

10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

.....-MADGARPSPRPAHAEVCGLMAKASETERSPGP-----TQPADAQTATSATVRPLST-----QAVFRPFDGFDEDNFPHPHTLG-PDTEPQDRMATTCSRVPVR-RLGGG-LVEIIPRAPDIDPDEALMTNPVVPSKRCWN-----CGRPVGRSDSE-----TKGASEGWCPYCGSPYSFL
 15839796.b ..-.MAKASETERSPGP-----TQPADAQTATSATVRPLST-----QAVFRPFDGFDEDNFPHPHTLG-PDTEPQDRMATTCSRVPVR-RLGGG-LVEIIPRAPDIDPDEALMTNPVVPSKRCWN-----CGRPVGRSDSE-----TKGASEGWCPYCGSPYSFL
 15607551.b ..-.MAKASETERSPGP-----TQPADAQTATSATVRPLST-----QAVFRPFDGFDEDNFPHPHTLG-PDTEPQDRMATTCSRVPVR-RLGGG-LVEIIPRAPDIDPDEALMTNPVVPSKRCWN-----CGRPVGRSDSE-----TKGASEGWCPYCGSPYSFL
 31791588.b ..-.MAKASETERSPGP-----TQPADAQTATSATVRPLST-----QAVFRPFDGFDEDNFPHPHTLG-PDTEPQDRMATTCSRVPVR-RLGGG-LVEIIPRAPDIDPDEALMTNPVVPSKRCWN-----CGRPVGRSDSE-----TKGASEGWCPYCGSPYSFL
 15827075.b ..-.MAESMKREIMDIDTEDVGQA-----AQRADPPSGTTEG-RLQST-----QAIFRNFDDDDLLHISVPSVTDPEQDRITPATRVLPIR-QLGGG-LVEIIRRVDIDPDEALMTNPVVPSKRCWN-----CGRPVGRSELQEADGAQGAKEGWCPYCGSPYSFL
 21221122.b ..-.MSEAGRITCQPGCCGTIEDMGGGELYCDTICGLAPVVAAGGALGATPTCTGVTTGGGGSGSRSRGSRAGSGGGSRSSARSRTSSQSRSKCCRVSGRSLRAVSRTGERSVSVRSSSSAGSTGRGRLGVG-LVEVPAPVPED-RVMVMDLPVEPRKRFCSRSRGCGAPVGRERGE-----RPGRTECFTCKGCHPYFSFV
 29831918.b ..-.MSEAQKQKCQPGCTGSYEDVGGGELYCDMCGVPAVVAAGGGMVGSQTPATGIGG-----RGSRGSGRSVSGRLSRALSGKTSGRSRLSGRSRSLGMV-LVQVPDPVDRPDRPMLVNEPVERKRFCSRSRGCGAPVGRERGE-----HPGRTEGFCFTCKGCHPYFSFV
 25029145.b ..-.TMRPTMIDNERKLNEVRNEDPGTSPPTEAVFKDFPFADDDDLDLDEVERALAPHTEGVAYDPAVSGTEAVKFDPFADDDDLDLVEELDHLLKLDLQLRATGQFPVPAEEEEEPTDVTSDEPITPAATFAS-----ADPSARSRRREAIYSTFERRGKTRQSRVADMGLVPLPFTKPE-----SELLIDPEAKLKPGKIKP
 19553944.b ..-.MKDXNDPDDP-----SPATEAVAFNFDDDDPDEDD-----SPATSAVAFNFEDDDDDDEPQEGCLEFLRLDNLNRATQGQMVVEQPAVEDSLGSASAHTETTAASLRPR-EVDPDSERSRQASLFRERVRVRSRPAVADMVLPFTKPE-----DELLLIDPEKKRKPGVAA
 38234610.b ..-.MNETEAVFPDFPADDTDDD-----MDELLSDLDLQLRMDVQG-----RSERAEISTFSRSGRNARTSRVANGMVTLPFTKPE-----SEVLLKSEEEYIASVGDE
 21219970.b ..-.MVTGFCDTFCFRRPAP-----EPTATPDDPDPDFAFGDARG-----PRPAQGQGAPAAGELDRGDLVLPHLPSPDPSSEAADTVARPTGGRGCVNDCACTGIVSYDG-----GPADHDGCFCECGTEYSR
 1mrn_PKN ..-.-----G
 2phk_PHK ..-.-----G
 113r_PKA ..-.-----G
 2erk_Erk2 ..-.-----G
 1jwh_CKII ..-.-----G
 1ias_TGFBR ..-.-----G

| | 210 | 220 | 230 | 240 | 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 | 360 | 370 | 380 | 390 | 40 | | | | | | | | | |
