

## Large Rearrangements

Int Num 317		E-value 1.1E-6	
1pho_A 007	DGNKLDVYGVKVKAMHYMSDNA-S-----KDGDQSYIRFGFKGETQINDQLTGYGRWEAEFAGNKA-----ESDTAQQKTRLAFAGLKYK-DLGSFDY	092	
5ldv_A 009	AIKDVVDVSGVLRIRYDTGNFDDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLYTTNEDVATSVIA	108	
1pho_A 093	GRNLGALYDVEAWTD-M-FPEF---G-GDSSAQTDNFM--TKRASGLATY-----RNTDFFGVIDGLNLTLYQYQK--NENRD-----	159	
5ldv_A 109	GKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDDLGGQSTYVGNKGNNNDSFKLDSIG--NLYGAAAVGSYDLAEGQFNPQLWL	206	
1pho_A 160	-VKKQNGDGFSTSLTYDFG---GSDFAISGAYTNSDRTNEQNLSRGTKRAEAWATGLKYDANNIYLATFYSETRKM-----T-----PI--	236	
5ldv_A 207	AYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELD--DKKTYANGNLFALKGSIEVNGWDASLGGLYYGDKKASTVVIEDQGNLGSLLAGEE	304	
1pho_A 237	-T-----GGFANKTQNFEEVAQYQDFGLRPSLGIVLSKKGDIIEG-IGDEDLVNYYIDVGATYYFNKNMSAFVDYKINQLSDSNK-LNINNDIDVAVGM	326	
5ldv_A 305	IFYTTGSRNLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPLNFSAFYSYVNLDDQGVNTNESADHSTVRLQA	404	
1pho_A 327	TYQF	330	
5ldv_A 405	LYKF	408	
Int Num 1308		E-value 9.8E-6	
2por_A 002	VKLSGDARMGMVYNGDDW-----NFSRSRVLFTMSGTTDSGLEFGASFKAHESV-----GAETGEDGTVFLSG--AFGKIEMGDAL	076	
5ldv_A 013	VDVSGVLRIRYDTGNFDDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLYTTNEDVATSVIAGKQ	112	
2por_A 077	GASEALFG--D-L-YE---VGYTDL---DDRGGNDIPYLTGDE-RLTAEDNP-----VILLYTY-SAGA-FSVAASMSDG--KVG-E-----TSEDD	146	
5ldv_A 113	LNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDDLGGQSTYVGNKGNNNDSFKLDSIGNLYGAAAVGSYDLAEGQFNPQLWLAYWDQV	212	
2por_A 147	AQEMAVAAAYTFG---N--YTVGLGYEKIDSPDT---ALMADMEQLELAAIAKEGATNVKAYYADGELDRD-----FARA--VF--DL--TP-VA	221	
5ldv_A 213	AFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELDKDKTYANGNLFALKGSIEVNGWDASLGGLYYGDKKASTVVIEDQGNLGSLLAGEEIFYTTGSR	312	
2por_A 222	AAATAVDHAKYGLSVDSFTFG-ATTVGGYVQVLDLDT-----IDDVYYGLGASYDLGGGASIVGGIADNLDLP-----NSDMVADLGVKKFF	301	
5ldv_A 313	LNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPLNFSAFYSYVNLDDQGVNTNESADHSTVRLQALYKF	408	
Int Num 1731		E-value 9.5E-6	
2zfg_A 007	DGNKVDLYGKA-VGLHYFSKNGGENS---YGGNGDMTYARLGFKGETQINSDLTGYGQWEYFQGNNS---GADAQTGNKTRLAFAGLKYA-DVGSFDY	098	
5ldv_A 009	AIKDVVDVSGVLRIRYDTGNFDDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLYTTNEDVATSVIA	108	
2zfg_A 099	GRNYGVVYDALG-YT-DMLPEFGGDTA-YSD----DFF--VGRVGGVAT-----YRNSNFGLVDGLNFAVQYLGK--NERDT-----	165	
5ldv_A 109	GKQQLNIIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDDLGGQSTYVGNKGNNNDSFKLDSIG--NLYGAAAVGSYDLAEGQFNPQLWL	206	
2zfg_A 166	-ARRSNGDGVGGSISYIE---GFGIVGAYGAADR TNLQEAQPLGNKGKAEQWATGLKYDANNIYLAANYGETRNA-----TPI--TNKFT-	245	
5ldv_A 207	AYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELD--KKTYANGNLFALKGSIEVNGWDASLGGLYYGDKKASTVVIEDQGNLGSLLAGEE	304	
2zfg_A 246	----N--TSGFANKTQDVLLVAQYQDFGLRPSIAYTKSKAKDVEG-IGDVLNYYFEVGATYYFNKNMSTYVDYIINQLSDSNK-LGVGSDDTVAVGI	336	
5ldv_A 305	IFYTTGSRNLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPLNFSAFYSYVNLDDQGVNTNESADHSTVRLQA	404	
2zfg_A 337	VYQF	340	
5ldv_A 404	LYKF	408	
Int Num 2194		E-value 3.7E-9	
3nsg_A 005	NKDGNKLDLYGKAVGRHVWTTTGDSK-----NADQTYAQIGFKGETQINTDLTGFGQWEYRTKADRAE-----GEQQNSNLVRLAFAGLKY--AEVGS	090	
5ldv_A 007	EEAIKDVVDVSGVLRIRYDTGNFDDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLYTTNEDVAT-S	105	
3nsg_A 091	IDYGRNYGIVYDVESYTDMAPIYFSGET-----WGGA-----YTDNYMTSRAGG-----LLTYRNSDFGLVDGLSFGIYQYQGN--	159	
5ldv_A 106	VIAGKQQLNIIWTDNGVDG-LVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDDLGGQSTYVGNKGNNNDSFKLDSIGNL-----YGAAAVGSYDLAEG	197	
3nsg_A 160	QDNHS-----INSQNGDGVGYTMAEYFD-----GFGVTAAYSNSKRTNDQQDRDNGDRAESRAVGAKYDANNVYLAAVYAETRNMS-----IVENT	241	
5ldv_A 198	GQFNPQLWLAYWDQVAFFYAVDAAYSTTIFDGINWTLEGAYLGNSLDSELD--KKTYYANGNLFALKGSIEVNGWDASLGGLYYGDKKASTVVIEDQGNL	296	
3nsg_A 242	----V-----TD---TVEMANKTONLEVVAAQYQDFGLRPAISYVQSKGQLNGAGGSADLAKYIQAGATYYFNKNMNVVVDYRFLNLLDENDYSSSYVG	328	
5ldv_A 297	GSLLAGEEIFYTTGSRNLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYSPLNFSAFYSYVNLDDQGVNT-NESA	395	
3nsg_A 329	TDDQAAVGITYQF	341	
5ldv_A 396	DHSTVRLQALYKF	408	
Int Num 2866		E-value 1.1E-8	
4d65_A 008	GNKLDVYQIDVRHYFADAKSGE-----DGDDSRVRLGFKGDTQITDQLIGFGRFEWETSTNKA-----ETSNDNQNRLAYAGLKFA-DYGSLLDYG	092	
5ldv_A 010	IKDVVDVSGVLRIRYDTGNFDDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVDGGTGVDNATNAEKGLFVRQLYLYTTNEDVATSVIAG	109	

4d65_A	093	RNYGV	VIYDTNAWTDVLP	WLGADT-----M-DQ-ED--TF--MMGRNRN-L--L-----TYRNNNGFGYIDG-L	SFALQYQGKN--GDQNKSTG	163
5ldv_A	110	KQQLNIIWTDNGVDG-LV	GTGVKVVNNSID	GLTLAAFAVDSFMAAEQGSDDLQGQSTYVGNKGNNNDSFKLDS---	IGNLYGAAAVGSYDLA	205
4d65_A	164	SSALDNN	GDGYGFSTAYELG---	WGLSIGGGYSNSSRTPSQNNIKTGATGKRAEAWN	VGSKLELDEL	245
5ldv_A	206	LAYWD	QVAFFYAVDAAYSTTIFDGIN	NWTLLEGAYLGNSLDSELD	---KTTYANGNLFALKGSIEVNGWDASLGGLYYGDK	302
4d65_A	246	-----D---	AEAIANKTENLEL	VALYSFDFGLTPSIGYNQSKGK	NLGN-YGNKDLVKYIAVGASYDE	335
5ldv_A	303	EEIFYTTGSRLNGDT	GRNIFGYVTGGYTFNET	VRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYS	PKLNFSAFYSYVNL	400
4d65_A	336	GLGLIYQF	343			
5ldv_A	401	RLQALYKF	408			

