
Rxy1 1228 -----MMEFEQILRSRGYRLTPQRRLVIVRELE-GE-RHLSA 34  
Rxy1 1140 -----MTPDPPPGSLSRVVEKFFQLGGDELEAVLGRMRGRGYVTPORLAVLEALA-----AER 55  
outgroup -----MWKERAMEEMKAGLRTPQRRLKLVIEIKIGGRHPTL 38  
ruler 1.....10.....20.....30.....40.....50.....60.....70.....80



SAV4029 DDILVEVRKKTASGVNISVYRTLELLEELGLVSHALHGAPTVHLAD---RHHHHLVCRDCTNVIEADIG-VAAEFTA 112  
SC04180 DDILVEVRKKTASGVNISVYRTLELLEELGLVSHALHGAPTVHLAD---RHHHHLVCRDCTNVIEADLS-VAAEFTA 112  
Franean1DRAFT\_3571 EAIVHVEVRQTASGVNISVYRTLDLLEELDLVSHALSHGAPTVHVTVG---VDPHVHLVCGACGAILLESPE-RLAGIVG 114  
Acel\_0061 EEILINVYREVASGVNMSVYRTLDLLEELSLVTHLHGAPTVHVAE---DAGHVHLVCSGCCGAVTEVSGE-VVQSLIQ 122  
Noca\_4251 DEVLAEVHAQSSAVNVSIYRTLELLEELGLVSHALSHGAPTVHVSVT---DREHFHLVCRNCHKVVSVDPE-VIGPLAE 111  
Acel\_2095 DEIATAVRRTLGAVSLQAVYNVLDALAGAGLVRRIEFLGHPARVESRV---SDNHHHLVCRVCGATADVCA-VGVVPLC 110  
Noca\_0839 DTIATAARARLQKVSQAQVYDVVHALTDAGLVRRIFPAGSPARFELAT---GDNHHHLVCRACHRIVDVACA-VGEAPCL 110  
Mfms\_4974 -----MREALQKVSQAQVYDVLRACVSAGLVRRIEPAGSSARVETRI---GDNHHHLVCRRCGRVADVDCI-VGAAPCL 70  
Mfms\_4885 -----MREALQKVSQAQVYDVLRACVSAGLVRRIEPAGSSARVETRI---GDNHHHLVCRRCGRVADVDCI-VGAAPCL 70  
Mjls\_5253 DDVAKQVREALQKVSQAQVYDVLRACVSAGLVRRIEPAGSSARVETRI---GDNHHHLVCRRCGRVADVDCI-VGAAPCL 115  
MSMEG\_6253 DDVAMAVRQNLGVSQAQVYDVLRACVAGLVRRIEPAGSSARVETRT---GDNHHHLVCRVCGRADVDCI-VGEAPCL 115  
FRAAL3168 DAVAERVRARLQKVSQAQVYDVVHALTDAGLVRRIFPAGSPARFETRT---ADNHHHLVCRVCGRADVDCV-VGEAPCL 111  
nfa3250 DTIAAEVRAALGVSVTQGIYDVLRACVAGLVRRIEPAGSPARVETRT---GDNHHHLVCRRCGADVDCI-VGAAPCL 114  
RHA1\_ro04308 DTAAVVREELGVSQAQVYDVLRACVAGLVRRIFPAGSPARFETRT---GDNHHHLVCRRCGADVDCI-VGAAPCL 113  
Tfu\_0145 DRVARAVREVRGHVSTQAVYDSLHALTAAGLVRRIEPAGSPARVETRV---GDNHHHLVCRACGVEVDIDCV-VGEAPCL 109  
MAV\_2752 ETIFSAVRMALPDVSRQAVYDVLRALTAAGLVRRIFPAGMVARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 101  
MAP1669c ETIFSAVRMALPDVSRQAVYDVLRALTAAGLVRRIFPAGMVARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 113  
MUL\_2189 ETIFSAVREILPDVSRQAVYDVLRALTAAGLVRRIFPAGSVARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 101  
Mjls\_2712 ETIFATVRRSLPDVSRQAVYDVLRALTAAGLVRRIFPAGSVARVETRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 116  
Mfms\_2681 ETIFATVRRSLPDVSRQAVYDVLRALTAAGLVRRIFPAGSVARVETRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 154  
Mfms\_2726 ETIFATVRRSLPDVSRQAVYDVLRALTAAGLVRRIFPAGSVARVETRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 116  
MSMEG\_3460 ETIFSVVRGSLPTVSRQAVYDVLRALTAAGLVRRIFPAGSARVEARV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 113  
Mb1944c ETIFGAVRFALPDVSRQAVYDVLRALTAAGLVRRIFPAGSVARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 116  
MT1960 ETIFGAVRFALPDVSRQAVYDVLRALTAAGLVRRIFPAGSVARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 116  
Rv1909c ETIFGAVRFALPDVSRQAVYDVLRALTAAGLVRRIFPAGSVARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 116  
BCG\_1948c ETIFGVVRFALPDVSRQAVYDVLRALTAAGLVRRIFPAGSVARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 116  
RHA1\_ro05274 ETIFGAVRTVLEGVSRQAVYDVLRALTAAGLVRRIFPAGSARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 110  
Mvan\_2983 DTIFGAVRTALPEVSRQAVYDVLRALTAAGLVRRIFPAGSARVETRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 111  
Franean1DRAFT\_1681 DSIVGVSREELPEVSHQAVYDSLHALTAAGLVRRIFPAGSARVESRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 134  
Noca\_0874 ESIIIGAVREGLPQVSHQAVYDSLHALTAAGLVRRIFPAGSARVEARV---GDNHHHLVCRACGIVADVDCI-VGGAPCL 117  
MSMEG\_6383 DTVIRAVREALPEVSHQAVYDSLHALAARLVRRIFPAGSVARVESRV---GDNHHHLVCRACGIVADVDCI-VGEAPCL 113  
Mvan\_3209 ELIINARELVPDVSQAQVYDVLRALTAAGLVRRIFPAGSARVETRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 116  
nfa29490 DSIILGRVRESVGAQVSHQAVYDVLRALTAAGLVRRIFPAGSARVETRV---DDNHHHLVCRDCGVIADVDCI-VGEAPCL 113  
SCO0561 EALTSQVRRNVGHVSLQAVYDVLRALTAAGLVRRIFPAGSARVEGRV---GDNHHHLVCRSCGTIADVDCI-VGEAPCL 118  
AAur\_3058 EGILAAARKELPELTAQSVYVVLSDLTDLQMLRRFEPHSPALVETRV---GDNHHHLVCRSCGTIADVDCI-VGHAPCL 117  
Arth\_3077 ESILAAARKELPELTAQSVYVVLSDLTDLQMLRRFEPHSPALVETRV---GDNHHHLVCRSCGTIADVDCI-VGHAPCL 117  
Lxx02790 ETVLAAVCPALPQSIQNIHNVLDLTLRMVRRIFPAHSPALVETRI---GDN-HHVVCTLCSTIADVDCI-VGHAPCL 111  
SAV3053 DEVHARAVKLPETISRAIVYNTLGLVSLGVELEVAIDKRAKRDENA---HRPHHLVCRACGAIADVDCI-VGAPCL 111  
SCO05206 DEVHARAVKLPETISRAIVYNTLGLVSLGVELEVAIDKRAKRDENA---HRPHHLVCRACGAIADVDCI-VGAPCL 111  
FRAAL2798 DDVLTTRADEIVPGLHRTVYRALETGLGLVTHVHPDHGPAVYHLASLHSGHLVCRRCGQISDVFPAD-LLDGVAD 142  
Franci3\_2661 DDVFAARETIVPQMHRTVYRALETGLGLVTHVHPDHGPAVYHLAALSGAHLVCRRCGQISDVFPAD-LLDGVAD 135  
Rxy1\_1144 ARIREAAREAPGVGRAIVYRALRTRREGGLVSVHLEPGEPAVYHLAALSGAHLVCRRCGQISDVFPAD-LLDGVAD 102  
FRAAL0074 QELHALLRSRGAAGVGLTVYRHLQVLRDGEVDMIRDDGETVYRRCAS---EAHHHLVCRCLCGRIVEIAGP-EIEAWTA 100  
Franci3\_0061 QDLHARLRQGAAGVGLTVYRHLQVLRDGEVDMIRDDGETVYRRCAS---DQHHHLVCRSCGRIIVEIAGP-EIEAWTA 112  
Franean1DRAFT\_4289 QDLHARLRQEGQSVGLTVYRHLQVLRDGEVDMIRDDGETVYRRCAS---DQHHHLVCRSCGRIIVEIAGP-EIEAWTA 151  
Tfu\_0856 QDLYASLRADGAKTGLTVYRALQALTDAGEVDVLTDEGEAVYRACST---PTHHHHLVCRDCGKAVEIEGP-AVESWAD 98  
MAV\_2036 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 110  
MAP2139 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 110  
Mb2380 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 104  
BCG\_2373 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 104  
MT2428 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 104  
Rv2359 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 104  
ML0824 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 105  
MUL\_3612 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 104  
MSMEG\_4487 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 103  
Mvan\_3820 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 103  
Mjls\_3458 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 104  
Mfms\_3510 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 104  
Mfms\_3447 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 104  
nfa14570 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 112  
RHA1\_ro01222 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 113  
SAV5631 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 109  
SCO2508 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 109  
Noca\_1934 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 110  
Acel\_2085 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 109  
BAD\_0517 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 103  
BL1128 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 107  
Lxx25010 QELHDEALRRRGENIGLTVYRQLQMAAAGLIDTLRDTGESVYRRCSS---EHHHHHLVCRSCGSIIEVGDH-EVEAWA 101  
AAur\_2630 QELYRLLQNKGISVSLAYRILQSLADDLGIDVLRNGDGEAVYRRCVAV---TGHHHLVCRNCGKAVEVEAP-AVETWAA 135  
Arth\_2638 QELYRMLQNGQTSVSLAYRILQSLADDLGIDVLRNGDGEAVYRRCVAV---TGHHHLVCRNCGKAVEVEAP-AVETWAA 122  
PPA0948 QVVDHQLRNRGDQVGLAVYRNLQMAAAGLIDTLRDTGESVYRRCSS---SAHHHLVCRNCGKAVEVEAP-AVETWAA 104  
CE2180 KAIHAELNAREHSGVGLTVYRQLQSLAIEGAVDVLTVTGGETLVRQCHD---EGHHHLVCRVCGRIVEIDGG-FVERWAG 142  
NCg12200 KEIHHELSTREHNVGLTVYRQLQSLADIEGAVDVLTVTGGETLVRQCHD---EGHHHLVCRVCGRIVEIDGG-FVERWAG 115  
DIP1710 KVIHQELTKRDLKVGGLTVYRQLQSLAIEGAVDVLTVTGGETLVRQCHD---DEHHHLVCRVCGRIVEIDGG-FVERWAG 113  
jrk0612 QDTHQELTKRDLKVGGLTVYRQLQSLAIEGAVDVLTVTGGETLVRQCHD---DEHHHLVCRVCGRIVEIDGG-FVERWAG 113  
FRAAL5117 AEVYERVRRASPRIGSAIVYRQLQSLAIEGAVDVLTVTGGETLVRQCHD---TRRHDAVCDGCRRAVDIDHP-VLDGMMMA 92  
Franci3\_3112 AEVYERVRTSPGIGSAIVYRQLQSLAIEGAVDVLTVTGGETLVRQCHD---TRRHDAVCDGCRRAVDIDHP-VLDGMMMA 105  
Franean1DRAFT\_4643 AEVYERVRLAAPGIGSAIVYRQLQSLAIEGAVDVLTVTGGETLVRQCHD---TSRHDAVCDGCRRAVDIDHP-VLDGMMMA 105  
Rxy1\_1228 EEIYERVKEHPELGLSIVYRQLQSLAIEGAVDVLTVTGGETLVRQCHD---ERMHHHLVCRVCGRIVEIDGG-FVERWAG 110  
Rxy1\_1140 HQSLEELRGCPEVGLAVLRTLDLTLGAVRRLGDDGPRVELAG---DGHHLVCRVCGRIVEIDGG-FVERWAG 127  
outgroup KEVYEEVVKFEPTMSFSILYSNLLIFRGLGLLDFFLGEGTRVEVNCPE---HFNVIER-----EETRDF-VDEELIG 107  
ruler .....90.....100.....110.....120.....130.....140.....150.....160



