Phyre2

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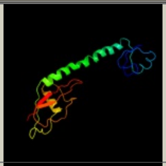
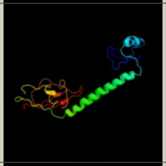
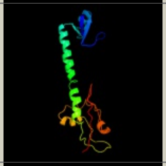
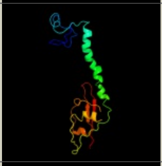
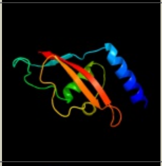
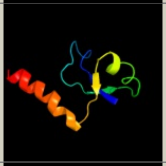
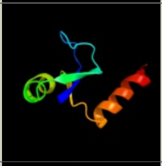
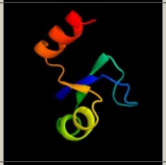
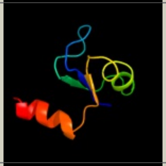
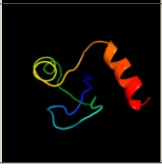
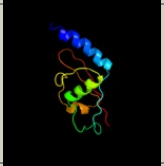
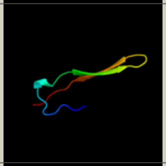
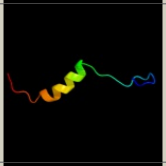
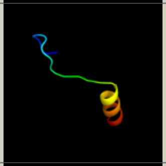
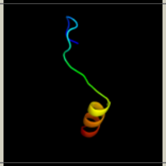
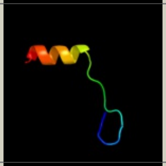
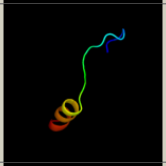
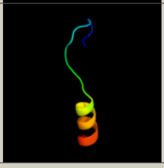
Description	P0A7R1
Date	Thu Jan 5 11:06:05 GMT 2012
Unique Job ID	f2ee4c7b60d85a6d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qbcH_	Alignment		100.0	100	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**50s ribosomal protein l9; **PDBTitle:** crystal structure of the bacterial ribosome from2 escherichia coli in complex with gentamicin. this file3 contains the 50s subunit of the second 70s ribosome, with4 gentamicin bound. the entire crystal structure contains5 two 70s ribosomes and is described in remark 400.
2	c2b66I_	Alignment		100.0	40	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**50s ribosomal protein l9; **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	c2v49I_	Alignment		100.0	41	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**50s ribosomal protein l9; **PDBTitle:** structure of the ribosome recycling factor bound to the2 thermus thermophilus 70s ribosome with mrna, asl-phe and3 trna-fmet (part 4 of 4). this file contains the 50s4 subunit of molecule 2.
4	c3bboJ_	Alignment		100.0	32	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**ribosomal protein l9; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
5	d2gycf1	Alignment		99.9	100	**Fold:**Ribosomal protein L9 C-domain **Superfamily:**Ribosomal protein L9 C-domain **Family:**Ribosomal protein L9 C-domain
6	d1diva1	Alignment		99.9	38	**Fold:**Ribosomal protein L9 C-domain **Superfamily:**Ribosomal protein L9 C-domain **Family:**Ribosomal protein L9 C-domain
7	d2gycf2	Alignment		99.8	100	**Fold:**MbtH/L9 domain-like **Superfamily:**L9 N-domain-like **Family:**Ribosomal protein L9 N-domain
8	d2j01i2	Alignment		99.8	51	**Fold:**MbtH/L9 domain-like **Superfamily:**L9 N-domain-like **Family:**Ribosomal protein L9 N-domain
9	d2hbaa1	Alignment		99.8	45	**Fold:**MbtH/L9 domain-like **Superfamily:**L9 N-domain-like **Family:**Ribosomal protein L9 N-domain
10	d1cqua_	Alignment		99.8	45	**Fold:**MbtH/L9 domain-like **Superfamily:**L9 N-domain-like **Family:**Ribosomal protein L9 N-domain
11	c1pnyF_	Alignment		99.8	55	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**50s ribosomal protein l9; **PDBTitle:** crystal structure of the wild type ribosome from e. coli,2 50s subunit of 70s ribosome. this file, 1pny, contains3 only molecules of the 50s ribosomal subunit. the 30s4 subunit is in the pdb file 1pnx.

12	c1sm1F_	Alignment		99.8	55	**PDB header:**ribosome/antibiotic **Chain:** F: **PDB Molecule:**50s ribosomal protein l9; **PDBTitle:** complex of the large ribosomal subunit from deinococcus radiodurans2 with quinupristin and dalfopristin
13	d2j01i1	Alignment		99.8	35	**Fold:**Ribosomal protein L9 C-domain **Superfamily:**Ribosomal protein L9 C-domain **Family:**Ribosomal protein L9 C-domain
14	c3rbgB_	Alignment		32.8	26	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cytotoxic and regulatory t-cell molecule; **PDBTitle:** crystal structure analysis of class-i mhc restricted t-cell associated2 molecule
15	c3ctuB_	Alignment		31.7	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
16	c3ddjA_	Alignment		30.4	22	**PDB header:**amp-binding protein **Chain:** A: **PDB Molecule:**cbs domain-containing protein; **PDBTitle:** crystal structure of a cbs domain-containing protein in complex with2 amp (sso3205) from sulfolobus solfataricus at 1.80 a resolution
17	d3ddja1	Alignment		30.2	22	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
18	d1vr9a3	Alignment		28.3	26	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
19	c3lqnA_	Alignment		26.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
20	d1o50a3	Alignment		26.2	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
21	c1vr9B_	Alignment	not modelled	26.2	26	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cbs domain protein/act domain protein; **PDBTitle:** crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
22	c3lhhA_	Alignment	not modelled	25.4	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
23	d2yzia1	Alignment	not modelled	24.8	23	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
24	c3gbyA_	Alignment	not modelled	23.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ct1051; **PDBTitle:** crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
25	c3kpbA_	Alignment	not modelled	23.6	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0100; **PDBTitle:** crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
26	c2emqA_	Alignment	not modelled	22.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** hypothetical conserved protein (gk1048) from geobacillus kaustophilus
27	c2k50A_	Alignment	not modelled	21.7	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
28	d2v8qe1	Alignment	not modelled	20.7	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair

						Family:CBS-domain pair
29	c2or7A_	Alignment	not modelled	20.6	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**t-cell immunoglobulin and mucin domain- **PDBTitle:** tim-2
30	d2j9la1	Alignment	not modelled	20.2	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
31	c3kxrA_	Alignment	not modelled	20.1	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**magnesium transporter, putative; **PDBTitle:** structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
32	c2p9mD_	Alignment	not modelled	19.5	27	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0922; **PDBTitle:** crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
33	d2ef7a1	Alignment	not modelled	19.3	41	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
34	c3i8nB_	Alignment	not modelled	19.1	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp2912; **PDBTitle:** a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633.
35	c3nqrD_	Alignment	not modelled	19.0	20	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**magnesium and cobalt efflux protein corc; **PDBTitle:** a putative cbs domain-containing protein from salmonella typhimurium2 lt2
36	d2ooxe2	Alignment	not modelled	18.5	25	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
37	c3fioB_	Alignment	not modelled	17.7	28	**PDB header:**nucleotide binding protein, metal bindin **Chain:** B: **PDB Molecule:**a cystathionine beta-synthase domain protein **PDBTitle:** crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
38	d1yava3	Alignment	not modelled	17.6	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
39	d1nksa_	Alignment	not modelled	17.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
40	c2v8qE_	Alignment	not modelled	17.5	21	**PDB header:**transferase **Chain:** E: **PDB Molecule:**5'-amp-activated protein kinase subunit gamma-1; **PDBTitle:** crystal structure of the regulatory fragment of mammalian2 ampk in complexes with amp
41	c3m45D_	Alignment	not modelled	17.2	15	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**cell adhesion molecule 2; **PDBTitle:** crystal structure of ig1 domain of mouse syncam 2
42	c2ouxB_	Alignment	not modelled	16.2	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium transporter; **PDBTitle:** crystal structure of the soluble part of a magnesium transporter
43	c3ocmA_	Alignment	not modelled	16.2	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
44	c2yvxD_	Alignment	not modelled	16.1	30	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
45	c2o8kA_	Alignment	not modelled	15.9	26	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
46	c3lfrB_	Alignment	not modelled	15.5	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative metal ion transporter; **PDBTitle:** the crystal structure of a cbs domain from a putative metal2 ion transporter bound to amp from pseudomonas syringae to3 1.55a
47	c3e0eA_	Alignment	not modelled	15.4	36	**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
48	c1yavB_	Alignment	not modelled	14.6	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14130; **PDBTitle:** crystal structure of cbs domain-containing protein ykul2 from bacillus subtilis
49	c2p9rA_	Alignment	not modelled	14.4	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**alpha-2-macroglobulin; **PDBTitle:** human alpha2-macroglogulin is composed of multiple domains,2 as predicted by homology with complement component c3
50	d1suxa_	Alignment	not modelled	14.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
51	c3jtfB_	Alignment	not modelled	13.9	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium and cobalt efflux protein; **PDBTitle:** the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp
52	d1zfja4	Alignment	not modelled	13.7	29	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
						Fold: Putative DNA-binding domain

53	d1jjcb1	Alignment	not modelled	13.5	11	**Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
54	d1k1xa1	Alignment	not modelled	13.1	43	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**4-alpha-glucanotransferase, domain 2
55	d1o7ia_	Alignment	not modelled	12.9	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
56	c2pfiA_	Alignment	not modelled	12.4	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chloride channel protein clc-ka; **PDBTitle:** crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
57	c3ocoB_	Alignment	not modelled	12.4	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hemolysin-like protein containing cbs domains; **PDBTitle:** the crystal structure of a hemolysin-like protein containing cbs2 domain of oenococcus oeni psu
58	d1ttja_	Alignment	not modelled	12.3	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
59	c3hf7A_	Alignment	not modelled	12.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cbs-domain protein; **PDBTitle:** the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
60	c2yvzA_	Alignment	not modelled	12.2	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
61	d1nunb2	Alignment	not modelled	12.1	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
62	c1z9mA_	Alignment	not modelled	11.9	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**gapa225; **PDBTitle:** crystal structure of nectin-like molecule-1 protein domain 1
63	d2d4za3	Alignment	not modelled	11.9	25	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
64	c1x37A_	Alignment	not modelled	11.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** structure of bacillus subtilis lon protease ssd domain
65	c2auvA_	Alignment	not modelled	11.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**potential nad-reducing hydrogenase subunit; **PDBTitle:** solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
66	d2nyca1	Alignment	not modelled	11.5	30	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
67	d1kv5a_	Alignment	not modelled	11.5	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
68	d1dkga1	Alignment	not modelled	11.4	22	**Fold:**Head domain of nucleotide exchange factor GrpE **Superfamily:**Head domain of nucleotide exchange factor GrpE **Family:**Head domain of nucleotide exchange factor GrpE
69	d1m55a_	Alignment	not modelled	11.4	30	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Replication protein Rep, nuclease domain
70	d2riha1	Alignment	not modelled	11.3	25	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
71	d1u2ca1	Alignment	not modelled	11.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cadherin-like **Family:**Dystroglycan, N-terminal domain
72	d2ouxa2	Alignment	not modelled	10.8	23	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
73	c2qstB_	Alignment	not modelled	10.7	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**carcinoembryonic antigen-related cell adhesion **PDBTitle:** crystal structure of the v39c mutant of the n-terminal2 domain of carcinoembryonic antigen (cea)
74	d2p5ka1	Alignment	not modelled	10.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
75	d2yzqa2	Alignment	not modelled	10.5	25	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
76	d1b4aa1	Alignment	not modelled	10.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
77	c2ds4A_	Alignment	not modelled	10.4	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 45; **PDBTitle:** solution structure of the filamin domain from human2 tripartite motif protein 45
78	d2yvxa2	Alignment	not modelled	10.4	32	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
79	d1ixla_	Alignment	not modelled	10.3	42	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase

						Family: PaaI/YdiI-like
80	d2e9ia1	Alignment	not modelled	10.1	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
81	d1qzma_	Alignment	not modelled	10.1	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
82	d1ncna_	Alignment	not modelled	9.9	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
83	c2dp3A_	Alignment	not modelled	9.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
84	c2ptvA_	Alignment	not modelled	9.6	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cd48 antigen; **PDBTitle:** structure of nk cell receptor ligand cd48
85	c3ocmB_	Alignment	not modelled	9.5	25	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
86	d1n55a_	Alignment	not modelled	9.4	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
87	c2k75A_	Alignment	not modelled	9.4	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ta0387; **PDBTitle:** solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
88	d1m2da_	Alignment	not modelled	9.3	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioredoxin-like 2Fe-2S ferredoxin
89	c2ednA_	Alignment	not modelled	9.3	17	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin-binding protein c, fast-type; **PDBTitle:** solution structure of the first ig-like domain from human2 myosin-binding protein c, fast-type
90	d1f9na1	Alignment	not modelled	9.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
91	d1sw3a_	Alignment	not modelled	8.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
92	d2b78a1	Alignment	not modelled	8.9	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
93	d1mo0a_	Alignment	not modelled	8.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
94	d2rc3a1	Alignment	not modelled	8.8	28	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
95	c3rghA_	Alignment	not modelled	8.7	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
96	c2d4zB_	Alignment	not modelled	8.6	25	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride channel protein; **PDBTitle:** crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
97	d2btma_	Alignment	not modelled	8.4	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
98	c3lv9A_	Alignment	not modelled	8.2	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative transporter; **PDBTitle:** crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
99	c1s1i0_	Alignment	not modelled	8.1	38	**PDB header:**ribosome **Chain:** 0: **PDB Molecule:**60s ribosomal protein l32; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.