Phyre2

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Description	RVBD1982c_(-)_2225421_2225840
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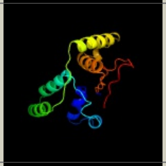
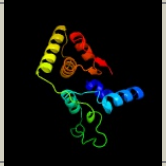
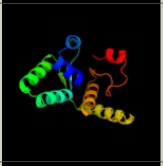
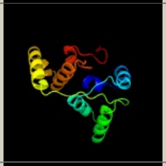
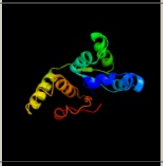
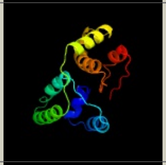
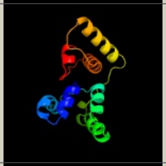
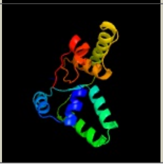
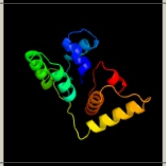
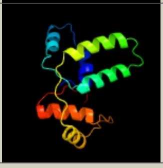
Unique Job ID	3adf6bdcae64c408

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xgrG_	Alignment		99.9	33	**PDB header:**toxin/antitoxin **Chain:** G: **PDB Molecule:**ribonuclease vapc30; **PDBTitle:** crystal structure of addiction module from mycobacterial species
2	d2h1ca1	Alignment		99.9	17	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
3	c3h87B_	Alignment		99.9	16	**PDB header:**toxin/antitoxin **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
4	c3zvkC_	Alignment		99.9	12	**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
5	c3dboB_	Alignment		99.8	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
6	c6nklA_	Alignment		99.8	15	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**ribonuclease vapc; **PDBTitle:** 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
7	c5sv2A_	Alignment		99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease vapc21; **PDBTitle:** toxin vapc21 from mycobacterium tuberculosis
8	d1v96a1	Alignment		99.8	12	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
9	c5l6mC_	Alignment		99.8	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease vapc; **PDBTitle:** structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
10	c4chgC_	Alignment		99.8	18	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**probable ribonuclease vapc15; **PDBTitle:** crystal structure of vapbc15 complex from mycobacterium tuberculosis
11	c3tndC_	Alignment		99.8	13	**PDB header:**translation, toxin **Chain:** C: **PDB Molecule:**trna(fmet)-specific endonuclease vapc; **PDBTitle:** crystal structure of shigella flexneri vapbc toxin-antitoxin complex

12	d1y82a1	Alignment		99.8	15	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
13	c6a7vG_	Alignment		99.8	18	**PDB header:**toxin/antitoxin **Chain:** G: **PDB Molecule:**ribonuclease vapc11; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
14	c5wzfB_	Alignment		99.8	18	**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
15	c5x3tD_	Alignment		99.7	23	**PDB header:**antitoxin/toxin **Chain:** D: **PDB Molecule:**ribonuclease vapc26; **PDBTitle:** vapbc from mycobacterium tuberculosis
16	c2fe1A_	Alignment		99.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein pae0151; **PDBTitle:** crystal structure of pae0151 from pyrobaculum aerophilum
17	d2fe1a1	Alignment		99.6	21	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
18	d1w8ia_	Alignment		99.3	16	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
19	d1v8pa_	Alignment		98.6	22	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
20	c1v8pK_	Alignment		98.6	22	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**hypothetical protein pae2754; **PDBTitle:** crystal structure of pae2754 from pyrobaculum aerophilum
21	c3ix7A_	Alignment	not modelled	98.1	14	**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	c3i8oA_	Alignment	not modelled	97.6	17	**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.
23	c2lcqA_	Alignment	not modelled	97.5	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
24	d1o4wa_	Alignment	not modelled	97.0	13	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
25	c5f4hF_	Alignment	not modelled	96.5	9	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nucleotide binding protein pinc; **PDBTitle:** archael ruvb-like holiday junction helicase
26	c5ywwA_	Alignment	not modelled	96.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotide binding protein pinc; **PDBTitle:** archael ruvb-like holiday junction helicase
27	c2hwwC_	Alignment	not modelled	94.4	14	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**telomerase-binding protein est1a; **PDBTitle:** structure of pin domain of human smg6
28	c5jpqd_	Alignment	not modelled	94.3	15	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**wd40 domain proteins; **PDBTitle:** cryo-em structure of the 90s pre-ribosome
						PDB header:hydrolase

