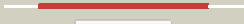



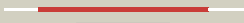






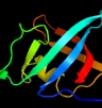












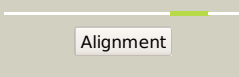
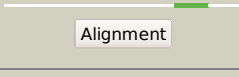
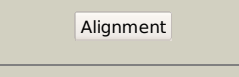
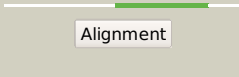
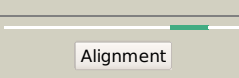
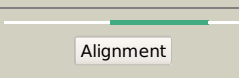
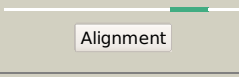

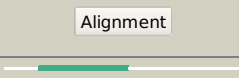
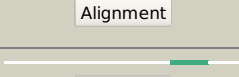
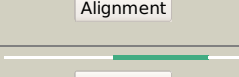
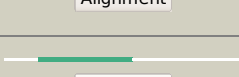
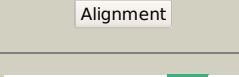
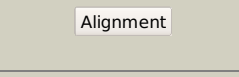
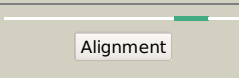
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3788 (- )_4234958_4235443
Date	Fri Aug 9 18:20:49 BST 2019
Unique Job ID	fbfdbeed45631f2

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2p4vA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor greb; <b>PDBTitle:</b> crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
2	<a href="#">c1grjA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> grea protein; <b>PDBTitle:</b> grea transcript cleavage factor from escherichia coli
3	<a href="#">c2etnA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anti-cleavage anti-grea transcription factor <b>PDBTitle:</b> crystal structure of thermus aquaticus gfh1
4	<a href="#">c2pn0D_</a>	 Alignment		99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> prokaryotic transcription elongation factor <b>PDBTitle:</b> prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
5	<a href="#">c3bmbB_</a>	 Alignment		99.9	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of nucleoside diphosphate kinase; <b>PDBTitle:</b> crystal structure of a new rna polymerase interacting2 protein
6	<a href="#">d2f23a2</a>	 Alignment		99.8	29	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
7	<a href="#">d2etna2</a>	 Alignment		99.8	29	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
8	<a href="#">d1grja1</a>	 Alignment		99.7	16	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> GreA transcript cleavage protein, N-terminal domain <b>Family:</b> GreA transcript cleavage protein, N-terminal domain
9	<a href="#">d1grja2</a>	 Alignment		99.7	20	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
10	<a href="#">d2f23a1</a>	 Alignment		99.7	21	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> GreA transcript cleavage protein, N-terminal domain <b>Family:</b> GreA transcript cleavage protein, N-terminal domain
11	<a href="#">d1t11a3</a>	 Alignment		91.0	15	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase

12	<a href="#">c3gtyX_</a>	Alignment		90.3	15	<b>PDB header:</b> chaperone/ribosomal protein <b>Chain:</b> X: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
13	<a href="#">d1w26a3</a>	Alignment		85.9	17	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
14	<a href="#">c2kfwA_</a>	Alignment		80.6	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase <b>PDBTitle:</b> solution structure of full-length slyd from e.coli
15	<a href="#">c1w26B_</a>	Alignment		79.5	18	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
16	<a href="#">c2k8iA_</a>	Alignment		76.4	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> solution structure of e.coli slyd
17	<a href="#">d1krha1</a>	Alignment		76.3	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
18	<a href="#">d1fdra1</a>	Alignment		75.0	16	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
19	<a href="#">c1t11A_</a>	Alignment		72.1	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> trigger factor
20	<a href="#">d1qx4a1</a>	Alignment		72.0	19	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
21	<a href="#">d1l1pa_</a>	Alignment	not modelled	71.5	17	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
22	<a href="#">d2piaa1</a>	Alignment	not modelled	68.4	21	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
23	<a href="#">c5udfB_</a>	Alignment	not modelled	68.2	18	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system transmembrane protein lole; <b>PDBTitle:</b> structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lole from acinetobacter baumannii
24	<a href="#">d1ndha1</a>	Alignment	not modelled	66.5	22	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
25	<a href="#">d2cnda1</a>	Alignment	not modelled	65.9	15	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
26	<a href="#">c5hu4A_</a>	Alignment	not modelled	64.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> crystal structure of listeria monocytogenes sortase a
27	<a href="#">d1umka1</a>	Alignment	not modelled	63.1	22	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
28	<a href="#">c2l66B_</a>	Alignment	not modelled	62.6	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, abrb family; <b>PDBTitle:</b> the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.

29	<a href="#">c2kw8A</a>	 Alignment	not modelled	61.3	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lpxtg-site transpeptidase family protein; <b>PDBTitle:</b> solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
30	<a href="#">c2ln7A</a>	 Alignment	not modelled	60.9	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lpxtg-site transpeptidase family protein; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for the catalytic2 domain of b. anthracis srtd
31	<a href="#">c2kr7A</a>	 Alignment	not modelled	58.4	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase slyd; <b>PDBTitle:</b> solution structure of helicobacter pylori slyd
32	<a href="#">d1e32a3</a>	 Alignment	not modelled	58.0	8	<b>Fold:</b> Cdc48 domain 2-like <b>Superfamily:</b> Cdc48 domain 2-like <b>Family:</b> Cdc48 domain 2-like
33	<a href="#">c5k9aA</a>	 Alignment	not modelled	52.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fimbrial associated sortase-like protein; <b>PDBTitle:</b> sortase a from corynebacterium diphtheriae
34	<a href="#">c1zeqX</a>	 Alignment	not modelled	51.7	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> cation efflux system protein cusf; <b>PDBTitle:</b> 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
35	<a href="#">c4dt4A</a>	 Alignment	not modelled	51.6	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type 16 kda peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> crystal structure of the ppiase-chaperone slpa with the chaperone2 binding site occupied by the linker of the purification tag
36	<a href="#">c3fn5B</a>	 Alignment	not modelled	50.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sortase a; <b>PDBTitle:</b> crystal structure of sortase a (spy1154) from streptococcus2 pyogenes serotype m1 strain sf370
37	<a href="#">c5zr0A</a>	 Alignment	not modelled	49.6	25	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,trigger factor; <b>PDBTitle:</b> solution structure of peptidyl-prolyl cis/trans isomerase domain of2 trigger factor in complex with mbp
38	<a href="#">c3re9A</a>	 Alignment	not modelled	48.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase-like protein; <b>PDBTitle:</b> crystal structure of sortasec1 from streptococcus suis
39	<a href="#">c4mspB</a>	 Alignment	not modelled	47.8	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp14; <b>PDBTitle:</b> crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp222 (aka fkbp14) containing two ef-hand motifs
40	<a href="#">c3cgnA</a>	 Alignment	not modelled	47.6	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> crystal structure of thermophilic slyd
41	<a href="#">d1t2wa</a>	 Alignment	not modelled	47.3	11	<b>Fold:</b> Sortase <b>Superfamily:</b> Sortase <b>Family:</b> Sortase
42	<a href="#">c5uttD</a>	 Alignment	not modelled	47.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sortase; <b>PDBTitle:</b> srta sortase from actinomyces oris
43	<a href="#">c3o0pA</a>	 Alignment	not modelled	46.2	19	<b>PDB header:</b> transferase , hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase family protein; <b>PDBTitle:</b> pilus-related sortase c of group b streptococcus
44	<a href="#">c4y66D</a>	 Alignment	not modelled	46.2	19	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> putative tbpip family protein; <b>PDBTitle:</b> crystal structure of giardia lamblia hop2-mnd1 complex
45	<a href="#">c2w1kB</a>	 Alignment	not modelled	45.7	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sortase; <b>PDBTitle:</b> crystal structure of sortase c-3 (srct-3) from2 streptococcus pneumoniae
46	<a href="#">c2pjhB</a>	 Alignment	not modelled	44.9	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> strctural model of the p97 n domain- npl4 ubd complex
47	<a href="#">c4d7wA</a>	 Alignment	not modelled	44.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase family protein; <b>PDBTitle:</b> crystal structure of sortase c1 (srct1) from streptococcus agalactiae
48	<a href="#">c1y698</a>	 Alignment	not modelled	43.9	15	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> ribosome-recycling factor; <b>PDB Fragment:</b> unp residues 1-30 and 106-185; <b>PDBTitle:</b> rrf domain i in complex with the 50s ribosomal subunit from2 deinococcus radiodurans
49	<a href="#">c3rccl</a>	 Alignment	not modelled	43.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> sortase srta; <b>PDBTitle:</b> crystal structure of the streptococcus agalactiae sortase a
50	<a href="#">c2l55A</a>	 Alignment	not modelled	42.8	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> silb,silver efflux protein, mfp component of the three <b>PDBTitle:</b> solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
51	<a href="#">c5i7pA</a>	 Alignment	not modelled	41.7	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp1a,fkbp-type <b>PDBTitle:</b> crystal structure of fkbp12-if(slyd), a chimeric protein of human2 fkbp12 and the insert in flap domain of ecoli slyd
52	<a href="#">c1cz5A</a>	 Alignment	not modelled	41.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
53	<a href="#">c5z81A</a>	 Alignment	not modelled	41.1	9	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 15; <b>PDBTitle:</b> trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution

54	<a href="#">c2xwgA</a>	Alignment	not modelled	40.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase; <b>PDBTitle:</b> crystal structure of sortase c-1 from actinomyces oris (formerly2 actinomyces naeslundii)
55	<a href="#">c5go5A</a>	Alignment	not modelled	40.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase; <b>PDBTitle:</b> structure of sortase e from streptomyces avermitilis
56	<a href="#">c3lssA</a>	Alignment	not modelled	40.1	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> trypanosoma brucei seryl-trna synthetase in complex with atp
57	<a href="#">d2csba1</a>	Alignment	not modelled	40.0	15	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
58	<a href="#">c4he5A</a>	Alignment	not modelled	39.6	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase family u32; <b>PDBTitle:</b> crystal structure of the selenomethionine variant of the c-terminal2 domain of geobacillus thermoleovorans putative u32 peptidase
59	<a href="#">c4d70A</a>	Alignment	not modelled	39.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase family protein; <b>PDBTitle:</b> structural, biophysical and biochemical analyses of a clostridium2 perfringens sortase d5 transpeptidase
60	<a href="#">d1hxva</a>	Alignment	not modelled	39.3	11	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
61	<a href="#">c1hxvA</a>	Alignment	not modelled	39.3	11	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> ppiase domain of the mycoplasma genitalium trigger factor
62	<a href="#">d1dm9a</a>	Alignment	not modelled	38.4	18	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Heat shock protein 15 kD
63	<a href="#">c1dm9A</a>	Alignment	not modelled	38.4	18	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 15.5 kd protein in mrca-pcka intergenic <b>PDBTitle:</b> heat shock protein 15 kd
64	<a href="#">c4tqxA</a>	Alignment	not modelled	38.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase; <b>PDBTitle:</b> molecular basis of streptococcus mutans sortase a inhibition by2 chalcone.
65	<a href="#">c3g66A</a>	Alignment	not modelled	38.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase c; <b>PDBTitle:</b> the crystal structure of streptococcus pneumoniae sortase c2 provides novel insights into catalysis as well as pilin3 substrate specificity
66	<a href="#">d2gp4a1</a>	Alignment	not modelled	37.1	23	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IIVD-like <b>Family:</b> IlvD/EDD C-terminal domain-like
67	<a href="#">c4o8tD</a>	Alignment	not modelled	35.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sortase; <b>PDBTitle:</b> structure of sortase a c207a mutant from streptococcus pneumoniae
68	<a href="#">d1sf9a</a>	Alignment	not modelled	35.1	18	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Hypothetical protein YfhH <b>Family:</b> Hypothetical protein YfhH
69	<a href="#">c4g1hA</a>	Alignment	not modelled	34.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sortase family protein; <b>PDBTitle:</b> group b streptococcus pilus island 1 sortase c2
70	<a href="#">c4djpD</a>	Alignment	not modelled	33.2	21	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp14; <b>PDBTitle:</b> crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp14
71	<a href="#">d1tvca1</a>	Alignment	not modelled	33.1	11	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
72	<a href="#">c2k6pA</a>	Alignment	not modelled	32.7	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp_1423; <b>PDBTitle:</b> solution structure of hypothetical protein, hp1423
73	<a href="#">c5oynB</a>	Alignment	not modelled	32.4	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydratase, ilvd/edd family; <b>PDBTitle:</b> crystal structure of d-xylonate dehydratase in holo-form
74	<a href="#">c5cuwA</a>	Alignment	not modelled	32.2	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> srte1; <b>PDBTitle:</b> crystal structure of sortase e1 from streptomyces coelicolor with2 tripeptide in the active site
75	<a href="#">d2es2a1</a>	Alignment	not modelled	32.0	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
76	<a href="#">c3j20G</a>	Alignment	not modelled	30.8	19	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 30s ribosomal protein s6e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
77	<a href="#">c3rbjB</a>	Alignment	not modelled	29.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sortase family protein; <b>PDBTitle:</b> crystal structure of the lid-mutant of streptococcus agalactiae2 sortase c1
78	<a href="#">c5uusB</a>	Alignment	not modelled	29.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> possible sortase-like protein; <b>PDBTitle:</b> srtf sortase from corynebacterium diphtheriae
79	<a href="#">c4lhzE</a>	Alignment	not modelled	29.1	16	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> rab-3a-interacting protein; <b>PDBTitle:</b> crystal structure of gtp-bound rab8:rabin8

