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Description	P46187
Date	Thu Jan 5 12:04:12 GMT 2012
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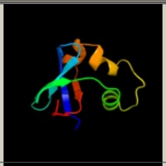
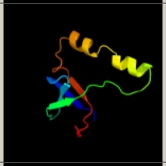
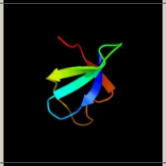
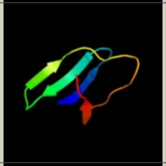
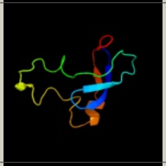
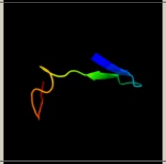
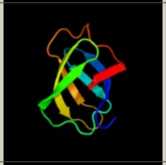
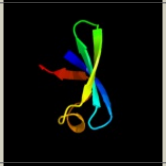
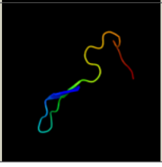
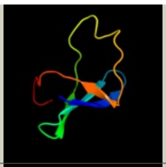
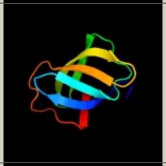
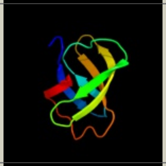
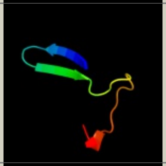
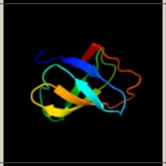
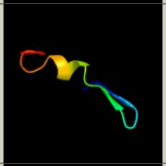
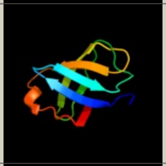
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u0la1	Alignment		91.2	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
2	d2z1ca1	Alignment		87.4	18	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
3	c1u0lB_	Alignment		87.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
4	d2ot2a1	Alignment		83.0	21	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
5	c3d3rA_	Alignment		73.7	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
6	d1t9ha1	Alignment		73.5	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
7	c2jnvA_	Alignment		66.1	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
8	c2r9vA_	Alignment		65.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
9	d2jdia2	Alignment		65.1	18	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
10	d3d3ra1	Alignment		65.0	26	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
11	d1xhja_	Alignment		62.9	25	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like

12	c2yv5A_	Alignment		61.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
13	d1skyb2	Alignment		53.7	12	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
14	c2w6fA_	Alignment		52.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha heart isoform, **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 2.
15	c1kmhA_	Alignment		52.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atpase alpha subunit; **PDBTitle:** crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
16	c2z51A_	Alignment		49.6	20	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast; **PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
17	c1w0jB_	Alignment		49.2	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase alpha chain heart isoform, **PDBTitle:** beryllium fluoride inhibited bovine f1-atpase
18	d1th5a1	Alignment		47.9	5	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
19	d1fx0a2	Alignment		47.9	11	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
20	c2qe7C_	Alignment		46.4	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
21	d2nqra1	Alignment	not modelled	41.9	13	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
22	d2gy9q1	Alignment	not modelled	40.2	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	c1s1hQ_	Alignment	not modelled	39.8	19	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**40s ribosomal protein s11; **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, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
24	d2uubq1	Alignment	not modelled	37.2	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
25	d1i94q_	Alignment	not modelled	37.0	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	d1uz5a1	Alignment	not modelled	36.1	21	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
27	d1xi8a1	Alignment	not modelled	34.9	21	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
28	d1te7a_	Alignment	not modelled	34.8	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**yqfB-like

29	d2do3a1	Alignment	not modelled	34.6	9	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
30	d1veha_	Alignment	not modelled	32.6	30	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
31	d1wu2a1	Alignment	not modelled	32.2	21	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
32	c2dpyA_	Alignment	not modelled	30.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flagellum-specific atp synthase; **PDBTitle:** crystal structure of the flagellar type iii atpase flii
33	c1t9hA_	Alignment	not modelled	29.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase.
34	d1qfja1	Alignment	not modelled	24.1	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
35	d1d7qa_	Alignment	not modelled	22.7	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
36	c1i18B_	Alignment	not modelled	22.3	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** solution structure of the n-terminal domain of riboflavin synthase2 from e. coli
37	c1hzeB_	Alignment	not modelled	22.3	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** solution structure of the n-terminal domain of riboflavin synthase2 from e. coli
38	c2oqkA_	Alignment	not modelled	21.4	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
39	d1maba2	Alignment	not modelled	21.2	18	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
40	c3oaaC_	Alignment	not modelled	20.4	16	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** structure of the e.coli f1-atp synthase inhibited by subunit epsilon
41	c3bbnQ_	Alignment	not modelled	20.3	14	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
42	c1skyE_	Alignment	not modelled	20.0	19	**PDB header:**atp synthase **Chain:** E: **PDB Molecule:**f1-atpase; **PDBTitle:** crystal structure of the nucleotide free alpha3beta3 sub-complex of2 f1-atpase from the thermophilic bacillus ps3
43	d1v43a2	Alignment	not modelled	19.5	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
44	d1kzla2	Alignment	not modelled	17.8	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
45	c2e6zA_	Alignment	not modelled	17.5	31	**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
46	d1mvfd_	Alignment	not modelled	17.4	20	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
47	d1rcqa1	Alignment	not modelled	17.3	26	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
48	c2rcnA_	Alignment	not modelled	17.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
49	d1kzla1	Alignment	not modelled	16.9	32	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
50	d1rl2a2	Alignment	not modelled	16.8	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	c2l55A_	Alignment	not modelled	16.7	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
52	d1nppa2	Alignment	not modelled	16.6	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
53	d1i8da1	Alignment	not modelled	16.4	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
54	d1udxa3	Alignment	not modelled	16.3	23	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
						PDB header:ribosome

55	c2xznQ_	Alignment	not modelled	16.2	17	**Chain:** Q: **PDB Molecule:**ribosomal protein s17 containing protein; **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 2
56	c2l66B_	Alignment	not modelled	16.0	19	**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.
57	d1oxxk1	Alignment	not modelled	15.6	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
58	d1nz9a_	Alignment	not modelled	15.5	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
59	d2ftsa1	Alignment	not modelled	15.4	15	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
60	c3ah7A_	Alignment	not modelled	15.0	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**[2fe-2s]ferredoxin; **PDBTitle:** crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
61	c2zkqq_	Alignment	not modelled	14.7	27	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
62	d1h9ra2	Alignment	not modelled	14.5	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
63	c2odoC_	Alignment	not modelled	14.1	26	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of pseudomonas fluorescens alanine racemase
64	d1vfsa1	Alignment	not modelled	14.1	6	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
65	d2z0sa1	Alignment	not modelled	13.2	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
66	c2po8A_	Alignment	not modelled	13.0	29	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**mcoti-ii; **PDBTitle:** the structure of a two-disulfide intermediate of mcoti-ii
67	d2ba0a1	Alignment	not modelled	13.0	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
68	c1zeqX_	Alignment	not modelled	12.9	11	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
69	c2d7gD_	Alignment	not modelled	12.8	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**primosomal protein n; **PDBTitle:** crystal structure of the aa complex of the n-terminal2 domain of pria
70	c1pkvB_	Alignment	not modelled	12.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin
71	c1pkvA_	Alignment	not modelled	12.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin
72	d1vqoa2	Alignment	not modelled	12.7	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
73	d2bs2b2	Alignment	not modelled	12.6	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
74	c2dgyA_	Alignment	not modelled	12.5	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
75	c2khiA_	Alignment	not modelled	12.5	13	**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
76	d1h9ra1	Alignment	not modelled	12.4	11	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
77	d1hr0w_	Alignment	not modelled	12.2	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
78	c2d0sA_	Alignment	not modelled	12.2	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
79	d1uufa1	Alignment	not modelled	12.1	29	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
80	c2l1tA_	Alignment	not modelled	11.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of the n-terminal domain of np_954075.1
						PDB header:antibiotic

81	c1s6wA_	Alignment	not modelled	11.4	38	**Chain:** A: **PDB Molecule:**hepcidin; **PDBTitle:** solution structure of hybrid white striped bass hepcidin
82	c2e70A_	Alignment	not modelled	11.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the fifth kow motif of human2 transcription elongation factor spt5
83	c2qf4A_	Alignment	not modelled	11.1	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cell shape determining protein mrec; **PDBTitle:** high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
84	c3iuwA_	Alignment	not modelled	11.1	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**activating signal cointegrator; **PDBTitle:** crystal structure of activating signal cointegrator (np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
85	c2rjgC_	Alignment	not modelled	10.6	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of biosynthetic alaine racemase from escherichia2 coli
86	d2qamc2	Alignment	not modelled	10.5	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
87	d2vv5a1	Alignment	not modelled	10.3	38	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
88	c3a5dB_	Alignment	not modelled	10.3	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase alpha chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
89	d2etna2	Alignment	not modelled	10.3	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
90	d2awna1	Alignment	not modelled	10.3	18	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
91	c2e7zA_	Alignment	not modelled	10.2	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
92	c3q87B_	Alignment	not modelled	10.1	10	**PDB header:**transferase activator/transferase **Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase; **PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
93	d1g2914	Alignment	not modelled	10.1	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
94	d2piaa1	Alignment	not modelled	10.1	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
95	c2etnA_	Alignment	not modelled	9.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
96	d1h9ma2	Alignment	not modelled	9.8	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
97	d2q07a1	Alignment	not modelled	9.7	27	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
98	d2f23a2	Alignment	not modelled	9.6	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
99	d2c34a1	Alignment	not modelled	9.5	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ICP-like **Family:**ICP-like