Phyre^2

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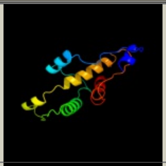
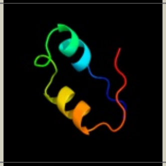
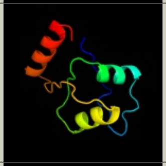
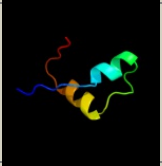
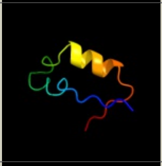
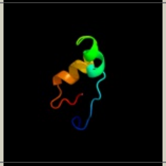
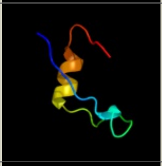
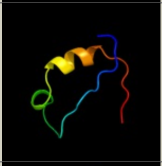
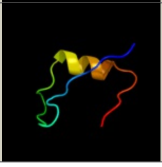
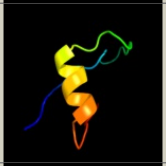
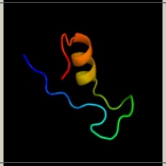
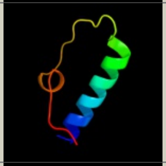
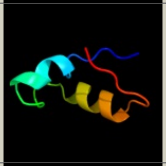
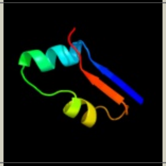
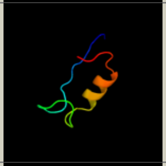
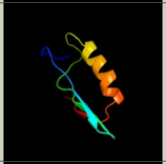
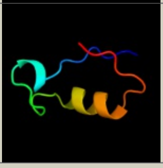
Description	P77301
Date	Thu Jan 5 12:27:28 GMT 2012
Unique Job ID	7b3c8a9c5c7e241e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2g5gx1	Alignment		94.9	12	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**ChaN-like
2	c3ndcB_	Alignment		61.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-4 c(11)-methyltransferase; **PDBTitle:** crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
3	c3hh1D_	Alignment		59.7	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**tetrapyrrole methylase family protein; **PDBTitle:** the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum tls
4	c2npnA_	Alignment		51.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative cobalamin synthesis related protein; **PDBTitle:** crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae
5	c3nd1B_	Alignment		45.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6a synthase/cobf protein; **PDBTitle:** crystal structure of precorrin-6a synthase from rhodobacter capsulatus
6	d1cbfa_	Alignment		37.8	24	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
7	c1cbfA_	Alignment		37.8	24	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**cobalt-precorrin-4 transmethylase; **PDBTitle:** the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
8	d1pjqa2	Alignment		36.9	26	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
9	d1wyza1	Alignment		36.7	16	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
10	c2qbuA_	Alignment		34.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 methyltransferase; **PDBTitle:** crystal structure of methanothermobacter thermautotrophicus cbil
11	c2e0kA_	Alignment		34.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis

12	c3kwpA_	Alignment		32.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from lactobacillus2 brevis
13	d1va0a1	Alignment		32.8	25	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
14	c2yboA_	Alignment		29.9	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
15	d2ebfx2	Alignment		29.8	10	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
16	d1vhva_	Alignment		27.5	26	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
17	d1zbsa2	Alignment		27.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
18	c2bb3B_	Alignment		25.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cobalamin biosynthesis precorrin-6y methylase (cbie); **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
19	d2az4a1	Alignment		22.5	12	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
20	d1s4da_	Alignment		20.8	25	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
21	d1vqqa1	Alignment	not modelled	19.7	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
22	d1wdea_	Alignment	not modelled	19.7	23	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
23	d1ve2a1	Alignment	not modelled	19.6	23	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
24	c1mwuA_	Alignment	not modelled	17.9	8	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 2a; **PDBTitle:** structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain3 27r at 2.60 a resolution.
25	c2ad5B_	Alignment	not modelled	17.7	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
26	d1ylqa1	Alignment	not modelled	17.5	30	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
27	c2vt2A_	Alignment	not modelled	17.4	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** structure and functional properties of the bacillus2 subtilis transcriptional repressor rex
28	c2fr1A_	Alignment	not modelled	16.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**erythromycin synthase, eryai; **PDBTitle:** the first ketoreductase of the erythromycin synthase2

						(crystal form 2)
29	d2fxta1	Alignment	not modelled	16.7	0	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**TIM44-like
30	d2cw9a1	Alignment	not modelled	16.6	2	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**TIM44-like
31	d2i7xa1	Alignment	not modelled	15.8	3	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
32	c2i7xA_	Alignment	not modelled	15.8	3	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
33	d1ybha3	Alignment	not modelled	14.6	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
34	d1s1ma2	Alignment	not modelled	14.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
35	d2dkfa1	Alignment	not modelled	13.5	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
36	d2deka1	Alignment	not modelled	13.0	26	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
37	c2z5lA_	Alignment	not modelled	12.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tylactone synthase starter module and modules 1 **PDBTitle:** the first ketoreductase of the tylosin pks
38	d1m6ia2	Alignment	not modelled	12.6	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
39	c3nutC_	Alignment	not modelled	12.6	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**precorrin-3 methylase; **PDBTitle:** crystal structure of the methyltransferase cobj
40	d2ewca1	Alignment	not modelled	12.4	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
41	c2zvbA_	Alignment	not modelled	12.3	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-3 c17-methyltransferase; **PDBTitle:** crystal structure of tt0207 from thermus thermophilus hb8
42	c3jz0B_	Alignment	not modelled	11.9	18	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**lincosamide nucleotidyltransferase; **PDBTitle:** linb complexed with clindamycin and ampcpp
43	c3mjsA_	Alignment	not modelled	11.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amphb; **PDBTitle:** structure of a-type ketoreductases from modular polyketide synthase
44	c1kbwA_	Alignment	not modelled	11.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**major outer membrane protein pan 1; **PDBTitle:** crystal structure of the soluble domain of ania from2 neisseria gonorrhoeae
45	c3qk9B_	Alignment	not modelled	11.1	3	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**mitochondrial import inner membrane translocase subunit **PDBTitle:** yeast tim44 c-terminal domain complexed with cymal-3
46	c3i4tA_	Alignment	not modelled	10.4	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**diphthine synthase; **PDBTitle:** crystal structure of putative diphthine synthase from2 entamoeba histolytica
47	c2xagA_	Alignment	not modelled	9.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
48	c2v1dA_	Alignment	not modelled	9.5	17	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
49	c1pjtB_	Alignment	not modelled	8.9	27	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
50	d2cxaa1	Alignment	not modelled	8.3	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**LFTR-like
51	c2cxaA_	Alignment	not modelled	8.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucyl/phenylalanyl-trna-protein transferase; **PDBTitle:** crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
52	d1ohpa1	Alignment	not modelled	8.2	3	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ketosteroid isomerase-like
53	c2q7xA_	Alignment	not modelled	8.1	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**upf0052 protein sp_1565; **PDBTitle:** crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
						Fold:P-loop containing nucleoside triphosphate hydrolases

54	d1vcoa2	Alignment	not modelled	7.6	18	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
55	d1h6la_	Alignment	not modelled	7.5	28	**Fold:**6-bladed beta-propeller **Superfamily:**Thermostable phytase (3-phytase) **Family:**Thermostable phytase (3-phytase)
56	c3d64A_	Alignment	not modelled	7.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
57	d2k54a1	Alignment	not modelled	7.3	4	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0742-like
58	d2bb3a1	Alignment	not modelled	6.6	18	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
59	d2cpga_	Alignment	not modelled	6.6	43	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
60	d2ok5a4	Alignment	not modelled	6.2	27	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
61	d2jfga1	Alignment	not modelled	6.2	13	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
62	d1wm1a_	Alignment	not modelled	6.1	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
63	d2o0qa1	Alignment	not modelled	6.1	15	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**CC0527-like
64	c2w8iG_	Alignment	not modelled	6.0	10	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**putative outer membrane lipoprotein wza; **PDBTitle:** crystal structure of wza24-345.
65	d2i7ta1	Alignment	not modelled	6.0	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
66	c3fh1A_	Alignment	not modelled	6.0	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (mll8193)2 from mesorhizobium loti at 1.60 a resolution
67	c3f8hA_	Alignment	not modelled	5.9	3	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
68	c3g5wC_	Alignment	not modelled	5.8	19	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**multicopper oxidase type 1; **PDBTitle:** crystal structure of blue copper oxidase from nitrosomonas europaea
69	d1no5a_	Alignment	not modelled	5.8	20	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
70	c2dbqA_	Alignment	not modelled	5.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
71	c3evtA_	Alignment	not modelled	5.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
72	d3b55a1	Alignment	not modelled	5.7	10	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**EreA-like
73	c3ff2A_	Alignment	not modelled	5.6	4	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized cystatin fold protein (yp_497570.1) from **PDBTitle:** crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution
74	c2yxwB_	Alignment	not modelled	5.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**blue copper oxidase cueo; **PDBTitle:** the deletion mutant of multicopper oxidase cueo
75	d2f99a1	Alignment	not modelled	5.5	5	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
76	d2ffea1	Alignment	not modelled	5.5	10	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
77	d1z1sa1	Alignment	not modelled	5.4	7	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like
78	c2zwnA_	Alignment	not modelled	5.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**two-domain type laccase; **PDBTitle:** crystal structure of the novel two-domain type laccase from a2 metagenome
79	d1t6aa_	Alignment	not modelled	5.3	13	**Fold:**TBP-like **Superfamily:**Rbstp2229 protein **Family:**Rbstp2229 protein
80	d3ec9a1	Alignment	not modelled	5.3	7	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like

81	c2j58G_	Alignment	not modelled	5.1	11	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**outer membrane lipoprotein wza; **PDBTitle:** the structure of wza
82	d2bnga1	Alignment	not modelled	5.1	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Limonene-1,2-epoxide hydrolase-like