Phyre^{2}

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Description	RVBD0549c_(-)_640231_640644
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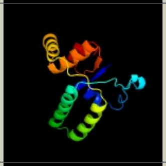
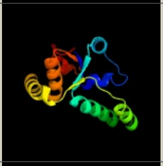
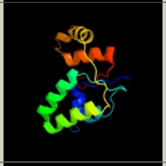
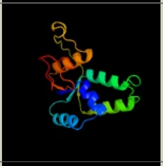
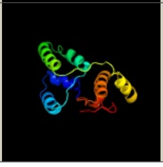
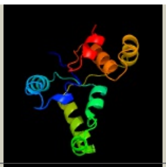
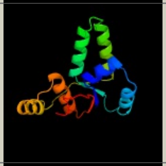
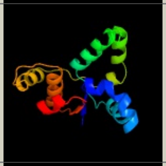
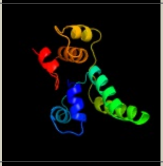
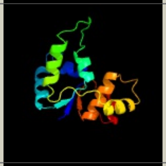
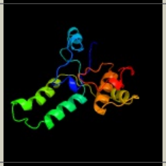
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v8pa_	Alignment		99.9	24	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
2	c1v8pK_	Alignment		99.9	24	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**hypothetical protein pae2754; **PDBTitle:** crystal structure of pae2754 from pyrobaculum aerophilum
3	c2fe1A_	Alignment		99.8	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein pae0151; **PDBTitle:** crystal structure of pae0151 from pyrobaculum aerophilum
4	d2fe1a1	Alignment		99.8	31	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
5	c4xgrG_	Alignment		99.6	23	**PDB header:**toxin/antitoxin **Chain:** G: **PDB Molecule:**ribonuclease vapc30; **PDBTitle:** crystal structure of addiction module from mycobacterial species
6	c5wzfB_	Alignment		99.4	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**23s rrna-specific endonuclease vapc20; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
7	c5x3tD_	Alignment		99.4	16	**PDB header:**antitoxin/toxin **Chain:** D: **PDB Molecule:**ribonuclease vapc26; **PDBTitle:** vapbc from mycobacterium tuberculosis
8	c3zvkC_	Alignment		99.3	13	**PDB header:**antitoxin/toxin/dna **Chain:** C: **PDB Molecule:**toxin of toxin-antitoxin system; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
9	c6a7vG_	Alignment		99.3	21	**PDB header:**toxin/antitoxin **Chain:** G: **PDB Molecule:**ribonuclease vapc11; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	c3tndC_	Alignment		99.2	12	**PDB header:**translation, toxin **Chain:** C: **PDB Molecule:**trna(fmet)-specific endonuclease vapc; **PDBTitle:** crystal structure of shigella flexneri vapbc toxin-antitoxin complex
11	c5l6mC_	Alignment		99.2	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease vapc; **PDBTitle:** structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)

12	c5sv2A_	Alignment		99.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease vapc21; **PDBTitle:** toxin vapc21 from mycobacterium tuberculosis
13	c6nklA_	Alignment		99.1	10	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**ribonuclease vapc; **PDBTitle:** 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
14	d2h1ca1	Alignment		99.1	12	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
15	c3h87B_	Alignment		99.1	22	**PDB header:**toxin/antitoxin **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
16	c4chgC_	Alignment		99.0	19	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**probable ribonuclease vapc15; **PDBTitle:** crystal structure of vapbc15 complex from mycobacterium tuberculosis
17	d1v96a1	Alignment		98.9	14	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
18	d1y82a1	Alignment		98.9	11	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
19	c3dboB_	Alignment		98.9	17	**PDB header:**toxin/antitoxin **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
20	c3i8oA_	Alignment		98.8	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh domain-containing protein mj1533; **PDBTitle:** a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
21	c3ix7A_	Alignment	not modelled	98.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ttha0540; **PDBTitle:** crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
22	c5ywwA_	Alignment	not modelled	98.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotide binding protein pinc; **PDBTitle:** archael ruvb-like holiday junction helicase
23	c5f4hF_	Alignment	not modelled	98.7	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nucleotide binding protein pinc; **PDBTitle:** archael ruvb-like holiday junction helicase
24	d1w8ia_	Alignment	not modelled	98.4	16	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
25	d1o4wa_	Alignment	not modelled	98.2	20	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
26	c2lcqA_	Alignment	not modelled	98.0	9	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
27	c2hwwC_	Alignment	not modelled	97.4	22	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**telomerase-binding protein est1a; **PDBTitle:** structure of pin domain of human smg6
28	c5yz4A_	Alignment	not modelled	96.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rrna-processing protein fcf1; **PDBTitle:** structure of the pin domain endonuclease utp24
29	c5jpqd_	Alignment	not modelled	95.4	19	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**wd40 domain proteins;

						PDBTitle: cryo-em structure of the 90s pre-ribosome
30	c2hwyB_	Alignment	not modelled	86.1	14	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein smg5; **PDBTitle:** structure of pin domain of human smg5.
31	c6g5iy_	Alignment	not modelled	86.0	23	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**40s ribosomal protein s24; **PDBTitle:** cryo-em structure of a late human pre-40s ribosomal subunit - state r
32	c4mj7B_	Alignment	not modelled	84.0	14	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**rrna-processing protein utp23; **PDBTitle:** crystal structure of the pin domain of saccharomyces cerevisiae utp23
33	c2mdtA_	Alignment	not modelled	83.0	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** a pilt n-terminus domain protein sso1118 from hyperthemophilic2 archaeon sulfolobus solfataricus p2
34	c3v33A_	Alignment	not modelled	69.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease zc3h12a; **PDBTitle:** crystal structure of mcpip1 conserved domain with zinc-finger motif
35	c3v32B_	Alignment	not modelled	63.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease zc3h12a; **PDBTitle:** crystal structure of mcpip1 n-terminal conserved domain
36	c1fw5A_	Alignment	not modelled	10.9	40	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nonstructural protein nsp1; **PDBTitle:** solution structure of membrane binding peptide of semliki2 forest virus mrna capping enzyme nsp1
37	c1jqsB_	Alignment	not modelled	10.6	14	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**elongation factor g; **PDBTitle:** fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
38	d1z9ha2	Alignment	not modelled	9.5	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
39	d3eeqa1	Alignment	not modelled	8.5	8	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
40	c3nfvA_	Alignment	not modelled	8.4	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alginate lyase; **PDBTitle:** crystal structure of an alginate lyase (bacova_01668) from bacteroides2 ovatus at 1.95 a resolution
41	c4g25A_	Alignment	not modelled	7.9	26	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**pentatricopeptide repeat-containing protein at2g32230, **PDBTitle:** crystal structure of proteinaceous rnase p 1 (prorp1) from a.2 thaliana, semet substituted form with sr
42	d1vjla_	Alignment	not modelled	7.8	18	**Fold:**Hypothetical protein TM0160 **Superfamily:**Hypothetical protein TM0160 **Family:**Hypothetical protein TM0160
43	d1hi9a_	Alignment	not modelled	7.6	21	**Fold:**Dipeptide transport protein **Superfamily:**Dipeptide transport protein **Family:**Dipeptide transport protein
44	c3by5A_	Alignment	not modelled	6.6	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein; **PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
45	d3by5a1	Alignment	not modelled	6.6	21	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
46	c2hsnA_	Alignment	not modelled	5.4	15	**PDB header:**ligase/rna binding protein **Chain:** A: **PDB Molecule:**methionyl-trna synthetase, cytoplasmic; **PDBTitle:** structural basis of yeast aminoacyl-trna synthetase complex2 formation revealed by crystal structures of two binary sub-3 complexes