80	<a href="#">d1h7ca_</a>	Alignment	not modelled	28.5	23	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Tubulin chaperone cofactor A <b>Family:</b> Tubulin chaperone cofactor A
81	<a href="#">c5j84A_</a>	Alignment	not modelled	28.2	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase; <b>PDBTitle:</b> crystal structure of l-arabinonate dehydratase in holo-form
82	<a href="#">c2eehA_</a>	Alignment	not modelled	28.0	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pdz domain-containing protein 7; <b>PDBTitle:</b> solution structure of first pdz domain of pdz domain2 containing protein 7
83	<a href="#">d1nbwa1</a>	Alignment	not modelled	28.0	41	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Swiveling domain of dehydratase reactivase alpha subunit <b>Family:</b> Swiveling domain of dehydratase reactivase alpha subunit
84	<a href="#">c3pr9A_</a>	Alignment	not modelled	27.6	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
85	<a href="#">c2gp4B_</a>	Alignment	not modelled	27.5	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
86	<a href="#">c2gpiA_</a>	Alignment	not modelled	27.5	13	<b>PDB header:</b> fad-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> siderophore-interacting protein; <b>PDBTitle:</b> crystal structure of a siderophore-interacting protein (sputc32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
87	<a href="#">c2gp4A_</a>	Alignment	not modelled	27.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
88	<a href="#">c2w1jB_</a>	Alignment	not modelled	26.4	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sortase; <b>PDBTitle:</b> crystal structure of sortase c-1 (src1) from streptococcus2 pneumoniae
89	<a href="#">c3if9A_</a>	Alignment	not modelled	25.6	9	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> 4e10_d0_1is1a_001_c (t161); <b>PDBTitle:</b> crystal structure of hiv epitope-scaffold 4e10_d0_1is1a_001_c
90	<a href="#">c5ym0A_</a>	Alignment	not modelled	25.4	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the crystal structure of dhad
91	<a href="#">c2pbC_D</a>	Alignment	not modelled	25.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> fk506-binding protein 2; <b>PDBTitle:</b> fk506-binding protein 2
92	<a href="#">d1ep3b1</a>	Alignment	not modelled	24.7	16	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
93	<a href="#">c6b4pB_</a>	Alignment	not modelled	24.4	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidylprolyl isomerase; <b>PDBTitle:</b> crystal structure of peptidylprolyl isomerase from naegleria fowleri
94	<a href="#">c3prdA_</a>	Alignment	not modelled	24.2	21	<b>PDB header:</b> chaperone, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp-type peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
95	<a href="#">d2d0oa1</a>	Alignment	not modelled	24.0	36	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Swiveling domain of dehydratase reactivase alpha subunit <b>Family:</b> Swiveling domain of dehydratase reactivase alpha subunit
96	<a href="#">c5ze4A_</a>	Alignment	not modelled	23.7	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the structure of holo- structure of dhad complex with [2fe-2s] cluster
97	<a href="#">c3k1rA_</a>	Alignment	not modelled	22.4	25	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> harmonin; <b>PDBTitle:</b> structure of harmonin npd21 in complex with the sampbm of2 sans
98	<a href="#">c2vcdA_</a>	Alignment	not modelled	22.3	38	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein mip; <b>PDBTitle:</b> solution structure of the fkbp-domain of legionella pneumophila mip in2 complex with rapamycin
99	<a href="#">c5naaB_</a>	Alignment	not modelled	22.2	20	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system transmembrane protein lolc; <b>PDBTitle:</b> lipoprotein-releasing system transmembrane protein lolc
100	<a href="#">c3u5cG_</a>	Alignment	not modelled	22.2	16	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 40s ribosomal protein s6-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
101	<a href="#">d1is1a_</a>	Alignment	not modelled	21.4	12	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF
102	<a href="#">c4bf8A_</a>	Alignment	not modelled	21.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fpr4; <b>PDBTitle:</b> fpr4 ppi domain
103	<a href="#">d2jioa1</a>	Alignment	not modelled	20.9	20	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
104	<a href="#">d1q1ca1</a>	Alignment	not modelled	20.9	12	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
						<b>Fold:</b> Reductase/isomerase/elongation factor common domain

105	<a href="#">d1gvha2</a>	Alignment	not modelled	20.8	15	<b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
106	<a href="#">c4l6rA_</a>	Alignment	not modelled	20.5	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562 and glucagon receptor chimera; <b>PDBTitle:</b> structure of the class b human glucagon g protein coupled receptor
107	<a href="#">d1eh1a_</a>	Alignment	not modelled	20.4	15	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF