

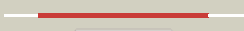



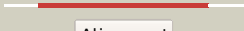





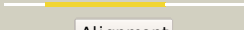

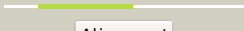

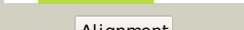



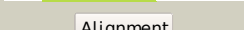




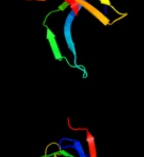

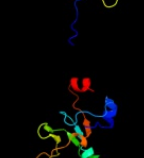
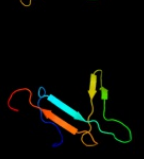

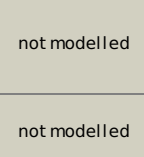


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2j01t1	 Alignment		100.0	46	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19
2	d2gycn1	 Alignment		100.0	100	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19
3	c1nwxN_	 Alignment		100.0	55	PDB header: ribosome Chain: N: PDB Molecule: ribosomal protein l19; PDBTitle: complex of the large ribosomal subunit from deinococcus2 radiodurans with abt-773
4	d2zjrm1	 Alignment		100.0	55	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19
5	c3bboR_	 Alignment		100.0	38	PDB header: ribosome Chain: R: PDB Molecule: ribosomal protein l19; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
6	c2ftcK_	 Alignment		100.0	26	PDB header: ribosome Chain: K: PDB Molecule: 39s ribosomal protein l19, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
7	c2e6zA_	 Alignment		73.6	29	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5
8	d1jb7a1	 Alignment		68.7	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
9	c2kvqG_	 Alignment		68.5	29	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
10	c2jvvA_	 Alignment		68.5	29	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
11	d1nppa2	 Alignment		67.1	31	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain

12	dlzqla1	Alignment		65.5	17	Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like
13	c3iz5Y_	Alignment		65.2	24	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l26 (l24p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
14	dlvqot1	Alignment		63.9	24	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
15	dlnz9a_	Alignment		58.3	36	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
16	clzqlB_	Alignment		57.3	16	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
17	c2f1lA_	Alignment		49.1	21	PDB header: unknown function Chain: A: PDB Molecule: 16s rna processing protein; PDBTitle: crystal structure of a putative 16s ribosomal rna processing protein2 rimm (pa3744) from pseudomonas aeruginosa at 2.46 a resolution
18	c4a1cS_	Alignment		49.1	16	PDB header: ribosome Chain: S: PDB Molecule: rpl26; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 4.
19	c1k8gC_	Alignment		45.3	18	PDB header: dna binding protein/dna Chain: C: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the n-terminal domain of oxytricha2 nova telomere end binding protein alpha subunit both3 uncomplexed and complexed with telomeric ssdna
20	c3p8bB_	Alignment		44.0	27	PDB header: transferase/transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
21	c1m1gB_	Alignment	not modelled	41.8	26	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
22	c2dxcG_	Alignment	not modelled	34.7	36	PDB header: hydrolase Chain: G: PDB Molecule: thiocyanate hydrolase subunit alpha; PDBTitle: recombinant thiocyanate hydrolase, fully-matured form
23	c1ph4A_	Alignment	not modelled	32.1	21	PDB header: dna binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggtttggcg
24	c1jb7A_	Alignment	not modelled	32.1	21	PDB header: dna-binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
25	d2d6fa1	Alignment	not modelled	31.7	23	Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like
26	dlugpb_	Alignment	not modelled	28.1	45	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
27	c3cnrA_	Alignment	not modelled	26.2	33	PDB header: unknown function Chain: A: PDB Molecule: type iv fimbriae assembly protein; PDBTitle: crystal structure of pilz (xac1133) from xanthomonas2 axonopodis pv citri
28	c3qz9D_	Alignment	not modelled	26.0	45	PDB header: lyase Chain: D: PDB Molecule: co-type nitrile hydratase beta subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.

29	d1hr0w_	Alignment	not modelled	25.9	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
30	c2zkrt	Alignment	not modelled	24.9	40	PDB header: ribosomal protein/rna Chain: T: PDB Molecule: rna expansion segment es39 part iii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
31	d1v29b_	Alignment	not modelled	24.8	27	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
32	c2eifA_	Alignment	not modelled	24.5	16	PDB header: gene regulation Chain: A: PDB Molecule: protein (eukaryotic translation initiation factor 5a); PDBTitle: eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
33	d1ah9a_	Alignment	not modelled	22.1	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
34	c2bi0A_	Alignment	not modelled	21.4	19	PDB header: hypothetical protein Chain: A: PDB Molecule: hypothetical protein rv0216; PDBTitle: rv0216, a conserved hypothetical protein from mycobacterium2 tuberculosis that is essential for bacterial survival3 during infection, has a double hotdogfold
35	c3i4oA_	Alignment	not modelled	21.0	29	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
36	d2qdyb1	Alignment	not modelled	20.8	36	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
37	c2v43A_	Alignment	not modelled	20.7	20	PDB header: regulator Chain: A: PDB Molecule: sigma-e factor regulatory protein rseb; PDBTitle: crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
38	d1kl9a2	Alignment	not modelled	20.5	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
39	d1qzga_	Alignment	not modelled	20.1	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
40	c2fhdA_	Alignment	not modelled	19.7	30	PDB header: cell cycle Chain: A: PDB Molecule: dna repair protein rhp9/crb2; PDBTitle: crystal structure of crb2 tandem tudor domains
41	c2kya_	Alignment	not modelled	19.7	38	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution struture of the h-rv107 n-terminal domain
42	d1je3a_	Alignment	not modelled	19.1	17	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
43	d1y14b1	Alignment	not modelled	19.0	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
44	d1vqoq1	Alignment	not modelled	18.9	18	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
45	d1ejxb_	Alignment	not modelled	17.5	26	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
46	c3e0eA_	Alignment	not modelled	17.4	35	PDB header: replication Chain: A: PDB Molecule: replication protein a; PDBTitle: crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
47	d2bi0a2	Alignment	not modelled	17.3	14	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
48	d1e9ya1	Alignment	not modelled	16.9	26	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
49	d4ubpb_	Alignment	not modelled	16.1	24	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
50	d1xjva1	Alignment	not modelled	15.8	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
51	d2do3a1	Alignment	not modelled	14.9	37	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
52	c2l66B_	Alignment	not modelled	14.3	35	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, abrb family; PDBTitle: the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
53	d2nn6i1	Alignment	not modelled	14.0	36	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
54	d2bi0a1	Alignment	not modelled	14.0	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
						PDB header: protein binding

55	c2rm4A_	Alignment	not modelled	14.0	21	Chain: A: PDB Molecule: cg6311-pb; PDBTitle: solution structure of the lsm domain of dm edc3 (enhancer2 of decapping 3)
56	c4a1aP_	Alignment	not modelled	13.5	19	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l21; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
57	c3izcU_	Alignment	not modelled	13.4	21	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein rpl21 (l21e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
58	c2wknE_	Alignment	not modelled	13.4	23	PDB header: hydrolase Chain: E: PDB Molecule: formamidase; PDBTitle: gamma lactamase from delftia acidovorans
59	c2d6fA_	Alignment	not modelled	13.3	25	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
60	d1is3a_	Alignment	not modelled	12.6	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
61	d1bf2a1	Alignment	not modelled	12.6	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
62	d2ahob2	Alignment	not modelled	12.1	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
63	c2nn6l_	Alignment	not modelled	12.0	36	PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
64	c2khjA_	Alignment	not modelled	11.9	26	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
65	c1e9zA_	Alignment	not modelled	11.7	24	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
66	d1q46a2	Alignment	not modelled	11.6	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
67	d1hh2p1	Alignment	not modelled	11.4	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
68	c3qgaD_	Alignment	not modelled	11.1	26	PDB header: hydrolase Chain: D: PDB Molecule: fusion of urease beta and gamma subunits; PDBTitle: 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
69	c2dbkA_	Alignment	not modelled	11.0	31	PDB header: signaling protein Chain: A: PDB Molecule: crk-like protein; PDBTitle: solution structures of the sh3 domain of human crk-like2 protein
70	c3u5gB_	Alignment	not modelled	10.6	13	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s1-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution
71	d1go3e1	Alignment	not modelled	10.4	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
72	c1y43B_	Alignment	not modelled	10.4	29	PDB header: hydrolase Chain: B: PDB Molecule: aspergillopepsin ii heavy chain; PDBTitle: crystal structure of aspergilloglutamic peptidase from2 aspergillus niger
73	c1xjvA_	Alignment	not modelled	10.2	21	PDB header: transcription/dna Chain: A: PDB Molecule: protection of telomeres 1; PDBTitle: crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggttag)
74	d2nn6h1	Alignment	not modelled	10.1	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
75	d2ifra1	Alignment	not modelled	9.9	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Peptidase A4
76	d1t0ha_	Alignment	not modelled	9.6	25	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
77	c1jsyA_	Alignment	not modelled	9.6	15	PDB header: signaling protein Chain: A: PDB Molecule: bovine arrestin-2 (full length); PDBTitle: crystal structure of bovine arrestin-2
78	d1vyva1	Alignment	not modelled	9.5	19	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
79	d2hbaa1	Alignment	not modelled	9.4	25	Fold: MbtH/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
80	c3dm3A_	Alignment	not modelled	9.3	26	PDB header: replication Chain: A: PDB Molecule: replication factor a; PDBTitle: crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural

						genomics target mjr118e
81	d2vv5a1	Alignment	not modelled	9.3	36	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
82	c3l53F	Alignment	not modelled	9.1	31	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative fumarylacetoacetate isomerase/hydrolase; PDBTitle: crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
83	d1cqua	Alignment	not modelled	9.1	25	Fold: MbtH/L9 domain-like Superfamily: L9 N-domain-like Family: Ribosomal protein L9 N-domain
84	c2xhcA	Alignment	not modelled	9.1	19	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
85	c2xzm4	Alignment	not modelled	8.9	16	PDB header: ribosome Chain: 4: PDB Molecule: 40s ribosomal protein s3a; PDBTitle: 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 1
86	c2ebpA	Alignment	not modelled	8.9	18	PDB header: cell adhesion Chain: A: PDB Molecule: sam and sh3 domain-containing protein 1; PDBTitle: solution structure of the sh3 domain from human sam and sh32 domain containing protein 1
87	c2k52A	Alignment	not modelled	8.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1198; PDBTitle: structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
88	d1gr3a	Alignment	not modelled	8.6	17	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
89	c1gr3A	Alignment	not modelled	8.6	17	PDB header: collagen Chain: A: PDB Molecule: collagen x; PDBTitle: structure of the human collagen x nc1 trimer
90	d2j01o1	Alignment	not modelled	8.2	22	Fold: Ribosomal protein L14 Superfamily: Ribosomal protein L14 Family: Ribosomal protein L14
91	c1t0ja	Alignment	not modelled	8.2	25	PDB header: signaling protein Chain: A: PDB Molecule: voltage-gated calcium channel subunit beta2a; PDBTitle: crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
92	d2je6i1	Alignment	not modelled	8.2	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
93	c3fxhA	Alignment	not modelled	8.1	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron gene cassette protein hfx_cass2; PDBTitle: crystal structure from the mobile metagenome of halifax2 harbour sewage outfall: integron cassette protein hfx_cass2
94	d1t3la1	Alignment	not modelled	7.6	45	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
95	c2eyxA	Alignment	not modelled	7.6	29	PDB header: signaling protein Chain: A: PDB Molecule: v-crK sarcoma virus ct10 oncogene homolog PDBTitle: c-terminal sh3 domain of ct10-regulated kinase
96	c3qiiA	Alignment	not modelled	7.5	24	PDB header: transcription regulator Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20
97	c3d0fA	Alignment	not modelled	7.5	50	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
98	c2khiA	Alignment	not modelled	7.5	33	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
99	d1vyua1	Alignment	not modelled	7.2	19	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain