Phyre^2

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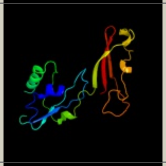
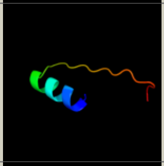
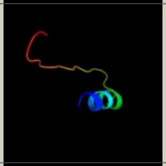
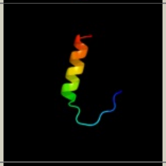
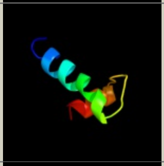
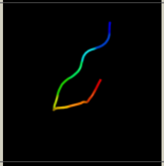
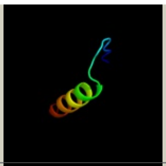
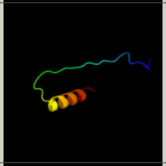
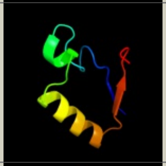
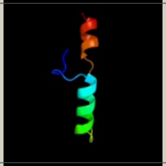
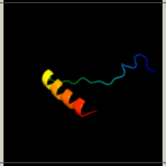
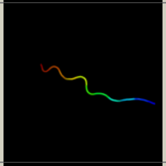
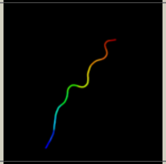
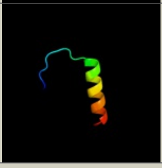
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dj0a_	Alignment		100.0	100	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase I TruA
2	c1vs3B_	Alignment		100.0	34	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trna pseudouridine synthase a; **PDBTitle:** crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
3	c2v9kA_	Alignment		91.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein flj32312; **PDBTitle:** crystal structure of human pus10, a novel pseudouridine2 synthase.
4	c1qysA_	Alignment		54.5	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
5	c2jvfA_	Alignment		49.5	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
6	d2hh8a1	Alignment		41.2	12	**Fold:**YdfO-like **Superfamily:**YdfO-like **Family:**YdfO-like
7	d1q9ja1	Alignment		21.9	15	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
8	c2kruA_	Alignment		20.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** solution nmr structure of the pcp_red domain of light-2 independent protochlorophyllide reductase subunit b from3 chlorobium tepidum. northeast structural genomics4 consortium target ctr69a (casp target)
9	d1e8ya3	Alignment		19.1	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
10	d1e88a3	Alignment		18.0	40	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
11	d1nija2	Alignment		17.3	11	**Fold:**Hypothetical protein YjiA, C-terminal domain **Superfamily:**Hypothetical protein YjiA, C-terminal domain **Family:**Hypothetical protein YjiA, C-terminal domain

12	d1l5aa1	Alignment		13.3	28	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
13	c2l09A_	Alignment		12.4	3	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**asr4154 protein; **PDBTitle:** solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
14	c1l5aA_	Alignment		12.1	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**amide synthase; **PDBTitle:** crystal structure of vibh, an nrps condensation enzyme
15	d1u02a_	Alignment		12.1	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
16	d1y6va1	Alignment		10.7	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
17	c2xhgA_	Alignment		9.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tyrocidine synthetase a; **PDBTitle:** crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
18	d2gjva1	Alignment		9.3	33	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**STM4215-like
19	c2gjvF_	Alignment		9.3	33	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** crystal structure of a protein of unknown function from salmonella2 typhimurium
20	c1q9jA_	Alignment		7.7	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**polyketide synthase associated protein 5; **PDBTitle:** structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
21	c3ni2A_	Alignment	not modelled	7.5	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**4-coumarate:coa ligase; **PDBTitle:** crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
22	c1e88A_	Alignment	not modelled	7.5	40	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fibronectin; **PDBTitle:** solution structure of 6f11f22f2, a compact three-module2 fragment of the gelatin-binding domain of human fibronectin
23	d2fbla1	Alignment	not modelled	7.4	21	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
24	c2wwaJ_	Alignment	not modelled	7.4	19	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l19; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
25	c2omlA_	Alignment	not modelled	7.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
26	c2jv4A_	Alignment	not modelled	6.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis/trans isomerase; **PDBTitle:** structure characterisation of pina ww domain and comparison2 with other group iv ww domains, pin1 and ess1
27	d1xb2b2	Alignment	not modelled	6.7	16	**Fold:**EF-Ts domain-like **Superfamily:**Elongation factor Ts (EF-Ts), dimerisation domain **Family:**Elongation factor Ts (EF-Ts), dimerisation domain
28	d1qlma_	Alignment	not modelled	6.3	31	**Fold:**Methenyltetrahydromethanopterin cyclohydrolase **Superfamily:**Methenyltetrahydromethanopterin cyclohydrolase **Family:**Methenyltetrahydromethanopterin cyclohydrolase

29	c3dh3C_	Alignment	not modelled	6.3	10	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
30	d2csha2	Alignment	not modelled	6.1	20	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
31	c1kskA_	Alignment	not modelled	6.1	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
32	d1owla1	Alignment	not modelled	5.9	33	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
33	d1dnpa1	Alignment	not modelled	5.7	27	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
34	c3l9aX_	Alignment	not modelled	5.6	32	**PDB header:**structural genomics, unknown function **Chain:** X: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of the c-terminal domain from a streptococcus2 mutans hypothetical
35	d1bdga2	Alignment	not modelled	5.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
36	d1czan2	Alignment	not modelled	5.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
37	c1unyA_	Alignment	not modelled	5.3	42	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
38	d1iwga1	Alignment	not modelled	5.3	14	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
39	c2cooA_	Alignment	not modelled	5.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
40	c3a52A_	Alignment	not modelled	5.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
41	c3umvB_	Alignment	not modelled	5.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photo-lyase; **PDBTitle:** eukaryotic class ii cpd photolyase structure reveals a basis for2 improved uv-tolerance in plants