Phyre²

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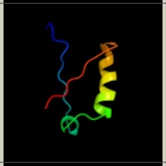
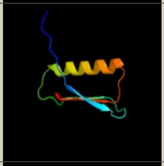
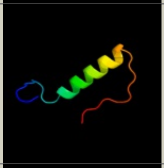
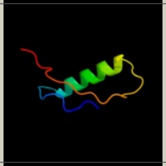
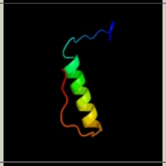
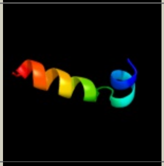
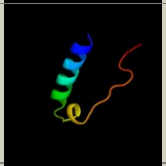
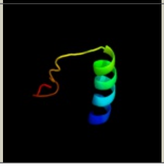
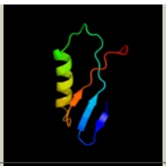
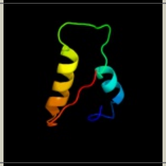
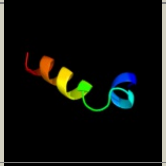
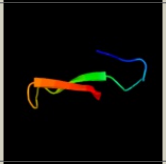
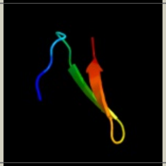
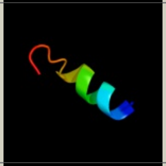
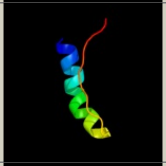
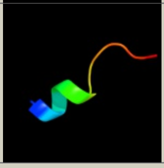
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ufwa_	Alignment		56.6	23	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
2	d2dy1a3	Alignment		51.1	29	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
3	c2dnrA_	Alignment		41.8	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**synaptojanin-1; **PDBTitle:** solution structure of rna binding domain in synaptojanin 1
4	d2bv3a3	Alignment		37.4	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
5	c1vbkA_	Alignment		32.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
6	d1mg7a1	Alignment		25.6	12	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Early switch protein XOL-1, N-terminal domain
7	d1vbka2	Alignment		24.1	14	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
8	c2nscA_	Alignment		22.1	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritima
9	d1am7a_	Alignment		21.1	37	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Lambda lysozyme
10	c1mg7B_	Alignment		20.0	13	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**early switch protein xol-1 2.2k splice form; **PDBTitle:** crystal structure of xol-1
11	c3jvnA_	Alignment		15.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** crystal structure of the acetyltransferase vf_1542 from vibrio2 fischeri, northeast structural genomics consortium target vfr136

12	d1uwda_	Alignment		15.4	10	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
13	d2cu6a1	Alignment		14.0	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
14	c3gtyX_	Alignment		12.8	19	**PDB header:**chaperone/ribosomal protein **Chain:** X: **PDB Molecule:**trigger factor; **PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
15	c3ffvA_	Alignment		12.7	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein syd; **PDBTitle:** crystal structure analysis of syd
16	d2nn6h2	Alignment		12.7	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
17	d1ttea1	Alignment		10.5	31	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
18	d1wina_	Alignment		10.2	17	**Fold:**EF-Ts domain-like **Superfamily:**Band 7/SPFH domain **Family:**Band 7/SPFH domain
19	c2zkqi_	Alignment		9.6	15	**PDB header:**ribosomal protein/rna **Chain:** I: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
20	d1regx_	Alignment		9.2	17	**Fold:**Ferredoxin-like **Superfamily:**Translational regulator protein regA **Family:**Translational regulator protein regA
21	d1z7ma1	Alignment	not modelled	9.1	9	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
22	d1yd9a1	Alignment	not modelled	8.8	15	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
23	c1fwlD_	Alignment	not modelled	8.7	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**homoserine kinase; **PDBTitle:** crystal structure of homoserine kinase
24	d1puga_	Alignment	not modelled	8.4	18	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
25	d1dwka2	Alignment	not modelled	8.3	7	**Fold:**Cyanase C-terminal domain **Superfamily:**Cyanase C-terminal domain **Family:**Cyanase C-terminal domain
26	d1w1oa1	Alignment	not modelled	8.1	16	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cytokinin dehydrogenase 1
27	c3m0zD_	Alignment	not modelled	7.6	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of putative aldolase from klebsiella2 pneumoniae.
28	c2kq1A_	Alignment	not modelled	7.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh0266 protein; **PDBTitle:** solution structure of protein bh0266 from bacillus2 halodurans. northeast structural genomics consortium target3 bhr97a
						PDB header:gene regulation

29	c1zr5B_	Alignment	not modelled	7.2	14	**Chain:** B: **PDB Molecule:**h2afy protein; **PDBTitle:** crystal structure of the macro-domain of human core histone variant2 macroh2a1.2
30	d1t11a2	Alignment	not modelled	6.9	32	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
31	c1ybxA_	Alignment	not modelled	6.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
32	c3lnoA_	Alignment	not modelled	6.5	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis
33	d1p97a_	Alignment	not modelled	6.5	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Hypoxia-inducible factor Hif2a, C-terminal domain
34	c2jo7A_	Alignment	not modelled	6.5	63	**PDB header:**surface active protein **Chain:** A: **PDB Molecule:**glycosylphosphatidylinositol-anchored merozoite **PDBTitle:** solution structure of the adhesion protein bd37 from2 babesia divergens
35	d1p42a1	Alignment	not modelled	6.4	30	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
36	c1usvB_	Alignment	not modelled	6.3	15	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**aha1; **PDBTitle:** the structure of the complex between aha1 and hsp90
37	c3ew5B_	Alignment	not modelled	6.2	11	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**macro domain of non-structural protein 3; **PDBTitle:** structure of the tetragonal crystal form of x (adrp) domain2 from fcov
38	d1o75a3	Alignment	not modelled	6.1	29	**Fold:**Tp47 lipoprotein, N-terminal domain **Superfamily:**Tp47 lipoprotein, N-terminal domain **Family:**Tp47 lipoprotein, N-terminal domain
39	c3h0gO_	Alignment	not modelled	6.0	23	**PDB header:**transcription **Chain:** O: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb3; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
40	d2q3la1	Alignment	not modelled	5.9	8	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Sfri0576-like
41	d1y14b2	Alignment	not modelled	5.9	18	**Fold:**Dodecin subunit-like **Superfamily:**N-terminal, heterodimerisation domain of RBP7 (RpoE) **Family:**N-terminal, heterodimerisation domain of RBP7 (RpoE)
42	c3q71A_	Alignment	not modelled	5.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose
43	c2rpbA_	Alignment	not modelled	5.7	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical membrane protein; **PDBTitle:** the solution structure of membrane protein
44	c1ta9A_	Alignment	not modelled	5.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
45	d1v54g_	Alignment	not modelled	5.5	25	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa
46	d1u0ua2	Alignment	not modelled	5.4	11	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
47	d1ee0a2	Alignment	not modelled	5.4	11	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
48	d1usub_	Alignment	not modelled	5.4	15	**Fold:**Aha1/BPI domain-like **Superfamily:**Activator of Hsp90 ATPase, Aha1 **Family:**Activator of Hsp90 ATPase, Aha1
49	c3imkA_	Alignment	not modelled	5.3	40	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative molybdenum carrier protein; **PDBTitle:** crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
50	d2ba0a2	Alignment	not modelled	5.3	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
51	d1mxaa3	Alignment	not modelled	5.2	40	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
52	d1wuda1	Alignment	not modelled	5.1	13	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases