Figure SX

Large Rearrangements

**Int Num 317**

**E-value 1.1E-6**

**1pho\_A 000 DGNKLDVYGKVKAMHYMSDNA-S--------KDGDQSYIRFGFKGETQINDQLTGYGRWEAEFAGNKA-----ESDTAQQKTRLAFAGLKYK-DLGSFDY 085**

**5ldv\_A 000 AIKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVIA 100**

**1pho\_A 086 GRNLGALYDVEAWTD-M-FPEF----G-GDSSAQTDNFM--TKRASGLATY----------------RNTDFFGVIDGLNLTLQYQGK--NENRD----- 153**

**5ldv\_A 101 GKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIG--NLYGAAAVGSYDLAGGQFNPQLWL 198**

**1pho\_A 154 -VKKQNGDGFGTSLTYDFG---GSDFAISGAYTNSDRTNEQNLQSRGTGKRAEAWATGLKYDANNIYLATFYSETRKM-----------T------PI-- 230**

**5ldv\_A 199 AYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELD--DKKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNLGSLLAGEE 296**

**1pho\_A 231 -T-------GGFANKTQNFEAVAQYQFDFGLRPSLGYVLSKGKDIEG-IGDEDLVNYIDVGATYYFNKNMSAFVDYKINQLDSDNK-LNINNDDIVAVGM 320**

**5ldv\_A 297 IFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNTNESADHSTVRLQA 396**

**1pho\_A 321 TYQF 324**

**5ldv\_A 397 LYKF 400**

**Int Num 1308**

**E-value 9.8E-6**

**2por\_A 000 VKLSGDARMGVMYNGDDW-----------NFSSRSRVLFTMSGTTDSGLEFGASFKAHESV------------GAETGEDGTVFLSG--AFGKIEMGDAL 075**

**5ldv\_A 000 VDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVIAGKQQ 100**

**2por\_A 076 GASEALFG--D-L-YE---VGYTDL---DDRGGNDIPYLTGDE-RLTAEDNP--------VLLYTY-SAGA-FSVAASMSDG--KVG-E------TSEDD 145**

**5ldv\_A 101 LNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIGNLYGAAAVGSYDLAGGQFNPQLWLAYWDQV 200**

**2por\_A 146 AQEMAVAAAYTFG---N--YTVGLGYEKIDSPDT----ALMADMEQLELAAIAKFGATNVKAYYADGELDRD--------FARA---VF--DL--TP-VA 220**

**5ldv\_A 201 AFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDDKKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNLGSLLAGEEIFYTTGSR 300**

**2por\_A 221 AAATAVDHKAYGLSVDSTFG-ATTVGGYVQVLDIDT-------IDDVTYYGLGASYDLGGGASIVGGIADNDLP--------NSDMVADLGVKFKF 300**

**5ldv\_A 301 LNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNTNESADHSTVRLQALYKF 396**

**Int Num 1731**

**E-value 9.5E-6**

**2zfg\_A 000 DGNKVDLYGKA-VGLHYFSKGNGENS---YGGNGDMTYARLGFKGETQINSDLTGYGQWEYNFQGNNSE---GADAQTGNKTRLAFAGLKYA-DVGSFDY 092**

**5ldv\_A 000 AIKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVIA 100**

**2zfg\_A 093 GRNYGVVYDALG-YT-DMLPEFGGDTA-YSD-----DFF--VGRVGGVAT----------------YRNSNFFGLVDGLNFAVQYLGK--NERDT----- 159**

**5ldv\_A 101 GKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIG--NLYGAAAVGSYDLAGGQFNPQLWL 198**

**2zfg\_A 160 -ARRSNGDGVGGSISYEYE-----GFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNA-----------TPI--TNKFT- 239**

**5ldv\_A 199 AYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDD--KKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNLGSLLAGEE 296**

**2zfg\_A 240 ----N---TSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEG-IGDVDLVNYFEVGATYYFNKNMSTYVDYIINQIDSDNK-LGVGSDDTVAVGI 330**

**5ldv\_A 297 IFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNTNESADHSTVRLQA 396**

**2zfg\_A 331 VYQF 334**

**5ldv\_A 397 LYKF 400**

**Int Num 2194**

**E-value 3.7E-9**

**3nsg\_A 000 NKDGNKLDLYGKAVGRHVWTTTGDSK--------NADQTYAQIGFKGETQINTDLTGFGQWEYRTKADRAE----GEQQNSNLVRLAFAGLKY--AEVGS 086**

**5ldv\_A 000 EEAIKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVAT-S 099**

**3nsg\_A 087 IDYGRNYGIVYDVESYTDMAPYFSGET-----WGGA-----YTDNYMTSRAGG-------------------LLTYRNSDFFGLVDGLSFGIQYQGKN-- 155**

**5ldv\_A 100 VIAGKQQLNIIWTDNGVDG-LVGTGVKVVNNSIDGLTLAAFAVDSF-MAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIGNL------YGAAAVGSYDLAG 191**

**3nsg\_A 156 QDNHS-----INSQNGDGVGYTMAYEFD-----GFGVTAAYSNSKRTNDQQDRDGNGDRAESRAVGAKYDANNVYLAAVYAETRNMS--------IVENT 237**

**5ldv\_A 192 GQFNPQLWLAYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDD-KKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNL 290**

**3nsg\_A 238 ----V------TD---TVEMANKTQNLEVVAQYQFDFGLRPAISYVQSKGKQLNGAGGSADLAKYIQAGATYYFNKNMNVWVDYRFNLLDENDYSSSYVG 324**

**5ldv\_A 291 GSLLAGEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNT-NESA 389**

**3nsg\_A 325 TDDQAAVGITYQF 337**

**5ldv\_A 390 DHSTVRLQALYKF 402**

**Int Num 2866**

**E-value 1.1E-8**

**4d65\_A 000 GNKLDVYGQIDVRHYFADAKSGE--------DGDDSRVRLGFKGDTQITDQLIGFGRFEWETSTNKA------ETSNDNQNRLAYAGLKFA-DYGSLDYG 085**

**5ldv\_A 000 IKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVIAG 100**

**4d65\_A 086 RNYGVIYDTNAWTDVLPLWGADT-----M-DQ-ED--TF--MMGRNRN-L--L------------TYRNNNGFGYIDG-LSFALQYQGKN--GDQNKSTG 156**

**5ldv\_A 101 KQQLNIIWTDNGVDG-LVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDS---IGNLYGAAAVGSYDLAGGQFNPQLW 196**

**4d65\_A 157 SSALDNNGDGYGFSTAYELG----WGLSIGGGYSNSSRTPSQNNIKTGATGKRAEAWNVGSKLELDELYLAAMYGQTLNT-----------TRF---GDD 238**

**5ldv\_A 197 LAYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDD---KKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNLGSLLAG 293**

**4d65\_A 239 ------D---AEAIANKTENLELVALYSFDFGLTPSIGYNQSKGKNLGN-YGNKDLVKYIAVGASYDFNKNMAAVIDYKINLLKDNQFTDDYGINTDNVL 328**

**5ldv\_A 294 EEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVN--TNESADHSTV 391**

**4d65\_A 329 GLGLIYQF 336**

**5ldv\_A 392 RLQALYKF 399**

**Int Num 3213**

**E-value 4.1E-9**

**5fvn\_A 000 NKDGNKLDLYGKVDGLHYFSDDDSQ---------DGDQTYMRLGFKGETQVNDQLTGYGQWEYQIQGNSG-----E-NENNSWTRVAFAGLKF--GDAGS 083**

**5ldv\_A 000 EEAIKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVAT-S 099**

**5fvn\_A 084 FDYGRNYGVVYDVTSWTD--VLPEFG---GDTYGS--D-NF---MQQRGN-G--FA------------TYRNSDFFGLVDG-LNFAVQYQGKNGSASGED 156**

**5ldv\_A 100 VIAGKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSI---GNLYGAAAVGSYDLAGGQFNP 196**

**5fvn\_A 157 QTNNGRTELRQNGDGVGGSITYNLG--E--GFGIGTAVSSSKRTSSQNDLTYGNGDRAETYTGGLKYDANNIYLAAQYTQTYNA-----------TRV-- 239**

**5ldv\_A 197 QLW--LAYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDD--KKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNLGS 292**

**5fvn\_A 240 --G------N-----LGWANKAQNFEVVAQYQFDFGLRPSVAYLQSKGKDLENGYGDQDLLKYVDVGATYYFNKNMSTYVDYKINLLDDKEFTRNAGIST 326**

**5ldv\_A 293 LLAGEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNT--NESAD 390**

**5fvn\_A 327 DDIVALGLVYQF 338**

**5ldv\_A 391 HSTVRLQALYKF 402**

**Int Num 3231**

**E-value 8.3E-9**

**5nxr\_A 000 KDGNKLDVYGKVDVRHYFASADKGKKS-----EDGDDSRVRLGVKGDTQITDQLTGFGRFEWETKTNKA------ENEGENKNRLAYAGLKFA-DFGSID 088**

**5ldv\_A 000 EAIKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVI 100**

**5nxr\_A 089 YGRNYGVVYDTNAWTD--VFPLW---GADTMA------QTDNFMTSRNRN-L--L------------TYRNNNAFGYVDG-LSFALQYQGKNGDNNKSSA 161**

**5ldv\_A 101 AGKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDS-FMAAEQGSDLLGQSTYVGNGKNNNDSFKLDS---IGNLYGAAAVGSYDLAGGQFNPQ 196**

**5nxr\_A 162 ---GMAKDNGDGYGFSTAYELGW----GVTLGGGYSSSSRTPNQKAGVVTSEGDSYYSATGKRAQAWNVGGKFDANNVYLAAMYGQTQNT---------- 244**

**5ldv\_A 197 LWLAYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDD-----------KKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIED 285**

**5nxr\_A 245 -SRY----GD----------LDLIANKTENVELVAQYLFDFGLKPSIGYNQSKGKNLGNGYDNQDLVKYISVGSYYYFNKNMSAVVDYKINLLKDNDFTK 329**

**5ldv\_A 286 QGNLGSLLAGEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNT- 384**

**5nxr\_A 330 EYGINTDNVLGLGLVYQF 347**

**5ldv\_A 385 -NESADHSTVRLQALYKF 401**

Loop to hairpin

**Int Num 380**

**E-value 6.7E-4**

**1prn\_A 000 DNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFG--ATTV-R-AYVSDIDRAGADTAYGIGADYQFA----EGVKVSGSVQSG 85**

**3szd\_A 000 DNRTVSALFSARYGLH-TLYLGLQKVSGDD---G----WMRVNGTSGGTLANDSYNASYD-NPGERSWQLRYDFDFVGLGLPGLTFMTRYLHG 84**

**Int Num 395**

**E-value 1.0E-3**

**1prn\_A 000 DNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGA-TTVRAYVSDIDR-AGADTAYGIGADYQFA----EGVKVSGSVQSG 85**

**4frx\_A 000 DNRAFSGLFTYTVSGH-SIGAGYQILNGDSDF-PFLNR-GDGEGSTAYLITDVQIGKFQRAGERTWQVRYGYDFATVGVPGLTFNTIYLSG 88**

**Int Num 910**

**E-value 2.8E-4**

**2fgr\_A 000 VGRYIGGYVAYDNGPLSASLGLAQQKTAVGGLATDRDEITLGASYNFGVAKLSGLLQQTKFKRDIGGDIKTNSYMLGASAPVG----GVGEVKLQYALYD 096**

**4frx\_A 000 DNRAFSGLFTYTVSGHSIGAGYQILNGDSD-----FPFLNRGDG-EGSTAYLITDVQIGKF-----QRAGERTWQVRYGYDFATVGVPGLTFNTIYLSGD 089**

**2fgr\_A 097 QKA---IDSKAHQITLGYVHNLS----KRTALYGNLAFLKNKD 132**

**4frx\_A 090 KIKTARGDQSEWERDISLAYVIPDGTFKGLGFTWKNASFRSGL 132**

**Int Num 922**

**E-value 6.8E-4**

**2fgr\_A 000 VGRYIGGYVAYDNGPLSASLGLAQQKTAVGGLATDRDEITLGASYNFGVAKLS-GLLQQTKFKRDIGGDIKTNSYMLGASAPVG-----GVGEVKLQYAL 094**

**5dl5\_A 000 TNNIWAISGTYATGPHSVMLAYQQNTGNVG-----Y-DYGQ-NA--DGFQSIYLPNSYMSDF-----IGNHEKSAQIQYNVDFGKLGVLPGLNWTTAFVY 086**

**2fgr\_A 095 YDQ-KA----IDSKAHQITLGYVHNLS----KRTALYGNLAFLKNKD 132**

**5dl5\_A 087 GWDIKVRNVTDDAQEREFFNQVKYTVQSGFAKDASLRIRNSYYRASD 133**

**Int Num 2791**

**E-value 2.8E-5**

**4aui\_A 000 AMADVTLYGTIKAGVETSRSVAHHGAQADRVKTATEIADLGSKIGFKGQEDLGNGLKAIWQLEQKAYVSG--------TDTGWGNRQSFIGLKG--GFGK 090**

**5ldv\_A 000 AIKDVDVSGVLRYRYDTGNFDKNFL-NNSNLNNSK--QDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATS 097**

**4aui\_A 091 VRVGRLNN--ILKDT----GNFNP-------WEGKSYY-SGLSNIAQ--PEE----------------------R-HVS----VRYDSP-EFAGFSGSVQ 146**

**5ldv\_A 098 VIAGKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIGNLYGAAAVGSYDLAGGQFNPQLW 197**

**4aui\_A 147 YVPNDNSGKNRSESYHAGFNYKND---GFFVQYAGSYKRHNYT--------TEKHQVHRLVGGYDHDALYASVAVQQQDAKL--------T-WRD----D 222**

**5ldv\_A 198 LAYWD----QVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDDKKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNLGSLLA 293**

**4aui\_A 223 N-------------SHNSQTEVATTVAYRFG-NVTPRVSYAHGFKGSVYD-ADHDNTYDQVVVGAEYDFSKRTSALVSAGWLQKGKGAE---KFVATVGG 304**

**5ldv\_A 294 GEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNTNESADHSTVR 393**

**4aui\_A 305 VGLRHKF 311**

**5ldv\_A 394 LQALYKF 400**

**Int Num 2965**

**E-value 1.2E-4**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRMEN-LYFAGLFTDGELAKDVDYTGYELAAGYKLG----Q-AAFTATYNNAETAK-----K 089**

**4fso\_A 000 DNRALSLLLAYAQG--GHTLSAGWQRMNGASSM----PYLDGSNPYLANYLQVNDF-ANPEERSWQLRYDFDLRSVGVPGLSFMTRYVNGDHIRLANGDE 093**

**6ehb\_A 090 TSADNFAIDATYYFK----PNFRSYISYQFNLLDSDKASKVASEDELAIGLRYDF 140**

**4fso\_A 094 GKEWERDIELKYIVQSGRFKDLSLRLRNATYRTDFER--SARDVDEVRLIASYNL 146**

**Int Num 2983**

**E-value 1.9E-4**

**6ehb\_A 000 GEDGYSLSAIYTF-GDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKDVDYTGYELAAGYKLGQ-----AAFTATYNNAETAK---- 088**

**4fsp\_A 000 DNRSFSGSLTYRLRN--GQAFGLGYQRMSGDHGF----PYLEGTDPYLVNF-GQYNDF-AEAGESSWQLRYDCDFAPLGVPGLSLMTRYFSGHGAKPKGA 092**

**6ehb\_A 089 -KTSADNFAIDATYYFK----PNFRSYISYQFNLLDSDKASKVASEDELAIGLRYDF 140**

**4fsp\_A 093 DGSREWERDSDLRYVLQGGALKGLGLVWRNATYRSAF-----SRDIDENRLYLTYEL 144**

**Int Num 3159**

**E-value 5.1E-4**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRMENLY-F-AGLFTDGELAKDVDYTGYELAAGYKLG---Q-AAFTATYNNAETA------- 087**

**5dl6\_A 000 DNDLYHAHFELKHQ--NHKFIFGTFQHHGDTAF----PYLTGGETGLLIDTWP-GEF-LNPKEKAYSFRYEYDFKEYVPGLCFMTRYTTGHNIYAPNLGG 092**

**6ehb\_A 088 KKTSADNFAIDATYYFK----PNFRSYISYQFNLLDSDKASKVASEDELAIGLRYDF 140**

**5dl6\_A 093 TNLKERETDFDLGYTVQSGWLKNLGLRARYAIYDNNMLSTANIKPVNETRINIDYTW 149**

**Int Num 3235**

**E-value 7.0E-9**

**6ehd\_A 000 KSDAGTVDFYGQLRTELKFLEDKDP---------TIGSGSSRAGVDANYTVNDSLALQGKVEFALKDS-----------GDMYVRNHILGVKT--NFGKF 078**

**5ldv\_A 000 EEAIKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSV 100**

**6ehd\_A 079 SFGKQWTT--SDDV--Y-G-AD---YSY-FFGGTGLR--Y-G---TLSDA-----------------------LHDSQ----VKYVY--EADSFWVKAGY 133**

**5ldv\_A 101 IAGKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIGNLYGAAAVGSYDLAGGQFNPQLWL 200**

**6ehd\_A 134 GFPEDNAKQELAELYVGATF--G-DLAVHAGGGQNRDKAFKVGSNTVGTTTTDIKADVTNSYFEVTGEYTIGDALIGVTYYNAELD-----------V-- 217**

**5ldv\_A 201 AYWDQ--VAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELD--------DKKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNL 290**

**6ehd\_A 218 ----EN-----------NPLVIDEDAISVAGTYKVADKTKLYAGYEYVMQEANT---GADEDGTLVYLGVEYKFASWARVYAEYGYGDGTTLGYTNKGSD 299**

**5ldv\_A 291 GSLLAGEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNT----- 385**

**6ehd\_A 300 AEVKATKVDSANNFGIGARYYW 321**

**5ldv\_A 386 -----NESADHSTVRLQALYKF 402**

Loop to hairpin with alternate alignments

**Int Num 378 – Loop to hairpin**

**E-value 1.9E-4**

**1prn\_A 000 DNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGAT--TVRAYVSDIDR-AGADTAYGIGADYQFA----EGVKVSGSVQSG 85**

**3sys\_A 000 DSHTVYGLFSAGIGLH-TFYLGLQKVGGDS-------GWQSVYGSSGRSMGNDMFNGNFTNADERSWQVRYDYDFVGLGWPGLIGMVRYGHG 84**

**Int Num 379 – Alternate alignment, also loop to hairpin**

**E-value 2.8E-4**

**1prn\_A 000 VTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVGAAYKFNDAGTVGLNWYDNGLS-TAGDQVTLYGNYAFG----A-TTVRAYVSDIDR------- 087**

**3sys\_A 000 DSHTVYGLFSAGIGLHTFYLGLQKVGGDS--GWQSVYG-SS---GR-SMGNDMFNGNFTNADERSWQVRYDYDFVGLGWPGLIGMVRYGHGSNATTKAGS 093**

**1prn\_A 088 AGADTAYGIGADYQFA----EGVKVSGSVQSG 115**

**3sys\_A 094 GGKEWERDVELGYTVQSGPLARLNVRLNHASN 125**

**Int Num 1628 - Loop to hairpin**

**E-value 9.1E-5**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKDVDYTGYELAAGYKLG----Q-AAFTATYNNAETAK----- 088**

**2y0l\_A 000 DNKSLNGMFTYSLG--NHAFGAAWQRMNGDDAF----PYLEGSNPYLVNFV-QVNDF-AGPKERSWQLRYDYDFVGLGIPGLTFMTRYVKGDNVELAGQS 092**

**6ehb\_A 089 -KTSADNFAIDATYYFK----PNFRSYISYQFNLLDSDKASKVASEDELAIGLRYDF 140**

**2y0l\_A 093 GEGREWERNTELQYVFQSGALKNLGIRWRNATFRSNF-----TRDIDENRLIVSYTL 144**

**Int Num 1627 – alternate alignment**

**E-value 1.0E-5**

**6ehb\_A 000 EDGYSLSAIYTFGDTGFNVGAGYADQDD-QNEYMLAASYRME----NLYFAGLFTDGELAK-----DVDYTGYELAAGYKLGQAAFTATYNNAETAK--- 087**

**2y0l\_A 000 DHFDLGGLDYKLTD-QLTASYHYSNLQDVYRQHFVGLLHSWPIGPGELTSDLRFARSTDSGSAKAGGIDNKSLNGMFTYSLGNHAFGAAWQRMNGDDAFP 099**

**6ehb\_A 088 -------------------KTSADNFAIDATYYFK----PNFRSYISYQFNLLD 118**

**2y0l\_A 100 YLEGSNPYLVNFVQVNDFAGPKERSWQLRYDYDFVGLGIPGLTFMTRYVKGDNV 153**

**Int Num 2550 – loop to hairpin**

**E-value 1.5E-4**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKDVDYTGYELAAGYKLG----Q-AAFTATYNNAETAK----- 088**

**3szv\_A 000 DNRAFGALFSLRLG--AHAVAAGYQRISGDDPYP----YIAGSDPYLVNF-IQIGDF-GNVDERSWQLRYDYDFGALGLPGLSFMSRYVSGDNVARGAAN 092**

**6ehb\_A 089 KTSADNFAIDATYYFK----PNFRSYISYQFNLLDSDKASKVASEDELAIGLRYDF 140**

**3szv\_A 093 DGKEWERNTDLGYVVQSGPLKNLGVKWRNATVRSNF-----ANDLDENRLILSYSL 143**

**Int Num 2551 – alternate alignment**

**E-value 2.8E-5**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDD-QNEYMLAASYRME-----NLYFAGLFTDGELAK---DVDYTGYELAAGYKLGQAAFTATYNNAETAK--- 088**

**3szv\_A 000 SDAFDFAGGDYRLTP-ALTASLHQGRLKDIYRQTFAGLVHTLDLGGQRSLKSDLRFARASEDGGFRELDNRAFGALFSLRLGAHAVAAGYQRISGDDPYP 099**

**6ehb\_A 089 -------------------KTSADNFAIDATYYFK----PNFRSYISYQFNLLDS 120**

**3szv\_A 100 YIAGSDPYLVNFIQIGDFGNVDERSWQLRYDYDFGALGLPGLSFMSRYVSGDNVA 154**

**Int Num 2948 – Loop to hairpin**

**E-value 4.1E-4**

**6ehb\_A 000 NGEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEY-MLAASYRM-ENLYFAGLFTDGELAKDVDYTGYELAAGYKLGQ-----AAFTATYNNAETAK---- 089**

**4frx\_A 000 VDNRAFSGLFTYTVS--GHSIGAGYQILNGDSDFPFLNRGDGEGSTAYLITDVQIGKF-QRAGERTWQVRYGYDFATVGVPGLTFNTIYLSGDKIKTARG 097**

**6ehb\_A 090 KTSADNFAIDATYYFK----PNFRSYISYQFNLLDSDKA---SKVASEDELAIGLRYDF 141**

**4frx\_A 098 DQSEWERDISLAYVIPDGTFKGLGFTWKNASFRSGLPAAGSSNNQRDQDENRLIVSYTL 156**

**Int Num 2948 – alternate alignment**

**E-value 1.0E-3**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDD-QNEYMLAASYRM--E--NLYFAGLFTDGELA-------------------------KDVDYTGYELAAGY 070**

**4frx\_A 000 SNKFYYAGGDYKVNK-DLTLQYYYGNLDDFYKQHFLGLIHNWQIGPGVLKTDLRAFDSSSDGKNGSRSGRADGYVSSGYYGSGVTKGEVDNRAFSGLFTY 099**

**6ehb\_A 071 KLGQAAFTATYNNAETAK---------------------------KTSADNFAIDATYYFK----PNFRSYISYQFNLLDS 120**

**4frx\_A 100 TVSGHSIGAGYQILNGDSDFPFLNRGDGEGSTAYLITDVQIGKFQRAGERTWQVRYGYDFATVGVPGLTFNTIYLSGDKIK 180**

**Int Num 3173 – Loop to hairpin**

**E-value 1.5E-4**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRME---NLYFAGLFTDGELAKDVDYTGYELAAGYKLGQ----------AAFTATYNNAETA 087**

**5dl7\_A 000 DNRHISGLFGLNYQ--NHTVSLGYMQSFGSTGL----PFLSGTESPVVLD--FMSSDY-SNKDEKVYSIRYEYDFKNARIGDVSLNGLRFMTRYAKGEDI 091**

**6ehb\_A 088 K-------KTSADNFAIDATYYFK----PNFRSYISYQFNLLDSDKASKVASEDELAIGLRYDF 140**

**5dl7\_A 092 DLLQYGDQRFKEDSLEFDLGYKIPEGKLKGLGMRARFSHYRNDMPTNMTFHSANETRLNVDYTF 155**

**Int Num 3174 – alternate alignment**

**E-value 7.4E-5**

**5dl7\_A 000 TDSFYTLGGSYQLK--DYRLRAYHAELKDIYQQQFLGFNGKQPLNDQLNFLSDVRFFNSEETGSKKIGEVDNRHISGLFGLNYQNHTVSLGYMQSFGSTG 098**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDD-QNEYMLAASYRME-----NLYFAGLFTDGELAK-----DVDYTGYELAAGYKLGQAAFTATYNNAETAK- 088**

**5dl7\_A 099 LPFLSGTESPVVLDFMSSDYSNKDEKVYSIRYEYDFKNARIGDVSLNGLRFMTRYAKGEDID 160**

**6ehb\_A 089 ---------------------KTSADNFAIDATYYFKP---------NFRSYISYQFNLLDS 120**

High E-values

**Int Num 373**

**E-value 1.8E-3**

**1prn\_A 000 VTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVGA--AYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFG----A-TTVRAYVSDIDR-A---- 088**

**3szd\_A 000 DNRTVSALFSARYGLHTLYLGLQKVSGDD--GWMRVNGTSGGTLA----N-DSYNASYDN-PGERSWQLRYDFDFVGLGLPGLTFMTRYLHGDHVRLAGV 092**

**1prn\_A 089 ---GADTAYGIGADYQF--A--EGVKVSGSVQSG 115**

**3szd\_A 093 TDDGSEWGRESELGYTLQSGAFKRLNVRWRNSSQ 126**

**Int Num 396**

**E-value 2.7E-3**

**1prn\_A 000 VTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFV-GAA-YKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFG----A-TTVRAYVSDIDR-A---- 088**

**4frx\_A 000 DNRAFSGLFTYTVSGHSIGAGYQILNGDS--DFPFLNRGDGEGST-AYLITDVQIGKFQR-AGERTWQVRYGYDFATVGVPGLTFNTIYLSGDKIKTARG 096**

**1prn\_A 089 -GADTAYGIGADYQFA----EGVKVSGSVQSG 115**

**4frx\_A 097 DQSEWERDISLAYVIPDGTFKGLGFTWKNASF 128**

**Int Num 410**

**E-value 1.1E-3**

**1prn\_A 000 DNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGATTVR-AYVSDIDR-AGADTAYGIGADYQFA-----EGVKVSGSVQSG 85**

**5dl5\_A 000 TNNIWAISGTYATGPH-SVMLAYQQNTGNV---GYDYGQN-ADGFQSIYLPNSYMSDFIGNHEKSAQIQYNVDFGKLGVLPGLNWTTAFVYG 87**

**Int Num 411**

**E-value 1.8E-3**

**1prn\_A 000 VTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVG-AAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFG-----A-TTVRAYVSDIDR------ 087**

**5dl5\_A 000 TNNIWAISGTYATGPHSVMLAYQQNTGN----VGYDYGQNADGFQSIYLPNSYMSDFIG-NHEKSAQIQYNVDFGKLGVLPGLNWTTAFVYGWDIKVRNV 095**

**1prn\_A 088 --AGADTAYGIGADYQFA----EGVKVSGSVQSG 115**

**5dl5\_A 096 TDDAQEREFFNQVKYTVQSGFAKDASLRIRNSYY 129**

**Int Num 413**

**E-value 1.4E-3**

**1prn\_A 000 VTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVGAAYKFNDA--GTVGLNWYDNGLSTAGDQVTLYGNYAFG---A-TTVRAYVSDIDR------- 087**

**5dl6\_A 000 DNDLYHAHFELKHQNHKFIFGTFQHHGD----TAF----PYLTGGETGLLIDTWPGEFL-NPKEKAYSFRYEYDFKEYVPGLCFMTRYTTGHNIYAPNLG 091**

**1prn\_A 088 --AGADTAYGIGADYQFA----EGVKVSGSVQSG 115**

**5dl6\_A 092 GTNLKERETDFDLGYTVQSGWLKNLGLRARYAIY 125**

**Int Num 924**

**E-value 3.0E-3**

**2fgr\_A 000 TDRDEITLGASYNFGVAKLSGLLQQTKFKRDIGGDIKTNSYMLGASAPVGGVGEVKLQYALYDQKAIDSKAHQITLGYVHNLS---KRTALYGNLAFLKN 97**

**5dl6\_A 000 VDNDLYHAHFELKHQNHKFIFGTFQHHGDTA-------------FPYLTGGETGLLID-TWPG-EFLNPKEKAYSFRYEYDFKEYVPGLCFMTRYTTGHN 85**

**Int Num 2051**

**E-value 3.0E-3**

**3jty\_A 000 ENRTWSGLFSAKYG--GNTFYVGLQKLTGDSAWMRVNG--TSGGTLANDSYNASY-DNAKEKSWQVRHDYNFAALGVPGLTLMNRYISGSNVHTATVSDG 095**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRMENLYFAGLFTDGELAKDVDYTGYELAAGYKLG----Q-AAFTATYNNAETAK-----KT 090**

**3jty\_A 096 KEWGRESEVAYTVQSGTLKNLNLKWRNSTMRRDF 129**

**6ehb\_A 091 SADNFAIDATYYFK----PNFRSYISYQFNLLDS 120**

**Int Num 2421**

**E-value 2.0E-3**

**3sy7\_A 000 SNTTWSLAAAYTLD--AHTFTLAYQKVHGDQPFDYIGFGRNGSGAGGDSIFLANSVQYSDF-NGPGEKSWQARYDLNLASYGVPGLTFMVRYINGKDIDG 097**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYM-LA-AS--YRMEN--LYFAGLFTDGELAKDVDYTGYELAAGYKLGQ-----AAFTATYNNAETAK- 088**

**3sy7\_A 098 TKMSDNNVGYKNYGYGEDGKHHETNLEAKYVVQSGPAKDLSFRIRQAWHRANA 150**

**6ehb\_A 089 -----------------KTSADNFAIDATYYF----KPNFRSYISYQFNLLDS 120**

**Int Num 2443**

**E-value 2.20E-3**

**3sy9\_A 000 DNNTYSLHFAVGYR--QHTVTAVLQKVNGNTPFDYINQ--GDSIFLDNSQQYSDF-NGPNEKSWKLQYDYDFVALGVPGLSASASYSRGKLDLTRVDPDS 095**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRMENLYFAGLFTDGELAKDVDYTGYELAAGYKLGQ-----AAFTATYNNAETA-------- 087**

**3sy9\_A 096 PGYGGWYSADGKNAKHWERDLDLQYVVQGGPAKDLSLRLRWATHRGTG 143**

**6ehb\_A 088 -----------KKTSADNFAIDATYYFK----PNFRSYISYQFNLLDS 120**

**Int Num 2471**

**E-value 2.7E-3**

**3syb\_A 000 DNDTWSLAFTLGHR--AHALTLAYQQVDGNEYFDYVHET-SAIFLANSM--LADY-NSPNEKSAQIRYETDWSYYGVPGLSTGVWYVKGWDIDGTHYDGD 094**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRMENLYFAGLFTDGELAKDVDYTGYELAAGYKLGQ-----AAFTATYNNAETAK------- 088**

**3syb\_A 095 RNGAYGNYAEVRAQDGEKHHELGLMAAYKVQNGPIKDSTFKLTYMMHKASQ 145**

**6ehb\_A 089 ---------------KTSADNFAIDATYYFK----PNFRSYISYQFNLLDS 120**

**Int Num 2576**

**E-value 3.4E-3**

**3t0s\_A 000 DNRNLNAMLTLRAG--AHAFGIGVQKMIGNDAFPVLNG--YTTPYVANLMAYQTF-TRPQEKSWQLRYDYDFAGLGLPGLNLMTRYVQGRDIDRGAGRAD 095**

**6ehb\_A 000 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRMENLYFAGLFTDGELAKDVDYTGYELAAGYKLGQ-----AAFTATYNNAETAK------K 089**

**3t0s\_A 096 DSEWERNTDLSYVIQSGPLKSVALKWRNITYRSR 129**

**6ehb\_A 090 TSADNFAIDATYYFK----PNFRSYISYQFNLLD 119**

**Int Num 3145**

**E-value 2.3E-3**

**5dl5\_A 000 KTNNIWAISGTYATG--PHSVMLAYQQNTGNVGYDYGQNADGFQSIYLP-NSYMSDF-IGNHEKSAQIQYNVDFGKLGVLPGLNWTTAFVYGWDIKVRNV 096**

**6ehb\_A 000 NGEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAAS-YRMENLYFAGLFTDGELAKDVDYTGYELAAGYKLG-----Q-AAFTATYNNAETA----- 088**

**5dl5\_A 097 TDDAQEREFFNQVKYTVQSGFAKDASLRIRNSYYRASDAYQGAYIGDTNEWRIFLDIPV 155**

**6ehb\_A 089 -KKTSADNFAIDATYYFK----PNFRSYISYQFNLLDSDKA-SKVASEDELAIGLRYDF 141**