Phyre2

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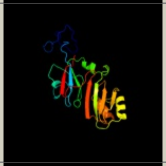
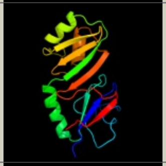
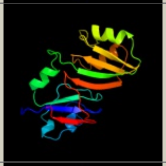
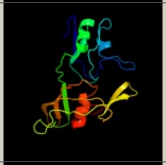
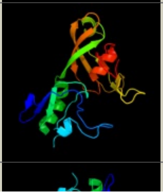
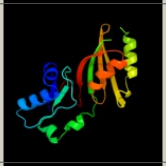
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2omlA_	Alignment		100.0	94	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
2	c2olwB_	Alignment		100.0	95	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
3	c3dh3C_	Alignment		100.0	31	**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
4	c1vioA_	Alignment		100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridylate synthase
5	c1kskA_	Alignment		100.0	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
6	c2gmlA_	Alignment		100.0	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of catalytic domain of e.coli rluf
7	d1vioa1	Alignment		100.0	29	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
8	d1kska4	Alignment		100.0	36	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
9	d1v9ka_	Alignment		100.0	17	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
10	c1v9fA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli
11	d1v9fa_	Alignment		100.0	21	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
						

12	c1qyuA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
13	c2i82D_	Alignment		100.0	20	**PDB header:**lyase/rna **Chain:** D: **PDB Molecule:**ribosomal large subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
14	d2apoa2	Alignment		98.8	13	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
15	d2ey4a2	Alignment		98.8	17	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
16	c2ey4A_	Alignment		98.7	15	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
17	d1r3ea2	Alignment		98.6	18	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
18	c2apoA_	Alignment		98.6	14	**PDB header:**isomerase/rna binding protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
19	c3uaiA_	Alignment		98.5	15	**PDB header:**isomerase/chaperone **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
20	d1sgva2	Alignment		98.5	18	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
21	d1k8wa5	Alignment	not modelled	98.5	20	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
22	c1sgvA_	Alignment	not modelled	98.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
23	c1k8wA_	Alignment	not modelled	98.0	21	**PDB header:**lyase/rna **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
24	c1ze2B_	Alignment	not modelled	95.4	18	**PDB header:**lyase/rna **Chain:** B: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
25	c2k6pA_	Alignment	not modelled	32.2	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
26	c2fo1A_	Alignment	not modelled	19.2	16	**PDB header:**gene regulation/signalling protein/dna **Chain:** A: **PDB Molecule:**lin-12 and glp-1 phenotype protein 1, isoform b; **PDBTitle:** crystal structure of the csl-notch-mastermind ternary2 complex bound to dna
27	d2ysca1	Alignment	not modelled	13.8	45	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
28	d1nkga1	Alignment	not modelled	12.4	14	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Rhamnogalacturonase B, RhgB, middle domain
29	c3cjsA	Alignment	not modelled	12.0	50	**PDB header:**transferase/ribosomal protein **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase;

29	c3cjsA_	Alignment	not modelled	12.0	30	**PDBTitle:** minimal recognition complex between prma and ribosomal protein l11
30	d2ho2a1	Alignment	not modelled	11.7	42	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
31	c2jmzA_	Alignment	not modelled	11.6	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein mj0781; **PDBTitle:** solution structure of a klba intein precursor from2 methanococcus jannaschii
32	c1f5nA_	Alignment	not modelled	11.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon-induced guanylate-binding protein 1; **PDBTitle:** human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
33	c3h7hA_	Alignment	not modelled	11.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
34	d1zhva1	Alignment	not modelled	9.4	31	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
35	c1mzwB_	Alignment	not modelled	8.3	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**u4/u6 snrnp 60kda protein; **PDBTitle:** crystal structure of a u4/u6 snrnp complex between human2 spliceosomal cyclophilin h and a u4/u6-60k peptide
36	d2hq4a1	Alignment	not modelled	7.9	33	**Fold:**PH1570-like **Superfamily:**PH1570-like **Family:**PH1570-like
37	c2voiB_	Alignment	not modelled	7.8	27	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bh3-interacting domain death agonist p13; **PDBTitle:** structure of mouse a1 bound to the bid bh3-domain
38	c2imzA_	Alignment	not modelled	6.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease pi-mtui; **PDBTitle:** crystal structure of mtu reca intein splicing domain
39	d1t6la1	Alignment	not modelled	6.4	19	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
40	c2exuA_	Alignment	not modelled	6.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation protein spt4/spt5; **PDBTitle:** crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
41	c1tlqA_	Alignment	not modelled	6.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ypjq; **PDBTitle:** crystal structure of protein ypjq from bacillus subtilis, pfam duf64
42	d1tlqa_	Alignment	not modelled	6.1	13	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
43	d1k4ta3	Alignment	not modelled	5.4	13	**Fold:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Superfamily:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Family:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
44	d1y9ia_	Alignment	not modelled	5.3	13	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
45	c3bbnD_	Alignment	not modelled	5.3	13	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
46	c1vs3B_	Alignment	not modelled	5.2	40	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trna pseudouridine synthase a; **PDBTitle:** crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
47	c2x5pA_	Alignment	not modelled	5.2	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b