Large rearrangements

**Int Num 313**

**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 1211**

**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 1639**

**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 2112**

**E-value 2.0E-5**

**CONTIGUOUS ALT ALIGNMENT**

**3nsg\_A 000 GNKLDLYGKAVGRHVWTTTGDS--------KNADQTYAQIGFKGETQINTDLTGFGQWEYRTKADRAE----GEQQNSNLVRLAFAGLKYA-EVGSIDYG 087**

**5ldv\_A 000 IKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVIAG 100**

**3nsg\_A 088 RNYGIVYDVESYTDMAPYFSGETWGGAYTDNYMTSRAGGLLTYRNSDFFGLVDGLSFGIQYQGKNQDNH---------------------SINSQNGDGV 166**

**5ldv\_A 101 KQQLNIIWTDNGVDG-LVGTGV-----------------KVVNNS--I----DGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIGNLY 176**

**3nsg\_A 167 GYTMAYEFD----GFGVTAAYSNSKRTNDQQDRDGNGDRAESRAVGAKYDA--N---NVYLAAVYAETRNMSIVENTVTDTVEMANKTQNLEVVAQYQFD 257**

**5ldv\_A 177 GAAAVGSYDLAGGQFNPQLWLAYWD------------QVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDD-----KKTYANGNLFALKGSIEVN 259**

**3nsg\_A 258 FGLRPAISYVQSKGKQLN---------G-----A------------GGSADLAKYIQAGATYYFNKNMNVWVD--YRFNLL 310**

**5ldv\_A 260 -GWDASLGGLYYGDKEKASTVVIEDQGNLGSLLAGEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKT 339**

**Int Num 2113**

**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 2855**

**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 3207**

**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 3225**

**E-value 8.3E-9**

**5ldv\_A 000 EAIKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVI 100**

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

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

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

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

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

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

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

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

**5nxr\_A 330 EYGINTDNVLGLGLVYQF 347**

Loop to hairpin

**Int Num 808**

**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 820**

**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 2225**

**E-value 4.6E-4**

**3prn\_A 000 TEEFGIAADWSND-----MISLAAAYTTDAGG------IVDNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAF--GAT-TVRAYV-SDID 085**

**3sy7\_A 000 YRQYYLNSNYTIPLASDQSLGFDFNIYRTNDEGKAKAGDISNTTWSLAAAYTLDAH-TFTLAYQKVHGDQPF-DYIGFGRNGSGAGGDSIFLANSVQYSD 098**

**3prn\_A 086 R-AGADTAYGIGADYQFA----EGVKVSGSVQSG 114**

**3sy7\_A 099 FNGPGEKSWQARYDLNLASYGVPGLTFMVRYING 132**

**Int Num 2232**

**E-value 7.3E-4**

**3prn\_A 000 TEEFGIAADWSN--DM--ISLAAAYTTDAGG------IVDNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFG--ATTVRA--YVSDIDR 086**

**3szd\_A 000 YRQQYLQLQHSQPLGDWLLGANLGGFRGRDAGSARAGKLDNRTVSALFSARYGLH-TLYLGLQKVSGDD---GW----MRVNGTSGGTLANDSYNASYD- 091**

**3prn\_A 087 AGADTAYGIGADYQFA----EGVKVSGSVQSG 114**

**3szd\_A 092 NPGERSWQLRYDFDFVGLGLPGLTFMTRYLHG 123**

**Int Num 2250**

**E-value 9.8E-4**

**3prn\_A 000 DNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGA-TTVRAYVSDIDR-AGADTAYGIGADYQFA----EGVKVSGSVQSG 85**

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

**Int Num 2278**

**E-value 6.4E-4**

**3prn\_A 000 ISLNGYGRFGLQYVEDRGVGLE-----DTIISSRLRINIVGTTETDQGVTFGAKLRMQWDDGDA--------FAGTAGNAAQFWTSY--NGVTVSVGNVD 085**

**5ldv\_A 000 VDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVIAGKQQ 100**

**3prn\_A 086 TAFDSVAL----TYDSEMGYE---WSSFGDAQSSFFAYNSKYDASGAL--------------------DNYNG-----IAVTY-SISGVNLYLSYVDPDQ 152**

**5ldv\_A 101 LNIIWTDNGVDGLVGTGVKVVNNSIDGLTLA-AFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIGNLYGAAAVGSYDLAGGQFNPQLWLAYWD- 198**

**3prn\_A 153 TVDSSLVTEEFGIAADWSNDM-----ISLAAAYTTDAGG--------IVDNDIAFVGAAYKFNDAGTVGLNWYDNGL----------------------- 216**

**5ldv\_A 199 -----QVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDDKKTYANGNLFALKGSIEV-NGWDASLGGLYYGDKEKASTVVIEDQGNLGSLLAGEE 292**

**3prn\_A 217 ------S------TAGDQVTLYGNYAFG-ATTVRAYVSDIDRA---------GADTAYGIGADYQFAEGVKVSGSVQSGF-AN--------E-TVADVGV 284**

**5ldv\_A 293 IFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNTNESADHSTVRLQA 392**

**3prn\_A 285 RFDF 288**

**5ldv\_A 393 LYKF 396**

**Int Num 2716**

**E-value 3.3E-6**

**3wi5\_A 000 VTLYGTIKAGVETSRSVFHQNGQVTEVTTATGIVDLGSKIGFKGQEDLGNGLKAIWQVEQKASIAG--------TDSGWGNRQSFIGLKG--GFGKLRVG 090**

**5ldv\_A 000 VDVSGVLRYRYDTGNFDKNFL-NNSNLNN--SKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSVIAG 097**

**3wi5\_A 091 RLNSV--LKDT--G--DIN-------PWDSK-S--DYLG-VNKIAEPE---------------------ARL-I----SVRYDSP-EFAGLSGSVQYALN 146**

**5ldv\_A 098 KQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIGNLYGAAAVGSYDLAGGQFNPQLWLAYW 197**

**3wi5\_A 147 DNAGRHNSESYHAGFNYKNG---GFFVQYGGAYKRHHQVQEG---LNIEKYQIHRLVSGYDNDALYASVAVQQQDAK-----------L------TD--- 220**

**5ldv\_A 198 D----QVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDDKKTYANGNLFALKGSIEVNGWDASLGGLYYGDKEKASTVVIEDQGNLGSLLAGEEI 293**

**3wi5\_A 221 A-------SNSHNSQTEVAATLAYRFG-NVTPRVSYAHGFKGLVAK-ADIGNRYDQVVVGAEYDFSKRTSALVSAGWLQEGKGE---NKFVATAGGVGLR 308**

**5ldv\_A 294 FYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNTNESADHSTVRLQAL 393**

**3wi5\_A 309 HKF 311**

**5ldv\_A 394 YKF 396**

**Int Num 2780**

**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 2955**

**E-value 1.2E-4**

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

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

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

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

**Int Num 3151**

**E-value 5.1E-4**

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

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

**5dl6\_A 093 TNLKERETDFDLGYTVQSGWLKNLGLRARYAIYDNNMLSTANIKPVNETRINIDYTW 149**

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

**Int Num 3229**

**E-value 7.0E-9**

**5ldv\_A 000 EEAIKDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLTYTNEDVATSV 100**

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

**5ldv\_A 101 IAGKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDLLGQSTYVGNGKNNNDSFKLDSIGNLYGAAAVGSYDLAGGQFNPQLWL 200**

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

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

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

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

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

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

**6ehd\_A 300 AEVKATKVDSANNFGIGARYYW 321**

Different patterns of insertion

**Int Num 1492**

**E-value 1.1E-4**

**LTH**

**2y0l\_A 000 DNKSLNGMFTYSLGNH-AFGAAWQRMNGDD-------AFPYLEGSNPYLVNFVQVNDFAGPKERSWQLRYDYDFVGLGIPGLTFMTRYVKG 83**

**3prn\_A 000 DNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGATTVRAYV-SDIDR-AGADTAYGIGADYQFA----EGVKVSGSVQSG 85**

**Int Num 1494**

**E-value 7.0E-5**

**ALT ALIGNMENT WITH CONTIG SECTION**

**2y0l\_A 000 KERSWQLRYDYDFVGLGIPGLTFMTRYVKGDNVELAGQSGEGREWERNTELQYVFQSGALKNLGIRWRNATFRSNFTRDIDENRLIVSYTL 91**

**3prn\_A 000 AGDQVTLYGNYAFG----A-TTVRAYVSDIDR--------AGADTAYGIGADYQFA----EGVKVSGSVQSGF----ANETVADVGVRFDF 70**

**Int Num 2229**

**E-value1.0E-4**

**ALT ALIGNMENT WITH LTH**

**3prn\_A 000 DNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGAT--TVRAYVSDIDR-AGADTAYGIGADYQFA----EGVKVSGSVQSG 85**

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

**Int Num 2230**

**E-value 2.0E-4**

**ALT ALIGNMENT WITH DIFF LTH**

**3prn\_A 000 VTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVGAAYKFNDAGTVGLNWYDNGLS-TAGDQVTLYGNYAFG----A-TTVRAYVSDIDR------- 087**

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

**3prn\_A 088 AGADTAYGIGADYQFA----EGVKVSGSVQSG 115**

**3sys\_A 094 GGKEWERDVELGYTVQSGPLARLNVRLNHASN 125**

**Int Num 2538**

**E-value 1.5E-4**

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

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

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

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

**Int Num 2539**

**E-value 2.8E-5**

**ALT ALIGNMENT WITH DOUBLE-HAIRPIN SHIFT FROM ABOVE**

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

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

**3szv\_A 100 YIAGSDPYLVNFIQIGDFGNVDERSWQLRYDYDFGALGLPGLSFMSRYVSGDNVA 154**

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

**Int Num 2937**

**E-value 4.1E-4**

**ALT ALIGNMENT WITH DOUBLE-HAIRPIN SHIFT FROM BELOW**

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

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

**4frx\_A 100 TVSGHSIGAGYQILNGDSDFPFLNRGDGEGSTAYLITDVQIGKFQRAGERTWQVRYGYDFATVGVPGLTFNTIYLSGDKIK 180**

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

**Int Num 2938**

**E-value 1.0E-3**

**LTH**

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

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

**4frx\_A 098 DQSEWERDISLAYVIPDGTFKGLGFTWKNASFRSGLPAAGSSNNQRDQDENRLIVSYTL 156**

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

**Int Num 3165**

**E-value 1.5E-4**

**LTH**

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

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

**5dl7\_A 092 DLLQYGDQRFKEDSLEFDLGYKIPEGKLKGLGMRARFSHYRNDMPTNMTFHSANETRLNVDYTF 155**

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

**Int Num 3166**

**E-value 7.4E-5**

**ALT ALIGNMENT WITH DOUBLE-HAIRPIN SHIFT FROM ABOVE**

**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**