
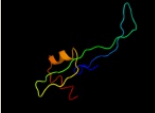

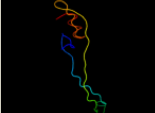
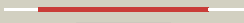
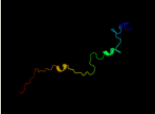

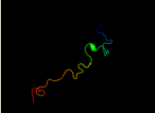

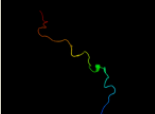





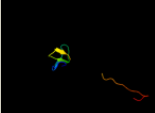





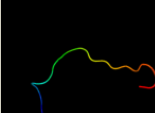
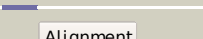

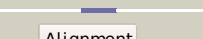
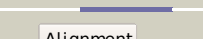
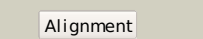
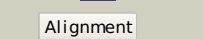



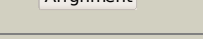





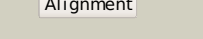
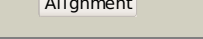




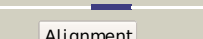





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlvs6z1	 Alignment		100.0	100	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
2	c2b664_	 Alignment		100.0	42	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
3	c3bbo1_	 Alignment		99.9	31	PDB header: ribosome Chain: 1: PDB Molecule: ribosomal protein l31; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
4	c2j034_	 Alignment		99.9	51	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
5	d2j0141	 Alignment		99.9	51	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
6	c3f1f4_	 Alignment		97.4	41	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: crystal structure of a translation termination complex2 formed with release factor rf2. this file contains the 50s3 subunit of one 70s ribosome. the entire crystal structure4 contains two 70s ribosomes as described in remark 400.
7	c2wh44_	 Alignment		97.4	41	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome
8	c3cngC_	 Alignment		38.9	26	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
9	d1iufa2	 Alignment		23.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
10	c3cucB_	 Alignment		20.7	54	PDB header: signaling protein Chain: B: PDB Molecule: protein of unknown function with a fic domain; PDBTitle: crystal structure of a fic domain containing signaling protein2 (bt_2513) from bacteroides thetaiotaomicron vpi-5482 at 2.71 a3 resolution
11	d1tqza1	 Alignment		19.8	25	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Necap1 N-terminal domain-like

12	c2ketA_	Alignment		18.6	60	PDB header: antibiotic Chain: A: PDB Molecule: cathelicidin-6; PDBTitle: solution structure of bmap-27
13	c3g66A_	Alignment		18.1	26	PDB header: transferase Chain: A: PDB Molecule: sortase c; PDBTitle: the crystal structure of streptococcus pneumoniae sortase c2 provides novel insights into catalysis as well as pilin3 substrate specificity
14	c3o0pA_	Alignment		16.3	26	PDB header: transferase , hydrolase Chain: A: PDB Molecule: sortase family protein; PDBTitle: pilus-related sortase c of group b streptococcus
15	d1x6ha1	Alignment		16.1	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
16	c1iufA_	Alignment		15.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: centromere abp1 protein; PDBTitle: low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
17	d1eb7a2	Alignment		14.5	42	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
18	c4a1eT_	Alignment		13.6	35	PDB header: ribosome Chain: T: PDB Molecule: rpl24; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
19	c2keqA_	Alignment		13.5	36	PDB header: splicing Chain: A: PDB Molecule: dna polymerase iii alpha subunit, nucleic acid PDBTitle: solution structure of dnae intein from nostoc punctiforme
20	c3izcZ_	Alignment		13.5	12	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein rpl24 (l24e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
21	c2kw8A_	Alignment	not modelled	13.3	26	PDB header: protein binding Chain: A: PDB Molecule: lpxtg-site transpeptidase family protein; PDBTitle: solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
22	c2w1jB_	Alignment	not modelled	13.1	26	PDB header: transferase Chain: B: PDB Molecule: putative sortase; PDBTitle: crystal structure of sortase c-1 (src1-1) from2 streptococcus pneumoniae
23	d1nmla2	Alignment	not modelled	12.5	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
24	c3n3vA_	Alignment	not modelled	11.9	46	PDB header: transferase Chain: A: PDB Molecule: adenosine monophosphate-protein transferase ibpa; PDBTitle: crystal structure of ibpafic2-h3717a in complex with adenylylated2 cdc42
25	c1zd7B_	Alignment	not modelled	11.8	25	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: 1.7 angstrom crystal structure of post-splicing form of a dnae intein2 from synechocystis sp. pcc 6803
26	d1mi8a_	Alignment	not modelled	11.7	25	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
27	d1oa8a_	Alignment	not modelled	11.3	31	Fold: AXH domain Superfamily: AXH domain Family: AXH domain
28	c1v0eB_	Alignment	not modelled	11.0	32	PDB header: hydrolase Chain: B: PDB Molecule: endo-alpha-sialidase; PDBTitle: endosialidase of bacteriophage k1f

29	d1e7la1		Alignment	not modelled	10.6	60	Fold: LEM/SAP HeH motif Superfamily: Recombination endonuclease VII, C-terminal and dimerization domains Family: Recombination endonuclease VII, C-terminal and dimerization domains
30	c1nmlA_		Alignment	not modelled	10.5	33	PDB header: oxidoreductase Chain: A: PDB Molecule: di-haem cytochrome c peroxidase; PDBTitle: di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
31	c2yiuE_		Alignment	not modelled	10.3	63	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
32	d1jz8a1		Alignment	not modelled	10.0	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
33	c3iz5Z_		Alignment	not modelled	10.0	23	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein l24 (l24e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
34	c3cwbQ_		Alignment	not modelled	9.6	71	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
35	c2w1kB_		Alignment	not modelled	9.4	32	PDB header: transferase Chain: B: PDB Molecule: putative sortase; PDBTitle: crystal structure of sortase c-3 (src-3) from2 streptococcus pneumoniae
36	c3rbjB_		Alignment	not modelled	9.3	21	PDB header: hydrolase Chain: B: PDB Molecule: sortase family protein; PDBTitle: crystal structure of the lid-mutant of streptococcus agalactiae2 sortase c1
37	d3cx5d1		Alignment	not modelled	9.2	57	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
38	c2fynH_		Alignment	not modelled	9.0	57	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
39	d1at0a_		Alignment	not modelled	8.9	10	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Hedgehog C-terminal (Hog) autoprocessing domain
40	c3hq7A_		Alignment	not modelled	8.9	33	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c551 peroxidase; PDBTitle: ccpa from g. sulfurreducens, g94k/k97q/r100i variant
41	d1am2a_		Alignment	not modelled	8.9	20	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
42	c3dd7A_		Alignment	not modelled	8.7	20	PDB header: ribosome inhibitor Chain: A: PDB Molecule: death on curing protein; PDBTitle: structure of doch66y in complex with the c-terminal domain of phd
43	c2lclA_		Alignment	not modelled	8.7	20	PDB header: hydrolase Chain: A: PDB Molecule: pab polc intein; PDBTitle: solution nmr structure of pab polii intein
44	c1p84D_		Alignment	not modelled	8.5	57	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
45	c3eqxB_		Alignment	not modelled	8.4	54	PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containing transcriptional regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
46	d1ppjd1		Alignment	not modelled	8.4	71	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
47	c2imzA_		Alignment	not modelled	8.2	17	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease pi-mtui; PDBTitle: crystal structure of mtu reca intein splicing domain
48	c1zrtD_		Alignment	not modelled	8.2	71	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
49	c3ltiA_		Alignment	not modelled	8.2	32	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta14 domains
50	d1wada_		Alignment	not modelled	7.9	67	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
51	d1lta_		Alignment	not modelled	7.4	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA replication initiator (cdc21/cdc54) N-terminal domain
52	c2in0A_		Alignment	not modelled	7.2	15	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease pi-mtui; PDBTitle: crystal structure of mtu reca intein splicing domain
53	d2cbpa_		Alignment	not modelled	7.2	25	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
54	c3ov7C_		Alignment	not modelled	6.7	17	PDB header: ribosomal protein Chain: C: PDB Molecule: 50s ribosomal protein l1;

54	c2ov7c	Alignment	not modelled	6.7	17	PDBTitle: the first domain of the ribosomal protein l1 from thermus2 thermophilus PDB header: unknown function
55	c2jmzA	Alignment	not modelled	6.6	20	Chain: A: PDB Molecule: hypothetical protein mj0781; PDBTitle: solution structure of a klba intein precursor from2 methanococcus jannaschii
56	c3mdnD	Alignment	not modelled	6.6	31	PDB header: transferase Chain: D: PDB Molecule: glutamine aminotransferase class-ii domain protein; PDBTitle: structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
57	c3re9A	Alignment	not modelled	6.6	26	PDB header: transferase Chain: A: PDB Molecule: sortase-like protein; PDBTitle: crystal structure of sortasec1 from streptococcus suis
58	c2cazB	Alignment	not modelled	6.4	30	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein PDBTitle: escrt-i core
59	d2cazb1	Alignment	not modelled	6.4	30	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
60	cliqcB	Alignment	not modelled	6.2	42	PDB header: oxidoreductase Chain: B: PDB Molecule: di-heme peroxidase; PDBTitle: crystal structure of di-heme peroxidase from nitrosomonas europaea
61	c2zkru	Alignment	not modelled	6.1	30	PDB header: ribosomal protein/rna Chain: U: PDB Molecule: rna expansion segment es41; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
62	c2xwgA	Alignment	not modelled	6.1	39	PDB header: hydrolase Chain: A: PDB Molecule: sortase; PDBTitle: crystal structure of sortase c-1 from actinomyces oris (formerly2 actinomyces naeslundii)
63	c2wg6L	Alignment	not modelled	6.1	9	PDB header: transcription,hydrolase Chain: L: PDB Molecule: general control protein gcn4, PDBTitle: proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
64	c3h43F	Alignment	not modelled	6.1	12	PDB header: hydrolase Chain: F: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
65	d1i77a	Alignment	not modelled	5.9	83	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
66	d1up9a	Alignment	not modelled	5.3	83	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
67	c1x0gA	Alignment	not modelled	5.2	23	PDB header: metal binding protein Chain: A: PDB Molecule: isca; PDBTitle: crystal structure of isca with the [2fe-2s] cluster
68	d2f6mb1	Alignment	not modelled	5.2	30	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
69	c2wcvl	Alignment	not modelled	5.2	36	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
70	d1j5ya2	Alignment	not modelled	5.2	16	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain