Phyre2

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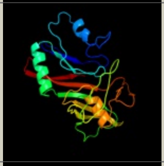
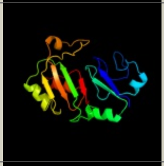
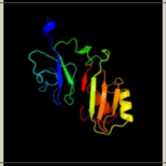
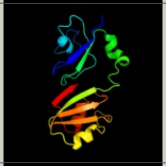
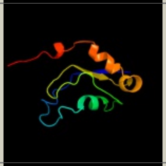
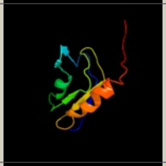
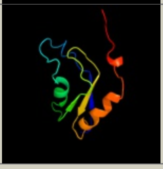
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2i82D_	Alignment		100.0	97	**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
2	d1v9fa_	Alignment		100.0	38	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
3	c1v9fA_	Alignment		100.0	38	**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
4	c1qyuA_	Alignment		100.0	36	**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
5	d1v9ka_	Alignment		100.0	39	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
6	c1vioA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridylate synthase
7	c1kskA_	Alignment		100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
8	c2omlA_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
9	c2olwB_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
10	c3dh3C_	Alignment		100.0	14	**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
11	d1vioa1	Alignment		100.0	19	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD

12	d1kska4	Alignment		100.0	17	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
13	c2gmlA_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of catalytic domain of e.coli rluf
14	d1k8wa5	Alignment		97.6	17	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
15	d2ey4a2	Alignment		97.6	30	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
16	d2apoa2	Alignment		97.5	32	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
17	d1sgva2	Alignment		97.5	29	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
18	c2ey4A_	Alignment		97.5	32	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
19	d1r3ea2	Alignment		97.5	22	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
20	c2apoA_	Alignment		97.3	30	**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
21	c3uaiA_	Alignment	not modelled	97.3	29	**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
22	c1k8wA_	Alignment	not modelled	97.2	19	**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
23	c1sgvA_	Alignment	not modelled	97.2	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
24	c1ze2B_	Alignment	not modelled	95.6	27	**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	94.6	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
26	c1f5nA_	Alignment	not modelled	31.0	12	**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.
27	c2zodB_	Alignment	not modelled	23.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
28	d2zoda2	Alignment	not modelled	22.1	17	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like

29	c2zauB_	Alignment	not modelled	21.1	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
30	c1mzwB_	Alignment	not modelled	16.9	38	**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
31	d1vjpa1	Alignment	not modelled	16.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
32	d1f46a_	Alignment	not modelled	14.6	18	**Fold:**TBP-like **Superfamily:**Cell-division protein ZipA, C-terminal domain **Family:**Cell-division protein ZipA, C-terminal domain
33	d1emsa1	Alignment	not modelled	13.2	29	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
34	d1gr0a1	Alignment	not modelled	12.4	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
35	d1fita_	Alignment	not modelled	11.7	6	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
36	d1k8ga2	Alignment	not modelled	11.6	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
37	c2p14A_	Alignment	not modelled	11.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**heterodimeric restriction endonuclease r.bspd6i small **PDBTitle:** crystal structure of small subunit (r.bspd6i2) of the heterodimeric2 restriction endonuclease r.bspd6i
38	d1jb7a2	Alignment	not modelled	10.9	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
39	c3n1tE_	Alignment	not modelled	9.7	38	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**hit-like protein hint; **PDBTitle:** crystal structure of the h101a mutant echint gmp complex
40	d1rzya_	Alignment	not modelled	9.7	25	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
41	c1u1iC_	Alignment	not modelled	9.5	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**myo-inositol-1-phosphate synthase; **PDBTitle:** myo-inositol phosphate synthase mips from a. fulgidus
42	c3l7xA_	Alignment	not modelled	9.3	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle **PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159
43	d1okia1	Alignment	not modelled	8.1	20	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
44	c2lkyA_	Alignment	not modelled	7.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
45	c1gr0A_	Alignment	not modelled	7.5	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**inositol-3-phosphate synthase; **PDBTitle:** myo-inositol 1-phosphate synthase from mycobacterium2 tuberculosis in complex with nad and zinc.
46	c2do5A_	Alignment	not modelled	7.5	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**splicing factor 3b subunit 2; **PDBTitle:** solution structure of the sap domain of human splicing2 factor 3b subunit 2
47	c3cinA_	Alignment	not modelled	7.4	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**myo-inositol-1-phosphate synthase-related protein; **PDBTitle:** crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
48	c3o0mB_	Alignment	not modelled	7.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
49	d1guqa2	Alignment	not modelled	7.2	17	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
50	d2al1a1	Alignment	not modelled	6.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
51	c2oi2A_	Alignment	not modelled	6.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
52	d2aaaa1	Alignment	not modelled	6.4	21	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
53	c3p0tB_	Alignment	not modelled	6.4	25	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an hit-like protein from

						mycobacterium2 paratuberculosis
54	c2kvcA_	Alignment	not modelled	6.0	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
55	c1emsB_	Alignment	not modelled	5.8	33	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
56	c2voiB_	Alignment	not modelled	5.8	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
57	d2dk4a1	Alignment	not modelled	5.7	23	**Fold:**LEM/SAP HeH motif **Superfamily:**PRP4-like **Family:**PRP4-like
58	d2oika1	Alignment	not modelled	5.5	50	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins