

Additional file 4. Alignment of all available ASP1 and ASP2 homologues from actinobacterial species.

				β1	αA	β2
SCO1997						
RSal33209_2429						
MAB_3033						
Noca_2852						
A20C1_03668						
Krad_1509						
CMS_1627						
Lxx10170						
nfa37830						
PPA1099						
JNB_00545						
DIP1417						
Mflv_3951						
SGR_5536						
AAur_1758						
Mvan_2446						
MUL_3357						
Rv2714						
RHA1_ro06805						
Sare_1722						
BLD_0447						
SSAG_03958						
BIFLAC_03242						
Tfu_0926						
SAV_6234						
BL0722						
Strop_1737						
CMM_1644						
Francci3_1247						
MSMEG_2746						
ML1009						
Acel_0028						
FRAAL1976						
Arth_1614						
Franean1_5208						
KRH_14390						
BIFDEN_02062						
cu0890						
jk1100						
NCgl1848						
cgR_1753						
MAP2831						
MMAR_1998						
ACTODO_01571						
MAV_3608						
Mb2733						
CE1815						
nfa31940						
RHA1_ro00860						
Rv2125						
Mtubh3_05282						
MT2184						
MUL_2357						
Mvan_3475						
MAP1860						
MAB_2128c						
Arth_2169						
ML1306						
Mflv_3052						
SGR_5841						
RSal33209_2043						
SCO1662						
Lxx08270						
A20C1_02494						
BlinB01000025						
SSAG_04705						
Rxyl_1077						
Noca_2630						
TWT317						
Mjls_3162						
MSMEG_4186						
Sare_2324						
FRAAL2860						
SAV_6650						
Strop_2170						
Francci3_2640						
Acel_1173						
Tfu_1826						
Krad_1842						
KRH_13910						
Franean1_4890						
SACE_2233						
JNB_03080						
CMM_1693						
CMS_1670						
PPA1200						
AAur_2170						
TW455						
BIFADO_01161						
BAD_0824						

SC01997 DHRLVLYRARRRPLLTFFK--RDTWSYDEEPTIE-----VRLVQDATGAPFLFSGPDPDVEERFAAAVQGIVERLGVRLSVSFHGIQPMGVPIHTPVGITHPHGSRITDL
 RSal33209_2429 DIDQLIDYRARRRPPISVF--EDHLLDTRQPEMV-----LYRMVDLGGQFPFLFLANPDLQWERFSAVVVERLDVNLVAVHVSIPMPVPHTRPIGVTVHGNRPDL
 MAB_3033 AIDDLDDYRARRRPPMTFK--SDHFTYEATPELNL-----LYALKDTKGTGTFLLLAGLEPDLKWERFVNAIRLLAEQLGVRKTIIGLGAIPMAVPHTRPIITLTAHGNDRKT
 Noca_2852 DVDFHDDYRARRRPPMSFV--RDHYDAYDAPRLV-----VRLLDATGGTFFLLHGGPDPDNRFEAFCAVRVVERFVGSRVVGMGSPMAVPHTRPIAITHHANSPDL
 A20C1_03668 DNDALLDYRARRRPIYFD--QDHLSDYRPAKLE-----VYLLAKDELGGQFPYLLTGPEPDRFEAFSAVLRVLEKFDVKSTTWHAIIMPVPHTRPSIGVTYSGNRSEL
 Krad_1509 DVDQLDDYRARRRPIYFD--QDHLSDYRPAKLE-----VYLLAKDELGGQFPYLLTGPEPDRFEAFSAVLRVLEKFDVKSTTWHAIIMPVPHTRPSIGVTYSGNRSEL
 CMS_1627 DTDLILLYRARRRPIYFD--QDHLSDYRPAKLE-----VYLLAKDELGGQFPYLLTGPEPDRFEAFSAVLRVLEKFDVKSTTWHAIIMPVPHTRPSIGVTYSGNRSEL
 Lxx10170 DADLILLYRARRRPIYFD--QDHLSDYRPAKLE-----VYLLAKDELGGQFPYLLTGPEPDRFEAFSAVLRVLEKFDVKSTTWHAIIMPVPHTRPSIGVTYSGNRSEL
 nFa37830 DVDDELLDYRARRRPLMTFK--TDHFSDYAEPELN-----LWALRDTAGTFFLLLAGLEPDLRWEKFTTAVRLLAEQLGVRRSIIGLSAIPMAIPIHTPRLGITAHSSDRSL
 PPA1099 DIDLDDLHRDSRQPIYFD--TDHFEGYERPLV-----LHEVTDQLGQAFLVLEGPDPALGWESLVSSLTSLVDSMGIRLTVITDSIPITPHTRPIAVTRWASRPEL
 JNB_00545 DVDALLDYRARRRPMVFD--TNRWESYADPSMV-----LYRMSDRDGGQTYLLTGPDPDFQWERTIEAIRQLIQLLGLSLVVTSHGIPMGVPHTRPVMGTAAHTADPRL
 DIP1417 NNDELIDYRARRRPAVTID--HNIIVVDANELKLS-----MDVLRDSNGTFPFLLSGPEPDLRWDAFSQAVADLVRRFVRRITICLYAAPMTVPHTRPILVSAHNSLDDL
 Mflv_3951 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALHDSVGTFFLLSGLMPPDLRWERFVTAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 SGR_5536 DHRLVLYRARRRPLMTFK--RDRTWSEFAPALE-----VRVQDATTGAPFLLSGLMPPDLRWERFVAAAVEQIVERLGVRLVNFHGIQPMGVPIHTPVGITHPHGSRITDL
 AAur_1758 DADQLIDYRARRRPIYFD--EDHLLDTRQPEMV-----LYKLDNGLGQFPFLLAGLEPDLQWERFSAVVVERLDVNLVAVHVSIPMPVPHTRPIGVTVHGNRPDL
 Mvan_2446 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALRDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 MUL_3357 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALRDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 Rv2714 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALRDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 RHA1_ro06805 AVDELVDYRARRRPLMTFK--ADHFSYDQPELN-----LYALKDTAGTFFLLLAGMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 Sare_1722 DLQQLFYRARRRPMVFD--EDHWESYDPALE-----LHLLRSDADTFFLLLTGPEPDLQWERFVAAVAGLSTRDLVRLTVGLNAIPMAVPHTRVGTAAHTRRREL
 BLD_0447 RCDDFYDQVARPMLCHVS--GRTNLIWPQTTFY-----DITLDAGKRIYAQIAPENPNRWKEYCSQSLATADELDVNRITITLGSMPDCHPTRLPIAVSDGDCQC
 SSAG_03958 DADRLLDYRARRPLMTFK--RDHWSEFEPRLE-----VRLVQDATTGAPFLLSGLMPPDLRWERFVAAVAGLSTRDLVRLTVGLNAIPMAVPHTRVGTAAHTRRREL
 BIFLAC_03242 NKDGYYDQVARPMTCTIQ--GSRCILWPQTVFY-----DIAVSDSLHILAQGLPEPNYQWLEYCRGSLRFAEQYDVECIITLGSMLAECPHTRPPLIDISNNGKPL
 Tfu_0926 DIDGLLYRARRRPIYFN--ETTWSYAEPEKLS-----LTLHLDELTGTFLLHGGLEPDRRWEFGTAAVRLVRLSVLTVCFYVIGMAVPHTRPVTATPHATRPEL
 SAV_6234 DHRLLDYRARRRPLMTFK--RDHWSEFEPRLE-----VRLVQDATTGAPFLLSGLMPPDLRWERFVAAVAGLSTRDLVRLTVGLNAIPMAVPHTRVGTAAHTRRREL
 BL0722 RCDDFYDQVARPMLCHVS--GRTNLIWPQTVFY-----DITLDAGKRIYAQIAPENPNRWKEYCSQSLATADELDVNRITITLGSMPDCHPTRLPIAVSDGDCQC
 Strop_1737 DLQQLFYRARRRPMVFD--EDHWESYDPALE-----LHLLRSDADTFFLLLTGPEPDLQWERFVAAVAGLSTRDLVRLTVGLNAIPMAVPHTRVGTAAHTRRREL
 CMM_1644 DTDLILLYRARRRPIYFD--QDHLSDYRPAKLE-----VYLLAKDELGGQFPYLLTGPEPDRFEAFSAVLRVLEKFDVKSTTWHAIIMPVPHTRPSIGVTYSGNRSEL
 Francci3_1247 DIDQLIDYRARRRPIYFD--EDHLLDTRQPEMV-----LYLLRDEAGTFFLLLAGLEPDLQWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPILVSAHNSDKEL
 MSMEG_2746 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALHDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 ML1009 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALRDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 Acel_0028 DIDQLFYRARRRPMVFD--EDHWESYDPALE-----VHAVTDGGGREFLLLTGPEPDTQWERFVAAVCTLLERYGVDVTVGLNAIPLATPHTRPIGVTRRHATSQDL
 FRAAL1976 DTDQLLYRARRRPIYFN--EDHLLDTRQPEMV-----LYQLRDSEDTFFLLTGGPEPDLQWERFVAAVAGLSTRDLVRLTVGLNAIPMAVPHTRPATIATGHSKPEL
 Arth_1614 DADQLIDYRARRRPIYFD--EDHLLDTRQPEMV-----LYRVLGDLGTFPLLAGLEPDLRWEKFTTAVRLLAEQLGVRQTIIGLGTIPMAVPHTRPVNLTSAHNSDKEL
 Franean1_5208 DVDQLDDYRARRRPMVFD--EDHWESYDPALE-----TELHDEAGTFFLLLGGPEPDLHWRKFTKAVQAQVMAELGVMSVGLNAIPMAVPHTRPCGVTAHATRKEKEL
 KRH_14390 DIDQLYDYRARRRPIYFN--EDHLLDTRQPEMV-----LHVVTDCGLDRHFLMLTGPDPDTQWERFSAVVVERLDVNLVAVHVSIPMPVPHTRPVLTVAHTRPRADL
 BIFDEN_02062 NDEGFYDQVARPMTCTIQ--GRKRIIWPQTVFY-----DITISPEATHFLAQIAPENPNRWKEYCSQSLATADELDVNRITITLGSMPDCHPTRLPIAVSDGDCQC
 cu0890 NLLDLLDYRARRRPIYFN--ENRITKSKLSDL-----VRIVKDVNRDFLLVAGGPEPDLKWEAFGHAVELVAQANVRAISFYSAPMTVPHTRPILVSAHNSDKEL
 jk1100 KVDLIDYRARRRPIYFN--ENRITKSKLSDL-----LHLLKDTQGRFFLLSGLPEPDLKWEAFGHAVELVAQANVRAISFYSAPMTVPHTRPILVSAHNSDKEL
 Ncgl1848 NNDELIDYRARRRPMVFD--HNEVTSMDLNGL-----LHVVRDNDKFPFLMSGLPEPDLRWDGFSNAVVDLVEKFGVNTICLYAAPMTVPHTRPVTVAHNSGSTR
 cgR_1753 NNDELIDYRARRRPMVFD--HNEVTSMDLNGL-----LHVVRDNDKFPFLMSGLPEPDLRWDGFSNAVVDLVEKFGVNTICLYAAPMTVPHTRPVTVAHNSGSTR
 MAP2831 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALRDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 MMAR_1998 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALRDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 ACTOD0_01571 DADALMDYRARRPIVTVDN--WASSPDMVMPETV-----LDLVEDDMGNPILVHGAEPDAHESFTNAINELCERAGVEITPFLHGVPSGVPHTRPVTVAHNSGSTR
 MAV_3608 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALRDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 Mb2733 AIDELLYRARRRPLMTFK--TDHFTHYDEPELN-----LYALRDSVGTFFLLSGLMPPDLRWERFITAIRLLAERLGVRRVIGLGSIPMAVPHTRPMTLTAHNSDKEL
 CE1815 NNDELIDYRARRRPIYFN--NNEVTEMEDLQLG-----LHVVRSDNKFPFLVLSGPEPDLRWDGFSNAVVDLVEKFGVNTICLYAAPMTVPHTRPVTVAHNSGSTR
 nfa31940 DSEYDYDQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 RHA1_ro00860 DSEYDYDQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Rv2125 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 MtubH3_05282 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 MT2184 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 MUL_2357 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Mvan_3475 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 MAP1860 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 MAB_2128c DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Arth_2169 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 ML1306 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Mflv_3052 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 SGR_5841 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 RSal33209_2043 EADYYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
SC01652 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Lxx08270 DPLEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 A20C1_02494 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 BlinB01000025 DTDGFYDFRFSPEEIVRDESNRAITAWPGIEVH-----RGQHMGTPTITIQGHEPGLKREFLSLITAEVTAED--CVLLGGLHAEVPHTRPPLVANTEDIRL
 SSAG_04705 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Rxy1_1077 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Noca_2630 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 TWT317 DADDYLDYHLRPRCESKD--GVRKIYWPAITVYKMS-----NEPGVPSGSAEDIYFLISPEPNMRRWRFKFAEIVDYAKANNISGIIFLGSMLTDIPIHTPFPVFLTSEEPK
 Mjls_3162 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 MSMEG_4186 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Sare_2324 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 FRAAL2860 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 SAV_6650 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Strop_2170 DDEAYDYQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Francci3_2640 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Acel_1173 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Tfu_1826 DSEYDYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Krad_1842 DPLEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 KRH_13910 ASDYYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 Franean1_4890 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 SACE_2233 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 JNB_03080 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 CMM_1693 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 CMS_1670 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 PPA1200 DPEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 AAur_2170 DAEYDFQVNRPIYRQVDGVTREIQWPSMTLS-----VCSPP--GSTRDVLVLRGIEPNMRRWFCADLEFVEQLGVTVVLGALLADTPHTRPVPVSGAAYSAA
 TW455 DADDYLDYHLRPRCESKD--GVRKIYWPAITVYKMS-----NEPGVPSGSAEDIYFLISPEPNMRRWRFKFAEIVDYAKANNISGIIFLGSMLTDIPIHTPFPVFLTSEEPK
 BIFADO_01161 DNEGFYDQVARPMTCTIQ--GRKRIIWPQTVFY-----DIAVSPMLHLLAQIAPENPNRWKEYCSQSLATADELDVNRITITLGSMPDCHPTRLPIAVSDGDCQC
 BAD_0824 DNEGFYDQVARPMTCTIQ--GRKRIIWPQTVFY-----DIAVSPMLHLLAQIAPENPNRWKEYCSQSLATADELDVNRITITLGSMPDCHPTRLPIAVSDGDCQC

SCO1997 TRG-N--MLAEPVEIPSADEITGREFERFLAE-----REGDG-----
 RSal33209_2429 RSL-L--AG-DGDELPADELGAAIEAYLAER-----DDTAERDDTTG-----
 MAB_3033 NRS----LLARDEELPSGDELAGEFERFLAEQAKFG-----DDPSGSPPEGPIL-----
 Noca_2852 SGT-S--LLARDQRLPTGEEITKEFERFLAGLDRPG-----DDEPQG-----
 A20C1_03668 RSP-L--TD-EDGELPSADEIAAELQKFLAIR-----RAGDDSTTGLPL-----
 Krad_1509 -----TGAASAFLLPTADELGEFERFLAQGE-----DEPDGDGPPGDRPGAG-----
