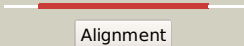

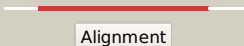

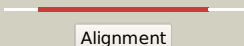






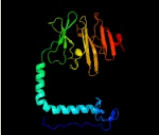
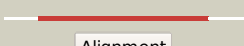









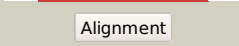


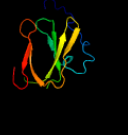

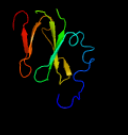

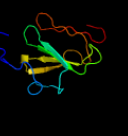


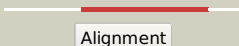

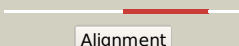
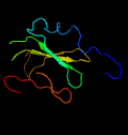


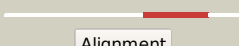
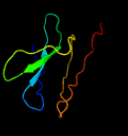


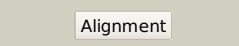
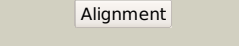
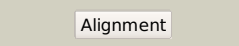

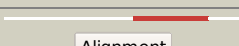



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0781\_ptrBa\_874236\_874946  
 Date Fri Jul 26 01:50:36 BST 2019  
 Unique Job ID b7928d9413ca89ba

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2xe4A_</a> |  Alignment   |    | 100.0      | 29     | <b>PDB header:</b> hydrolase/inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptidase b;<br><b>PDBTitle:</b> structure of oligopeptidase b from leishmania major  |
| 2  | <a href="#">d1qfma1</a> |  Alignment   |    | 100.0      | 21     | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> Peptidase/esterase 'gauge' domain<br><b>Family:</b> Prolyl oligopeptidase, N-terminal domain   |
| 3  | <a href="#">c4bp9A_</a> |  Alignment   |    | 100.0      | 33     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptidase b;<br><b>PDBTitle:</b> oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form   |
| 4  | <a href="#">c1yr2A_</a> |  Alignment   |   | 100.0      | 29     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prolyl oligopeptidase;<br><b>PDBTitle:</b> structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity |
| 5  | <a href="#">c3iumA_</a> |  Alignment |  | 100.0      | 22     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prolyl endopeptidase;<br><b>PDBTitle:</b> appep_wtx opened state   |
| 6  | <a href="#">c5uzwD_</a> |  Alignment |  | 100.0      | 21     | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> peptide cyclase 1;<br><b>PDBTitle:</b> pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp   |
| 7  | <a href="#">c2bklB_</a> |  Alignment |  | 100.0      | 28     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prolyl endopeptidase;<br><b>PDBTitle:</b> structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity |
| 8  | <a href="#">c1qfmA_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (prolyl oligopeptidase);<br><b>PDBTitle:</b> prolyl oligopeptidase from porcine muscle   |
| 9  | <a href="#">c5uw7B_</a> |  Alignment |  | 100.0      | 20     | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> peptide cyclase 1;<br><b>PDBTitle:</b> pcy1 y481f variant in complex with follower peptide   |
| 10 | <a href="#">c5n4dA_</a> |  Alignment |  | 100.0      | 19     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prolyl oligopeptidase;<br><b>PDBTitle:</b> prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant                     |
| 11 | <a href="#">c4hvtA_</a> |  Alignment |  | 100.0      | 14     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> post-proline cleaving enzyme;<br><b>PDBTitle:</b> structure of a post-proline cleaving enzyme from rickettsia typhi  |

|    |                         |   |   |       |    |  |
|----|-------------------------|---|---|-------|----|--|
| 12 | <a href="#">c5t88B_</a> |  Alignment   |     | 100.0 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prolyl endopeptidase;<br><b>PDBTitle:</b> prolyl oligopeptidase from pyrococcus furiosus   |
| 13 | <a href="#">c2g5tA_</a> |  Alignment   |    | 98.6  | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase 4;<br><b>PDBTitle:</b> crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag                            |
| 14 | <a href="#">c2qtbB_</a> |  Alignment   |    | 98.5  | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl peptidase 4;<br><b>PDBTitle:</b> human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor   |
| 15 | <a href="#">c5oljA_</a> |  Alignment   |    | 98.5  | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase iv;<br><b>PDBTitle:</b> crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4  |
| 16 | <a href="#">c1z68A_</a> |  Alignment   |    | 98.2  | 16 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fibroblast activation protein, alpha subunit;<br><b>PDBTitle:</b> crystal structure of human fibroblast activation protein alpha   |
| 17 | <a href="#">c2gopB_</a> |  Alignment   |   | 98.2  | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> trilobed protease;<br><b>PDBTitle:</b> the beta-propeller domain of the trilobed protease from pyrococcus2 furiosus reveals an open velcro topology  |
| 18 | <a href="#">c4wjlB_</a> |  Alignment |  | 98.2  | 19 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> inactive dipeptidyl peptidase 10;<br><b>PDBTitle:</b> structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels  |
| 19 | <a href="#">c5l8sD_</a> |  Alignment |  | 98.1  | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> amino acyl peptidase;<br><b>PDBTitle:</b> the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism        |
| 20 | <a href="#">c5yznA_</a> |  Alignment |  | 98.1  | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acyl-peptide hydrolase, putative;<br><b>PDBTitle:</b> crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1   |
| 21 | <a href="#">c5jrlC_</a> |  Alignment | not modelled  | 98.1  | 12 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like<br><b>PDBTitle:</b> crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)                             |
| 22 | <a href="#">d2bgra1</a> |  Alignment | not modelled  | 98.0  | 16 | <b>Fold:</b> 8-bladed beta-propeller<br><b>Superfamily:</b> DPP6 N-terminal domain-like<br><b>Family:</b> DPP6 N-terminal domain-like  |
| 23 | <a href="#">c5f30B_</a> |  Alignment | not modelled  | 98.0  | 4  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thiocyanate dehydrogenase;<br><b>PDBTitle:</b> thiocyanate dehydrogenase from thioalkalivibrio paradoxus  |
| 24 | <a href="#">c5tztT_</a> |  Alignment | not modelled  | 98.0  | 14 | <b>PDB header:</b> translation<br><b>Chain:</b> T: <b>PDB Molecule:</b> utp21;<br><b>PDBTitle:</b> architecture of the yeast small subunit processome  |
| 25 | <a href="#">c4nsxA_</a> |  Alignment | not modelled  | 98.0  | 22 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar rna-associated protein 21;<br><b>PDBTitle:</b> crystal structure of the utp21 tandem wd domain  |
| 26 | <a href="#">c1xfdD_</a> |  Alignment | not modelled  | 98.0  | 12 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl aminopeptidase-like protein 6;<br><b>PDBTitle:</b> structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family |
| 27 | <a href="#">c5c2vB_</a> |  Alignment | not modelled  | 98.0  | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> hydrazine synthase beta subunit;<br><b>PDBTitle:</b> kueningenia stuttgartiensis hydrazine synthase   |
| 28 | <a href="#">d1orva1</a> |  Alignment | not modelled  | 97.9  | 16 | <b>Fold:</b> 8-bladed beta-propeller<br><b>Superfamily:</b> DPP6 N-terminal domain-like<br><b>Family:</b> DPP6 N-terminal domain-like  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">c4hxgl_</a> | Alignment | not modelled | 97.9 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> J; <b>PDB Molecule:</b> putative uncharacterized protein ph0594;<br><b>PDBTitle:</b> pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)  |
| 30 | <a href="#">c1n6dE_</a> | Alignment | not modelled | 97.9 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> E; <b>PDB Molecule:</b> tricorn protease;<br><b>PDBTitle:</b> tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative  |
| 31 | <a href="#">c1k32E_</a> | Alignment | not modelled | 97.9 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> E; <b>PDB Molecule:</b> tricorn protease;<br><b>PDBTitle:</b> crystal structure of the tricorn protease  |
| 32 | <a href="#">c3pe7A_</a> | Alignment | not modelled | 97.9 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> oligogalacturonate lyase;<br><b>PDBTitle:</b> oligogalacturonate lyase in complex with manganese   |
| 33 | <a href="#">c2w8bB_</a> | Alignment | not modelled | 97.9 | 21 | <b>PDB header:</b> protein transport/membrane protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> protein tolB;<br><b>PDBTitle:</b> crystal structure of processed tolB in complex with pal   |
| 34 | <a href="#">c3wj9A_</a> | Alignment | not modelled | 97.9 | 16 | <b>PDB header:</b> translation<br><b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 2a;<br><b>PDBTitle:</b> crystal structure of the eukaryotic initiation factor   |
| 35 | <a href="#">c3c5mC_</a> | Alignment | not modelled | 97.9 | 11 | <b>PDB header:</b> lyase<br><b>Chain:</b> C; <b>PDB Molecule:</b> oligogalacturonate lyase;<br><b>PDBTitle:</b> crystal structure of oligogalacturonate lyase (vpa0088)2 from vibrio parahaemolyticus. northeast structural3 genomics consortium target vpr199   |
| 36 | <a href="#">c5a1vK_</a> | Alignment | not modelled | 97.8 | 6  | <b>PDB header:</b> transport protein<br><b>Chain:</b> K; <b>PDB Molecule:</b> coatomer subunit alpha;<br><b>PDBTitle:</b> the structure of the copI coat linkage i   |
| 37 | <a href="#">c3dm0A_</a> | Alignment | not modelled | 97.8 | 12 | <b>PDB header:</b> sugar binding protein,signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> maltose-binding periplasmic protein fused with rack1;<br><b>PDBTitle:</b> maltose binding protein fusion with rack1 from a. thaliana   |
| 38 | <a href="#">c4nlmA_</a> | Alignment | not modelled | 97.8 | 10 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> lmo1340 protein;<br><b>PDBTitle:</b> 1.18 angstrom resolution crystal structure of uncharacterized protein2 lmo1340 from listeria monocytogenes egd-e  |
| 39 | <a href="#">c5ov3B_</a> | Alignment | not modelled | 97.8 | 18 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> retinoblastoma-binding protein 5;<br><b>PDBTitle:</b> structure of the rbbp5 beta-propeller domain  |
| 40 | <a href="#">c2ecfA_</a> | Alignment | not modelled | 97.8 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> dipeptidyl peptidase iv;<br><b>PDBTitle:</b> crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia  |
| 41 | <a href="#">c3jb9K_</a> | Alignment | not modelled | 97.8 | 12 | <b>PDB header:</b> rna binding protein/rna<br><b>Chain:</b> K; <b>PDB Molecule:</b> pre-mrna-splicing factor prp5;<br><b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution   |
| 42 | <a href="#">c3mmyE_</a> | Alignment | not modelled | 97.7 | 10 | <b>PDB header:</b> nuclear protein<br><b>Chain:</b> E; <b>PDB Molecule:</b> mrna export factor;<br><b>PDBTitle:</b> structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1   |
| 43 | <a href="#">c5i2tA_</a> | Alignment | not modelled | 97.7 | 13 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> periodic tryptophan protein 2;<br><b>PDBTitle:</b> domain characterization of the wd protein pwp2 and their relevance in2 ribosome biogenesis   |
| 44 | <a href="#">c5mzhB_</a> | Alignment | not modelled | 97.7 | 10 | <b>PDB header:</b> motor protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> dynein assembly factor with wdr repeat domains 1;<br><b>PDBTitle:</b> crystal structure of oda16 from chlamydomonas reinhardtii  |
| 45 | <a href="#">c5a5uB_</a> | Alignment | not modelled | 97.7 | 11 | <b>PDB header:</b> translation<br><b>Chain:</b> B; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b;<br><b>PDBTitle:</b> structure of mammalian eif3 in the context of the 43s preinitiation2 complex   |
| 46 | <a href="#">c4wjsA_</a> | Alignment | not modelled | 97.7 | 26 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> rsa4;<br><b>PDBTitle:</b> crystal structure of rsa4 from chaetomium thermophilum  |
| 47 | <a href="#">c2ivzD_</a> | Alignment | not modelled | 97.7 | 21 | <b>PDB header:</b> protein transport/hydrolase<br><b>Chain:</b> D; <b>PDB Molecule:</b> protein tolB;<br><b>PDBTitle:</b> structure of tolB in complex with a peptide of the colicin2 e9 t-domain  |
| 48 | <a href="#">c2hu7A_</a> | Alignment | not modelled | 97.7 | 8  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> acylamino-acid-releasing enzyme;<br><b>PDBTitle:</b> binding of inhibitors by acylaminoacyl peptidase  |
| 49 | <a href="#">c6chgD_</a> | Alignment | not modelled | 97.7 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> D; <b>PDB Molecule:</b> klla0a08800p;<br><b>PDBTitle:</b> crystal structure of the yeast compass catalytic module  |
| 50 | <a href="#">c6nd4L_</a> | Alignment | not modelled | 97.7 | 10 | <b>PDB header:</b> ribosome<br><b>Chain:</b> L; <b>PDB Molecule:</b> utp5;<br><b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit   |
| 51 | <a href="#">c4wjuB_</a> | Alignment | not modelled | 97.7 | 23 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> ribosome assembly protein 4;<br><b>PDBTitle:</b> crystal structure of rsa4 from saccharomyces cerevisiae  |
| 52 | <a href="#">c4noxA_</a> | Alignment | not modelled | 97.7 | 9  | <b>PDB header:</b> translation<br><b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b;<br><b>PDBTitle:</b> structure of the nine-bladed beta-propeller of eif3b   |
| 53 | <a href="#">c5k0yT_</a> | Alignment | not modelled | 97.7 | 11 | <b>PDB header:</b> translation<br><b>Chain:</b> T; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit i;<br><b>PDBTitle:</b> m48s late-stage initiation complex, purified from rabbit reticulocytes2 lysates, displaying eif2 ternary complex and eif3 i and g subunits3 relocated to the intersubunit face |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 54 | <a href="#">c5a1vL_</a> | Alignment | not modelled | 97.7 | 10 | <b>PDB header:</b> transport protein<br><b>Chain:</b> L: <b>PDB Molecule:</b> coatomer subunit beta;<br><b>PDBTitle:</b> the structure of the copi coat linkage i  |
| 55 | <a href="#">d1k8kc_</a> | Alignment | not modelled | 97.6 | 15 | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> WD40 repeat-like<br><b>Family:</b> WD40-repeat   |
| 56 | <a href="#">c6nd4S_</a> | Alignment | not modelled | 97.6 | 14 | <b>PDB header:</b> ribosome<br><b>Chain:</b> S: <b>PDB Molecule:</b> utp18;<br><b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit  |
| 57 | <a href="#">c6nd4T_</a> | Alignment | not modelled | 97.6 | 22 | <b>PDB header:</b> ribosome<br><b>Chain:</b> T: <b>PDB Molecule:</b> utp21;<br><b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit  |