|------------|---------------|------------|----------------|--------------|-------------|-------------|-------------|-------------|-------------|--------------|---------------|--------------|------------|------------|------------|--------------|--------------|-----------|-----------|---------|-----------|---------|--------|--------|----------|---------|-------|-------|------------|
| 15839796.b | POLINP_GDIVAG | QYBVK_CIA | GGLG_WIYLADRN | VNCRPVVLLKG | HSG_DAEQA | AMAMAEROFLA | EYHPSIVQIFN | FVEHTD | R_HGD | FVGIVYMEYYGG | SLKRS | KG_QKL | VBAIA | YEL | EIPALSYLHS | IQLVYNDL | KPKENIML | TEE | QLKLID | GAVS | RIN | | | | | | | | |
| 15607551.b | POLINP_GDIVAG | QYBVK_CIA | GGLG_WIYLADRN | VNCRPVVLLKG | HSG_DAEQA | AMAMAEROFLA | EYHPSIVQIFN | FVEHTD | R_HGD | FVGIVYMEYYGG | SLKRS | KG_QKL | VBAIA | YEL | EIPALSYLHS | IQLVYNDL | KPKENIML | TEE | QLKLID | GAVS | RIN | | | | | | | | |
| 31791588.b | POLINP_GDIVAG | QYBVK_CIA | GGLG_WIYLADRN | VNCRPVVLLKG | HSG_DAEQA | AMAMAEROFLA | EYHPSIVQIFN | FVEHTD | R_HGD | FVGIVYMEYYGG | SLKRS | KG_QKL | VBAIA | YEL | EIPALSYLHS | IQLVYNDL | KPKENIML | TEE | QLKLID | GAVS | RIN | | | | | | | | |
| 15827075.b | POLSP_GDIVAG | QYBVK_CIA | GGLG_WIYLADRN | VNCRPVVLLKG | HSG_DAEQA | OSASA | VAEROFLA | EYHPSIVQIFN | FVEHTD | R_HGD | FVGIVYMEYYGG | SLKRS | KG_QKL | VBAIA | YEL | EIPALSYLHS | IQLVYNDL | KPKENIML | TEE | QLKLID | GAVS | RIN | | | | | | | |
| 21221122.b | PKLKA_GDIVVG | QYEWV_GCL | GGLG_WIYLADRN | VNSRPAVVLKG | DIG_DODAMAA | SISERELAE | EHANIV | EYHPSIVQIFN | FVEHLD | QRTGS | LSDGIVYMEYYGG | CSLKEIANARR | -SPQRGRDPL | VEACAY | GIEAEALCHL | ESLRSRILLYCD | IKVNNAI | TED | QLKLID | GAVS | RIN | | | | | | | | |
| 29831918.b | PKLKA_GDIVVG | QYEWV_GCL | GGLG_WIYLADRN | VNSRPAVVLKG | DIG_DODAMAA | SISERELAE | EHANIV | EYHPSIVQIFN | FVEHLD | QRTGS | LSDGIVYMEYYGG | CSLKEIANARR | -SPQRGRDPL | VEACAY | GIEAEALCHL | ESLRSRILLYCD | IKVNNAI | TED | QLKLID | GAVS | RIN | | | | | | | | |
| 25029145.b | POLQAD_GDIVAE | QYEVLS_VIA | GGGMG_WIYLADRN | VNCRPVVLLKG | MAQT_SA | QDTQTA | EAERAF | LA | THPGCIVRAYN | FIDD | RV | FGGFIVMEYYNG | SLDRRK | -TPTGKRDPL | VEACAY | GIEAEALCHL | ESLRSRILLYCD | IKVNNAI | TEN | QLKLID | GAVS | RIN | | | | | | | |
| 19553944.b | POLVA_GDIVAE | QYEVLS_VIA | GGGMG_WIYLADRN | VNSCRPVVLLKG | MAQS_SVQD | QDTQTA | EAERAF | LA | THPGCIVRAYN | FIDD | RV | FGGFIVMEYYNG | SLDRRK | -TPTGKRDPL | VEACAY | GIEAEALCHL | ESLRSRILLYCD | IKVNNAI | TEN | QLKLID | GAVS | RIN | | | | | | | |
| 38234610.b | PALKP_GDLAG | QYEVLS_VIA | GGGMG_WIYLADRN | VNSCRPVVLLKG | RDKA_K | QDQDYGA | AAVAAKE | ELAD | THPGCIVRAYN | FIDD | RV | FGGFIVMEYYNG | SLDRRK | -AQPDGVL | FRVDAI | YIYEL | EADYDYL | HORVVVNDL | KPKENII | TE | QLKLID | GAVS | GJ | | | | | | |
| 21219970.b | PKFRP_GDIVVG | HYEWL_VIA | GGGMG_WIYLADRN | VNSCRPVVLLKG | RDKA_K | QDQDYGA | AAVAAKE | ELAD | THPGCIVRAYN | FIDD | RV | FGGFIVMEYYNG | SLDRRK | -AQPDGVL | FRVDAI | YIYEL | EADYDYL | HORVVVNDL | KPKENII | TE | QLKLID | GAVS | GJ | | | | | | |
| 1mrn_PKN | SHMTPPSHLSD | RYELGEI | GGGM_WIYLADRN | VNSCRPVVLLKG | RDKA_K | QDQDYGA | AAVAAKE | ELAD | THPGCIVRAYN | FIDD | RV | FGGFIVMEYYNG | SLDRRK | -AQPDGVL | FRVDAI | YIYEL | EADYDYL | HORVVVNDL | KPKENII | TE | QLKLID | GAVS | GJ | | | | | | |
| 2phk_PKA | GPFYE | NYSEKEI | GGGSVSV | RRCIN | TCKEYA | KVII | GGGSFS | AEV | ELREAT | KEVDIL | KKGELFDYLT | EKVTID | SEKETR | KMRLAE | EVICM | AKR | YIYEL | EADYDYL | HORVVVNDL | KPKENII | TE | QLKLID | GAVS | GJ | | | | | |
| 113r_PKA | ETPSQNTAQOLD | OFTRIKL | GGGSFGRVM | WKEH | YHNMAYK | MLDQKV | VKKLQ | QIEH | NEKR | QANW | FPLV | DIM | KKGELFDYLT | EKVTID | SEKETR | KMRLAE | EVICM | AKR | YIYEL | EADYDYL | HORVVVNDL | KPKENII | TE | QLKLID | GAVS | GJ | | | |
| 2erk_Erk2 | PEMVR_GDIVVG | RYINLNSV | GGCA | YMC | AVD | -LNKVR | YK | SPF | HEQTY | CORID | KEID | LRF | HN | IND | HIRAP | TIEQKMD | VIV | DIMETDYL | RLLKT | QBS | END | ICVFL | YHNSAN | VLKPK | NLNLNTTC | DLKLCID | GLARV | PLDHD | HIFGLXEVAT |
| 1jwh_CKII | SEWVGNQDD | YOLVRLK | GGCA | YMC | AVD | -LNKVR | YK | SPF | HEQTY | CORID | KEID | LRF | HN | IND | HIRAP | TIEQKMD | VIV | DIMETDYL | RLLKT | QBS | END | ICVFL | YHNSAN | VLKPK | NLNLNTTC | DLKLCID | GLARV | PLDHD | HIFGLXEVAT |
| 1ias_TGFbR | PLHIVQTIA | RTIVLQES | GGCA | YMC | AVD | -LNKVR | YK | SPF | HEQTY | CORID | KEID | LRF | HN | IND | HIRAP | TIEQKMD | VIV | DIMETDYL | RLLKT | QBS | END | ICVFL | YHNSAN | VLKPK | NLNLNTTC | DLKLCID | GLARV | PLDHD | HIFGLXEVAT |

| | 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 | 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 | 570 | 580 | 590 | 60 |
|------------|--|---|---|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| 15839796.b | IVRIGEPTVADITYTVIRTEAAFLDLPLTRNGRYVGDPLEDD-- | PVLKTYDSDYGRILRRAIDPDPROFRTTAEEMSAQLTQVLR | EVVADDTGVPRPGLSTIRSPRSRTFGVDLLVAHT-DVY | -LDGQVH-AEKLTANEIVT | | | | | | | | | | | | | | | | |
| 15607551.b | IVRIGEPTVADITYTVIRTEAAFLDLPLTRNGRYVGDPLEDD-- | PVLKTYDSDYGRILRRAIDPDPROFRTTAEEMSAQLTQVLR | EVVADDTGVPRPGLSTIRSPRSRTFGVDLLVAHT-DVY | -LDGQVH-AEKLTANEIVT | | | | | | | | | | | | | | | | |
| 31791588.b | IVRIGEPTVADITYTVIRTEAAFLDLPLTRNGRYVGDPLEDD-- | PVLKTYDSDYGRILRRAIDPDPROFRTTAEEMSAQLTQVLR | EVVADDTGVPRPGLSTIRSPRSRTFGVDLLVAHT-DVY | -LDGQVH-AEKLTANEIVT | | | | | | | | | | | | | | | | |
| 15827075.b | IVRIGEPTVADITYTVIRTEAAFLDLPLTRNGRYVGDPLEDD-- | PVLKTYDSDYGRILRRAIDPDPROFRTTAEEMSAQLTQVLR | EVVADDTGVPRPGLSTIRSPRSRTFGVDLLVAHT-DVY | -LDGQVH-AEKLTANEIVT | | | | | | | | | | | | | | | | |
| 21221122.b | VADYGESVAIDLTVVSRTEAVLSDFPGQGYTTVVADSLPPDIEVEFRQYESFYRLLVTAATDPDPARFRASQAEMAEQLTQVLR | BVVSLQTGRAPRPAVSTLGPVPRVRVUDTELFRLDGEVSR | -LGARVPPPARCRGGSGAALPGGGSPAVAGPGTVAHAPPVGAGTFVAASGGASASLPGAVSSA | | | | | | | | | | | | | | | | | |
| 29831918.b | VADYGESVAIDLTVVSRTEAVLSDFPGQGYTTVVADSLPPDIEVEFRQYESFYRLLVTAATDPDPARFRASQAEMAEQLTQVLR | BVVSLQTGRAPRPAVSTLGPVPRVRVUDTELFRLDGEVSR | -LGARVPPPARCRGGSGAALPGGGSPAVAGPGTVAHAPPVGAGTFVAASGGASASLPGAVSSA | | | | | | | | | | | | | | | | | |
| 25029145.b | VATQGESVAIDIYTICRTEAAFLKLPLVEDGVLAQGIPSPNDQPKLRRHLSFYRLLRATAEKPEDRFTSVEAELRTOFVCLR | BVVSLQTGRAPRPAVSTLGPVPRVRVUDTELFRLDGEVSR | -LGARVPPVGKR-QVRITAPEIIVS | | | | | | | | | | | | | | | | | |
| 19553944.b | VATHQGESISSDITTCRTEAAFLTMLPLVEDGVLAQGIPSPKNSPLLRRHLSFYRLLRATAADDPOHRFRVSELRTOFVCLR | BVVSLQTGRAPRPAVSTLGPVPRVRVUDTELFRLDGEVSR | -G-IER-CARITAPEIIVS | | | | | | | | | | | | | | | | | |
| 38234610.b | VASDGESVAISDIYTICRTEAAFLTMLPLVEDGVLAQGIPSPKNSPLLRRHLSFYRLLRATAADDPOHRFRVSELRTOFVCLR | BVVSLQTGRAPRPAVSTLGPVPRVRVUDTELFRLDGEVSR | -G-IER-CARITAPEIIVS | | | | | | | | | | | | | | | | | |
| 21219970.b | RDRRGLEDVSDSLTVVSRTEVPLERAAARPT | LAARSPFEALIRPATHEPAAFRSRAAESMRNLNBVRLEBODAQLGREPFYPERTRIEPATAAVFGAALGTVPALQWTRTPGTGTP | -NVRITSEEVNA-ELFAGAPEPRAARR | | | | | | | | | | | | | | | | | |
| 1mrw_PKN | -DSCGSVQTAAVIC | -IAQVLSPEQARGDSDVARSDVYSLGCVLYVWLT-GEPPTFTGDSPPSVAYQHVRRED- | | | | | | | | | | | | | | | | | | |
| 2phk_PHK | | -PGCBLREVECGTPSYLAELHII-ECSTMNDNHPGYKBEVDMISTG- | | | | | | | | | | | | | | | | | | |
| 1l3r_PKA | | -EIILSKCGYNAWDWALGVILYKEMAA-GYPVFFADCPQIYKEIVSFKGVR- | | | | | | | | | | | | | | | | | | |
| 2erk_Erk2 | | -PKYRAPEMILNSKCYTISIDIWVSGCLLAMEMS-NRPPIFFGHYLDQQLNHLIGILGSPSQED- | | | | | | | | | | | | | | | | | | |
| 1jwh_CKII | | -GPELLWDYQMDYSLDMWISLGCMLAALMIFRK-BEPFFHGHDNYDQLVRIAKLVGLSP | | | | | | | | | | | | | | | | | | |
| 1ias_TGFbR | | -TKRYMAPEVLDSSINMKHFEFKRADYIAMGLVF-EIARR | | | | | | | | | | | | | | | | | | |

810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990
 15839796.b -EHKFYQTWNSTNDGVISAAFQILARQSAEGDRVCAVRILDEVPPTSRHFITTARITSAVTLLSGRSTSEVTEEQIRD--AARRVEAIP--PTEPRLQIRALVLLGGADWLKD--KASTNEILGFPTTSHLRLGV-EASISRSARVAPTORQRYILVDWANKVREPTSTF--
 15607551.b -EHKFYQTWNSTNDGVISAAFQILARQSAEGDRVCAVRILDEVPPTSRHFITTARITSAVTLLSGRSTSEVTEEQIRD--AARRVEAIP--PTEPRLQIRALVLLGGADWLKD--KASTNEILGFPTTSHLRLGV-EASISRSARVAPTORQRYILVDWANKVREPTSTF--
 31791588.b -EHKFYQTWNSTNDGVISAAFQILARQSAEGDRVCAVRILDEVPPTSRHFITTARITSAVTLLSGRSTSEVTEEQIRD--AARRVEAIP--PTEPRLQIRALVLLGGADWLKD--KASTNEILGFPTTSHLRLGV-EASISRSARVAPTORQRYILVDWANKVREPTSTF--
 15827075.b -EHKFYRTVNWTNDGVVSAAFQILARQSAEGDRVCAVRILDEVPPTSRHFITTARITSAVTLLSGRSTSEVTEEQIRD--AARRVEAIP--PTEPRLQIRALVLLGGADWLKD--KASTNEILGFPTTSHLRLGV-EASISRSARVAPTORQRYILVDWANKVREPTSTF--
 21221122.b -AAEYRIVVNSDESHVSAAFQILARVQLAAQDRRAJAVRULLESVPESVHCTAARVAAVRARLRC-TAAAGDLRFLLDDIIAAAROVEDVVGLDPARREQISABVLCARDWVLSGGRGSVPFAAQRILLGFDLDERGLRFGERSYRDTARJARGGERRIDLVEPANRYRPTTVW--
 29831918.b -AAEYRIVVNTDPSYVGSAAFQILARVQLAAQDRRAJAVRULLESVPESVHCTAARVAAVRARLRC-TNEAPEASFLDDLGAAGCWEAINGYGLDAVRRQISTEVLCACDWVLSGSQQGSAAPPDGGRALLCNELDERGLRFGERSYRDTARJAGGERRIDLVEPANRYRPTTVW--
 25029145.b HSLRVYADVWLINTTVSSAFQILARQIMAEQGQIEAVQALDKLSPASRHRMAGLTILLLLSSNLSESRIRR--AARRVEAIP--TNDPREFNIKIAIMSAGDSWLRD--LQSAAASPNTLFYPPFTQRLRREGISSEARVQCARSAFFARFRYLVDWANAVRPFITWF--
 19553944.b HSLRLYADVWATNTTVSSAFQILARQIMAEQGQIEAVQALDKLPOSSEHYRMALITILLLVSSNLSESRIRR--AARRVEAIP--TNEPREFNIKIAIMSAGDSWLRERK--LKASASANLFFYPPSSQKLRLTGISEAIRICARSAPPFHRYALVDWANAVRPLSWF--
 38234610.b KAIYLYALVNRTNITIVSSAFQILARQIQAENQIDIAVSTLDPVPONSHRRMAETAILHLLG-DLSEARLRR--AARRVEAIP--TNEPREFLQIQIAIMNAABQWLRTG--GEAANDLIFYPPFTQRLRNGSATRQJARASAPSS-IFYALVDWANAVRPMWF--
 21219970.b QAEFFPEAVVRRDPTQGSAAFQILARVRLRRAQRRIAVDVLDQVPTTSRHYDAARVAAVRILTGRLPDRPAPLAELR--EAAERIAQCHLD--GSGSWDRIVTEPREHALACRPPGGWG--SGFPAGEICGPQDTEEAIRRLISASIRRIADAGGVGRGDLDFAYAVLPAPAGLRELVRGWRRTA
 1mrPKN
 2phk_PHK
 113r_PKA
 2erk_Erk2
 1jwh_CKII
 lias_TGFbR