 CMS_1627 KSP-L--TD-EDGALPTADEIAAELEKFLARR-----RPGDGDAA-----
 Lxx10170 RSP-L--TD-RDGEPLPSADEIAAELENFLAFLR-----RHGDEDNSRGRD-----
 nfa37830 RQS-S--LLAADGDLPSGEELGAEFERFLAEQGGYDG-----DKD-----
 PPA1099 -----LGTQVAVPDAEIDIAEVEDFLRSIDEDDGPNS-----DDPDTQSGSPRRSSDDTSDDDKPDYHPRGGDLN-----
 JNB_00545 RPS-L--LATEAEDLPSADELGADIEEFLRNVSD-----GSDD-----
 DIP1417 NPK-A--LEIAEDDLPADELGEFERFLANIDEEN-----GDDQPREGL-----
 Mflv_3951 NRS----LLARDEDLPSGEELGAEFERFLAQQAAGEKKRKD-----GDDQPREGL-----
 SGR_5536 TRG-N--LVAEPVLDPSADEITGREFERFLAE-----REGEG-----
 AAur_1758 RSL-L--AD-ENDELNAEDIGAAVEAYLARK-----DSAQ-----
 Mvan_2446 NRS----LLARDEDLPSGEELGAEFERFLAQQAAGEKKRKD-----GDD-PREGL-----
 MUL_3357 NRS----LLTRDEDLPSGDELGAEFERFLAQQAEEK-----FDDDDQP-----
 Rv2714 NRS----LLTRDEDLPSGDELGAEFERFLAQQAEEK-----SDDPT-----
 RHA1_ro06805 QQS-T--LLASEDLPSGDELGAEFERFLAEQALQDGE-----GSDDEGGSPGGA-----
 Sare_1722 PNL-L--NTG-AGSLPTADELGAELERFLAEQ-----TRPND-NPGG-----
 BLD_0447 ---QQKAEAEASLGAPQAEQLVKEAEAFLRQMGN-----
 SSAG_03958 TRG-N--MLAEPVEIPSADEITGREFERFLAE-----REGEG-----
 BIFLAC_03242 ---HQHAKELSSAGTMAEQLVQEAFAFLRDQD-----
 Tfu_0926 VDA-L--LAGDESRLPTADELGAELERFLAEHGRGSAEHD-----RGSEG-----
 SAV_6234 TRG-N--MLAEPVEIPSADEITGREFERFLAE-----REGEG-----
 BL0722 ---QQKAEAEASLGAPQAEQLVKEAEAFLRQMGN-----
 Strop_1737 PNL-L--STG-TEALPTADELGAELERFLAEQ-----TRPND-NPGG-----
 CMM_1644 KSP-L--TD-EDGALPTADEIAAELEKFLARR-----RPGDGDAA-----
 Francii_1247 PSL-P--AADDVQPLPTADELGDALERFLAEQ-----TEPDGPTPNP-----
 MSMEG_2746 NRS----LLARDEDLPSGDELGAEFERFLAQQAAGEKFKDDKYKDGHEGFGGRIRGTVTTDDVDVQD-----
 ML1009 NRS----LLRRDEDLPSGDELGAEFERFLAQQAEEK-----RDDLDT-----
 Acel_0028 ESP-L--GGG-TDNLPSADELGAELERFLAEQ-----ARRHRDRDQ-----
 FRAAL1976 PSL-P--TIDAEQKLPPTADELGAELERFLAEQ-----SEPGGPNPLS-----
 Arth_1614 RSL-L--AD-ENDELPNADALGAAVEAYLARE-----EPRQ-----
 Franeanl_5208 EHL-P--VVDDSEPLPTGEEILGAELERFLAEQ-----SEPGGPQPT-----
 KRH_14390 RSI-L--AGPDDADLPDADLGAEEAFLLAAQ-----SDPAHED-----
 BIFDEN_02062 ---NVKAREIASNGTPACEQLIQEAEAFLRNQPFAEH-----
 cu0890 K-S-S--LLEPGQDIPPTGEEILGAEFEAFLLRNMNDAA-----DTDSEADGEDPKKPGDSNDPHDDGEGDTQ-----
 jk1100 REN-N--LLKPGQDIPPTGEEILGAEFEAFLLNMSDGD-----LSD-ENGADN--SADSDEQEEN-----
 NCg11848 HPQ-A--VMPGESELPSGDEITGAEFEKFLADLDDQ-----GSDHKETPEA-----
 cgR_1753 HPQ-A--VMPGESELPSGDEITGAEFEKFLADLDDQ-----GSDHKETPEA-----
 MAP2831 NRS----LLTRDGLDPSGDELGAEFERFLAQQAEEK-----FDDDDQA-----
 MMAR_1998 NRS----LLTRDEDLPSGDELGAEFERFLAQQAEEK-----FDDDDQP-----
 ACTODO_01571 LPG-LGQRPSAGGEEKTPKIDVIEAYLAQVSRQAQDEEIESVQR-----APRTEESEEPKPDITIEDVLARIEARRNGKGTGPSAPRHRA-----
 MAV_3608 NRS----LLTRDGLDPSGDELGAEFERFLAQQAEEK-----FDDDDQA-----
 Mb2733 NRS----LLTRDEDLPSGDELGAEFERFLAQQAEEK-----SDDPT-----
