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Description	P0AFX9
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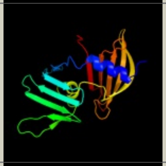
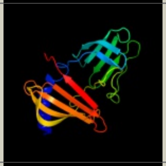
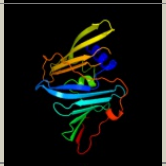
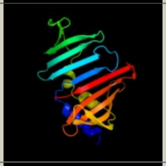
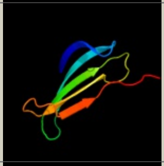
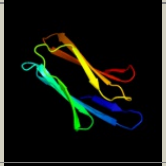
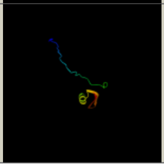
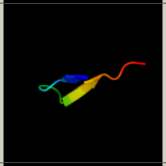
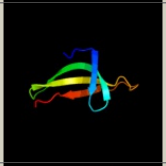
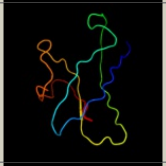
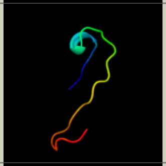
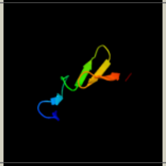
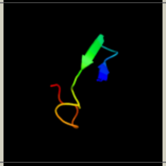
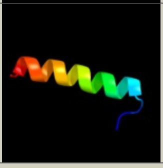
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v43A_	Alignment		100.0	100	**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
2	c3buuB_	Alignment		99.9	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized lola superfamily protein ne2245; **PDBTitle:** crystal structure of lola superfamily protein ne2245 from2 nitrosomonas europaea
3	c3bk5A_	Alignment		99.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative outer membrane lipoprotein-sorting protein; **PDBTitle:** crystal structure of putative outer membrane lipoprotein-sorting2 protein domain from vibrio parahaemolyticus
4	c2w7qB_	Alignment		99.7	10	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**outer-membrane lipoprotein carrier protein; **PDBTitle:** structure of pseudomonas aeruginosa lola
5	d1iwla_	Alignment		99.6	10	**Fold:**LolA-like prokaryotic lipoproteins and lipoprotein localization factors **Superfamily:**Prokaryotic lipoproteins and lipoprotein localization factors **Family:**Outer-membrane lipoproteins carrier protein LolA
6	c2yzyA_	Alignment		98.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1012; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
7	c3mhaB_	Alignment		98.1	14	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**lipoprotein lprg; **PDBTitle:** crystal structure of lprg from mycobacterium tuberculosis bound to pim
8	d2byoa1	Alignment		97.1	16	**Fold:**LolA-like prokaryotic lipoproteins and lipoprotein localization factors **Superfamily:**Prokaryotic lipoproteins and lipoprotein localization factors **Family:**LppX-like
9	c3fzxA_	Alignment		90.0	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of a putative exported protein with ymcc-like fold2 (bf2203) from bacteroides fragilis nctc 9343 at 2.22 a resolution
10	c3mx7A_	Alignment		77.1	18	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
11	d2jnaa1	Alignment		34.4	21	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like

12	c3h4rA_	Alignment		24.7	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease 8; **PDBTitle:** crystal structure of e. coli rece exonuclease
13	d1ei5a1	Alignment		18.9	31	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
14	d1khia1	Alignment		18.6	23	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
15	d1f15a_	Alignment		18.4	15	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
16	c3m7aA_	Alignment		17.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of saro_0823 (yp_496102.1) a protein of2 unknown function from novosphingobium aromaticivorans dsm3 12444 at 1.22 a resolution
17	c2vy8A_	Alignment		12.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** the 627-domain from influenza a virus polymerase pb22 subunit with glu-627
18	c2jcmA_	Alignment		12.4	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic purine 5'-nucleotidase; **PDBTitle:** crystal structure of human cytosolic 5'-nucleotidase ii in2 complex with beryllium trifluoride
19	d1fe0a_	Alignment		12.0	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
20	d1u5da1	Alignment		11.3	13	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
21	d1bcca1	Alignment	not modelled	11.3	14	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
22	d2bdea1	Alignment	not modelled	10.8	7	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**5' nucleotidase-like
23	d3cx5a1	Alignment	not modelled	10.7	18	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
24	c3rd4A_	Alignment	not modelled	10.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of propen_03304 from proteus penneri atcc 351982 northeast structural genomics consortium target id pvr55
25	d1ufza_	Alignment	not modelled	9.2	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**HBS1-like domain **Family:**HBS1-like domain
26	c3pjyB_	Alignment	not modelled	8.9	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hypothetical signal peptide protein; **PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
27	d1ci3m1	Alignment	not modelled	8.3	42	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
28	c1jmtB_	Alignment	not modelled	8.3	27	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**splicing factor u2af 65 kda subunit; **PDBTitle:** x-ray structure of a core u2af65/u2af35 heterodimer
						PDB header:chaperone

29	c2crlA_	Alignment	not modelled	8.2	21	**Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase
30	d1e2wa1	Alignment	not modelled	8.2	42	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
31	c2opdA_	Alignment	not modelled	8.0	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pilx; **PDBTitle:** structure of the neisseria meningitidis minor type iv pilin,2 pilx
32	d1tu2b1	Alignment	not modelled	8.0	42	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
33	d1hcza1	Alignment	not modelled	7.9	42	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
34	d1vf5c1	Alignment	not modelled	7.8	42	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
35	d1q2la1	Alignment	not modelled	7.2	18	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
36	c2jxmB_	Alignment	not modelled	7.1	42	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
37	c3nqyA_	Alignment	not modelled	7.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed complex of vibriolysin mcp-022 with a single point mutation e346a
38	c1tu2B_	Alignment	not modelled	7.0	42	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**apocytochrome f; **PDBTitle:** the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
39	c1ctmA_	Alignment	not modelled	6.9	42	**PDB header:**electron transport(cytochrome) **Chain:** A: **PDB Molecule:**cytochrome f; **PDBTitle:** crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
40	c1e2vB_	Alignment	not modelled	6.8	42	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
41	d1tafb_	Alignment	not modelled	6.3	35	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
42	d1hr6b1	Alignment	not modelled	5.9	14	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
43	c1q90A_	Alignment	not modelled	5.7	42	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii