Phyre2

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Description	P0AAS5
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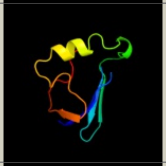
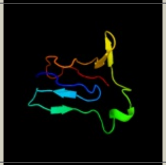
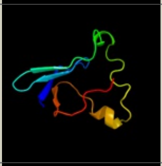
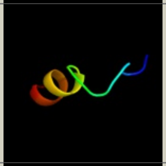
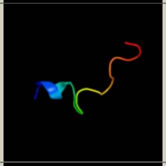
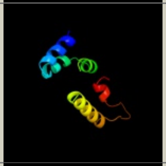
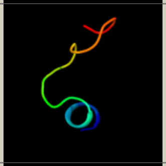
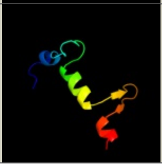
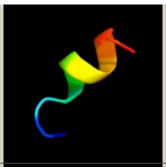
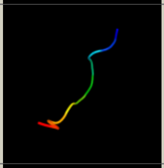
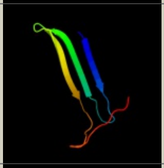
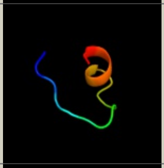
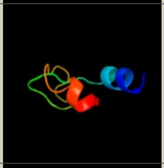
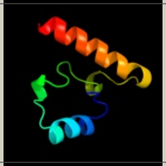
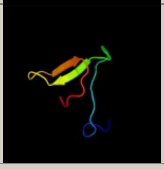
Unique Job ID	7d983361948f1f1f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l55A_	Alignment		39.5	16	**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
2	d1gpra_	Alignment		29.7	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
3	d2f3ga_	Alignment		28.6	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
4	d2gpra_	Alignment		27.5	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
5	c2dchX_	Alignment		26.8	44	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**putative homing endonuclease; **PDBTitle:** crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
6	d1glaf_	Alignment		24.6	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
7	d1apja_	Alignment		23.8	26	**Fold:**TB module/8-cys domain **Superfamily:**TB module/8-cys domain **Family:**TB module/8-cys domain
8	c2xgyA_	Alignment		19.0	17	**PDB header:**viral protein/isomerase **Chain:** A: **PDB Molecule:**relik capsid n-terminal domain; **PDBTitle:** complex of rabbit endogenous lentivirus (relik)capsid with2 cyclophilin a
9	d1ksqa_	Alignment		17.7	22	**Fold:**TB module/8-cys domain **Superfamily:**TB module/8-cys domain **Family:**TB module/8-cys domain
10	c1zeqX_	Alignment		13.6	3	**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
11	c2j5dA_	Alignment		12.4	39	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles

12	c2d1kC_	Alignment		11.9	36	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**metastasis suppressor protein 1; **PDBTitle:** ternary complex of the wh2 domain of mim with actin-dnase i
13	d2cbra_	Alignment		11.1	27	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
14	d1gl4a1	Alignment		10.6	13	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Domain G2 of nidogen-1
15	d1fasa_	Alignment		10.0	57	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
16	d1u0ma2	Alignment		9.9	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
17	d1ve2a1	Alignment		9.8	41	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
18	c3h41A_	Alignment		9.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nlp/p60 family protein; **PDBTitle:** crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
19	c1wl5A_	Alignment		9.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyl-coenzyme a acetyltransferase 2; **PDBTitle:** human cytosolic acetoacetyl-coa thiolase
20	c2e4mC_	Alignment		8.7	20	**PDB header:**toxin **Chain:** C: **PDB Molecule:**ha-17; **PDBTitle:** crystal structure of hemagglutinin subcomponent complex (ha-2 33/ha-17) from clostridium botulinum serotype d strain 4947
21	c2e0kA_	Alignment	not modelled	8.5	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
22	c3nutC_	Alignment	not modelled	8.2	41	**PDB header:**transferase **Chain:** C: **PDB Molecule:**precorrin-3 methylase; **PDBTitle:** crystal structure of the methyltransferase cobj
23	d1twda_	Alignment	not modelled	8.1	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
24	c1h4uA_	Alignment	not modelled	8.1	13	**PDB header:**extracellular matrix protein **Chain:** A: **PDB Molecule:**nidogen-1; **PDBTitle:** domain g2 of mouse nidogen-1
25	c3iwpK_	Alignment	not modelled	7.6	80	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
26	c2bb3B_	Alignment	not modelled	7.4	22	**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
27	d1drsa_	Alignment	not modelled	7.0	38	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Dendroaspin
28	d1cnza_	Alignment	not modelled	6.9	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases

29	c2kzqA_	Alignment	not modelled	6.8	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**envelope glycoprotein e2 peptide; **PDBTitle:** s34r structure
30	c2vu2D_	Alignment	not modelled	6.7	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** biosynthetic thiolase from z. ramigera. complex with s-2 pantetheine-11-pivalate.
31	d1va0a1	Alignment	not modelled	6.6	41	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
32	d1wyza1	Alignment	not modelled	6.6	18	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
33	d2eiaa2	Alignment	not modelled	6.6	16	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
34	d1ycna_	Alignment	not modelled	6.4	11	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
35	c1cbfA_	Alignment	not modelled	6.3	35	**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
36	d1cbfa_	Alignment	not modelled	6.3	35	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
37	d1niya_	Alignment	not modelled	6.3	58	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
38	d1mb6a_	Alignment	not modelled	6.3	33	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
39	c2npnA_	Alignment	not modelled	6.3	35	**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
40	c3ndcB_	Alignment	not modelled	6.2	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-4 c(11)-methyltransferase; **PDBTitle:** crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
41	d1cm7a_	Alignment	not modelled	6.1	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
42	d2bb3a1	Alignment	not modelled	6.0	25	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
43	c2avuF_	Alignment	not modelled	6.0	18	**PDB header:**transcription activator **Chain:** F: **PDB Molecule:**flagellar transcriptional activator flhc; **PDBTitle:** structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription
44	d1pkla1	Alignment	not modelled	5.9	6	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
45	d1v53a1	Alignment	not modelled	5.8	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
46	d1dq3a3	Alignment	not modelled	5.8	31	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
47	c4a1cX_	Alignment	not modelled	5.6	27	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**60s ribosomal protein l32; **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 4.
48	d1pjqa2	Alignment	not modelled	5.6	41	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
49	d1q90g_	Alignment	not modelled	5.5	44	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
50	c1q90G_	Alignment	not modelled	5.5	44	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**cytochrome b6f complex subunit petg; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
51	d2d0oa1	Alignment	not modelled	5.4	80	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Swiveling domain of dehydratase reactivase alpha subunit **Family:**Swiveling domain of dehydratase reactivase alpha subunit
52	d1vhva_	Alignment	not modelled	5.3	12	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
53	c3u1hA_	Alignment	not modelled	5.2	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
54	c2zvbA_	Alignment	not modelled	5.2	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-3 c17-methyltransferase; **PDBTitle:** crystal structure of tt0207 from thermus thermophilus hb8
55	d1y7ma1	Alignment	not modelled	5.1	8	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like

						Family:L,D-transpeptidase catalytic domain-like
56	d1ep3b2_	Alignment	not modelled	5.1	40	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
57	c3kwpA_	Alignment	not modelled	5.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from lactobacillus2 brevis