 CE1815 NPQ-A--VLPGETVPVPSGDEITGAEFERFLANLDDSG-----DPDGPEDNGQ-----
 nfa31940 ---AVDMKEAIAKIDGDALAAEFERYLRRRGGPSFGL-----
 RHA1_ro00860 ---ETDISDAISKIDGDALAAEFERYLRRRGGPSFGL-----
 Rv2125 ---AVDMNEALGNIDGDALAAEFERYLRRRRPG-FGR-----
 Mtubh3_05282 ---AVDMNEALGNIDGDALAAEFERYLRRRRPG-SGARGRLRCGGRRCQPGGPGSPESP-----
 MT2184 ---AVDMNEALGNIDGDALAAEFERYLRRRRPG-FGR-----
 MUL_2357 ---AVEMNDALGKIDGDALAAEFERYLRRRRPG-FGL-----
 Mvan_3475 ---EVDMNEALGKIDGDALAAEFERYLRRRGGP-FRG-----
 MAP1860 ---EVDMDALGKIDGDALAAEFERYLRRRRPG-FGR-----
 MAB_2128c ---EVDTTTEMLSKIDGDALAAEFERYLRRRGGP-FGG-----
 Arth_2169 ---TADLPEASGEATAREFERYLKRRGKDKQ-----
 ML1306 ---EVDVNDALGKIDGDALAAEFERYLRRRRPG-FGR-----
 Mflv_3052 ---EVDMNEALGKIDGDALAAEFERYLRRRGR-----
 SGR_5841 ---TAELEASGEATAREFERYLRRRDGGPG---QPGGHATESGD---IPYLRDPATGRTRPKP-PRTEPGRGRDADQGAEGPDETPGKDPNGSGETPDED
 RSal33209_2043 ---TAELEATGESIAREFERYLRRRGGKEK-----PKAGGDDE-----ESSED-----
SCO1662 ---TAELEASGEATAREFERYLRRRDGAGPGGPGGHHATADGGDGPAGAPFRRDNPGRARPPK-----
 Lxx08270 ---TVDSPEASGEATAQEFERYLRRRD---GRAGDD-PRRG-----
 A20C1_02494 ---TVDSPEASGEATAQEFERYLRRGDDKDPQGSAGDE-PWRGKD-----
 BlinB01000025 ---TELPEASGDATAAEFERYLKRRGRER-----
 SSAG_04705 ---TADLPEASGDATAAEFERYLRRRD--P---AGPS--STEPGD---GSYLRDTSGLPRPMMRRDPPEPGRVRRARSRTIR---TPRR---
 Rxyl_1077 ---SQEEGGGQIRHLPSGDELARELEDFLRRQGEDEQ-----
 Noca_2630 ---TDLPEASGEATAREFERYLKRRQGE-----
 TWT317 ---VALSSTANDHLVKSLELYLSSIRRESEFPPTISRLRELPE-----
 Mjls_3162 ---EVDMTVEVLGKIDGDALAAEFERYLRRRGGP-FRS-----
 MSMEG_4186 ---EVDLHEVLGKIDGDALAAEFERYLRRRGR-----
 Sare_2324 ---VGDAGITPLTGDETAQEFERYLRRRGGSGAGTAGSW-----
 FRAAL2860 ---EPETALPEASGDATAAEFERYLRRRGG-----
 SAV_6650 ---TAELEASGEATAREFERYLRRRDGGGP---AAGGHATADGSDGTS---YLRDAPGGTRTRPKP---PKPEAEDDGPADGEGSDSSSED-----
 Strop_2170 ---VGDAGITPLTGDETAQEFERYLRRRGGSGAGTAGSW-----
 Francii_2640 ---EPETALPEASGDATAAEFERYLRRRGG-----
 Acel_1173 ---DDVPEGAGEATAREFERYLRRHREGQS-----
 Tfu_1826 ---AAELPEASGEATAREFERYLRRRGGG-----
 Krad_1842 ---TAELEASGEATAREFERYLRRRDPPRRG-----
 KRH_13910 ---TVDLPEATGDATAAEFERYLRRRDDRG-----
 Franeanl_4890 ---EPETALPEASGDATAAEFERYLRRRGE-----
 SACE_2233 ---EVLTTETS---GDATAAEFERYLRRRGGGKPKGPGPG-----
 JNB_03080 ---TAELEASGDATAAEFERYLKRRGTDD-----
 CMM_1693 ---TVDSPEASGEATAQEFERYLRRGDGPRGRGDRPEEPWRPKDKPKDQ-----
 CMS_1670 ---TVDSPEASGEATAQEFERYLRRGDGPRGRGDRPEEPWRPKDKPKDQ-----
 PPA1200 ---ALSEGLTGDVLAVEFQSYLRHRHG-----
 AAur_2170 ---TADLPEASGESIAREFERYLKRRGKERP-----
 TW455 ---VALSSTANDHLVKSLELYLSSIRRESEFPPTISRLRELPE-----
 BIFADO_01161 ---DARAKRIASNGMPACEELLRAEESLNRNV-----
 BAD_0824 ---DARAKRIASNGMPACEELLRAEESLNRNV-----

Note: Conserved residues colored in Additional file 2 are also highlighted here. Unexpected amino acids at conserved positions are highlighted in cyan.