Int Num 3213  
E-value 4.1E-9

5fvn_A	005	NKDGNK	LDLYGKVDGLHYFSDDDSQ-----	DGDQTYMRLGFKGETQ	NDQLTGYGQWEYQIQGNSG-----	E-NENNSWTRVAFAGLKF--GDAGS	087
5ldv_A	007	EEAIKDV	DVSGVLRIRYDTGNF	DKNFLNNSNLNNSKQDHKYRAQVNFSA	AIADNFKAFVQFDYNAVDGGTGVDNATNAE	GLFVRQLYLTYNEDVAT-S	105
5fvn_A	088	FDYGRNY	GVVDVTSWTD--VLPEFG--	GDTYGS--D-NF--MQQRGN-G--FA-----	TYRNSDFFG	LDVG-LNFAVQYQGKNGSASGED	160
5ldv_A	106	VIAGK	QQLNIIWTDNGVDGLVGTGVKVVNNSID	GLTLAAFAVDSFMAAEQGSDDLQGQSTYVGNKGNNNDSFKLDSI---	IGNLYGAAAVGSYDLA	GGQFNF	202
5fvn_A	161	QTNNGR	TELRQNGDGVGGSITYNLG--E--	GFGIGTAVSSSKRTSSQNDLTYGNGDRAET	YTGGKLYDANNIYLAAQYTQTYNA-----	TRV--	243
5ldv_A	203	QLW--	LAYWDQVAFFYAVDAAYSTTIFDGIN	NWTLLEGAYLGNSLDSELD	---KTTYANGNLFALKGSIEVNGWDASLGGLYYGDK	KEASTVVIEDQGNLGS	298
5fvn_A	244	--G-----N-----	LGWANKAQNFEVVAQYQFDFGL	RPSVAYLQSKGKDL	LENGYGDQDLKYVDVGATYYFNK	NMSTYVDYKINLLDDKEFTRNAGIST	330
5ldv_A	299	LLAGEE	IFYTTGSRLNGDTGRNIFGYVTGGYTFNET	VRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYS	PKLNFSAFYSYVNL	DQGVNT--NESAD	396
5fvn_A	331	DD	IVALGLVYQF	332			
5ldv_A	397	HSTVRL	QALYKF	408			

Int Num 3231  
E-value 8.3E-9

5nxxr_A	006	KDGNK	LDVYGKVDVRHYFASADK	GKKS-----EDGDDSRVRLGVKGD	QTIDQLTGFRFEWE	TKNKA-----ENEGENKNRLAYAGLKFA-D	FGSID	093
5ldv_A	008	EAIKDV	DVSGVLRIRYDTGNF	DKNFLNNSNLNNSKQDHKYRAQVNFSA	AIADNFKAFVQFDYNAVDGGTGVDNATNAE	GLFVRQLYLTYNEDVATSVI		107
5nxxr_A	094	YGRNYG	VVYDTNAWTD--VFPLW--	GADTMA-----QTDNFM	TSRNRN-L--L-----TYRNNNAFGYVDG-L	SFALQYQGKN	GDNNKSSA	166
5ldv_A	108	AGKQQLNIIWTDNGVDGLVGTGVKVVNNSID	GLTLAAFAVDSFMAAEQGSDDLQGQSTYVGNKGNNNDSFKLDS---	IGNLYGAAAVGSYDLA	GGQFNF			203
5nxxr_A	167	---GMAKD	NGDGYGFSTAYELG---	GVTILGGGYSNSSRTPNQKAGVVTSE	SGDYSYATGKRAQAWN	VGGKFANNVYLAAMYQGTQNT-----		249
5ldv_A	204	LWLAYWD	QVAFFYAVDAAYSTTIFDGIN	NWTLLEGAYLGNSLDSELD	---KTTYANGNLFALKGSIEVNGWDASLGGLYYGDK	KEASTVVIED		292
5nxxr_A	250	-SRY-----GD-----	LDLIANKTENVELVAQYIFDFGL	KPSIGYNQSKGKNLNGYDN	QDLVKYISVGSYYYFNK	NMSAVVDYKINLLKDNDFTK		334
5ldv_A	293	QGNLGS	LLAGEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNET	VRVGADFVYGGTKTEATTHLGGGKKLEAVARVDYKYS	PKLNFSAFYSYVNL	DQGVNT--		391
5nxxr_A	335	EYGINTDN	VLGLGLVYQF	352				
5ldv_A	392	-NESADHSTVRL	QALYKF	408				

## Loop to hairpin

Int Num 372  
E-value 4.6E-4

1prn_A	161	TEEF	GIAADWSND-----MI	SLAAAYTTDAGG-----IVDND	IAFVGAAAYKFNDAGTVGLN	WYDNLSTAGDQVTLYGNYAF--GAT-TV	RAYVSD	ID	245
3sy7_A	210	VRQYYL	NSNYTIPLASDQSLGF	DFNIYRTNDEGAKAGDISNTTWSLAAAYT	LDLDAH-TFTLAYQKVHGDQ-PFDYIGFGRNGSGAGGDS	SIFLANSVQ	SD		307
1prn_A	246	R-AGADT	AYGIGADYQFA---	EGVKVSGSVQSG	274				
3sy7_A	308	FNGP	GKESWQARYDLNLASYGV	PGLTFMVR	YING	341			

Int Num 380  
E-value 6.7E-4

1prn_A	190	DND	IAFVGAAAYKFNDAGTVGLN	WYDNLSTAGDQVTLYGNYAFG--ATTV-R-AYVSD	IDRAGADTAYGIGADYQFA---	EGVKVSGSVQSG	274	
3szd_A	248	DNRTVS	ALFSARYGLH-TLYLGLQK	VS	GDD---G---WMRVNGTSGGTLANDSYNASYD-NP	GERSWQLRYDF	FVGLGLPGLTFMTRYLHG	331

Int Num 385  
E-value 6.7E-4

1prn_A	160	VTE	EF	GIAADWSNDMI	SLAAAYTTDAGGIVDND	IAFVGAAAYKFNDAGTVGLN	WYDNLSTAGDQVTLYGNYAFG--A-TV	RAYVSD	IDR-----	247
3t0s_A	244	DNRRNL	NAMLTIRAGAHAFGIGVQ	KMIGN---DAFPVLNGYT-TPY-VANILMAQ	YTFTR-PQEKSWQLRYDYDFAGLGLPGLNLMTRYVQGR	IDR	GAGR		336	
1prn_A	248	-AGADT	AYGIGADYQFA---	EGVKVSGSVQSG	274					
3t0s_A	337	ADD	SEWERNTDLSYVIQSGPLKSV	ALKWRNITY	369					

Int Num 395  
E-value 1.0E-3

1prn_A	190	DND	IAFVGAAAYKFNDAGTVGLN	WYDNLSTAGDQVTLYGNYAFGA-TV	RAYVSD	IDR-AGADTAYGIGADYQFA---	EGVKVSGSVQSG	264	
4frx_A	280	DNRAF	SGLFTTYT	VS	GH-SIGAGYQILNGDSDF-PFLNR-G	BEGEGSTAYLITDVQIGKFQ	RAGERTWQVRYGYDFATVGV	PGLTFNTIYLSG	367

Int Num 910  
E-value 2.8E-4

2fgr\_A 168 VGRYIGGYVAYDNGPLSASLGLAQQKTAVGGLATDRDEITLGASYNFGVAKLSGLLQQTQKFRDIGGDIKTNSYMLGASAPVG---GVGEVKLQYALYD 267  
4frx\_A 280 DNRAFSGLFTYTVSGHSIGAGYQILNGSD-----FPFLNRGDG-EGSTAYLITDVQIGKF-----QRAGERTWQVRYGYDFAATVGVPGLTFNTIYLSGD 370

2fgr\_A 266 QKA---IDSKAHQITLGIVHNLNLS-----KRTALYGNLAFLKND 299  
4frx\_A 369 KIKTARGDQSEWERDISLAYVIPDGTFKGLGFTWKNASFRSGL 279

Int Num 922  
E-value 6.8E-4

2fgr\_A 168 VGRYIGGYVAYDNGPLSASLGLAQQKTAVGGLATDRDEITLGASYNFGVAKLSGLLQQTQKFRDIGGDIKTNSYMLGASAPVG---GVGEVKLQYALYD 261  
5dl5\_A 274 TNNIWAISGTYATGPHSVMLAYQQNTGNVG-----Y-DYGQ-NA--DGFQSIYLPNSYMSDF-----IGNHEKSAQIQYNVDFGKLGVLPLNLTWTFVY 359

2fgr\_A 262 YDQ-KA---IDSKAHQITLGIVHNLNLS-----KRTALYGNLAFLKND 299  
5dl5\_A 360 GWDIKVRNVTTDDAQEREFFNQVKYTVQSGFAKDAFLRIRNSYRASD 273

Int Num 2791  
E-value 2.8E-5

4aui\_A 017 AMADVTLTYGTIKAGVETSRSAHHAQAQDRVKTATEIADLGSKIGKQEDLGNGLKAIWQLEQKAYVSG-----TDTGWGNRQSFGLKQ--GFGK 106  
5ldv\_A 009 AIKVDVDSGVLRYRYDTGNFDKNFL--NNSNLNNSK--QDHKYRAQVNFSAAIADNFKAFVQFDYNAVGGTGVNDATNAEKGLFVRQLYLYTNTEDVATS 105

4aui\_A 107 VRVGRLLNN--ILKDT---GNFNP-----WEGKSY-SGLSNIAQ--PEE-----R-HVS---VRIDSP-EFAGFSGSVQ 162  
5ldv\_A 106 VIAGKQQLNIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDDLQGSYTVNGKNNNSFKLDSIGNLYGAAAVGSYDLAEGQFNPQLW 205

4aui\_A 163 VVPNDNSGKNRSESYHAGFNKYND---EFFVQYAGSYKRNYT-----TEKHQVHRLVGGYDHDALYASVAVQQQDAKL-----T-WRD---D 238  
5ldv\_A 206 LAYWE---QVAFYAVDAAYSTTIFDGINWTLLEGAYLGNSLDSELDKKTYSANGNLFALKGSIEVNGWDASLGGLYGDKEKASTVVIEDQGNLGLLA 301

4aui\_A 239 N-----SHNSQTEVATTVAIRFG-NVTPRVSYAHGFKGSVYD-ADHDNTYDQVVVGAEXDFSKRTSALVSAGWLQKKGAE---KFWATVGG 320  
5ldv\_A 302 GEEIFYTTGSRNLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATHTLGGGKKLEAVARVDYKSPKLNFSAFYSYVNLDDQGVNTNESADHSTVR 401

4aui\_A 321 VGLRHKF 327  
5ldv\_A 402 LQALYKF 408

Int Num 2965  
E-value 1.2E-4

6ehb\_A 181 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRMEN-LYFAGLFTDGELAKDVDYTGYLEAAGYKLG---Q-AAFTATYNNAE TAK-----K 269  
4fso\_A 258 DNRAISLLLAYAQG--GHTLSAGWQRMNGASSM----PYLDGSNPLYANYLQVNDF-ANPEERSWQLRYDFDLRSVGVPGLSFMTRYVNGDHIRLANGDE 350

6ehb\_A 270 TSADNFAIDATYYFK----PNFRSYISYQFNLLSDSKASKVASEDELAIGLRYDF 320  
4fso\_A 351 GKWERDIELKYIVQSGRFKDLRLRLNATYRTDFER--SARDVDEVRLIASYNL 403

Int Num 2983  
E-value 1.9E-4

6ehb\_A 181 GEDGYSLSAIYTF-GDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKDVDYTGYLEAAGYKLGQ-----AAFTATYNNAE TAK----- 268  
4fsp\_A 262 DNRSFSGSLTYRLRN--GQAFGLGYQRMNGDHF----PYLEGTDPLYLVNF-GQYNDF-AEAGESSWQLRYDCDFAPLGVPLGLSLMTRYFSGHGAKPKGA 353

6ehb\_A 269 -KTSADNFAIDATYYFK----PNFRSYISYQFNLLSDSKASKVASEDELAIGLRYDF 320  
4fsp\_A 354 DGSREWERDSDLRYVLQGGALKGLGLVWRNATYRSF-----SRDIDENRLYLYTEL 405

Int Num 3159  
E-value 5.1E-4

6ehb\_A 181 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRMENLY-F-AGLFTDGELAKDVDYTGYLEAAGYKLG---Q-AAFTATYNNAE TA----- 245  
5dl6\_A 187 DNDLYHAHFEKHKQ--NHKFIFGTFQHHGDTAF----PYLTGGETGLLIDTWP-GEF-LNPKEKAYSFRYEYDKEYVPGLCFMTRYTGHNIYAPNLGG 305

6ehb\_A 246 KKTSAADNFAIDATYYFK----PNFRSYISYQFNLLSDSKASKVASEDELAIGLRYDF 298  
5dl6\_A 306 TNLKEREIDFDLGYTVQSGWLKNLGLRLARYAIYDNMMLSTANIKPVNETRINIDYTW 362

Int Num 3235  
E-value 7.0E-9

6ehd\_A 005 KSDAGTVDFYQGLRTELKFLFLEDKDP-----TIGSGSSRAGVDANYTVNDSLALQGVKVEFLKDS-----GDMYVRNHILGVKT--NFGKF 082  
5ldv\_A 007 EEAKIDVDVSGVLRYRYDTGNFDKNFLNNSNLNNSKQDHKYRAQVNFSAAIADNFKAFVQFDYNAVGGTGVNDATNAEKGLFVRQLYLYTNTEDVATS 106

6ehd\_A 083 SFGKQWTT--SDDV--Y-G-AD---YSY-FFGGTGLR--Y-G--TLSDA-----LHDSQ---VKYVY--EADSFVWKAGY 137  
5ldv\_A 107 IAGKQQLNIWTDNGVDGLVGTGVKVVNNSIDGLTLAAFAVDSFMAAEQGSDDLQGSYTVNGKNNNSFKLDSIGNLYGAAAVGSYDLAEGQFNPQLWL 206

6ehd\_A 138 GFPEDNAKQELAELYVGAFTF--G-DLAVHAGGGQNRDAKFKVGSNTVGTTTIDIKADVNTNSYFEVTGEYTGIDALIGVTTYNAELD-----V-- 221  
5ldv\_A 207 AYWDQ--VAFYAVDAAYSTTIFDGINWTLLEGAYLGNSLDSELD-----DKKTYANGNLFALKGSIEVNGWDASLGGLYGDKEKASTVVIEDQGNL 296

6ehd\_A 222 ----EN-----NPLVIDEDAISVAGTYKVADKTKLYAGYEYVMQEANT--GADEDGTLVLYLVGEYKFASWARVYAEYGYGDGTTLYGNTKGS 303  
5ldv\_A 297 GSLLAGEEIFYTTGSRNLNGDTGRNIFGYVTGGYTFNETVRVGADFVYGGTKTEATHTLGGGKKLEAVARVDYKSPKLNFSAFYSYVNLDDQGVNT----- 391

6ehd\_A 304 AEVKATKVDSANNFGIGARYYW 325  
5ldv\_A 392 ----NESADHSTVRLQALYKF 408

## Loop to hairpin with alternate alignments

Int Num 378 - Loop to hairpin

E-value 1.9E-4

```
1prn_A 190 DNDIAFVGAAAYKFNDAGTVGLNWDNGLSTAGDQVTLYGNYAFGAT--TVRAYVSDIDR-AGADTAYGIGADYQFA---EGVKVSGSVQSG 274
3sys_A 245 DSHTVYGLFSAGIGLH-TFYLGLQKVGGDS-----GWQSVYGSGRSMGNDMFNGNFTNADERSWQVRYDYDFVGLGWPGLIGMVRVYGHG 328
```

Int Num 379 - Alternate alignment, also loop to hairpin

E-value 2.8E-4

```
1prn_A 160 VTEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVGAAAYKFNDAGTVGLNWDNGLS-TAGDQVTLYGNYAFG---A-TTVRAYVSDIDR----- 246
3sys_A 245 DSHTVYGLFSAGIGLH-TFYLGLQKVGGDS--GWQSVYG-SS---GR-SMGNDMFNGNFTNADERSWQVRYDYDFVGLGWPGLIGMVRVYGHGNSNATTKAGS 337

1prn_A 247 AGADTAYGIGADYQFA---EGVKVSGSVQSG 274
3sys_A 338 GGKEWERDVELGYTVQSGPLARLNVRLNHASN 369
```

Int Num 1628 - Loop to hairpin

E-value 9.1E-5

```
6ehb_A 181 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKDVDYTGYLEAAGYKLG---Q-AAFTATYNNAE TAK----- 268
2y0l_A 256 DNKSLNGMFTYSLG--NHAFGAAWQRMNGDDAF----PYLEGSNPYLVNFV-QVNDF-AGPKERSWQLRYDYDFVGLGLPGLTFMTRYVKGDNVELAGQS 347

6ehb_A 269 -KTSADNFAIDATYYFK----PNFRSYISYQFNLLDSKASKVASEDELAIGLRYDF 320
2y0l_A 348 GEGREWERNTLQVVFQSGALKNLGIRWRNATFRSNF-----TRDIDENRLIVSYTL 399
```

Int Num 1627 - alternate alignment

E-value 1.0E-5

```
6ehb_A 182 EDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKD---DVDYTGYLEAAGYKLGQAFTATYNNAE TAK--- 268
2y0l_A 189 DHFDLGGLDYKLT-DLTASYHYHSLQDVYRQHFVGLLHWPPIGPELTSDLRFARSTDGSAKAGGIDNKSLNGMFTYSLGNHAFGAAWQRMNGDDAF 287

6ehb_A 269 -----KTSADNFAIDATYYFK----PNFRSYISYQFNLLD 299
2y0l_A 288 YLEGSNPYLVNFVQVNDFAGPKERSWQLRYDYDFVGLGLPGLTFMTRYVKGDNV 341
```

Int Num 2550 - loop to hairpin

E-value 1.5E-4

```
6ehb_A 181 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKDVDYTGYLEAAGYKLG---Q-AAFTATYNNAE TAK----- 268
3szv_A 256 DNRAFGALFSLRLG--AHAVAAGYQRISGDDPYP---YIAGSDPYLVNF-IQIGDF-GNVDERSWQLRYDYDFGALCLPGLSFMSRVVSGD NVARGAAN 347

6ehb_A 269 KTSADNFAIDATYYFK----PNFRSYISYQFNLLDSKASKVASEDELAIGLRYDF 320
3szv_A 348 DGKEWERNTDLGYVQSGPLKNLGKWRNATVRSNF-----ANDIDENRLILSYSL 398
```

Int Num 2551 - alternate alignment

E-value 2.8E-5

```
6ehb_A 181 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKD---DVDYTGYLEAAGYKLGQAFTATYNNAE TAK--- 268
3szv_A 189 SDAFDFAGGDRYLTTP-ALTASLHQRLNDIYRQTFAGLVHTLDLGGQRLSKSDLRFRASEDGGFRELDNRAFGALFSLRLGAHAVAAGYQRISGDDPYP 287

6ehb_A 269 -----KTSADNFAIDATYYFK----PNFRSYISYQFNLLDS 300
3szv_A 288 YIAGSDPYLVNFIQIGDFGNVDERSWQLRYDYDFGALCLPGLSFMSRVVSGDNVA 342
```

Int Num 2948 - Loop to hairpin

E-value 1.0E-3

```
6ehb_A 180 NGEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEY-MLAASYRM-ENLYFAGLFTDGELAKDVDYTGYLEAAGYKLGQ-----AAFTATYNNAE TAK--- 268
4frx_A 279 VDNRAFGSLFTYTVS--GHSIGAGYQILNGDSDFPFLNRGDGEGSTAYLITDVQIGKF-QRAGERTWQVRYGYDFATVGVPGLTFNTIYLSGDKIKTARG 375

6ehb_A 269 KTSADNFAIDATYYFK----PNFRSYISYQFNLLDSKA---SKVASEDELAIGLRYDF 320
4frx_A 376 DQSEWERDISLAYVIPDGTFFKGLGFTWKNASFRSGLPAAGSSNNQRDQDENRLIVSYTL 434
```

Int Num 2947 - alternate alignment

E-value 4.1E-4

```
6ehb_A 181 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRM--E--NLYFAGLFTDGELAKD---DVDYTGYLEAAGYKLGQ-----AAFTATYNNAE TAK 250
4frx_A 192 SNKFYYAGGDYKVNK-DLTLLQYYYGNLDFYKQHFGLLIHNWQIGPGVLKTDLRAFDSSSDGKNRSRSGRADGYVSSGYGSGVTKGEVDNRAFGSLFTY 290

6ehb_A 251 XLGQAFTATYNNAE TAK-----KTSADNFAIDATYYFK----PNFRSYISYQFNLLDS 300
4frx_A 291 TVSGHSIGAGYQILNGSDFPFLNRGDGEGSTAYLITDVQIGKFRACERTWQVRYGYDFATVGVPGLTFNTIYLSGDKIK 371
```

Int Num 3173 - Loop to hairpin

E-value 1.5E-4

```
6ehb_A 181 GEDGYSLSAIYTFGDTGFNVGAGYADQDDQNEYMLAASYRME--NLYFAGLFTDGELAKDVDYTGYLEAAGYKLGQ-----AAFTATYNNAE TAK 267
5dl7_A 263 DNRHISGLFGLNYQ--NHTVSLGYMQSFGSTGL-----PFLSGTESPPVLD--FMSSDY-SNKDEKVYSIRYEYDFKNAIRIGDVSINGLRFMTRYAKGEDI 353
```

6ehb\_A 268 K-----KT**SADNFAIDATYYF**K---P**NFRSYISYQFN**LLSDKASKVASE**ELAIGLRYDF** 320  
5dl7\_A 354 **ILLQYGDQRFKEDSLEFDLG**YKIPEGKLG**LGMRRARFSHYRND**MPTNMTFHS**ANETRLNVDYTF** 417

Int Num 3174 - alternate alignment

E-value 7.4E-5  
6ehb\_A 181 **GEDGYSLSAIYTF**GD**TGFNVGAGYAD**QDD-Q**NEYMLAASYRME**-----**NLYFAGLFTD**GELAK-----**VDY**TGYELAAGYKL**GQA**AFTATYN**NAETAK**- 268  
5dl7\_A 195 **TDSFYTLGGSYQLK**--**DYRLRAYHAELE****DIYQQQFLGFNGKQPLNDQ****LNFLSDVRFFNSEE**TGSKKIGE**VDNRHISGLFGLNYQ****NHTVSLGYMQSFGSTG** 292  
  
6ehb\_A 269 -----KT**SADNFAIDATYYFKP**-----**NFRSYISYQFN**LLDS 300  
5dl7\_A 293 LPFLSGTESPVVLD**FMSSDYSNKDEKVYSIRYEYDFKNA**RIGDVS**LNGLRFMTRYAKGEDID** 354