Structure of a pseudokinase domain switch that controls oncogenic activation of Jak kinases

Angela V. Toms, Anagha Deshpande, Randall McNally, Youngjee Jeong, Julia M. Rogers, Sol M. Gruner, Chae Un Kim, Scott B. Ficarro, Jarrod A. Marto, Martin Sattler, James D. Griffin and Michael J. Eck

Supplementary File ConSurf_Alignment.pdf

Aligned sequences of 89 vertebrate Jak-family pseudokinase domains analyzed using the ConSurf server (http://consurf.tau.ac.il/). Sequences are shaded according to conservation, from teal (most variable) to dark magenta (most conserved). Species annotations are provided at the end of the alignment. Sequences were extracted from the Uniref90 database, and were chosen to have a minimal identity of 32% and a maximal identity of 95%. Sequence selection and conservation analysis is based on a fragment of human Jak1 including both the pseudokinase and kinase domains to assure selection of authentic Jak pseudokinase sequences. Numbering above the alignment corresponds to human Jak1, with human Jak2 numbering in parentheses. Excerpts from the alignment highlighting the F-F-V triad are presented first, followed by the complete alignment.

Excerpts from Jak pseudokinase sequence alignment highlighting the F-F-V triad

	F |575 (537)	F |636(595)	V |658(617)
Jak2_human_529_1116	VFHKIRNE	FFEAASMM	NYGVCV
H2V1W4_515_1120	VFHKIRKE	FFEAASMM	NYGVCV
I3KJT0_513_1117	VFHKIRKE	FFEAASMM	NYGVCV
G1PKC8_569_1171	SFHRVCQD	FYETASLM	VHGVCV
G3STB4_577_1153	SFHRVCRE	FYEIASLM	VHGICV
O12990_562_1150	SFDRILKE	FFETASMM	LYGVCV
G3WN84_561_1153	SFHRILKE	FFEAASMM	LYGVCV
Q6W5B1_355_948	IFHKIHRE	FFESASMM	NYGICV
G1KI54_559_1153	SFHQIRKE	FFETASMM	LHGICV
H3DDQ1_395_969	VFHKIRKE	FFEAASMM	NYGVCV
G5B225_576_1168	SFHRVQQD	FYETASLM	LHGVCV
H0VSL1_499_1098	TFQKIPPH	FLEAASLM	LHGVCM
F8W4H3_558_1147	SFNPIKDK	FFETASLM	VHGLSV
O57612_578_1166	SFHRILKE	FFETASMM	LYGVCV
H3ABD2_524_1119	VFHKIRNE	FFEAASMI	NYGVCV
H0V2Z6_556_1148	SFHRVQQD	FYETASLM	VHGVCV
H2LQD3_521_1110	QFQMIKYE	FFEAASLM	VYGVSV
Q6GPK5_575_1163	SFHQIRKH	FFETASLM	VHGVCV
G3PKI3_511_1116	VFHKIRKE	FFEAASMM	NYGVCV
B0V237_509_1091	QFHMIKHE	LFEAASLM	VYGISV
G1N138_441_1047	CFLSMIFG	FFHVVSYS	LLCTVL
H2TE39_530_1116	QVPYIPDK	FIESVGTM	VHGLSV
H2VE41_574_1180	SFHRILKE	FFETASMM	LYGVCV
H1A3H7_27_589	MFHKIDPQ	FLEAASTM	LHGVS-
C7ATY9_562_1151	RFHQIKDR	FFETASLM	VHGVSV
H2SBF4_355_996	VFHKIRRE	FYEAASMM	SYGVCV
H3B0L6_509_1107	IFHKIKKE	FFEAASVM	VYGICV
G3PKV8_559_1147	RFHQIKER	FLETASLM	VHGVSV
I3K428_523_1114	QFHMIKYE	FFEAASLM	VYGVSV
I3IZB2_589_1184	MFPQIKDK	FFETASLM	VYGVSV
O42291_505_1097	SFHKIDPE	FLEAASIM	LHGVS-
H0X425_574_1168	SFHRVGQD	FYETASLM	VHGVCV
G1P7K0_396_981	TFHKIAAD	FLEAASLM	LHGVCM
G3TF05_473_1068	TFHKIPSD	FLEAASLM	LHGVCM
F1NMJ9_554_1150	SFHRIRKE	FFEAASMM	LHGVCV
P29597_576_1171	SFHRVDQK	FYETASLM	VHGVCV
Q75R65_529_1123	VFHKIRNE	FFEAASMM	NYGVCV
D2GV17_503_1098	TFHKIPPE	FLEAASLM	LHGVCM
Q9PTN6_498_1097	QFHMIKHE	FFEAASLM	VYGISV
Tyk2_human_576_1166	SFHRVDQK	FYETASLM	VHGVCV
F7EV03_508_1101	TFHKIHLK	FLEAASIM	VHGVCV
Jak3_human_503_1091	TFHKIPAD	FLEAASLM	LHGVCM
G5BSN6_723_1350	SFDRILKK	FFEAASMM	LYGVCV
G1LYZ3_576_1170	SFHRVCRD	FYETASLM	VHGICV
H2M2I1_581_1165	SFIRILKE	FFETASMM	LYGVCV
F1MCX4_575_1169	SFYRVRQE	FYETASLM	VHGVFV
H2SBF2_535_1131	VFHKIRRE	FYEAASMM	SYGVCV
G3NVW0_582_1174	SFHRILKE	FFETASMM	LYGVCV
Q9PWD0_515_1100	QFQMIKYE	FFEAASLM	VYGVTL
I3MAE0_504_1097	TFHKIPAD	FLEAASLM	LHGVCM
H2TE42_495_1102	QVPYIPDK	FIESVGTM	VHGLSV
C7ATY6_576_1168	SFHRILKE	FFETASMM	LYGVCV
D3Z4S5_718_1310	SFHTIPTD	FLEAASLM	LHGVCM
I3JQC0_567_1148	SFPRILKE	FFETASKM	LYGVCV
Q9R117_572_1164	SFHRVHQD	FYEXASLM	LHGVCV
H0VRI8_531_1132	VFHKIRNE	FFEAASMM	NYGVCV
Jak1_human_561_1154	SFDRILKK	FFEAASMM	LYGVCV
H2VE42_579_1162	SFHRILKE	FFETASMM	LYGVCV
F6V3I2_589_1182	SFYQIRKD	FFETASLM	VHGVCV

Jak Pseudokinase Sequence Conservation

```
                                                |575(537)
Q6Y4Q0_534_1126          -------ISQM--VFHKIRREDLV--LDNSLGQGTFTKIFRGVR-KE
F1PBD0_595_1189          -------VSQL--SFHRICQADVT--QLSHLGQGTRTNVYEGVL-RV
H3ADK6_22_610            -S----YTLSQL--SFHRILKEEIK--QEAHLGTGTRTNIFEGTL-NY
G1KHZ7_606_1200          -------LTQL--SFHQIRKNEIT--QRAHLGQGTLTNIYDGVL-HV
Q6DDJ0_546_1139          -ALEWQPVYHLSQL--SFHRILKEEIT--QLEHLGRGTRTQIYAGKL-NY
Jak2_human_529_1116      -------MNQM--VFHKIRNEDLI--FNESLGQGTFTKIFKGVR-RE
H2V1W4_515_1120          PLSPSTNRHNISQM--VFHKIRKEDLE--FNESLGQGTFTKIFKGIR-KE
I3KJT0_513_1117          PLSPSLHRHNISQM--VFHKIRKEDLE--FMESLGQGTFTKIFKGVR-KE
G1PKC8_569_1171          -QASARSLNLSQL--SFHRVCQDDLT--QLSHLGQGTRTNVYEGLL-RV
G3STB4_577_1153          -------LSQL--SFHRVCREEIT--QLSHLGQGTRTNVYEGLL-RV
O12990_562_1150          ----QKKTQVSQL--SFDRILKEEIV--QGEHLGRGTRTNIYAGIL-KP
G3WN84_561_1153          -AQECQPVYTMSQL--SFHRILKEDII--QGEHMGRGTRTQIYSGTL-DY
Q6W5B1_355_948           -------VNQM--IFHKIHREDLQ--TTEGLGQGTFTQVFRGIR-RE
G1KI54_559_1153          -SQECKPIYPLSQL--SFHQIRKEEII--QGEHLGRGTKTQIYSGIL-NY
H3DDQ1_395_969           PLSPSTNRHNISQM--VFHKIRKEDLE--FNESLGQGTFTKIFKGVR-KE
G5B225_576_1168          -------LSQL--SFHRVQQDDIT--QLSHLGQGTRTNVYEGLL-RV
H0VSL1_499_1098          -PVQPSVQPKLSQL--TFQKIPPHSLQ--WHENLGHGSFTKIYRGSR-HE
F8W4H3_558_1147          -------LSKL--SFNPIKDKEIT--KEQHLGRGTRTNIYSGWL-KI
O57612_578_1166          -----P-----DSQL--SFHRILKEDIE--QEEHLGRGTRTNIYSGTL-RV
H3ABD2_524_1119          ----QRHNNISQM--VFHKIRNEDLS--FGESLGQGTFTKIFKGVR-KE
H0V2Z6_556_1148          -------LSQL--SFHRVQQDDIT--QLSHLGQGTRTNVYEGLL-RV
H2LQD3_521_1110          -------FSHI--QFQMIKYEDLK--WVESLGQGSFTRIFKGYK-TY
Q6GPK5_575_1163          -------LSQL--SFHQIRKHEIL--QKAHLGQGTRTNIYDGML-LV
G3PKI3_511_1116          PLSPTLHRHNINQM--VFHKIRKEDLE--FMESLGQGTFTKIFKGVR-KE
B0V237_509_1091          --------SHM--QFHMIKHEDLI--WSESLGQGSFTHIFRGSK-ID
G1N138_441_1047          -AESYQIYSTLPQVPSCFLSMIFGDLL--MEESLGQGTFTKIFKGIR-KE
H2TE39_530_1116          ---FQPSSKTSRV--QVPYIPDKDLV--QGQHLGSGPITNIYRGLL-LV
H2VE41_574_1180          -----P-----DSQL--SFHRILKEDIE--QEEHLGRGTRTNIYSGTL-RV
H1A3H7_27_589            ----RSLQQM--MFHKIDPQSLT--RGESLGQGSFTQIYKGVK-RE
C7ATY9_562_1151          -------MTQL--RFHQIKDREIV--QEQHLGRGTRTNIYSGRL-LV
H2SBF4_355_996           --PHTHISQM--VFHKIRREDLV--LNESLGQGTFTKIFRGVR-KE
H3B0L6_509_1107          ----RAVSQM--IFHKIKKEDLI--WGENLGMGSFTKIYKGTK-VS
G3PKV8_559_1147          --------TQL--RFHQIKERDIV--QKQHLGRGTRTHIFSGHL-LV
I3K428_523_1114          -------FSHI--QFHMIKYEELS--CDESLGKGSFTRIFKGKK-ID
I3IZB2_589_1184          ---PLSQTYKTRL--MFPQIKDKDIK--QEQHLGRGTRTNIYTGRL-LT
O42291_505_1097          --------NQM--SFHKIDPESLI--RGESLGQGSFTHIYKGIK-RD
H0X425_574_1168          -------LSQL--SFHRVGQDEIT--QLSHLGQGTRTNVYEGLL-RV
G1P7K0_396_981           -PVQPHSGCQLSQM--TFHKIAADSLE--WCENLGHGSFTKIYRGCR-HE
G3TF05_473_1068          Q---PQFQCQLSQM--TFHKIPSDSLE--WHENLGHGSFTKIYRGHR-HE
F1NMJ9_554_1150          -AQECQPAYHLGQL--SFHRIRKEEIM--QGEHLGRGTRTQIYSGIL-NY
P29597_576_1171          -------LSQL--SFHRVDQKEIT--QLSHLGQGTRTNVYEGRL-RV
Q75R65_529_1123          -------VSQM--VFHKIRNEDLI--FEESLGQGTFTKIFKGIR-KE
D2GV17_503_1098          ----QSQCQLSQM--TFHKIPPESLE--WHENLGHGSFTKIYRGCR-HE
Q9PTN6_498_1097          PSSPMLQRHKPSHM--QFHMIKHEDLT--WSESLGQGSFTHIFRGSK-TD
Tyk2_human_576_1166      -------LSQL--SFHRVDQKEIT--QLSHLGQGTRTNVYEGRL-RV
F7EV03_508_1101          ----RNLQSL--TFHKIHLKDIT--FMESLGKGSFTKIFRGLR-TD
Jak3_human_503_1091      ----QSQYQLSQM--TFHKIPADSLE--WHENLGHGSFTKIYRGCR-HE
G5BSN6_723_1350          -AQEWQPVYPMSQL--SFDRILKKDIM--QGEHLGRGTRTHIYSGTLVDY
G1LYZ3_576_1170          -------LSQL--SFHRVCRDDIT--QLSHLGQGTRTNVYEGIL-RV
H2M2I1_581_1165          --------SQL--SFIRILKEDIQ--QDEHLGTGTKTNIYSGNL-RA
F1MCX4_575_1169          -------LSHL--SFYRVRQEDIT--QLSHLGQGTRTNVYEGLL-RV
H2SBF2_535_1131          --PHTHISQM--VFHKIRREDLV--LNESLGQGTFTKIFRGVR-KE
G3NVW0_582_1174          ----QTPMQESQL--SFHRILKEEIE--QEEHLGPGTRTNIFSGTL-RV
Q9PWD0_515_1100          --------HI--QFQMIKYEDLQ--WGESHGQGSFTRLFKGYK-SN
I3MAE0_504_1097          ----QSQHKLNQM--TFHKIPADSLE--WHENLGHGSFTKIYRGCR-HE
H2TE42_495_1102          ---FQPSSKTSRV--QVPYIPDKDLV--QGQHLGSGPITNIYRGLL-LV
C7ATY6_576_1168          ---PQTPMQESQL--SFHRILKEEIE--QEEHLGRGTRTNIYSGTL-RV
D3Z4S5_718_1310          -------LTQL--SFHTIPTDSLE--WHENLGHGSFTKIFRGRR-RE
I3JQC0_567_1148          -----P-----GNQV--SFPRILKEDIE--QEEHLGIGTKTNIYSGTL-KV
Q9R117_572_1164          -------LSQL--SFHRVHQDEIT--QLSHLGQGTRTNVYEGLL-RV
H0VRI8_531_1132          ----QRHNNVNQM--VFHKIRNEDLI--FNESLGQGTFTKIFKGIR-RE
Jak1_human_561_1154      -AQEWQPVYPMSQL--SFDRILKKDLV--QGEHLGRGTRTHIYSGTLMDY
H2VE42_579_1162          -----P-----DSQL--SFHRILKEDIE--QEEHLGRGTRTNIYSGTL-RV
F6V3I2_589_1182          --------LSQL--SFYQIRKDEIT--QLAHLGQGTRTNIYEGLL-HV
Q9PWD1_530_1117          ----QPLSNKTQV--QVRHIKETEIV--QGRHLGCGTKTNIHKGSL-QV
F1S3L9_566_1169          --QACTRPLNLSHL--SFHRVHQEDIT--QLSHLGQGTRTNVYEGLL-RV
G3VR92_504_1104          AQAWPHPQRQLSQM--MFHKIPPDSLE--WHENLGHGSFTKIYRGSR-LD
F6X8E5_508_1068          ----QPRLQLSHM--MFHTIQPESLQ--WHENLGHGSFTKIYRGTR-RD
H2L7P7_514_1119          PLTPSLQRHNISQM--VFHKISKDDLE--FMESLGQGTFTKIFKGVR-KE
I3M210_601_1192          -------LSQL--SFHRIHQDEIT--QLSHLGQGTRTNVYEGLL-RV
G1KCE0_530_1126          -------INQM--VFHKIRNEDLI--FNESLGQGTFTKIFKGVR-KE
Q09178_563_1153          -D--SQRQPQVSQL--SFHRILKEEIV--QGEHLGRGTRTNIYSGVL-KL
D3ZUV6_649_1241          -------LTKL--SFHTIPADSLE--WHENLGHGSFTKIFHGHR-RE
G9KW41_102_676           -------LSQL--SFHRISQDDIT--QLSHLGQGITRTNVYEGIL-RV
H2LLN7_568_1156          -------LTKL--RFNRIKEKNIT--PEVHLGRGTRTNIYSGRL-LV
H3C837_398_1006          PLSPSTNRHNISQM--VFHKIRKEDLE--FNESLGQGTFTKIFKGVR-KE
F7EAS1_502_1096          AQAWPQSQRQLSQM--MFHKIPADSLE--WHENLGHGTFTKIYRGSR-LD
H2M2B1_532_1128          ----RHISQM--VFHKIRREDLI--IKASLGQGTFTKIFCGVR-KE
H2TCV2_510_1100          -------LSHI--QFQMIKYEDLQ--WGESLGQGSFTRLFKGYK-SD
G3P1H3_515_1105          -------FSHI--EFHMIKYKDLD--LGESLGQGSFTRNFKGYK-TD
A0JM01_530_1122          -------VNQM--VFHKIRSEDLH--FLENLGQGTFTKIFKGKR-EE
G3PZA6_518_1120          PLTPSLHKHNISQM--VFHKIRKEDLV--IKESLGQGTFTKIFCGVR-KE
I3J7Z7_537_1129          -------ISQM--VFHKIRKEDLI--IKESLGQGTFTKIFCGVR-KE
G1MVV3_535_1025          -------LTQL--SFHQIRKDEITQPQRAHLGQGTRTNIYDGVL-NV
F7B2N9_488_1076          ------QLSQM--TFHKIPADSLE--WHENLGHGSFTKIYRGHR-HE
Q4T1R9_364_1003          -------ISQM--VFHKIRREDLV--LDNSLGQGTFTKIFRGVR-KE
C7ATY8_513_1104          -------FSHI--QFHMIKYGDLK--WGESLGQGSFTRIFKGYK-TD
H0ZIA6_541_1134          -AQEWQPVYPMGQL--SFHRIRKEEIV--QGEHLGRGTRTQIYSGML-SL
C0RW38_515_1112          -------ISQM--VFHKIKKEDLE--LGESQGQGTFTKIFKGIR-KE
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                                                                                  |621(580)
Q6Y4Q0_534_1126          -LGD-----------------------------YGEVHQMDVVVKILDKAHCNFSE---
F1PBD0_595_1189          -GARAPKEGA---ADGED-PPTPSEDSGLELRVVLKVLDPSHHDIAL---
H3ADK6_22_610            -KEDEDNE-E-----------------------FYSAKEVKVVLKVLDPRYRDISL---
G1KHZ7_606_1200          -CGGASGDDE-----TEY-FSTEQNNNNREVHVVLKMLDPSHRDIAL---
Q6DDJ0_546_1139          -KDDNDSE-S-----------------------YSTEKEIKVILKVLHPSHRDISL---
Jak2_human_529_1116      -VGD-----------------------------YGQLHETEVLLKVLDKAHRNYSE---
H2V1W4_515_1120          -LGD-----------------------------YGLMHQTEVVMKVLDQAHRNFSE---
I3KJT0_513_1117          -LRD-----------------------------YG-EHQTEVVMKVLDQSHRNFSE---
G1PKC8_569_1171          -GGGGPEEDE---AYVGD-PTLPGGGHGQELRVVLKVLDTSHHDIAL---
G3STB4_577_1153          -KGRDSEEDK---EEGGD-PLSPSRGSGQELRVVLKVLDPSHHDITL---
O12990_562_1150          -KSDDEDDLG-----------------------GYS-QEVKVVLKVLGSGHRDISL---
G3WN84_561_1153          -KDD-E---G-----------------------SSDEKKMKVILKVLDPSHRDISL---
Q6W5B1_355_948           -VGD-----------------------------YGEVHKMEVVMKILDKSHRNYTE---
G1KI54_559_1153          -KDD-ES---------------------------YQSEKEIKVLLKVLDPNHRDISL---
H3DDQ1_395_969           -LGD-----------------------------YGLMHQTEVVMKVLDQAHRNYSE---
G5B225_576_1168          -G--TPEEDK---EDSMG-PVEPSGGCGQELRVVLKVLDPGHHDITL---
H0VSL1_499_1098          -DVD-----------------------------GEARETEVLLKVLDAEHRNLVE---
F8W4H3_558_1147          -RGSLE-DED-------D-ESNNNHCKTKGIRVVLKILEQSQKDKAL---
O57612_578_1166          -KSEEDEDAG-----------------------YSSFQEVKVVLKLLSYGHRDISL---
H3ABD2_524_1119          -VGD-----------------------------YGHLHETEVLLKVLDRAHRNYSE---
H0V2Z6_556_1148          -G--TPEEDK---EDGVD-SGEPSGGRGQELRVVLKVLDPGHHDIML---
H2LQD3_521_1110          -TLD-----------------------------GEKHQTEVLLKELDAAHKNYWE---
Q6GPK5_575_1163          -SEGSEQESD---FESGE-----LNNNSHDLRVVLKVLDPSHRDIAL---
G3PKI3_511_1116          -LGD-----------------------------YGLVHQTEVVMKVLDQAHRNYSE---
B0V237_509_1091          -QRD-----------------------------GGTHSTEVLLKVLDANHKNCWE---
G1N138_441_1047          -VGD-----------------------------YGQLHQTEVLLKVLDKVHRNYSE---
H2TE39_530_1116          -HGGGDNGEE-------D-KFNNNASSQTGIPVVLKILNPNHDELSL---
H2VE41_574_1180          -KSEEDEDAG-----------------------YSSFQEVKVVLKLLSYGHRDISL---
H1A3H7_27_589            -QDE-----------------------------EDGPRQTPVVLKVMDSSHRNCLE---
C7ATY9_562_1151          -RGAGENDED-------D-EFNNNFTDRKGIQVVLKILDQSHQDIAL---
H2SBF4_355_996           -LGD-----------------------------YGEVHQMDVVVKILDKTYRNFSEVSV
H3B0L6_509_1107          -KKN-----------------------------EDETHQTEVLLKVLENIHKNCSE---
G3PKV8_559_1147          -QGGGENDQD-------D-EFNNNSGGRKEIQVVLKILDQSDKDIDL---
I3K428_523_1114          -IHD-----------------------------GEKRMTEVLLKELDATHKNCWE---
I3IZB2_589_1184          -QEREEND-N-------D-EFNNN--SHRGHRVVLKILDQTHEDIAL---
O42291_505_1097          -Q-K-----------------------------DDEFYQTPVVLKVMDSSHRNCSE---
H0X425_574_1168          -EGGDPEEGK---VDGRD-PPMPCRNCGQELRVVLKVLDPSHHDIAL---
G1P7K0_396_981           -TVD-----------------------------GEPRETEVLLKVLDAKHKHCME---
G3TF05_473_1068          -TVD-----------------------------GEVWETEVLLKVMDAKHKNCME---
F1NMJ9_554_1150          -KDD-ENE-G-----------------------YQNEKEIKVLLKVLDPSHRDISLAS-
P29597_576_1171          EGSGDPEEGK---MDDED-PLVPGRDRGQELRVVLKVLDPSHHDIAL---
Q75R65_529_1123          -VGD-----------------------------YGQLHQTEVLLKVLDKVHRNYSE---
D2GV17_503_1098          -VVE-----------------------------GEARETEVLLKVMDAKHKNCME---
Q9PTN6_498_1097          -QRD-----------------------------GVTHTTEVLLKVLDANHKNCWE---
Tyk2_human_576_1166      EGSGDPEEGK---MDDED-PLVPGRDRGQELRVVLKVLDPSHHDIAL---
F7EV03_508_1101          -E-E-----------------------------RDERCEVEVLLKVLDPTYGHYQE---
Jak3_human_503_1091      -VVD-----------------------------GEARKTEVLLKVMDAKHKNCME---
G5BSN6_723_1350          -RDD-E---G-----------------------TAEEKRIKVILKVLDPSHRDISL---
G1LYZ3_576_1170          -GGRSPEEGM---ADGED-PPTPSGDRGQELRVVLKVLDPSHHDIAL---
H2M2I1_581_1165          -KNEEDEDVG-----------------------YTSFQEVKVVLKVLGSGHRDISL---
F1MCX4_575_1169          -GGGGPEEDK---ADGEE-PPTPAGDRGQELRVVLKVLDPSHHDIAL---
H2SBF2_535_1131          -LGD-----------------------------YGEVHQMDVVVKILDKTYRNFSE---
G3NVW0_582_1174          -KSEEEEDAG-----------------------YSSFQEVKVVLKVLGSGHRDISL---
Q9PWD0_515_1100          -LSE-----------------------------GGKRVS-VFLKELDVNHRNLWE---
I3MAE0_504_1097          -AVD-----------------------------GEARATEVLLKVMDAKHRNCME---
H2TE42_495_1102          -HGGGDNGEE-------D-KFNNNASSQTGIPVVLKILNPNHDELSL---
C7ATY6_576_1168          -KSEEEEDAG-----------------------YSSFQEVKVVLKVLGSGHRDISL---
D3Z4S5_718_1310          -VVD-----------------------------GETHDSEVLLKVMDSRHRNCME---
I3JQC0_567_1148          -KGEEEEDAG-----------------------YTSFQEVKVVLKVLGSGHRDISM---
Q9R117_572_1164          ---GGPDEGK---VDNGC-PPEPGGTSGQQLRVVLKVLDPSHHDIAL---
H0VRI8_531_1132          -VGD-----------------------------YGQLHETEVLLKVLDKAHRNYSE---
Jak1_human_561_1154      -KDD-E---G-----------------------TSEEKKIKVILKVLDPSHRDISL---
H2VE42_579_1162          -KSEEDEDAG-----------------------YSSFQEVKVVLKLLSYGHRDISL---
F6V3I2_589_1182          -GGGMEAEDE---EEENI-PSEPNNNH-RELRVVLKVLDPSHRDIAL---
Q9PWD1_530_1117          -RSTEDGDQE-------N-EFNNN-SSGLDIPVVLKIPHQNL-EVSL---
F1S3L9_566_1169          -GGGGPEEEK---SDGRD-PSPSSGDRGQELRVVLKVLDPSHHDIAL---
G3VR92_504_1104          -NVD-----------------------------GETHKIEVLLKVMDSTHQNCIE---
F6X8E5_508_1068          -MAD-----------------------------EETRETEVLLKVMDSTHQNCSE---
H2L7P7_514_1119          -LGD-----------------------------YGCMHQTEVIMKVLDLAHRNYSE---
I3M210_601_1192          -G--GPEEGK---ADGGD-SPKPGGGCGQQLRVVLKVLDPSHHDIAL---
G1KCE0_530_1126          -VGD-----------------------------YGKLYQTEVLLKVLDKVHRNYSE---
Q09178_563_1153          -KSEDDDDMG-----------------------GYS-QEVKVILKVLGSGHRDISL---
D3ZUV6_649_1241          -VVD-----------------------------GETHDTEVLLKVMDSRHQNCME---
G9KW41_102_676           -GGRDPKEGTADRADSED-PPTPSGDCGQELRVVLKVLDPSHHDIAL---
H2LLN7_568_1156          ---GGEDDGN-------DVEFNNNSSKQKGIRVVLKILDRSHEDIAL---
H3C837_398_1006          -LGD-----------------------------YGLMHQTEVVMKVLDQAHRNYSE---
F7EAS1_502_1096          -KVE-----------------------------RETHKVEVLLKVMDGTHQNCIE---
H2M2B1_532_1128          -LGD-----------------------------YGEMHQIDVVVKILDKAHRNYSE---
H2TCV2_510_1100          -MRN-----------------------------GGKYMS-IFLKELDVSHRNLWE---
G3P1H3_515_1105          -IRD-----------------------------GEKYVTPVFLKELDVIHKHRWE---
A0JM01_530_1122          -LGD-----------------------------YNKIHVTEVLLKVLDKTHRSFSE---
G3PZA6_518_1120          -LGD-----------------------------YGEIHTIDVVIKILDKAHRDYSE---
I3J7Z7_537_1129          -LGD-----------------------------YGEIHQMDVVVKILDKAHRSYSE---
G1MVV3_535_1025          RGAAGPDEAE---YFSTE---QNNNSDGREMHVVLKVLDPTHRDIAL---
F7B2N9_488_1076          -AVD-----------------------------GEARETEVLLKVMDAKHKNCME---
Q4T1R9_364_1003          -LGD-----------------------------YGEVHQMDVVVKILDKAHCNFSEVSL
C7ATY8_513_1104          -IRD-----------------------------GEKHVTEVFLKELDVVHKNCWE---
H0ZIA6_541_1134          -KDD-ENE-G-----------------------YQNEREIRVLLKVLDPSHRDISL---
C0RW38_515_1112          -QGD-----------------------------YGETHKTEVIVKVLDKAHRNYSE---
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                                                                  |636(595)                                  |658(617)
Q6Y4Q0_534_1126          ----------------------S--FYEAASMMSQL--SHKHL-LLSYGVCV
F1PBD0_595_1189          ----------------------A--FYETASLMSQV--SHVHL-AFVHGICV
H3ADK6_22_610            ----------------------A--FFETASMMKQV--CHKHI-VLLHGVCV
G1KHZ7_606_1200          ----------------------A--FFETASLMSQV--SHIHL-AFVHGVCV
Q6DDJ0_546_1139          ----------------------A--FFETASMMRQV--SHKHI-VLLHGVCV
Jak2_human_529_1116      ----------------------S--FFEAASMMSKL--SHKHL-VLNYGVCV
H2V1W4_515_1120          ----------------------S--FFEAASMMTQL--SYKHL-ILNYGVCV
I3KJT0_513_1117          ----------------------S--FFEAASMMSQL--SHVHL-ILNYGVCV
G1PKC8_569_1171          ----------------------A--FYETASLMSQV--SHVHL-TFVHGVCV
G3STB4_577_1153          ----------------------A--FYEIASLMSQV--SHVHL-AFVHGICV
O12990_562_1150          ----------------------A--FFETASMMRQI--SHKHT-ALLYGVCV
G3WN84_561_1153          ----------------------A--FFEAASMMRQV--SHKHI-VYLYGVCV
Q6W5B1_355_948           ----------------------S--FFESASMMSQL--SHKHL-LLNYGICV
G1KI54_559_1153          ----------------------A--FFETASMMRQI--SHKHI-VLLHGICV
H3DDQ1_395_969           ----------------------S--FFEAASMMTQL--SHVHL-ILNYGVCV
G5B225_576_1168          ----------------------A--FYETASLMSQV--SHAHL-AFLHGVCV
H0VSL1_499_1098          ----------------------S--FLEAASLMSQV--SYPHL-VLLHGVCM
F8W4H3_558_1147          ----------------------A--FFETASLMSQV--SHCHL-IFVHGLSV
O57612_578_1166          ----------------------A--FFETASMMRQV--SHKHI-VLLYGVCV
H3ABD2_524_1119          ----------------------S--FFEAASMISQL--SYKHL-VLNYGVCV
H0V2Z6_556_1148          ----------------------A--FYETASLMSQV--SHVHL-AFVHGVCV
H2LQD3_521_1110          ----------------------S--FFEAASLMTQI--SHKHL-LFVYGVSV
Q6GPK5_575_1163          ----------------------A--FFETASLMSQV--SHIHL-VFVHGVCV
G3PKI3_511_1116          ----------------------S--FFEAASMMSQL--SHKHL-VLNYGVCV
B0V237_509_1091          ----------------------S--LFEAASLMSQI--SHRHL-LLVYGISV
G1N138_441_1047          ----------------------KSLFFHVVSYSSSKIGDYKHLRIMLLCTVL
H2TE39_530_1116          ----------------------T--FIESVGTMSQV--SHRHL-VHVHGLSV
H2VE41_574_1180          ----------------------A--FFETASMMRQV--SHKHI-VLLYGVCV
H1A3H7_27_589            ----------------------S--FLEAASTMSQL--SCKHL-VLLHGVS-
C7ATY9_562_1151          ----------------------A--FFETASLMSQV--SHCHL-VFVHGVSV
H2SBF4_355_996           RSVCV---SDDKKLRVFGFRS--FYEAASMMSQI--SHKHL-LLSYGVCV
H3B0L6_509_1107          ----------------------S--FFEAASVMSQI--SHKHL-ILVYGICV
G3PKV8_559_1147          ----------------------G--FLETASLMSQV--SHNHL-VFVHGVSV
I3K428_523_1114          ----------------------S--FFEAASLMSQI--AHRHL-LLVYGVSV
I3IZB2_589_1184          ----------------------V--FFETASLMCQV--SHRHL-VFVYGVSV
O42291_505_1097          ----------------------S--FLEAASIMSQL--SHKHL-VLLHGVS-
H0X425_574_1168          ----------------------A--FYETASLMSQV--SHVHL-AFVHGVCV
G1P7K0_396_981           ----------------------S--FLEAASLMSQV--SYQHL-VLLHGVCM
G3TF05_473_1068          ----------------------S--FLEAASLMSQV--SYQHL-VLLHGVCM
F1NMJ9_554_1150          ----------------------A--FFEAASMMRQV--SHKHI-VFLHGVCV
P29597_576_1171          ----------------------A--FYETASLMSQV--SHTHL-AFVHGVCV
Q75R65_529_1123          ----------------------S--FFEAASMMSQL--SYKHL-VLNYGVCV
D2GV17_503_1098          ----------------------S--FLEAASLMSQV--SYQHL-VLLHGVCM
Q9PTN6_498_1097          ----------------------S--FFEAASLMSQI--SHKHL-LLVYGISV
Tyk2_human_576_1166      ----------------------A--FYETASLMSQV--SHTHL-AFVHGVCV
F7EV03_508_1101          ----------------------S--FLEAASIMNQI--SHKHH-ILVHGVCV
Jak3_human_503_1091      ----------------------S--FLEAASLMSQV--SYRHL-VLLHGVCM
G5BSN6_723_1350          ----------------------A--FFEAASMMRQV--SHKHI-VYLYGVCV
G1LYZ3_576_1170          ----------------------A--FYETASLMSQV--SHVHL-AFVHGICV
H2M2I1_581_1165          ----------------------A--FFETASMMRQV--SHKHI-VLLYGVCV
F1MCX4_575_1169          ----------------------A--FYETASLMSQV--SHVHL-AFVHGVFV
H2SBF2_535_1131          ----------------------S--FYEAASMMSQI--SHKHL-LLSYGVCV
G3NVW0_582_1174          ----------------------A--FFETASMMRQV--SHKHI-VLLYGVCV
Q9PWD0_515_1100          ----------------------S--FFEAASLMSQF--SHKHL-ILVYGVTL
I3MAE0_504_1097          ----------------------S--FLEAASLMSQV--SYPHL-VLLHGVCM
H2TE42_495_1102          ----------------------T--FIESVGTMSQV--SHRHL-VHVHGLSV
C7ATY6_576_1168          ----------------------A--FFETASMMRQV--SHKHI-VLLYGVCV
D3Z4S5_718_1310          ----------------------S--FLEAASLMSQV--SYPHL-VLLHGVCM
I3JQC0_567_1148          ----------------------A--FFETASKMQQV--SHKHI-VLLYGVCV

Q9R117_572_1164          ----------------------A--FYEXASLMSQV--SHMHL-AFLHGVCV

H0VRI8_531_1132          ----------------------S--FFEAASMMSQL--SHKHL-VLNYGVCV
Jak1_human_561_1154      ----------------------A--FFEAASMMRQV--SHKHI-VYLYGVCV
H2VE42_579_1162          ----------------------A--FFETASMMRQV--SHKHI-VLLYGVCV
F6V3I2_589_1182          ----------------------A--FFETASLMSQV--SHIHL-AFVHGVCV
Q9PWD1_530_1117          ----------------------A--FIETVGIMGQL--SHSHL-VRVHGLSV
F1S3L9_566_1169          ----------------------A--FYETASLMSQV--SHVHL-VFVHGVYV
G3VR92_504_1104          ----------------------S--FLEAASVMSQV--SHQHL-VLLHGVCM
F6X8E5_508_1068          ----------------------E--GLQLSSKLPRV--SFISP-LLWDP---
H2L7P7_514_1119          ----------------------S--FFEAASMMSQL--SHKHL-ILNYGVCV
I3M210_601_1192          ----------------------A--FYETASLMSQV--SHAHL-AFVHGVCV
G1KCE0_530_1126          ----------------------S--FFEAASMMSQL--SYKHL-VLNYGVCV
Q09178_563_1153          ----------------------A--FFETASMMRQI--SHKHI-ALLYGVCV
D3ZUV6_649_1241          ----------------------S--FLEAASLMSQV--SYPHL-VLLHGVCM
G9KW41_102_676           ----------------------A--FYETASLMSQV--SHVHL-AFVHGICV
H2LLN7_568_1156          ----------------------A--FFETASLMSKV--SHSHL-VFVHGVSV
H3C837_398_1006          ----------------------S--FFEAASMMTQL--SHVHL-ILNYGVCV
F7EAS1_502_1096          ----------------------S--FLEAASIMSQV--SHQHL-VLLHGVCM
H2M2B1_532_1128          ----------------------S--FFEAASMMSQL--SHKHL-LLNYGVCV
H2TCV2_510_1100          ----------------------S--FFEAASLMSQI--SHKHL-ILTHGVSV
G3P1H3_515_1105          ----------------------S--FFEAASVMSQI--SHSHL-LLVYGVSV
A0JM01_530_1122          ----------------------S--FFEAASMMSQL--SYKHL-ILNYGVCV
G3PZA6_518_1120          ----------------------S--FFEAASMMSQL--SHKHL-LLNFGVCV
I3J7Z7_537_1129          ----------------------S--FFEAASIMSQL--SHKHL-LLTYGVCV
G1MVV3_535_1025          ----------------------A--FFETASLMSQV--SHVHL-AFVHGVCV
F7B2N9_488_1076          ----------------------S--FLEAASLMSQV--SYQHL-VFLHGVCM
Q4T1R9_364_1003          SAKSRFFGSEEKPSGLFSLQS--FYEAASMMSQL--SHKHL-LLSYGVCV
C7ATY8_513_1104          ----------------------S--FFESASLMSQI--SHKHL-LLVYGVSV
H0ZIA6_541_1134          ----------------------A--FFETASMMRQV--SHKHI-VLLHGVCV
C0RW38_515_1112          ----------------------S--FFEAASMMSQL--THKHL-VLTYGICV
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                                                  |671(630)                                  |691(650)
Q6Y4Q0_534_1126          CGDEN--MMVQEYGKFGSLDTYLKKKKG--CVNITWKLEVAKQLSWAMHY
F1PBD0_595_1189          YGSEN--IMVTEYVEHGPLDVWLRREKG--HVPVAWKVAVAQQLASALSY
H3ADK6_22_610            KDLEN--IIVEEYVQFGPLDLFMRRKSE--FLTTPWKFQVAKQLASALSY
G1KHZ7_606_1200          WGSEN--IMVEEYVEHGPLDVFLRKNKG--RIMVGWKFTVAAQLASALSY
Q6DDJ0_546_1139          RDVEN--IMVEEFVDFGPLDLFMHRKSD--VLTTPWKFKVAKQLASALSY
Jak2_human_529_1116      CGDEN--ILVQEFVKFGSLDTYLKKNKN--CINILWKLEVAKQLAWAMHF
H2V1W4_515_1120          CGEEN--IMVQEFVKFGSLDTYLKKNKN--SVNILWKLEVAKQLAQAMNF
I3KJT0_513_1117          CGEEN--IMVQEYVKFGSLDTYLKKNKN--SINLLWKLEVAKQLAWAMNF
G1PKC8_569_1171          HGSQN--IMVTEYVEHGPLDVWLRRERG--RVPVAWKVAVAQQLASALSY
G3STB4_577_1153          HGSES-------------ECPLPLLI-GQLP--LIPSPWPVVAIPEPLTCTPY
O12990_562_1150          RHQEN--IMVEEFVQYGPLDLFMRRQTT--PLSTAWKFQVAKQLASALSY
G3WN84_561_1153          RDVEN--IMVEEYMEFGPLDLFMHRKSE--LLTTPWKFKVAKQLASALSY
Q6W5B1_355_948           CADEH--IMVQEYVRFGSLDTYLKRNRN--TINITWKLEVAKQLAWALHH
G1KI54_559_1153          RDVEN--IMVEEYVEFGPLDLFMRRKSV--LLTTPWKFKVAKQLASALSY
H3DDQ1_395_969           CGEEN--IMVQEYVKFGSLDTYLKKNKN--SVNILWKLEVAKQLAQAMNF
G5B225_576_1168          RGSEN--VIVTEFVEHGPLDVWLRRERG--CVPLAWKLVVAQQLASALSY
H0VSL1_499_1098          AG-DS--TMVQEFVPLGAIDTYLRKRSH--LVPASWKLQVTKQLAYALNY
F8W4H3_558_1147          KGTEN--IMVEEFVEFGPLDVFLHRERA--HVSPQWKFTVAKQLASALCY
O57612_578_1166          HHQEN--IMVEEFVQLGPLDVFMRRQQS--PLSIPWKFQVAKQLASALSY
H3ABD2_524_1119          CGEEN--IMVQEYVKFGSLDTYLKKNKN--TVNIMWKLEVAKQLAWVMHF
H0V2Z6_556_1148          RGSEN--IMVTEFVEHGPLDVWLRRERG--RVPLAWKLVVAQQLASALSY
H2LQD3_521_1110          HGVKN--IIVQEFVKHGALDLYLKRAR---SVSVSWKLNVAKQLACALSF
Q6GPK5_575_1163          RESEN--IMVEEFIEHGPLDVCLRKDKL--RIKTEWKFTVARQLASALSY
G3PKI3_511_1116          CGEEN--IMVQEYVKFGTLDTYLKKNRN--LINILWKLEVAKQLAWAMNF
B0V237_509_1091          HKSKN--IMVQEFVKHGALDLYLKRSM---CVSVSWKLDVAKQLACALNF
G1N138_441_1047          CLPED--ILVQEYVKFGSLDTYLKKNKN--VINILWKLEVAKQLALAMHF
H2TE39_530_1116          KEHQH--IMVEEFVKFGPLDVFLHKEKA--SISGRWKFIVAIQLASALSY
H2VE41_574_1180          HHQEN--IMVEEFVQLGPLDVYMRRQQS--PLSIPWKFQVAKQLASALSY
H1A3H7_27_589            LGKDS--VMVQEYVRHGPLDLYVRKN--RGMVTTGWKLTVAKQLAYALNY
C7ATY9_562_1151          KGSEN--IMVEEFVEFGPLDVFLRKEKA--SVTPQWKFIVARQLASALNY
H2SBF4_355_996           CGDESEYMMVQEYGKFGSLDTYLKKNKS--RVNITWKLEVAKQLSWAMHY
H3B0L6_509_1107          INIGN--VMVQEFVKYGALDTYLKKKKNTGTVTASWKLEVAKQLAYALNF
G3PKV8_559_1147          KGSEN--IMVEEFVEFGPLDVFLRKEKG--SVNSQWKFIVAKQLASALNY
I3K428_523_1114          HGAKN--IMVQEYVKYGALDLYLKRGR---SVSVSWKLDVAKQLASALNF
I3IZB2_589_1184          KGSEN--IMVEEFVDFGPLDVFLRREK---NVSPGWKFIVAKQLASALDY
O42291_505_1097          LGKDS--IMVQEYIRHGPLDLYLKKNHSEGKVTTSWKLQVAKQLAYALNY
H0X425_574_1168          RGSEN--IMVTEYVEHGPIDVWLRRERG--RVPVAWKVVVAQQLASALSY
G1P7K0_396_981           AG-DS--IMVQEFVRLGALDTYLRKCGH--LVPASWKLQVIKQLAYALNY
G3TF05_473_1068          AG-DS--IMVQEFVLLGALDTYLRKRGH--LVPASWKLQVVKQLAYALNY
F1NMJ9_554_1150          RDLEN--IMVEEFVEFGPLDLFMHRKSE--LLTTPWKFNVAKQLASALSY
P29597_576_1171          RGPEN--IMVTEYVEHGPLDVWLRRERG--HVPMAWKMVVAQQLASALSY
Q75R65_529_1123          CGEEN--ILVQEYVKFGSLDTYLKKNKN--VINILWKLEVAKQLALAMHF
D2GV17_503_1098          AG-DS--IMVQEFVHLGALDTYLLKSGH--LVPASWKLQVIKQLAYALNY
Q9PTN6_498_1097          HKSKN--IMVQEFVKHGALDLYLKKST---SVSVSWKLDVAKQLACALNF
Tyk2_human_576_1166      RGPEN--IMVTEYVEHGPLDVWLRRERG--HVPMAWKMVVAQQLASALSY
F7EV03_508_1101          -GKQI--IMIQEFVCHGALDLYLKRQQQKGPIAISWKLEVVRQLAYALCY
Jak3_human_503_1091      AG-DS--TMVQEFVHLGAIDMYLRKRGH--LVPASWKLQVVKQLAYALNY
G5BSN6_723_1350          RDVEN--IMVEEFVEGGPLDLFMHRKSD--VLTTPWKFKVAKQLASALSY
G1LYZ3_576_1170          HGSEN--IMVTEYVEHGPLDVWLRREKG--HTPVAWKVAVAQQLASALSY
H2M2I1_581_1165          HHQEN--IMVEEFVQLGPLDVFMKRQQS---LSTPWKFQVAKQLASALSY
F1MCX4_575_1169          HGSEN--IMVTEYVEHGPLDVWLRRERG--RVPLAWKLAVAQQLASALSY
H2SBF2_535_1131          CGDEN--MMVQEYGKFGSLDTYLKKNKS--RVNITWKLEVAKQLSWAMHY
G3NVW0_582_1174          RHQEN--IMVEEFVQPGPLDLFMKRQQS--PLDTLWKFQVAKQLASALSY
Q9PWD0_515_1100          -AVKN--IMVQEFVEYGALDLYLKRGR---SVSVSWKLDVAKQLASVLTF
I3MAE0_504_1097          AG-DS--IMVQEFVLLGAIDTYLRKHGH--LVPASWKLQVVKQLAYALNY
H2TE42_495_1102          KEHQH--IMVEEFVKFGPLDVFLHKEKA--SISGRWKFIVAIQLASALSY
C7ATY6_576_1168          RHQEN--IMVEEFVQLGPLDLFMRRQQS--PLSTPWKFQVAKQLASALSY
D3Z4S5_718_1310          AG-DS--IMVQEFVYLGAIDMYLRKRGH--LVSASWKLQVTKQLAYALNY
I3JQC0_567_1148          HHQEN--IMVEEFVQLGPLDVFMRRQQT--PLSTSWKFQVALQLASALSY
Q9R117_572_1164          RGSEN--IIVTEFVEHGPLDVWLRRQRG--QVPMTWKMVVAQQLASALSY
H0VRI8_531_1132          CGEEN--ILVQEFVKFGSLDTYLKKNKN--SINILWKLEVAKQLAWAMHF
Jak1_human_561_1154      RDVEN--IMVEEFVEGGPLDLFMHRKSD--VLTTPWKFKVAKQLASALSY
H2VE42_579_1162          HHQEN--IMVEEFVQLGPLDVYMRRQQS--PLSIPWKFQVAKQLASALSY
F6V3I2_589_1182          RGSEN--IMVAEYVEHGPLDVCLRREKG--HVPVAWKITVAQQLASALSY
Q9PWD1_530_1117          --LKH--IMVEEWVKFGPLDVFLHREKA--SVSAHWKLIVAMQLASALRY
F1S3L9_566_1169          HGSEN--IMVTEYVEHGPLDVWLRRERG--HVPLAWKLAVAQQLASALSY
G3VR92_504_1104          AG-DS--IMVQEFVRWGALDTHLRKCGP--LVPASWKLQVAKQLSYALNY
F6X8E5_508_1068          -SPPG--IMVQEFVRFGALDTHLKKHTP--NITASWKLQVAKQLAYALNY
H2L7P7_514_1119          CGEEN--IMVQEYVKFGSLDTYLKKNKS--SINIMWKLEVAKQLAWAMNF
I3M210_601_1192          RGSEN--IMVTEYVENGPLDVWLRREKG--HVPMTWKVAVAQQLASALSY
G1KCE0_530_1126          CGEEN--ILVQEYVKFGALDTYLKKNKN--SINILWKLEVAKQLAMAMHF
Q09178_563_1153          RHQEN--IMVEEFVQYGPLDLFMRRQSI--PLSTAWKFQVAKQLAGALSY
D3ZUV6_649_1241          AG-DS--IMVQEFVYLGAIDTYLRKRGH--LVPASWKLQVTKQLAYALNY
G9KW41_102_676           HGSEN--IMVAEYVEHGPLDVWLRREKG--HVPVAWKVVVAQQLASALSY
H2LLN7_568_1156          KGSEN--IMVEEFVEFGPLDVFLRKHKA--AVNAKWKFIVSIQLASALSY
H3C837_398_1006          CGEEN--IMVQEYVKFGSLDTYLKKNKN--SVNILWKLEVAKQLAQAMNF
F7EAS1_502_1096          AG-DS--IMVQEFVRWGALDTHLRKCGP--LVPASWKLQVAKQLSYALNY
H2M2B1_532_1128          CGDQN--MMVQEYGKFGSLDTYLKKKKS--CVNITWKLEVAKQLAWAMHY
H2TCV2_510_1100          HGVKN--IIVQEFMEYGALDLYLKRGR---SVSVSWKLDVAKQLASVLNF
G3P1H3_515_1105          HGVQN--IMVQEFVEYGALDLYLKRRR---SLSMSWKLDVAKQLASALLF
A0JM01_530_1122          CGDES--ILVQEYAKYGSLDTYLKRNKN--AINIMWKLEVSKQLAWAMHF
G3PZA6_518_1120          CGNEN--MMVQEYGKFGSLDTYLKKNKS--RVNITWKLEVAKQLSWAMHY
I3J7Z7_537_1129          CGDEN--MMVQEYGKFGSLDTYLKKNKS--CVNITWKLEVAKQLSWAMHY
G1MVV3_535_1025          RGSEN--IMVEEFVEHGPLDVLLRKEKG--RVPVGWKITVAKQLASALSY
F7B2N9_488_1076          AG-DS--IMVQEFVRLGALDTYLRKCGH--LVPASWKLQVIKQLAYALNY
Q4T1R9_364_1003          CGDESKYMMVQEYGKFGSLDTYLKKKKG--CVNITWKLEVAKQLSWAMHY
C7ATY8_513_1104          HGVKN--IMVQEFVEYGALDLYLMRGR---SVSVSWKLDVAKQLASVLNF
H0ZIA6_541_1134          RDLEN--IMVEEFVECGPLDLFMHKKSE--VLTTPWKFKVAKQLASALSY
C0RW38_515_1112          CGDEN--IMVQEYVKFGSLDTYLKKNKSSVSVNILWKLEVAKQLAWAMLY
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                                                  |711(670)                                  |735(695)
Q6Y4Q0_534_1126          --------LEDKNLVHGNLCAKNVLLIREEDRMSGSPPFVKLSDPGISVG
F1PBD0_595_1189          --------LEDKSLVHGNVCGRNILLARLGLE-EGTSPFIKLSDPGVGLG
H3ADK6_22_610            --------LEDKNLVHGNVCTKNILLARQGID-NEVGPFIKLSDQGIPVT
G1KHZ7_606_1200          --------LEGKNLVHGSVCAKNILLARKGLE-DGMLPFIKLSDPGVSFT
Q6DDJ0_546_1139          --------LEDKDLVHGNVCTKNILLAREGID-NDCGPFIKLSDPGIPIT
Jak2_human_529_1116      --------LEENTLIHGNVCAKNILLIREEDRKTGNPPFIKLSDPGISIT
H2V1W4_515_1120          --------LEEKHLVHGNVCAKNVLLIREDDWKAGNPPFIKLSDPGISIT
I3KJT0_513_1117          --------LEEKHLVHGNVCAKNVLLIREEDRRAGNPPFIKLSDPGISIT
G1PKC8_569_1171          --------LEDKRLAHGNVCGRNILLARLGLA-EGTSPFIKLSDPGMGLG
G3STB4_577_1153          PGYTPTLNLRPFPWLHLNSQIRPQLLT-------TPPQASLYP------
O12990_562_1150          --------LEDKKMVHGYVCSKNILVARDGLD-GEGGPFIKLSDPGIPIT
G3WN84_561_1153          --------LEDKDLVHGNVCAKNVLLAREGLD-GECSPFIKLSDPSIPIT
Q6W5B1_355_948           --------LEEKSLTHGNVCARNVLVTREEDRKTGTPPFIKLSDPGISIT
G1KI54_559_1153          --------LEDKDLVHGNVCTKNILLAREGID-NEYGPFIKLSDPGISVT
H3DDQ1_395_969           --------LEEKNLVHGNVCAKNVLLIREDDWRAGNPPFIKLSDPGISIT
G5B225_576_1168          --------LEDKNLVHGNVCGRNILLARLGLA-DGTSPFIKLSDPGVGLA
H0VSL1_499_1098          --------LEDKGLPHGNVSARKVLLAREG--ADGSPPFIKLSDPGVSPT
F8W4H3_558_1147          --------LETKRLVHGNVCGKNILVVRKGLE-EGTSPFVKLSDPGISLS
O57612_578_1166          --------LEDKKLVHGFVCAKNILLARDGMGTDEGGPFIKLSDPGIPIT
H3ABD2_524_1119          --------LEDKNLMHGNVCAKNILLIREGDRRSGNPPFIKLSDPGISIT
H0V2Z6_556_1148          --------LEDKNLVHGNVCGRNILLARLGLA-EGTSPFIKLSDPGVGLG
H2LQD3_521_1110          --------LEEHNIVHGNICAKNLLLAREGD--KGSSPFIKLSDPGISVA
Q6GPK5_575_1163          --------LEDKNLVHGNVCAKNILLARKGLE-ENSSPFIKLSDPGVTFT
G3PKI3_511_1116          --------LEEKQLVHGNVCGKNVLLIREEDRRAGNPPFIKLSDPGIGIT
B0V237_509_1091          --------LEEKNIAHGNICAKNLLLVREGD-----SPFIKLSDPGVSMS
G1N138_441_1047          --------LEDKGLVHGNVCAKNILLIREEDRKSGNLPFIKLSDPGISIT
H2TE39_530_1116          --------LENKQLIHGNVCARNILLARCGLD-TGTAPFIKLSDPGIPIS
H2VE41_574_1180          --------LEDKKLVHGFVCAKNILLARDGLGIDEGGPFIKLSDPGIPIT
H1A3H7_27_589            --------LEDKKIPHGNVSAKKVLLAREGDTARGSPPFIKLNDPGVSVT
C7ATY9_562_1151          --------LETKRLVHGNVCAKNILVARRGLE-HGTTPFVKLSDPGIALS
H2SBF4_355_996           --------LEDKNLIHGKVCAKNVILIREEDRTTGSLPFIKLSDPGISVG
H3B0L6_509_1107          --------LEDKNIIHGNVCAKNILLTREGDAMNGSPPFIKLSDPGISIT
G3PKV8_559_1147          --------LETKRLVHGNVCAKNILVARRGLE-SGTSPFVKLSDPGVSLS
I3K428_523_1114          --------LEEKNIVHGNICAKNLLLAREGDPSQGSSPFIKLSDPGISMA
I3IZB2_589_1184          --------LETNGLVHGNVCAKNILLVKNGLE-PNTTPFIKLSDPGIALS
O42291_505_1097          --------LEDKKITHGNVSAKKVLLTREGDAASSSPPFIKLNDPGVSIT
H0X425_574_1168          --------LEDKNLIHGNVCGRNILLARLGLV-EGTSPFIKLSDPGVGLS
G1P7K0_396_981           --------LVSAPLP----APSSILRGGVG-----------------GVEGG
G3TF05_473_1068          --------LEDKGLPHGNVSARKVLLAREG--AEGSPPFIKLSDPGVSPT

F1NMJ9_554_1150          --------LEDKDLVHGNVCTKNILLAREGID-TEYGPFIKLSDPGIPIT

P29597_576_1171          --------LENKNLVHGNVCGRNILLARLGLA-EGTSPFIKLSDPGVGLG
Q75R65_529_1123          --------LEDKGLVHGNVCAKNILLIREEDRKSGNLPFIKLSDPGISIT
D2GV17_503_1098          --------LEDKGLPHGNVSARKVLLAREG--ADGNLPFIKLSDPGVSPT
Q9PTN6_498_1097          --------LEEKNIAHGNICAKNLLLAREGDPSTDNSPFIKLSDPGINMA
Tyk2_human_576_1166      --------LENKNLVHGNVCGRNILLARLGLA-EGTSPFIKLSDPGVGLG
F7EV03_508_1101          --------LEDKQLVHGNISAKKILLSREGD--KGNPPFIKLSDRGVSIK
Jak3_human_503_1091      --------LEDKGLPHGNVSARKVLLAREG--ADGSPPFIKLSDPGVSPA
G5BSN6_723_1350          --------LEDKDLVHGNVCTKNLLLAREGVD-SEIGPFIKLSDPGIPVT
G1LYZ3_576_1170          --------LEDKNLVHGNVCGRNILLARLGLA-EGTSPFIKLSDPGVGLG
H2M2I1_581_1165          --------LEDKKLVHGYVCAKNILLARDGLDADEGGPFIKLSDPGIPIT
F1MCX4_575_1169          --------LEDKSLVHGNVCGRNILLARLGLA-EGTSPFIKLSDPGVGLS
H2SBF2_535_1131          --------LEDKNLIHGKVCAKNVILIREEDRTTGSLPFIKLSDPGISVG
G3NVW0_582_1174          --------LEDKKLVHGFVCAKNI-LARDGLDADMGGPFIKLSDPGIPIT
Q9PWD0_515_1100          --------LEQNNIVHGNICAKNLLLAREGDPSQSIPPFIKLSDPGISVL
I3MAE0_504_1097          --------LEDKGLPHGNVSARKVLLAREG--ADGSSPFIKLSDPGVSPT
H2TE42_495_1102          --------LENKQLIHGNVCARNILLARCGLD-TGTAPFIKLSDPGIPIS
C7ATY6_576_1168          --------LEDKKLVHGFVCAKNILLARDGLGTDEGGPFIKLSDPGIPIT
D3Z4S5_718_1310          --------LEDKGLPHGNVSARKVLLAREG--GDGNPPFIKLSDPGVSPT
I3JQC0_567_1148          --------LEDKKLVHGFVCAKNILLARDGLGNDEGGPFIKLSDPGIPIT
Q9R117_572_1164          --------LEDKNLVHGNVCGRNILLARLGLE-EGTNPFIKLSDPGVGQG
H0VRI8_531_1132          --------LEEKNRIHGNVCAKNILLIREEDRKTGNPPFIKLSDPGISIT
Jak1_human_561_1154      --------LEDKDLVHGNVCTKNLLLAREGID-SECGPFIKLSDPGIPIT
H2VE42_579_1162          --------LEDKKLVHGFVCAKNILLARDGLGIDEGGPFIKLSDPGIPIT
F6V3I2_589_1182          --------LEDKNLVHGNVCAKNILLARRGLG-DGTQPFIKLSDPGVSVT
Q9PWD1_530_1117          --------QESKQLVHGNVCLKNILVARHGLE-EGCTPCIKLSDPGIAMS
F1S3L9_566_1169          --------LEDKSLVHGNVCGRNILLARLGQA-EGTSPFIKLSDPGVGLN
G3VR92_504_1104          --------LEDKGIIHGNISSKKVLLAREG--AGGSPPFIKLSDPGVSPT
F6X8E5_508_1068          --------LEDRRIVHGNVSAKKVLLAREGDGASGSPPFIKLSDPGVSPA
H2L7P7_514_1119          --------LEDKQLVHGNVCAKNVLLIREEDRRAGNPPFIKLSDPGICIT
I3M210_601_1192          --------LEDKNLVHGNVCGRNILLARLGLA-EGTSPFIKLSDPGVGLG
G1KCE0_530_1126          --------LEDKNLVHGNVCAKNILLIREEDRKSGNLPFIKLSDPGIGIT
Q09178_563_1153          --------LEDKKLVHGNVCSKNILVARDGLD-GEGGPFIKLSDPGIPIT
D3ZUV6_649_1241          --------LEDKGLPHGNVSARKVLLAREG--VDGNPPFIKLSDPGVSPT
G9KW41_102_676           --------LEDKSLVHGNVCGRNILLARLGLT-EGTSPFIKLSDPGVGLG
H2LLN7_568_1156          --------LEAKQLVHGNVCAKNILVARRGLE-RDTTPFIKLSDPGISLN
H3C837_398_1006          --------LEEKNLVHGNVCAKNVLLIREDDWRAGNPPFIKLSDPGISIT
F7EAS1_502_1096          --------LEDKGIIHGNISSKKVLLARKG--AGGSPPFIKLSDPGVSPT
H2M2B1_532_1128          --------LEDKNLIHGNVCAKNVLLIREEDRKSGSVPFVKLSDPGISLT
H2TCV2_510_1100          --------LEQNNIIHGNICAKNLLLAREGDPSKSVPPFIKLSDPGISVM
G3P1H3_515_1105          --------LEEKNIVHGNICAKNLLLAREDDPSQGISPFIKLSDPGISVA
A0JM01_530_1122          --------LEDRNLVHGNVCSKNILLIREEDRKTGNPPFIKLSDPGISIT
G3PZA6_518_1120          --------LEDKNLVHGNVCAKNVLLIREEDRMTGSLPFIKLSDPGISIT
I3J7Z7_537_1129          --------LEDKNVIHGNVCAKNVLLIREEDRKTGSLPFIKLSDPGISIT
G1MVV3_535_1025          --------LEDKSLVHGNVCAKNVLLARTGLG-DGTQPFVKLSDPGVSFT
F7B2N9_488_1076          --------LEDKGLPHGNVSARKVLLAREG--ADGSPPFIKLSDPGVSPA
Q4T1R9_364_1003          --------LEDKNLVHGNLCAKNVLLIREEDRMSGSPPFVKLSDPGISVG
C7ATY8_513_1104          --------LEEKNIVHGNICAKNLLLAREGDLSQGSSPFIKLSDPGISVA
H0ZIA6_541_1134          --------L-DKDLVHGNVCTKNILLAREGID-TEYGPFIKLSDPGIPIT
C0RW38_515_1112          --------LEEKSLAHGNVCAKNILLIREEDRALGNTPFIKLSDPGISIT
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                                                  |761(721)                                  |785(745)
Q6Y4Q0_534_1126          VLPLD--VLADRIP-WVPPECIENP-QNLSLAADKWSFGTTLWE--ICSG
F1PBD0_595_1189          ALSRE--ERIERIP-WIAPECLTGGANSLTTAADKWGFGATLLE--ICFD
H3ADK6_22_610            VLSRE--ECVERIP-RIAPECIGEY-KNLSIAADKWSFGTALWE--ICYN
G1KHZ7_606_1200          VLSREGKERVDRIP-WIAPECVRDV-SNLSTAADKWSFGTTLLE--ICFD
Q6DDJ0_546_1139          VLTRQ--ERVERIP-WIAPECVEDS-RVLSVAADKWSFGTTLWE--ICFN
Jak2_human_529_1116      VLPKD--ILQERIP-WVPPECIENP-KNLNLATDKWSFGTTLWE--ICSG
H2V1W4_515_1120          VLPKE--ILVERIP-WVPPECLTDP-ANLSLAADKWSFGTTLWE--ICSG
I3KJT0_513_1117          VLPKE--ILIERIP-WVPPECIEDP-AKLSLAADKWSFGTTLWE--ICSG
G1PKC8_569_1171          ALSRE--ERVERIP-WMAPECLFGGANSLSTAADKWGFGATLLE--ICFD
G3STB4_577_1153          ---------DPTP-WLHHECLHLPPKTLYNPAPIFPLTSLALT--LCDT
O12990_562_1150          VLSRE--ECVDRIP-WIAPECVKDT-ANLTIAADKWSFGTTLWE--ICYN
G3WN84_561_1153          VLSRQ--ECVERIP-WIAPECVDDS-KNLSVAADKWSFGTTLWE--ICYN
Q6W5B1_355_948           VQPRE--ILLERIP-WVPPECVKDS-RNLSLAADKWSFGTTLWE--IYCG
G1KI54_559_1153          VLSKQ--ECVERIP-WLAPECVKDS-KNLSVAADKWSFGTTLWE--ICYN
H3DDQ1_395_969           VLPKE--ILVERIP-WVPPECVNDP-ANLSLAADKWSFGTTLWE--ICSG
G5B225_576_1168          ALSRE--ERVERIP-WTAPESLLAGASSLSTTTDKWGFGATLLE--ICFN
H0VSL1_499_1098          VLSLE--MLTDRIP-WVAPECLDEA-RTLGLEADKWGFGATVWE--VFSG
F8W4H3_558_1147          ALSQG--ERVERIP-WIAPECVADG-TRIGSAADKWSFGATLLE--ICNN
O57612_578_1166          VLTRE--ECVHRIP-WIAPECVKNV-SALSVAADKWGFGTTLWE--ICYD
H3ABD2_524_1119          VLPKD--ILIERIP-WVPPECIEDA-KNLNQAVDKWSFGTTLWE--ICSG
H0V2Z6_556_1148          ALSRE--ERVERIP-WTAPESLPTGAGSLSTAVDKWGFGATLLE--ICFD
H2LQD3_521_1110          MLDKD--VILDRIP-WVAPEVLEAP-ENLILESDKWSFGATVWE--IFNN
Q6GPK5_575_1163          VLSRE--ERVERIP-WIAPECVR-NISSLSTAADKWSFGTTLLE--ICFN
G3PKI3_511_1116          VLPKE--ILIERVP-WISPECVEDP-ANLSLAADKWSFGATLWE--ICSG
B0V237_509_1091          LLGKD--VVLDRIP-WVAPEVLDTL-E-IELECDKWSFGTTLWE--IFNG
G1N138_441_1047          VLPRD--ILLERIP-WVPPECIENP-KQLSLATDKWSFGTTLWE--ICSG
H2TE39_530_1116          ALERE--ERLERIP-WIAPECIDGG-ESNQSATDQWSFGATFLE--ICYN
H2VE41_574_1180          VLTRE--ECVHRIP-WIAPECVKNM-SSLSVAADKWGFGTTLWE--ICYD

H1A3H7_27_589            VLARD--TLGSRIP-WVAPECVSNP-GSLALPADKWGFGATLWE--IFSG

C7ATY9_562_1151          VLSRE--ERLERIP-WIAPECVDSG-ASIGSAADQWGFGATLLE--ICNN
H2SBF4_355_996           VLPRE--ILVDHIP-WVPPECIDNP-QNLSLAADKWSFGTTLWE--ICSS
H3B0L6_509_1107          VLAKE--MCIDRIP-WVAPECINDS-NNLSLESDKWSYGTTLWE--IFSG
G3PKV8_559_1147          VLSRE--ERLERIP-WIAPECVDTG-SHAANAADQWSFGVTLLE--ICYD
I3K428_523_1114          MVGKD--VILDRIP-WVAPEVLDAP-EKLTLECDKWSFGATVWE--IFNN
I3IZB2_589_1184          VLSRE--ERLERIP-WIAPECIDSG-SNIGSHADQWSFGVTVLE--IYNN
O42291_505_1097          VLAKE--WLVERIP-WVAPECLSDP-QSLALPADKWGFGATLWE--IFSG
H0X425_574_1168          ALSRE--ERVERIP-WMAPECLPGRTSSLSTATDKWGFGATLLE--ICFD
G1P7K0_396_981           LCCMD--RSLARVPGWRAKHMYGLR-DDLCLYPEANGEPATGWETSIREG
G3TF05_473_1068          VLSLE--MLTDRIP-WVAPECLQEA-RMLGLEADKWGFGATVWE--VFSG
F1NMJ9_554_1150          VLSRQ--ECVERIP-WIAPECVEDS-KNLSIAADKWSFGTTLWE--ICYN
P29597_576_1171          ALSRE--ERVERIP-WLAPECLPGGANSLSTAMDKWGFGATLLE--ICFD
Q75R65_529_1123          VLPRD--ILLERIP-WVPPECIENP-RQLSLATDKWSFGTTLWE--ICSG
D2GV17_503_1098          VLNRE--MLTDRIP-WVAPECLQEA-RTLGLEADKWGFGATVWE--VFSG
Q9PTN6_498_1097          LLGKD--VVLDRIP-WVAPEVLDTL-E-IELECDKWSFGTTLWE--IFNN
Tyk2_human_576_1166      ALSRE--ERVERIP-WLAPECLPGGANSLSTAMDKWGFGATLLE--ICFD
F7EV03_508_1101          VLDEE--LLAERIP-WLSPECVSDP-NNLALESDRWSFGVTLWE--IFND
Jak3_human_503_1091      VLSLE--MLTDRIP-WVAPECLREA-QTLSLEADKWGFGATVWE--VFSG
G5BSN6_723_1350          VLSRQ--ECIERIP-WIAPECVEDS-KNLSVAADKWSFGTTLWE--ICYN
G1LYZ3_576_1170          ALSRE--ERVERIP-WIAPECLSGGANSLTTAADKWGFGATLLE--ICFD
H2M2I1_581_1165          VLTRE--ECVHRIP-WIAPECVKSV-SSLSVAADKWGFGTTLWE--ICYD
F1MCX4_575_1169          ALSRE--ERVERIP-WTAPECLSGGANSLSTAADKWGFGATLLE--ICFD
H2SBF2_535_1131          VLPRE--ILVDHIP-WVPPECIDNP-QNLSLAADKWSFGTTLWE--ICSS
G3NVW0_582_1174          VLTRE--ECVRRIP-WIAPECVKSA-SSLSVAADKWGFGTTLWE--ICYD
Q9PWD0_515_1100          MLGKD--VIVDRIP-WVAPEVLASP-ENLTLESDKWSFGATLWE--LFNN
I3MAE0_504_1097          VLSLE--MLTDRIP-WVAPECLQET-QTLGLEADKWGFGATVWE--VFSG
H2TE42_495_1102          ALERE--ERLERIP-WIAPECIDGG-ESNQSATDQWSFGATFLE--ICYN
C7ATY6_576_1168          VLTRE--ECVHRIP-WIAPECVKSV-SSLSVAADKWGFGTTLWE--ICYD
D3Z4S5_718_1310          VLSLE--MLTDRIP-WVAPECLQEA-QTLGLEADKWGFGATTWE--VFSG
I3JQC0_567_1148          VLTRE--ECVHRIP-WIAPECVRNA-SSLGVAADKWGFGTTLWE--ICYD
Q9R117_572_1164          ALSRE--ERVERIP-WTAPECLSGGTSSLGTATDMWGFGATLLE--ICFD
H0VRI8_531_1132          VLPKD--ILQERIP-WVPPECIENP-KNLNLATDKWSFGTTLWE--ICSG
Jak1_human_561_1154      VLSRQ--ECIERIP-WIAPECVEDS-KNLSVAADKWSFGTTLWE--ICYN
H2VE42_579_1162          VLTRE--ECVHRIP-WIAPECVKNM-SSLSVAADKWGFGTTLWE--ICYD
F6V3I2_589_1182          ALSRE--ERVERIP-WIAPECVPSG-TGLSTAADKWSFGTTLLE--ICFD
Q9PWD1_530_1117          VLTRE--ERLERIP-WIAPECIDGG-VSIRSNPDQWSFGATFLE--ICYN
F1S3L9_566_1169          ALSRE--ERVERIP-WTAPECLSGGANSLSTAADKWGFGATLLE--ICFD
G3VR92_504_1104          VLTKE--MLTDRIP-WVAPECLWDA-KLLSLESDKWSFGATLWE--IFSG
F6X8E5_508_1068          VLAKE--LLTDRIP-WVAPECLWDP-KSLSLEADKWSFGATVWE--IFSG
H2L7P7_514_1119          VLPKE--IVIERIP-WVPPEYIKEP-GKLCLAADKWSFGTTLWE--ICSG
I3M210_601_1192          ALSRE--ERVERIP-WTAPECLPAGATSLCTAADKWGFGATLLE--ICFD
G1KCE0_530_1126          VLPKD--ILLERIP-WVPPECIENP-KRLSLATDKWSFGTTLWE--ICSG
Q09178_563_1153          VLSRE--ECVDRLP-WIAPECVQDT-ANLSIAADKWGFGTTLWE--ICYN
D3ZUV6_649_1241          VLSLE--MLTDRIP-WVAPECLQEA-GTLNLEADKWGFGATTWE--VFSG
G9KW41_102_676           ALSRE--ERVERIP-WTAPECLSGGANSLTTAADKWGFGATLLE--ICFD
H2LLN7_568_1156          ALTRE--ERLDRIP-WIAPECVDGS-APIGNTADQWSFGITLLE--ICNN
H3C837_398_1006          VLPKT--VLVERIP-WVPPECVNDP-ANLSLAADKWSFGTTLWE--ICSG
F7EAS1_502_1096          VLTKE--MLTDRIP-WVAPEYLWDT-KLLSLESDKWSFGATLWE--IFSG
H2M2B1_532_1128          VLPRE--VLVERIP-WVPPECIETP-QKASLATDKWSFGTTLWE--ICSG
H2TCV2_510_1100          MLGKD--VVVDRIP-WVAPEVLLSP-DNMTLECDKWSFGATLWE--LFNN
G3P1H3_515_1105          MLGKE--VTLDRIP-WVAPELLDSP-ENLTLGCDKWSFGATVWE--IFNN
A0JM01_530_1122          VLPKE--ILLERIP-WVPPECIDNS-KHLTQASDKWSFGTTLWE--IYSG
G3PZA6_518_1120          VLPRE--VLVERIP-WVPPECIGKP-QNLSLATDKWGFGTTLWE--ICSG
I3J7Z7_537_1129          VLPRE--VLVERIP-WVPPECIENP-QNLSLATDKWSFGTTLWE--ICSG
G1MVV3_535_1025          ALTRE--ERVDRIP-WIAPECIQDV-GNLHPAADKWSFGTTLLE--ICFD
F7B2N9_488_1076          VLSLE--MLTDRIP-WVAPECLQEA-HTLGLEADKWGFGATVWE--VFSG
Q4T1R9_364_1003          VLPLD--VLADRIP-WVPPECIENP-QNLSLAADKWSFGTTLWE--ICSG
C7ATY8_513_1104          MLGKD--VILDRIP-WVAPEVLEDP-DNLTLECDKWSFGATVWE--IFNN
H0ZIA6_541_1134          VLSRQ--ERVERIP-WIAPECVEDS-KNLSIAADKWSFGTTLWE--ICYN
C0RW38_515_1112          VLPRE--ILVERIP-WVPPECILDP-KNLSLATDKWSFGTTLWE--ICSG
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                                                  |805(765)                                                  |830(790)
Q6Y4Q0_534_1126        GKKPLSTLDSSK-KRLF---YEDRHQLPAPKWTELANLIH-SCMDYEPLH
F1PBD0_595_1189        GEAPLQGRGPSE-KECF---YQKQHLLPQPSCPELATLIS-QCLTYEPAQ
H3ADK6_22_610          GEIPLKDKTLAE-KEMF---YVGHFILAPPSCEELADLIK-RCMNYDPHQ
G1KHZ7_606_1200        ADVPLKERTPSE-KERF---YEKKHRLPEPSFKELATLIS-QCLNYAPAE
Q6DDJ0_546_1139        GEVPLKDRTLAE-KERF---YGGCFMLVAPSCKELADLIN-HCMNYDPNR
Jak2_human_529_1116    GDKPLSALDSQR-KLQF---YEDRHQLPAPKWAELANLIN-NCMDYEPDF
H2V1W4_515_1120        GEKPLASLDNTK-KILF---YEDRYQLPAPKWIELANLIT-SCMDYEPTF
I3KJT0_513_1117        GDKPLATLDNSK-KTLF---YMDHHQLPAPKWTELANLIS-SCMDYEPTF
G1PKC8_569_1171        GEAPLQDRSPAE-KEYF---YQKQHQLPEPSCPELATLTS-QCLTYEPAQ
G3STB4_577_1153        ALTSALQFNPAQ-SPLYLYPYCVSLKIPVLSTPSPASITSYECLTYEPAQ
O12990_562_1150        GEIPLKDKKLSE-KERF---YAAQCQLATPDCDELAKLMT-HCMTYDPRQ
G3WN84_561_1153        GEIPLKDKTLAE-KERF---YEGRVMPVTPSCKELADLMT-QCMNYDPSQ
Q6W5B1_355_948         GEQPLAAYDTAK-KLLF---YEDKHQLPAPKWTELASVIN-SCMDYEPLH
G1KI54_559_1153        GEIPLKDKTLAE-KERF---YDGHFTLRTPSCKELADLMK-QCMHYDPNQ
H3DDQ1_395_969         GEKPLASLDNTN-KTLF---YEDRHQLPAPKWIELANLIT-SCMDYEPTF
G5B225_576_1168        GEVPLQGHTPSE-KERF---YQKQHQLPKPLCPELASITS-QCLSYEQAQ
H0VSL1_499_1098        APVPTRSLDPAK-KLRF---YEERRQLPAPRWTELAALIR-QCMDYEPGR
F8W4H3_558_1147        GDLHVSNSTLSE-KQRF---YETQSRLAVPSSQELASFIS-RCLTYDAAA
O57612_578_1166        GEVPLKEKKLTEQKERF---YETECQLATPDCTELAELMT-HCMNYDPKK
H3ABD2_524_1119        GDKPLGTLDSST-KLQF---YKDRHQLPAPKWTELANLIN-NCMDYEPEF
H0V2Z6_556_1148        GEVPLQGRAPSE-KERF---YQKQHQLPEPACPELAAVTS-QCLSYERAQ
H2LQD3_521_1110        GNSLLQGWNLEK-KQKF---YEKRHHLPPSQWTELADLID-QCMDYEAAF
Q6GPK5_575_1163        GEVPLKERTPPE-KERF---YEKELGLPEPSCKELADLIG-QCHNYNAEG
G3PKI3_511_1116        GERPLASLDNSK-KTLF---YEDHHQLPAPKWTELANLIT-SCMDYEPSF
B0V237_509_1091        GEAPLQGLDLMQ-KLQF---YENFSNLPTLEWTELAELIS-HCMQYQPEL
G1N138_441_1047        GDKPLSALDSSR-KLQF---YEDRHQLPAPNWTELANLIN-NCMDYEPDF
H2TE39_530_1116        GTLPISTS--SE-KERF---YQQKGRLPVLSSQEVSNFIN-TCLAYDPMD
H2VE41_574_1180        GEVPLKEKKLTE-KERF---YETKCQLATPDCKELAELMT-HCMNYDPKK
H1A3H7_27_589          GNMPLSLLEPQR-KLEF---YQGCQQLPAPKWPELAVLVA-QCMEYEPQR
C7ATY9_562_1151        GDLPLSGSTLSE-KERF---YQQKGRLAEPSSQELASFIS-MCLTYEPVE
H2SBF4_355_996         GDKPLSTLDSSK-KRLF---YEDRHQLPAPKWTELANLIN-SCMDYEPSH
H3B0L6_509_1107        GVLPLSALEPSR-KLEF---YKNSLQLPAPKWTELANLIN-QCMDYQVYL
G3PKV8_559_1147        GDLPMSGGTLSE-KERF---YQQKGRLAEPLSPELAKFFS-MCLTYEPLE
I3K428_523_1114        GNSLLRGWNLDQ-KKQF---YESFQQLPPSQWTELADLIS-QCMDYQADF
I3IZB2_589_1184        GDLPFNFNTLSE-KERF---YQQKGHLAEPSSPELARFIN-MCLTYEPEE
O42291_505_1097        GNMPVSLLEPQK-KLQF---YDSRLQLPAPRWSELAALIA-QCI-YAPSR
H0X425_574_1168        GEAPLQGRGPSE-KERF---YQKQHRLPEPSCPELATLTS-QCLTYDPAQ
G1P7K0_396_981         GGMPISTLEPAK-KLQF---YEDRQQLPAPKWMELALLIQ-QCMAYEPGH
G3TF05_473_1068        VPMPISALDPAK-KLQF---YEDQQQLPAPKWMELALLIQ-QCMAYEPKH
F1NMJ9_554_1150        GETPLKDKTLAE-KERF---YEGHFMLITPSCKELADLMK-QCMNYDPHQ
P29597_576_1171        GEAPLQSRSPSE-KEHF---YQRQHRLPEPSCPQLATLTS-QCLTYEPTQ
Q75R65_529_1123        GDKPLSALDSSR-KLQF---YEDRHQLPAPNWTELANLIN-NCMDYEPDF
D2GV17_503_1098        IPMPISTLDPAK-KLQF---YEEQQQLPAPKWMELATLIQ-QCMAYESGQ
Q9PTN6_498_1097        GEAPLQGQDLIH-KQQF---YEHFSNLPALEWTELADLIA-QCMQYQPEL
Tyk2_human_576_1166    GEAPLQSRSPSE-KEHF---YQRQHRLPEPSCPQLATLTS-QCLTYEPTQ
F7EV03_508_1101        GHVPLSAEDPST-KLQF---YNDHKTLPSPHWIELASLEQ-QCMSYNPLL
Jak3_human_503_1091    VTMPISALDPAK-KLQF---YEDRQQLPAPKWTELALLIQ-QCMAYEPVQ
G5BSN6_723_1350        GEIPLKDKTLIE-KERF---YESRCRPVTPSCKELADLMT-RCLNYDPNQ
G1LYZ3_576_1170        GEAPLQGRGPSE-KECF---YQKQHRLPQPSCPELATLTS-QCLTYEPAQ
H2M2I1_581_1165        GEVPLKQKKLTEQKERF---YETECQLVTPDCTELAKLMT-DCMNYDPKK
F1MCX4_575_1169        GEAPLQGRSPSE-KERF---YQKQHKLPEPSCPELATLTS-QCLTYEPAQ
H2SBF2_535_1131        GDKPLSTLDSSK-KRLF---YEDRHQLPAPKWTELANLIN-SCMDYEPSH
G3NVW0_582_1174        GEVPLKDKKLTEQKEMF---YVSECQLATPECKELAELMT-HCMTYDPKK
Q9PWD0_515_1100        GNNPLLGWDLDM--KF---YESFQQLPPSQWTELADLIN-QCMDYQADF
I3MAE0_504_1097        IPMPLINLDPPK-KLKF---YEDRQQLPAPKWTELALLIQ-QCMAYEPGQ
H2TE42_495_1102        GTLPISTSFLVQ-KERF---YQQKGRLPVLSSQEVSNFIN-TCLAYDPMD
C7ATY6_576_1168        GEVPLKDKKLTE-KERF---YETECQLATPDCRELAELMT-HCMNYDPKK
D3Z4S5_718_1310        GPAHITSLEPAK-KLKF---YEDQGQLPALKWTELAGLIT-QCMAYDPGR
I3JQC0_567_1148        GEVPLKDKKLTE-KERF---YETECQLATPDCTELAELMT-HCMNYDPKK
Q9R117_572_1164        GEAPLQGRGPSE-KERF---YTKKHQLPEPSCPELATLTR-QCLTYEPAQ
H0VRI8_531_1132        GDKPLSALDSQR-KLQF---YEDRHQLPAPKWTELANLIN-NCMDYEPDF
Jak1_human_561_1154    GEIPLKDKTLIE-KERF---YESRCRPVTPSCKELADLMT-RCMNYDPNQ
H2VE42_579_1162        GEVPLKEKKLTE-KERF---YETKCQLATPDCKELAELMT-HCMNYDPKK
F6V3I2_589_1182        GEAPLQGRTPSE-KERF---YEKKHRLQEPSCKELATLIS-QCLTYEANQ
Q9PWD1_530_1117        GNLPMSTITLSE-KERF---YQQKGRLPVLSSKTVSNFIN-TCLAYDPTE
F1S3L9_566_1169        GEAPLQGRGPSE-KERF---YQKQHKLPEPSCPELATLTS-QCLTYEPAQ
G3VR92_504_1104        GTMPLSTLEPAK-KLQF---YKEKQQLPALKWTELATLIG-QCMEYTPHL
F6X8E5_508_1068        GTMPLSTLEPAE-KLQF---YKKQHQLPAPKWTELANLIG-QCMDYSPPR
H2L7P7_514_1119        AEKPLGTLDNFK-KIQF---YENHHHLPAPKWTELANIIS-SCMDYEPAF
I3M210_601_1192        GEAPLQGRGPSE-KERF---YQKQHRLPEPSCPELATITS-QCLTYERAL
G1KCE0_530_1126        GDKPLGALDLQR-KLQF---YEDRHQLPAPNWTELANLIN-NCMDYEPDF
Q09178_563_1153        GEIPLKDKKLTE-KERF---YAAQCQLASPDCEELAKLMT-HCMTYDPRQ
D3ZUV6_649_1241        APMHITSLEPAK-KLKF---YEDRGQLPALKWTELEGLIA-QCMAYDPGR
G9KW41_102_676         GEAPLQGRGPSE-KECF---YQKQHQLPQPSCPELATLTS-QCLTYEPTQ
H2LLN7_568_1156        GEVPISGCTLPE-KELF---YRERHHLTEPSSEELAKFIS-MCLTYEPEE
H3C837_398_1006        GEKPLASLDNTN-KTLF---YEDRHQLPAPKWIELANLIT-SCMDYEPTF
F7EAS1_502_1096        GTMPISTLEPAK-KLQF---YKEKQQLPALKWTELATLIG-QCMEYTPHL
H2M2B1_532_1128        GDKPLSTLDCSK-KFLF---YEDRHQLPAPKWTELANLIN-SCMDYEPSH
H2TCV2_510_1100        GNNPLLGWDLDM-KQKF---YESFQQLPPSQWTELADLIN-QCMDYQADF
G3P1H3_515_1105        GNTPLLGWELEK-KEQF---YKSFQQLPPSQWTELADLVS-QCMDYQAVF
A0JM01_530_1122        GDKPLTALDSQR-KLQF---YEDRHQLPAPKWIELANLIN-SCMDYEPDF
G3PZA6_518_1120        GDKPLSTLDCSK-KNLF---YEDRHQLPAPKWTELANLIN-SCMDYEPSH
I3J7Z7_537_1129        GDKPLSTLDCSK-KNLF---YEDRHQLPAPKWTELANLIN-SCMDYEPLH
G1MVV3_535_1025        ADVPLKERTPAE-KERF---YEKKHRLPEPSCQDLAALIQ-QCLSYAPAE
F7B2N9_488_1076        VTMPISMLDPAK-KLQF---YQERQQLPAPKWTELALLIQ-QCMAYERGL
Q4T1R9_364_1003        GKKPLSTLDSSK-KRLF---YEDRHQLPAPKWTELANLIH-SCMDYEPLH
C7ATY8_513_1104        GNTPLRGWDLDQ-KRLF---YDNFQQLPPSEWTELADLIS-QCMDYQAAF
H0ZIA6_541_1134        GETPLKDKTLAE-KERF---YEGHFVLATPSCKELADLMK-QCMNYDPHQ
C0RW38_515_1112        GEQPLANMDNSK-KHLF---YENHHQLPAPKWTELANLIN-SCMDYEPTF
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Q6Y4Q0_534_1126          RPSFKAVIRDLNSLF----TP--------------------DYELLVDSDI
F1PBD0_595_1189          RPSFRTILRDLTQLQ----PQ--------------------NLADVLAVN-
H3ADK6_22_610            RPFFRAIMRDITRLE----EQ--------------------NPDIVLEST-
G1KHZ7_606_1200          RPSFRTILRDLTQLQ----PH--------------------NPLDISSVN-
Q6DDJ0_546_1139          RPFFRAIMREINKLE----EQ--------------------NPDIVSEKS-
Jak2_human_529_1116      RPSFRAIIRDLNSLF----TP--------------------DYELLTENDM
H2V1W4_515_1120          RPTFRAVIRDLHSLF----TP--------------------DYELIVDSDI
I3KJT0_513_1117          RPTFRAVIRDLHSLF----TP--------------------DYELIVDSDI

G1PKC8_569_1171          RPSFRTILRDLTHLQ----PQ--------------------NLVEILCVN-
G3STB4_577_1153          RPSFRIILRDLTRLQ----PH--------------------NLVDVSAVS-
O12990_562_1150          RLFFRAIVRDIVMVE----KQ--------------------NPSI--QPV-
G3WN84_561_1153          RPFFRAIMRDINRLE----EQ--------------------NPDILSEKQ-
Q6W5B1_355_948           RPSFRALIRDLNSLY----TP--------------------DYELLVESDT
G1KI54_559_1153          RPFFRAIMRDINKLE----EQ--------------------NPEIVSEKK-
H3DDQ1_395_969           RPTFRAIIRDLHSLF----TP------------------------------
G5B225_576_1168          RPSFRTILRDLTRLQ----PH--------------------SLVDVSALN-
H0VSL1_499_1098          RPSFRAVIRDLNSLS----TS--------------------DYELLSDPAP
F8W4H3_558_1147          RPSFRTILRELTEIQ----IK--------------------NP-DISSEC-
O57612_578_1166          RPFFRAIVRDIDMLG----EQ--------------------NPSI--KPK-
H3ABD2_524_1119          RPSFRAIIRDLNSLF----TP--------------------DYELLAESDM
H0V2Z6_556_1148          RPSFRTILRDLTRLQ----PH--------------------SLADISTVN-
H2LQD3_521_1110          RPSCRSIIRQLNSLI----TS--------------------DYEILHSTEP
Q6GPK5_575_1163          RPSFRTILRELTQLQ----PD--------------------VLPDIAAIS-
G3PKI3_511_1116          RPTFRAVIRDLHSLF----TP--------------------DYELIVDSDI
B0V237_509_1091          RPSCRSIIRQLNSLI----TS--------------------DYEILHATDT
G1N138_441_1047          RPSFRAIIRDLNSLF----TP--------------------DYELLTENDM
H2TE39_530_1116          RPSFCIVLRELSEFM----NK--------------------NL-DISP-S-
H2VE41_574_1180          RPFFRAIVRDIDMLG----EKTHSCGCSKDVCISTCLHSSDPSI--KPK-
H1A3H7_27_589            RPCFRALIRDLNSLI----TS--------------------DYELLSDLSP
C7ATY9_562_1151          RPSFLTVLRVLTEIM----IK--------------------NP-DISP-S-
H2SBF4_355_996           RPSFRAIIRDLNSLF----TP--------------------DYELLVESDM
H3B0L6_509_1107          RPSFRAIIRDLNSLI----TS--------------------DYELLCDMSP
G3PKV8_559_1147          RPSFRTVLRELTGLI----II--------------------NP-NISP-S-
I3K428_523_1114          RPSCRSIIRQLNSLI----TS--------------------DYVILHATEP
I3IZB2_589_1184          RPSFRKVLRELIELMRKGFVI--------------------QS-VMPS-S-
O42291_505_1097          RPCFRAIIRDINSLI----SS--------------------DYELLSELSP
H0X425_574_1168          RPSFRTILRDLTRLQ----PQ--------------------NLTDILTVN-
G1P7K0_396_981           RPSFRAVIRDLNNLI----TS--------------------DYELLSDPTP
G3TF05_473_1068          RPSFRAVIRDLNSLI----TS--------------------DYELLSDPTP
F1NMJ9_554_1150          RPFFRAIMRDINKLE----EQ--------------------NPDIVSEKK-
P29597_576_1171          RPSFRTILRDLTRLQ----PH--------------------NLADVLTVN-
Q75R65_529_1123          RPSFRAIIRDLNSLF----TP--------------------DYELLTENDM
D2GV17_503_1098          RPSFRAIIRDLNSLI----TS--------------------DYELLSDPTP
Q9PTN6_498_1097          RPSCRSIIRQLNSLI----TS--------------------DYEILHATGT
Tyk2_human_576_1166      RPSFRTILRDLTRLQ----PH--------------------NLADVLTVN-
F7EV03_508_1101          RPSFRSIMRELNNII----AF--------------------DYELLVDSKG
Jak3_human_503_1091      RPSFRAVIRDLNSLI----SS--------------------DYELLSDPTP
G5BSN6_723_1350          RPFFRAIMRDINKLE----EQ--------------------NPDIVSEKT-
G1LYZ3_576_1170          RPSFRTILRDLTQLQ----PQ--------------------NLADVLAVN-
H2M2I1_581_1165          RPFFRAIVRELDDLL----PI--------------------SDLL--ITK-
F1MCX4_575_1169          RPSFRTILRDFTQLQ----PQ--------------------NLADVLSVS-
H2SBF2_535_1131          RPSFRAIIRDLNSLF----TP--------------------DYELLVESDM
G3NVW0_582_1174          RPFFRAIVRDIDMLE----EK--------------------NPSI--KPQ-
Q9PWD0_515_1100          RPSCRSIIRQLFSLI----TS--------------------DYVILFATEP
I3MAE0_504_1097          RPSFRAVIRDLNSLI----TS--------------------DYELLSDPTP
H2TE42_495_1102          RPSFCIVLRELSEFM----NK--SIYFFLPFIFVFLYQRHNL-DISP-S-
C7ATY6_576_1168          RPFFRAIVRDIDMLE----EK--------------------NPLI--KPK-
D3Z4S5_718_1310          RPSFRAILRDLNGLI----TS--------------------DYELLSDPTP
I3JQC0_567_1148          RPFFRAIVREMDQLI----EK--------------------NPSI--KPQ-
Q9R117_572_1164          RPSFRTILRDLTRLQ----PQ--------------------NLVGTSAVN-
H0VRI8_531_1132          RPSFRAIIRDLNSLF----TP--------------------DYELLTENDM
Jak1_human_561_1154      RPFFRAIMRDINKLE----EQ--------------------NPDIVSEKK-
H2VE42_579_1162          RPFFRAIVRDIDMLG----EK----------------IMASDPSI--KPK-
F6V3I2_589_1182          RPSFRTILRDLTQLQ----PQ--------------------NLSDITTMS-
Q9PWD1_530_1117          RPSFRIELRELSEFM----KT--------------------TP-DLSP-S-
F1S3L9_566_1169          RPSFRTILRDLTQLQ----PQ--------------------NLADVLSVN-
G3VR92_504_1104          RPSFRAIIRDLNSLI----TS--------------------DYELLSDLSP
F6X8E5_508_1068          RPSFRAVIRDLNSLI----TS--------------------DYELLSDLSP
H2L7P7_514_1119          RPTFRAVIRDLHSLI----TP--------------------DYELIMDSDI
I3M210_601_1192          RPSFRTILRDLTQLQ----PH--------------------DLVDVSTIN-
G1KCE0_530_1126          RPSFRAIIRDLNSLF----TP--------------------DYELLTENDM
Q09178_563_1153          RLFFRAIVRDIDMVE----KQ--------------------NPSI--QPV-
D3ZUV6_649_1241          RPSFRAILRDLNGLI----TS--------------------DYELLSDPTP
G9KW41_102_676           RPSFRTILRDLTQLQ----PQ--------------------NLADVLAVN-
H2LLN7_568_1156          RPSFRAVLRELTEMM----MK--------------------NL-DIPD-T-
H3C837_398_1006          RPTFRAIIRDLHSLF----TP------------------------------
F7EAS1_502_1096          RPSFRAIIRDLNSLI----TS--------------------DYELLSDLSP
H2M2B1_532_1128          RPSFRAIIRDLNSLF----TP--------------------DYELLVESDM
H2TCV2_510_1100          RPSCRSIIRQLNSLI----TS--------------------DYVILFATEP
G3P1H3_515_1105          RPSCRCIIRQLNSLI----TS--------------------DYVILHATEP
A0JM01_530_1122          RPSFRAIIRDLNSLF----TP--------------------DYELLAETDF
G3PZA6_518_1120          RPSFRAIIRDLNSLF----TP--------------------DYELLVESDM
I3J7Z7_537_1129          RPSFRTIIRDLNSLF----TP--------------------DYELLVESDM
G1MVV3_535_1025          RPSFRTVLRDLTQLQ----PH--------------------SLMDVSSVN-
F7B2N9_488_1076          RPSFRGIIRDLNSLI----TS--------------------DYELLSDPTP
Q4T1R9_364_1003          RPSFKAVIRDLNSLF----TP--------------------DYELLVDSDI
C7ATY8_513_1104          RPSCLSIIRQLNNLI----TS--------------------DYVILHAAEP
H0ZIA6_541_1134          RPFFRAIMRDINKLE----EQ--------------------NPDIVSEKK-
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> UniRef90_G3P1H3
<http://www.uniprot.org/uniref/UniRef90_G3P1H3>_515_1105 |
Tyrosine-protein kinase n=1 Tax=Gasterosteus aculeatus RepID=G3P1H3_GASAC

> UniRef90_I3JQC0
<http://www.uniprot.org/uniref/UniRef90_I3JQC0>_567_1148 |
Uncharacterized protein n=2 Tax=Oreochromis niloticus RepID=I3JQC0_ORENI

> UniRef90_Q9PTN6
<http://www.uniprot.org/uniref/UniRef90_Q9PTN6>_498_1097 |
Tyrosine-protein kinase n=1 Tax=Cyprinus carpio RepID=Q9PTN6_CYPCA

> UniRef90_G1KI54
<http://www.uniprot.org/uniref/UniRef90_G1KI54>_559_1153 |
Uncharacterized protein (Fragment) n=2 Tax=Anolis carolinensis RepID=G1KI54_ANOCA

> UniRef90_G3WN84
<http://www.uniprot.org/uniref/UniRef90_G3WN84>_561_1153 |
Tyrosine-protein kinase n=4 Tax=Metatheria RepID=G3WN84_SARHA

> UniRef90_Q9PWD1
<http://www.uniprot.org/uniref/UniRef90_Q9PWD1>_530_1117 |
Tyrosine-protein kinase n=3 Tax=Tetraodon RepID=Q9PWD1_TETFL

> UniRef90_H2V1W4
<http://www.uniprot.org/uniref/UniRef90_H2V1W4>_515_1120 |
Tyrosine-protein kinase n=2 Tax=Tetraodontidae RepID=H2V1W4_TAKRU

> UniRef90_F6V3I2
<http://www.uniprot.org/uniref/UniRef90_F6V3I2>_589_1182 |
Tyrosine-protein kinase n=3 Tax=Metatheria RepID=F6V3I2_MONDO

> UniRef90_F1NMJ9
<http://www.uniprot.org/uniref/UniRef90_F1NMJ9>_554_1150 |
Tyrosine-protein kinase n=5 Tax=Phasianidae RepID=F1NMJ9_CHICK

> UniRef90_Q6GPK5
<http://www.uniprot.org/uniref/UniRef90_Q6GPK5>_575_1163 |
Tyrosine-protein kinase n=3 Tax=Xenopus RepID=Q6GPK5_XENLA

> UniRef90_H2TCV2
<http://www.uniprot.org/uniref/UniRef90_H2TCV2>_510_1100 |
Tyrosine-protein kinase (Fragment) n=3 Tax=Takifugu rubripes RepID=H2TCV2_TAKRU

> UniRef90_H2SBF2
<http://www.uniprot.org/uniref/UniRef90_H2SBF2>_535_1131 |
Tyrosine-protein kinase (Fragment) n=3 Tax=Takifugu rubripes RepID=H2SBF2_TAKRU

> UniRef90_F1PBD0
<http://www.uniprot.org/uniref/UniRef90_F1PBD0>_595_1189 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Canis lupus familiaris
RepID=F1PBD0_CANFA

> UniRef90_C0RW38
<http://www.uniprot.org/uniref/UniRef90_C0RW38>_515_1112 |
Tyrosine-protein kinase n=7 Tax=root RepID=C0RW38_DANRE

> UniRef90_C7ATY6
<http://www.uniprot.org/uniref/UniRef90_C7ATY6>_576_1168 |
Tyrosine-protein kinase n=1 Tax=Siniperca chuatsi RepID=C7ATY6_SINCH

> UniRef90_P29597
<http://www.uniprot.org/uniref/UniRef90_P29597>_576_1171 | Non-receptor
tyrosine-protein kinase TYK2 n=21 Tax=Simiiformes RepID=TYK2_HUMAN

> UniRef90_I3M210
<http://www.uniprot.org/uniref/UniRef90_I3M210>_601_1192 |
Uncharacterized protein (Fragment) n=2 Tax=Eutheria RepID=I3M210_SPETR

> UniRef90_A0JM01
<http://www.uniprot.org/uniref/UniRef90_A0JM01>_530_1122 |
Tyrosine-protein kinase n=4 Tax=Xenopus RepID=A0JM01_XENTR

> UniRef90_H2VE42
<http://www.uniprot.org/uniref/UniRef90_H2VE42>_579_1162 |
Tyrosine-protein kinase n=1 Tax=Takifugu rubripes RepID=H2VE42_TAKRU

> UniRef90_H2L7P7
<http://www.uniprot.org/uniref/UniRef90_H2L7P7>_514_1119 |
Tyrosine-protein kinase n=2 Tax=Oryzias latipes RepID=H2L7P7_ORYLA

> UniRef90_I3J7Z7
<http://www.uniprot.org/uniref/UniRef90_I3J7Z7>_537_1129 |

> UniRef90_Q6Y4Q0
<http://www.uniprot.org/uniref/UniRef90_Q6Y4Q0>_534_1126 |
Tyrosine-protein kinase n=3 Tax=Tetraodon RepID=Q6Y4Q0_TETFL

> UniRef90_H2LQD3
<http://www.uniprot.org/uniref/UniRef90_H2LQD3>_521_1110 |
Tyrosine-protein kinase n=1 Tax=Oryzias latipes RepID=H2LQD3_ORYLA

> UniRef90_Q6DDJ0
<http://www.uniprot.org/uniref/UniRef90_Q6DDJ0>_546_1139 |
Tyrosine-protein kinase n=3 Tax=Xenopus RepID=Q6DDJ0_XENLA

> UniRef90_G1KHZ7
<http://www.uniprot.org/uniref/UniRef90_G1KHZ7>_606_1200 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Anolis carolinensisRepID=G1KHZ7_ANOCA

> UniRef90_H2M2B1
<http://www.uniprot.org/uniref/UniRef90_H2M2B1>_532_1128 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Oryzias latipes RepID=H2M2B1_ORYLA

> UniRef90_G5BSN6
<http://www.uniprot.org/uniref/UniRef90_G5BSN6>_723_1350 |
Tyrosine-protein kinase JAK1 n=4 Tax=Theria RepID=G5BSN6_HETGA

> UniRef90_G9KW41
<http://www.uniprot.org/uniref/UniRef90_G9KW41>_102_676 |
Tyrosine kinase 2 (Fragment) n=1 Tax=Mustela putorius furo RepID=G9KW41_MUSPF

> UniRef90_G3VR92
<http://www.uniprot.org/uniref/UniRef90_G3VR92>_504_1104 |
Tyrosine-protein kinase n=1 Tax=Sarcophilus harrisii RepID=G3VR92_SARHA

> UniRef90_G3TF05
<http://www.uniprot.org/uniref/UniRef90_G3TF05>_473_1068 |
Tyrosine-protein kinase (Fragment) n=2 Tax=Loxodonta africana RepID=G3TF05_LOXAF

> UniRef90_I3IZB2
<http://www.uniprot.org/uniref/UniRef90_I3IZB2>_589_1184 |
Uncharacterized protein (Fragment) n=1 Tax=Oreochromis niloticus RepID=I3IZB2_ORENI

> UniRef90_H2M2I1
<http://www.uniprot.org/uniref/UniRef90_H2M2I1>_581_1165 |
Tyrosine-protein kinase n=1 Tax=Oryzias latipes RepID=H2M2I1_ORYLA

> UniRef90_H3ADK6
<http://www.uniprot.org/uniref/UniRef90_H3ADK6>_22_610 |
Uncharacterized protein (Fragment) n=1 Tax=Latimeria chalumnae RepID=H3ADK6_LATCH

> UniRef90_O12990
<http://www.uniprot.org/uniref/UniRef90_O12990>_562_1150 |
Tyrosine-protein kinase JAK1 n=5 Tax=Danio rerio RepID=JAK1_DANRE

> UniRef90_B0V237
<http://www.uniprot.org/uniref/UniRef90_B0V237>_509_1091 |
Tyrosine-protein kinase (Fragment) n=2 Tax=Danio rerio RepID=B0V237_DANRE

> UniRef90_H3C837
<http://www.uniprot.org/uniref/UniRef90_H3C837>_398_1006 |
Uncharacterized protein (Fragment) n=1 Tax=Tetraodon nigroviridis
RepID=H3C837_TETNG

> UniRef90_H2TE42
<http://www.uniprot.org/uniref/UniRef90_H2TE42>_495_1102 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Takifugu rubripes RepID=H2TE42_TAKRU

> UniRef90_G1LYZ3
<http://www.uniprot.org/uniref/UniRef90_G1LYZ3>_576_1170 |
Tyrosine-protein kinase (Fragment) n=4 Tax=Caniformia RepID=G1LYZ3_AILME

> UniRef90_C7ATY8
<http://www.uniprot.org/uniref/UniRef90_C7ATY8>_513_1104 |
Tyrosine-protein kinase n=2 Tax=Percoidei RepID=C7ATY8_SINCH

> UniRef90_F7EAS1
<http://www.uniprot.org/uniref/UniRef90_F7EAS1>_502_1096 |
Uncharacterized protein n=4 Tax=Monodelphis domestica RepID=F7EAS1_MONDO

> UniRef90_O42291
<http://www.uniprot.org/uniref/UniRef90_O42291>_505_1097 |
Tyrosine-protein kinase n=3 Tax=Phasianidae RepID=O42291_CHICK

> UniRef90_F1MCX4
<http://www.uniprot.org/uniref/UniRef90_F1MCX4>_575_1169 |
Tyrosine-protein kinase n=1 Tax=Bos taurus RepID=F1MCX4_BOVIN

> UniRef90_F7B2N9
<http://www.uniprot.org/uniref/UniRef90_F7B2N9>_488_1076 |
Uncharacterized protein n=1 Tax=Equus caballus RepID=F7B2N9_HORSE

> UniRef90_H0VSL1
<http://www.uniprot.org/uniref/UniRef90_H0VSL1>_499_1098 |

Tyrosine-protein kinase n=2 Tax=Cavia porcellus RepID=H0VSL1_CAVPO

> UniRef90_G3PKI3
<http://www.uniprot.org/uniref/UniRef90_G3PKI3>_511_1116 |
Tyrosine-protein kinase n=1 Tax=Gasterosteus aculeatus RepID=G3PKI3_GASAC

> UniRef90_Q09178
<http://www.uniprot.org/uniref/UniRef90_Q09178>_563_1153 |
Tyrosine-protein kinase JAK1 n=1 Tax=Cyprinus carpio RepID=JAK1_CYPCA

> UniRef90_I3K428
<http://www.uniprot.org/uniref/UniRef90_I3K428>_523_1114 |
Uncharacterized protein n=2 Tax=Oreochromis niloticus RepID=I3K428_ORENI

> UniRef90_Q4T1R9
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SCAF10492, whole genome shotgun sequence. (Fragment) n=1 Tax=Tetraodon nigroviridis
RepID=Q4T1R9_TETNG

> UniRef90_I3KJT0
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> UniRef90_H2SBF4
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Uncharacterized protein n=1 Tax=Takifugu rubripes RepID=H2SBF4_TAKRU

> UniRef90_H3DDQ1
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Tyrosine-protein kinase (Fragment) n=1 Tax=Tetraodon nigroviridis
RepID=H3DDQ1_TETNG

> UniRef90_Q6W5B1
<http://www.uniprot.org/uniref/UniRef90_Q6W5B1>_355_948 | TEL/JAK2
fusion protein n=1 Tax=Danio rerio RepID=Q6W5B1_DANRE

> UniRef90_Q9PWD0
<http://www.uniprot.org/uniref/UniRef90_Q9PWD0>_515_1100 |
Tyrosine-protein kinase n=3 Tax=Tetraodon RepID=Q9PWD0_TETFL

> UniRef90_H0X425
<http://www.uniprot.org/uniref/UniRef90_H0X425>_574_1168 |
Tyrosine-protein kinase n=1 Tax=Otolemur garnettii RepID=H0X425_OTOGA

> UniRef90_Q9R117
<http://www.uniprot.org/uniref/UniRef90_Q9R117>_572_1164 | Non-receptor
tyrosine-protein kinase TYK2 n=10 Tax=Muroidea RepID=TYK2_MOUSE

> UniRef90_G1P7K0
<http://www.uniprot.org/uniref/UniRef90_G1P7K0>_396_981 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Myotis lucifugus RepID=G1P7K0_MYOLU

> UniRef90_H0ZIA6
<http://www.uniprot.org/uniref/UniRef90_H0ZIA6>_541_1134 |
Uncharacterized protein n=2 Tax=Taeniopygia guttata RepID=H0ZIA6_TAEGU

> UniRef90_G5B225
<http://www.uniprot.org/uniref/UniRef90_G5B225>_576_1168 |
Tyrosine-protein kinase n=1 Tax=Heterocephalus glaber RepID=G5B225_HETGA

> UniRef90_D3ZUV6
<http://www.uniprot.org/uniref/UniRef90_D3ZUV6>_649_1241 |
Tyrosine-protein kinase n=1 Tax=Rattus norvegicus RepID=D3ZUV6_RAT

> UniRef90_O57612
<http://www.uniprot.org/uniref/UniRef90_O57612>_578_1166 |
Tyrosine-protein kinase n=4 Tax=Tetraodontidae RepID=O57612_TETFL

> UniRef90_H0V2Z6
<http://www.uniprot.org/uniref/UniRef90_H0V2Z6>_556_1148 |
Tyrosine-protein kinase (Fragment) n=2 Tax=Cavia porcellus RepID=H0V2Z6_CAVPO

> UniRef90_F1S3L9
<http://www.uniprot.org/uniref/UniRef90_F1S3L9>_566_1169 |
Uncharacterized protein n=3 Tax=Sus scrofa RepID=F1S3L9_PIG

> UniRef90_G3PKV8
<http://www.uniprot.org/uniref/UniRef90_G3PKV8>_559_1147 |
Tyrosine-protein kinase n=2 Tax=Gasterosteus aculeatus RepID=G3PKV8_GASAC

> UniRef90_G1KCE0
<http://www.uniprot.org/uniref/UniRef90_G1KCE0>_530_1126 |
Tyrosine-protein kinase n=2 Tax=Anolis carolinensis RepID=G1KCE0_ANOCA

> UniRef90_C7ATY9
<http://www.uniprot.org/uniref/UniRef90_C7ATY9>_562_1151 |
Tyrosine-protein kinase n=1 Tax=Siniperca chuatsi RepID=C7ATY9_SINCH

> UniRef90_H3ABD2
<http://www.uniprot.org/uniref/UniRef90_H3ABD2>_524_1119 |
Tyrosine-protein kinase n=1 Tax=Latimeria chalumnae RepID=H3ABD2_LATCH

> UniRef90_G3NVW0
<http://www.uniprot.org/uniref/UniRef90_G3NVW0>_582_1174 |
Tyrosine-protein kinase n=1 Tax=Gasterosteus aculeatus RepID=G3NVW0_GASAC

> UniRef90_H2VE41
<http://www.uniprot.org/uniref/UniRef90_H2VE41>_574_1180 |
Tyrosine-protein kinase n=2 Tax=Tetraodontidae RepID=H2VE41_TAKRU

> UniRef90_I3MAE0
<http://www.uniprot.org/uniref/UniRef90_I3MAE0>_504_1097 |
Uncharacterized protein n=1 Tax=Ictidomys tridecemlineatus RepID=I3MAE0_SPETR

> UniRef90_D3Z4S5
<http://www.uniprot.org/uniref/UniRef90_D3Z4S5>_718_1310 |
Tyrosine-protein kinase n=2 Tax=Mus musculus RepID=D3Z4S5_MOUSE

> UniRef90_F8W4H3
<http://www.uniprot.org/uniref/UniRef90_F8W4H3>_558_1147 |
Tyrosine-protein kinase n=3 Tax=Danio rerio RepID=F8W4H3_DANRE

> UniRef90_F7EV03
<http://www.uniprot.org/uniref/UniRef90_F7EV03>_508_1101 |
Tyrosine-protein kinase n=3 Tax=Xenopus (Silurana) tropicalis RepID=F7EV03_XENTR

> UniRef90_Q75R65
<http://www.uniprot.org/uniref/UniRef90_Q75R65>_529_1123 |

Tyrosine-protein kinase JAK2 n=7 Tax=Neognathae RepID=JAK2_CHICK

> UniRef90_H0VRI8
<http://www.uniprot.org/uniref/UniRef90_H0VRI8>_531_1132 |
Tyrosine-protein kinase n=1 Tax=Cavia porcellus RepID=H0VRI8_CAVPO

> UniRef90_G1PKC8
<http://www.uniprot.org/uniref/UniRef90_G1PKC8>_569_1171 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Myotis lucifugus RepID=G1PKC8_MYOLU

> UniRef90_G1N138
<http://www.uniprot.org/uniref/UniRef90_G1N138>_441_1047 |
Uncharacterized protein (Fragment) n=2 Tax=Meleagris gallopavo RepID=G1N138_MELGA

> UniRef90_H2LLN7
<http://www.uniprot.org/uniref/UniRef90_H2LLN7>_568_1156 |
Tyrosine-protein kinase n=1 Tax=Oryzias latipes RepID=H2LLN7_ORYLA

> UniRef90_D2GV17
<http://www.uniprot.org/uniref/UniRef90_D2GV17>_503_1098 |
Tyrosine-protein kinase (Fragment) n=5 Tax=Caniformia RepID=D2GV17_AILME

> UniRef90_H2TE39
<http://www.uniprot.org/uniref/UniRef90_H2TE39>_530_1116 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Takifugu rubripes RepID=H2TE39_TAKRU

> UniRef90_H3B0L6
<http://www.uniprot.org/uniref/UniRef90_H3B0L6>_509_1107 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Latimeria chalumnae RepID=H3B0L6_LATCH

> UniRef90_G3PZA6
<http://www.uniprot.org/uniref/UniRef90_G3PZA6>_518_1120 |
Tyrosine-protein kinase n=1 Tax=Gasterosteus aculeatus RepID=G3PZA6_GASAC

> UniRef90_H1A3H7
<http://www.uniprot.org/uniref/UniRef90_H1A3H7>_27_589 |
Uncharacterized protein (Fragment) n=1 Tax=Taeniopygia guttata RepID=H1A3H7_TAEGU

> UniRef90_G3STB4
<http://www.uniprot.org/uniref/UniRef90_G3STB4>_577_1153 |
Tyrosine-protein kinase (Fragment) n=1 Tax=Loxodonta africana RepID=G3STB4_LOXAF

> UniRef90_G1MVV3
<http://www.uniprot.org/uniref/UniRef90_G1MVV3>_535_1025 |
Tyrosine-protein kinase (Fragment) n=4 Tax=Phasianidae RepID=G1MVV3_MELGA