29	c5yz4A_	Alignment	not modelled	93.8	18	**Chain:** A: **PDB Molecule:**rrna-processing protein fcf1; **PDBTitle:** structure of the pin domain endonuclease utp24
30	c6g5iy_	Alignment	not modelled	89.1	17	**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
31	c2hwyB_	Alignment	not modelled	81.5	17	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein smg5; **PDBTitle:** structure of pin domain of human smg5.
32	c4mj7B_	Alignment	not modelled	72.9	10	**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	c3v32B_	Alignment	not modelled	71.8	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease zc3h12a; **PDBTitle:** crystal structure of mcpip1 n-terminal conserved domain
34	c3v33A_	Alignment	not modelled	67.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease zc3h12a; **PDBTitle:** crystal structure of mcpip1 conserved domain with zinc-finger motif
35	d1cmwa2	Alignment	not modelled	61.2	19	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
36	d1tfra2	Alignment	not modelled	56.3	16	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
37	c3zddA_	Alignment	not modelled	42.6	12	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein xni; **PDBTitle:** structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
38	d1xo1a2	Alignment	not modelled	42.3	19	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
39	c2ihnA_	Alignment	not modelled	35.7	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
40	c1jqsB_	Alignment	not modelled	28.6	23	**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
41	c1ut8B_	Alignment	not modelled	20.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** divalent metal ions (zinc) bound to t5 5'-exonuclease
42	c1cmwA_	Alignment	not modelled	18.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
43	d1qf6a1	Alignment	not modelled	14.8	7	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
44	d1a77a2	Alignment	not modelled	12.7	17	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
45	c4mitG_	Alignment	not modelled	12.6	30	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**serine/threonine protein kinase pak, putative; **PDBTitle:** crystal structure of e. histolytica racc bound to the ehpak4 pbd
46	c4rodA_	Alignment	not modelled	12.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor iiib 50 kda subunit; **PDBTitle:** human tfiib-related factor 2 (brf2) and tbp bound to trnau1 promoter
47	d1o8bb1	Alignment	not modelled	10.3	8	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
48	c5fa0B_	Alignment	not modelled	10.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative n-acetyl glucosaminyl transferase; **PDBTitle:** the structure of the beta-3-deoxy-d-manno-oct-2-ulosonic acid2 transferase domain from wbbb
49	d1ul1x2	Alignment	not modelled	9.7	13	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
50	c6n2bA_	Alignment	not modelled	9.1	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tapirin; **PDBTitle:** the crystal structure of caldicellulosiruptor kristjanssonii tapirin2 c-terminal domain
51	c3l7oB_	Alignment	not modelled	8.9	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
52	c5j6qA_	Alignment	not modelled	8.9	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell wall binding protein cwp8; **PDBTitle:** cwp8 from clostridium difficile
53	c4x23V_	Alignment	not modelled	8.1	43	**PDB header:**structural protein/dna **Chain:** V: **PDB Molecule:**cenp-c; **PDBTitle:** crystal structure of cenp-c in complex with the nucleosome core2 particle
54	c4inmV_	Alignment	not modelled	8.1	43	**PDB header:**structural protein/dna **Chain:** V: **PDB Molecule:**cenp-c; **PDBTitle:** crystal structure of cenp-c in complex with the nucleosome core2 particle
						PDB header:isomerase

55	c4x84C_	Alignment	not modelled	7.2	12	**Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
56	c3q8lA_	Alignment	not modelled	6.6	13	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
57	c4inmX_	Alignment	not modelled	6.6	43	**PDB header:**structural protein/dna **Chain:** X: **PDB Molecule:**cenp-c; **PDBTitle:** crystal structure of cenp-c in complex with the nucleosome core2 particle
58	c4x23X_	Alignment	not modelled	6.6	43	**PDB header:**structural protein/dna **Chain:** X: **PDB Molecule:**cenp-c; **PDBTitle:** crystal structure of cenp-c in complex with the nucleosome core2 particle
59	d1lmb3_	Alignment	not modelled	6.4	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
60	d1qd1a1	Alignment	not modelled	6.3	25	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
61	c6iz4G_	Alignment	not modelled	6.2	9	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**trimeric intracellular cation channel type b-b; **PDBTitle:** crystal structure analysis of tric counter-ion channels in calcium2 release
62	c6f42V_	Alignment	not modelled	6.0	5	**PDB header:**transcription **Chain:** V: **PDB Molecule:**transcription factor iiib 70 kda subunit; **PDBTitle:** rna polymerase iii closed complex cc1.
63	c5egiB_	Alignment	not modelled	6.0	8	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**uncharacterized protein y57a10a.10; **PDBTitle:** structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
64	d1l1ya_	Alignment	not modelled	5.9	35	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
65	c1l2aD_	Alignment	not modelled	5.9	35	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
66	d1kmma1	Alignment	not modelled	5.7	12	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
67	c4mitE_	Alignment	not modelled	5.7	38	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**serine/threonine protein kinase pak, putative; **PDBTitle:** crystal structure of e. histolytica racc bound to the ehpak4 pbd
68	d2diga1	Alignment	not modelled	5.5	50	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
69	c3iefA_	Alignment	not modelled	5.5	24	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from bartonella2 henselae using mpcs.
70	c5eikA_	Alignment	not modelled	5.5	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein y57a10a.28; **PDBTitle:** structure of a trimeric intracellular cation channel from c. elegans2 in the absence of ca2+
71	c6iz0A_	Alignment	not modelled	5.3	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**trimeric intracellular cation channel type a; **PDBTitle:** crystal structure analysis of a eukaryotic membrane protein
72	c4el8A_	Alignment	not modelled	5.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 48; **PDBTitle:** the unliganded structure of c.bescii cela gh48 module