| 58 | <a href="#">d1k32a2</a> | Alignment | not modelled | 97.6 | 15 | <b>Fold:</b> 6-bladed beta-propeller<br><b>Superfamily:</b> Tricorn protease N-terminal domain<br><b>Family:</b> Tricorn protease N-terminal domain  |
| 59 | <a href="#">c5gmkq_</a> | Alignment | not modelled | 97.6 | 17 | <b>PDB header:</b> rna binding protein/rna<br><b>Chain:</b> Q: <b>PDB Molecule:</b> pre-mrna-splicing factor slt11;<br><b>PDBTitle:</b> cryo-em structure of the catalytic step i spliceosome (c complex) at2 3.4 angstrom resolution                                      |
| 60 | <a href="#">c4zovB_</a> | Alignment | not modelled | 97.6 | 7  | <b>PDB header:</b> chaperone<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribosome assembly protein sqt1;<br><b>PDBTitle:</b> crystal structure of the saccharomyces cerevisiae sqt1   |
| 61 | <a href="#">c6e29C_</a> | Alignment | not modelled | 97.6 | 15 | <b>PDB header:</b> protein binding<br><b>Chain:</b> C: <b>PDB Molecule:</b> swd1-like protein;<br><b>PDBTitle:</b> crystal structure of myceliophtheria_thermophila cps50 (swd1) beta-2 propeller domain   |
| 62 | <a href="#">c1nr0A_</a> | Alignment | not modelled | 97.6 | 15 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> actin interacting protein 1;<br><b>PDBTitle:</b> two seven-bladed beta-propeller domains revealed by the2 structure of a c. elegans homologue of yeast actin3 interacting protein 1 (aip1). |
| 63 | <a href="#">c3mkqA_</a> | Alignment | not modelled | 97.6 | 11 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> coatomer beta'-subunit;<br><b>PDBTitle:</b> crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat  |
| 64 | <a href="#">c4lg9A_</a> | Alignment | not modelled | 97.6 | 18 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> f-box-like/wd repeat-containing protein tbl1xr1;<br><b>PDBTitle:</b> crystal structure of tbl1xr1 wd40 repeats  |
| 65 | <a href="#">c4yhCA_</a> | Alignment | not modelled | 97.5 | 14 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sterol regulatory element-binding protein cleavage-<br><b>PDBTitle:</b> crystal structure of the wd40 domain of scap from fission yeast   |
| 66 | <a href="#">c2ymuA_</a> | Alignment | not modelled | 97.5 | 10 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> wd-40 repeat protein;<br><b>PDBTitle:</b> structure of a highly repetitive propeller structure  |
| 67 | <a href="#">d1gxra_</a> | Alignment | not modelled | 97.5 | 12 | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> WD40 repeat-like<br><b>Family:</b> WD40-repeat   |
| 68 | <a href="#">c5a1uC_</a> | Alignment | not modelled | 97.5 | 6  | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> coatomer subunit alpha;<br><b>PDBTitle:</b> the structure of the copi coat triad   |
| 69 | <a href="#">c4jspC_</a> | Alignment | not modelled | 97.5 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> target of rapamycin complex subunit lst8;<br><b>PDBTitle:</b> structure of mtordeltan-mist8-atpgammas-mg complex   |
| 70 | <a href="#">c4o9dA_</a> | Alignment | not modelled | 97.5 | 21 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> rik1-associated factor 1;<br><b>PDBTitle:</b> structure of dos1 propeller  |
| 71 | <a href="#">c4u1fA_</a> | Alignment | not modelled | 97.5 | 5  | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b;<br><b>PDBTitle:</b> crystal structure of middle domain of eukaryotic translation2 initiation factor eif3b                                    |
| 72 | <a href="#">c5txeA_</a> | Alignment | not modelled | 97.4 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> atxe2;<br><b>PDBTitle:</b> atxe2 isopeptidase - s527a variant with astexin3-dc4 bound  |
| 73 | <a href="#">c6nd4O_</a> | Alignment | not modelled | 97.4 | 13 | <b>PDB header:</b> ribosome<br><b>Chain:</b> O: <b>PDB Molecule:</b> utp1;<br><b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit   |
| 74 | <a href="#">c3c75J_</a> | Alignment | not modelled | 97.4 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> J: <b>PDB Molecule:</b> methylamine dehydrogenase heavy chain;<br><b>PDBTitle:</b> paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin   |
| 75 | <a href="#">c4h5jB_</a> | Alignment | not modelled | 97.4 | 11 | <b>PDB header:</b> protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> guanine nucleotide-exchange factor sec12;<br><b>PDBTitle:</b> crystal structure of the guanine nucleotide exchange factor sec12 (p642 form)  |
| 76 | <a href="#">c6nd4H_</a> | Alignment | not modelled | 97.4 | 12 | <b>PDB header:</b> ribosome<br><b>Chain:</b> H: <b>PDB Molecule:</b> utp17;<br><b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit  |
| 77 | <a href="#">c3zwlB_</a> | Alignment | not modelled | 97.4 | 12 | <b>PDB header:</b> translation<br><b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit i;<br><b>PDBTitle:</b> structure of eukaryotic translation initiation factor eif3i complex2 with eif3b c-terminus (655-700)                     |
| 78 | <a href="#">c3bwsA_</a> | Alignment | not modelled | 97.4 | 18 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein lp49;<br><b>PDBTitle:</b> crystal structure of the leptospiral antigen lp49   |
|    |                         |           |              |      |    | <b>PDB header:</b> transcription   |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
| 79  | <a href="#">c3jcmB_</a> | Alignment | not modelled | 97.4 | 20 | <b>Chain:</b> B: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp4;<br><b>PDBTitle:</b> cryo-em structure of the spliceosomal u4/u6.u5 tri-snrrp   |
| 80  | <a href="#">c6chgA_</a> | Alignment | not modelled | 97.4 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> klla0e24487p;<br><b>PDBTitle:</b> crystal structure of the yeast compass catalytic module  |
| 81  | <a href="#">c2pbiB_</a> | Alignment | not modelled | 97.4 | 16 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> guanine nucleotide-binding protein subunit beta 5;<br><b>PDBTitle:</b> the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure  |
| 82  | <a href="#">d1tt2a_</a> | Alignment | not modelled | 97.4 | 11 | <b>Fold:</b> 5-bladed beta-propeller<br><b>Superfamily:</b> Tachylectin-2<br><b>Family:</b> Tachylectin-2  |
| 83  | <a href="#">c2eepA_</a> | Alignment | not modelled | 97.4 | 11 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl aminopeptidase iv, putative;<br><b>PDBTitle:</b> prolyl tripeptidyl aminopeptidase complexed with an inhibitor  |
| 84  | <a href="#">d1nira2</a> | Alignment | not modelled | 97.4 | 8  | <b>Fold:</b> 8-bladed beta-propeller<br><b>Superfamily:</b> C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase<br><b>Family:</b> C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase  |
| 85  | <a href="#">c3iytG_</a> | Alignment | not modelled | 97.3 | 13 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> G: <b>PDB Molecule:</b> apoptotic protease-activating factor 1;<br><b>PDBTitle:</b> structure of an apoptosome-procaspase-9 card complex   |
| 86  | <a href="#">c3j65q_</a> | Alignment | not modelled | 97.3 | 23 | <b>PDB header:</b> ribosome<br><b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l18;<br><b>PDBTitle:</b> arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.   |
| 87  | <a href="#">c6fqIA_</a> | Alignment | not modelled | 97.3 | 5  | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase trim71;<br><b>PDBTitle:</b> crystal structure of danio rerio lin41 filamin-nhl domains in complex2 with mab-10 3'utr 13mer rna                                 |
| 88  | <a href="#">c4uerb_</a> | Alignment | not modelled | 97.3 | 5  | <b>PDB header:</b> translation<br><b>Chain:</b> B: <b>PDB Molecule:</b> us2;<br><b>PDBTitle:</b> 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri   |
| 89  | <a href="#">d1nr0a1</a> | Alignment | not modelled | 97.3 | 5  | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> WD40 repeat-like<br><b>Family:</b> WD40-repeat   |
| 90  | <a href="#">d1qksa2</a> | Alignment | not modelled | 97.3 | 14 | <b>Fold:</b> 8-bladed beta-propeller<br><b>Superfamily:</b> C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase<br><b>Family:</b> C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase  |
| 91  | <a href="#">c5nnzB_</a> | Alignment | not modelled | 97.3 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> dynein assembly factor with wdr repeat domains 1;<br><b>PDBTitle:</b> crystal structure of human oda16   |
| 92  | <a href="#">d1tbga_</a> | Alignment | not modelled | 97.3 | 11 | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> WD40 repeat-like<br><b>Family:</b> WD40-repeat   |
| 93  | <a href="#">c4cc9A_</a> | Alignment | not modelled | 97.3 | 13 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein vprbp;<br><b>PDBTitle:</b> crystal structure of human samhd1 (amino acid residues 582-626) bound2 to vpx isolated from sooty mangabey and human dcaf1 (amino acid3 residues 1058-1396) |
| 94  | <a href="#">d2bbkh_</a> | Alignment | not modelled | 97.3 | 12 | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> YVTN repeat-like/Quinoprotein amine dehydrogenase<br><b>Family:</b> Methylamine dehydrogenase, H-chain   |
| 95  | <a href="#">c5nzvC_</a> | Alignment | not modelled | 97.3 | 10 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> coatomer subunit beta';<br><b>PDBTitle:</b> the structure of the copi coat linkage iv  |
| 96  | <a href="#">c6cb1s_</a> | Alignment | not modelled | 97.3 | 22 | <b>PDB header:</b> ribosome<br><b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein l20-a;<br><b>PDBTitle:</b> yeast nucleolar pre-60s ribosomal subunit (state 3)  |
| 97  | <a href="#">d1xfda1</a> | Alignment | not modelled | 97.2 | 14 | <b>Fold:</b> 8-bladed beta-propeller<br><b>Superfamily:</b> DPP6 N-terminal domain-like<br><b>Family:</b> DPP6 N-terminal domain-like  |
| 98  | <a href="#">c6iyyA_</a> | Alignment | not modelled | 97.2 | 19 | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> wd repeat domain phosphoinositide-interacting protein 3;<br><b>PDBTitle:</b> crystal structure of human wipi3,loop deletion mutant   |
| 99  | <a href="#">c6nd4Q_</a> | Alignment | not modelled | 97.2 | 12 | <b>PDB header:</b> ribosome<br><b>Chain:</b> Q: <b>PDB Molecule:</b> utp12;<br><b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit  |
| 100 | <a href="#">c3iz6a_</a> | Alignment | not modelled | 97.2 | 12 | <b>PDB header:</b> ribosome<br><b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa (s2p);<br><b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome                      |
| 101 | <a href="#">d1k32a3</a> | Alignment | not modelled | 97.2 | 13 | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> Tricorn protease domain 2<br><b>Family:</b> Tricorn protease domain 2  |
| 102 | <a href="#">c5thaA_</a> | Alignment | not modelled | 97.2 | 11 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gem-associated protein 5;<br><b>PDBTitle:</b> gemin5 wd40 repeats in complex with a guanosyl moiety  |
| 103 | <a href="#">c6mzcG_</a> | Alignment | not modelled | 97.2 | 14 | <b>PDB header:</b> transcription<br><b>Chain:</b> G: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 5;<br><b>PDBTitle:</b> human tfiid bc core   |
| 104 | <a href="#">c4ci8B_</a> | Alignment | not modelled | 97.2 | 13 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> echinoderm microtubule-associated protein-like 1;   |

|     |                         |           |              |      |    |   |
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|     |                         |           |              |      |    | <b>PDBTitle:</b> crystal structure of the tandem atypical beta-propeller domain of eml1   |
| 105 | <a href="#">d1ospo_</a> | Alignment | not modelled | 97.2 | 8  | <b>Fold:</b> open-sided beta-meander<br><b>Superfamily:</b> Outer surface protein<br><b>Family:</b> Outer surface protein   |
| 106 | <a href="#">c3dwIH_</a> | Alignment | not modelled | 97.2 | 10 | <b>PDB header:</b> structural protein<br><b>Chain:</b> H: <b>PDB Molecule:</b> actin-related protein 2/3 complex subunit 1;<br><b>PDBTitle:</b> crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit   |
| 107 | <a href="#">d1yfqA_</a> | Alignment | not modelled | 97.2 | 13 | <b>Fold:</b> 7-bladed beta-propeller<br><b>Superfamily:</b> WD40 repeat-like<br><b>Family:</b> Cell cycle arrest protein BUB3   |
| 108 | <a href="#">c4jxmA_</a> | Alignment | not modelled | 97.1 | 11 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar rna-interacting protein 2;<br><b>PDBTitle:</b> crystal structure of rrp9 wd40 repeats  |
| 109 | <a href="#">c3dw8B_</a> | Alignment | not modelled | 97.1 | 12 | <b>PDB header:</b> hydrolase/hydrolase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein phosphatase 2a 55 kda regulatory<br><b>PDBTitle:</b> structure of a protein phosphatase 2a holoenzyme with b55 subunit                                 |
| 110 | <a href="#">c5cykB_</a> | Alignment | not modelled | 97.1 | 22 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribosome biogenesis protein erb1;<br><b>PDBTitle:</b> structure of ytm1 bound to the c-terminal domain of erb1-r486e  |
| 111 | <a href="#">c2ojhA_</a> | Alignment | not modelled | 97.1 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1656/agr_c_3050;<br><b>PDBTitle:</b> the structure of putative tolB from agrobacterium tumefaciens   |
| 112 | <a href="#">c5juyB_</a> | Alignment | not modelled | 97.1 | 13 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> B: <b>PDB Molecule:</b> apoptotic protease-activating factor 1;<br><b>PDBTitle:</b> active human apoptosome with procaspase-9   |
| 113 | <a href="#">c2xznR_</a> | Alignment | not modelled | 97.1 | 15 | <b>PDB header:</b> ribosome<br><b>Chain:</b> R: <b>PDB Molecule:</b> rack1;<br><b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |
| 114 | <a href="#">c3fm0A_</a> | Alignment | not modelled | 97.1 | 9  | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein ciao1;<br><b>PDBTitle:</b> crystal structure of wd40 protein ciao1   |
| 115 | <a href="#">c5jk7C_</a> | Alignment | not modelled | 97.1 | 13 | <b>PDB header:</b> viral protein/dna binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein vprbp;<br><b>PDBTitle:</b> the x-ray structure of the ddb1-dcaf1-vpr-ung2 complex   |
| 116 | <a href="#">c4bh6H_</a> | Alignment | not modelled | 97.1 | 20 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> H: <b>PDB Molecule:</b> apc/c activator protein cdh1;<br><b>PDBTitle:</b> insights into degron recognition by apc coactivators from2 the structure of an acm1-cdh1 complex   |
| 117 | <a href="#">c6nd4U_</a> | Alignment | not modelled | 97.0 | 14 | <b>PDB header:</b> ribosome<br><b>Chain:</b> U: <b>PDB Molecule:</b> sof1;<br><b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit  |
| 118 | <a href="#">c6bx3B_</a> | Alignment | not modelled | 97.0 | 16 | <b>PDB header:</b> gene regulation/transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> compass component swd1;<br><b>PDBTitle:</b> structure of histone h3k4 methyltransferase   |
| 119 | <a href="#">c6em5m_</a> | Alignment | not modelled | 97.0 | 22 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14-a;<br><b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes                                 |
| 120 | <a href="#">c5ganH_</a> | Alignment | not modelled | 97.0 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> H: <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp4;<br><b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom   |