Phyre^2

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Description	P64536
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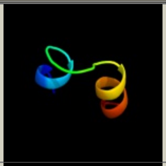
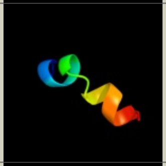
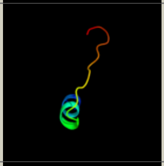
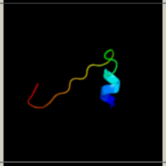
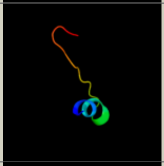
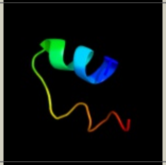
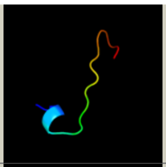
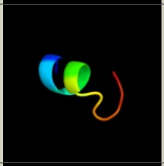
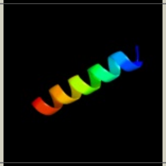
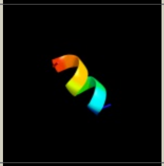
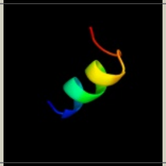
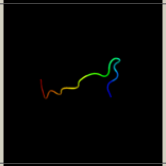
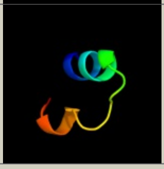
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qp6B_	Alignment		30.7	50	**PDB header:** de novo protein **Chain:** B: **PDB Molecule:** protein (alpha2d); **PDBTitle:** solution structure of alpha2d
2	d1xfja_	Alignment		23.3	27	**Fold:** CNF1/YfiH-like putative cysteine hydrolases **Superfamily:** CNF1/YfiH-like putative cysteine hydrolases **Family:** YfiH-like
3	d1rw0a_	Alignment		19.8	27	**Fold:** CNF1/YfiH-like putative cysteine hydrolases **Superfamily:** CNF1/YfiH-like putative cysteine hydrolases **Family:** YfiH-like
4	d2a6qb1	Alignment		17.8	14	**Fold:** YefM-like **Superfamily:** YefM-like **Family:** YefM-like
5	d1xafa_	Alignment		17.5	33	**Fold:** CNF1/YfiH-like putative cysteine hydrolases **Superfamily:** CNF1/YfiH-like putative cysteine hydrolases **Family:** YfiH-like
6	d1t8ha_	Alignment		16.6	27	**Fold:** CNF1/YfiH-like putative cysteine hydrolases **Superfamily:** CNF1/YfiH-like putative cysteine hydrolases **Family:** YfiH-like
7	c3hs2H_	Alignment		16.3	14	**PDB header:** antitoxin **Chain:** H: **PDB Molecule:** prevent host death protein; **PDBTitle:** crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
8	c3hryA_	Alignment		16.3	14	**PDB header:** antitoxin **Chain:** A: **PDB Molecule:** prevent host death protein; **PDBTitle:** crystal structure of phd in a trigonal space group and partially2 disordered
9	d1bxna1	Alignment		13.8	9	**Fold:** TIM beta/alpha-barrel **Superfamily:** RuBisCo, C-terminal domain **Family:** RuBisCo, large subunit, C-terminal domain
10	d1ykwa1	Alignment		13.2	32	**Fold:** TIM beta/alpha-barrel **Superfamily:** RuBisCo, C-terminal domain **Family:** RuBisCo, large subunit, C-terminal domain
11	d1rv9a_	Alignment		12.9	20	**Fold:** CNF1/YfiH-like putative cysteine hydrolases **Superfamily:** CNF1/YfiH-like putative cysteine hydrolases **Family:** YfiH-like

12	c3g5oA_	Alignment		11.1	11	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein rv2865; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
13	c2ip6A_	Alignment		10.9	33	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**papb; **PDBTitle:** crystal structure of pedb
14	c2zt9E_	Alignment		10.8	50	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
15	c2j5dA_	Alignment		9.6	40	**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
16	c2jobA_	Alignment		9.3	30	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
17	c3fy6A_	Alignment		9.2	57	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass3
18	d1ldda_	Alignment		8.8	0	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
19	d1wwca_	Alignment		8.6	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
20	c1rcxH_	Alignment		8.2	32	**PDB header:**lyase (carbon-carbon) **Chain:** H: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase; **PDBTitle:** non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
21	d2q9oa1	Alignment	not modelled	8.1	42	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
22	d2a6qa1	Alignment	not modelled	7.9	11	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
23	c1bwvA_	Alignment	not modelled	7.6	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ribulose bisphosphate carboxylase); **PDBTitle:** activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
24	d1vcaa2	Alignment	not modelled	7.3	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
25	d1geha1	Alignment	not modelled	6.8	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
26	d1bwva1	Alignment	not modelled	6.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
27	d8ruca1	Alignment	not modelled	6.6	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
28	d1wdda1	Alignment	not modelled	6.5	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain

29	c2jmvA_	Alignment	not modelled	6.5	41	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**scytovirin; **PDBTitle:** solution structure of scytovirin refined against residual2 dipolar couplings
30	d1ej7l1	Alignment	not modelled	6.2	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
31	d1svda1	Alignment	not modelled	6.2	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
32	c1vf5R_	Alignment	not modelled	6.2	16	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
33	c2e75E_	Alignment	not modelled	6.2	16	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
34	c2e74E_	Alignment	not modelled	6.2	16	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
35	d2e74e1	Alignment	not modelled	6.2	16	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
36	c2e76E_	Alignment	not modelled	6.2	16	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
37	d1wwwx_	Alignment	not modelled	6.1	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
38	c1telA_	Alignment	not modelled	6.0	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase, large subunit; **PDBTitle:** crystal structure of a rubisco-like protein from chlorobium2 tepidum
39	c2w0cR_	Alignment	not modelled	5.9	31	**PDB header:**virus **Chain:** R: **PDB Molecule:**protein p3; **PDBTitle:** x-ray structure of the entire lipid-containing2 bacteriophage pm2
40	c3nwrA_	Alignment	not modelled	5.9	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**a rubisco-like protein; **PDBTitle:** crystal structure of a rubisco-like protein from burkholderia fungorum
41	d1kbva1	Alignment	not modelled	5.8	33	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
42	c2qygC_	Alignment	not modelled	5.7	32	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**ribulose bisphosphate carboxylase-like protein 2; **PDBTitle:** crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
43	c2rq2A_	Alignment	not modelled	5.6	45	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**big defensin; **PDBTitle:** the solution structure of the n-terminal fragment of big2 defensin