Phyre^2

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Description	RVBD3182_(-)_3550371_3550715
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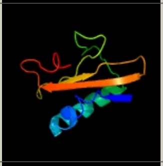
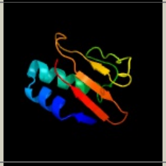
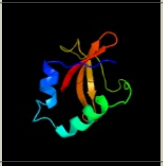
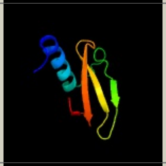
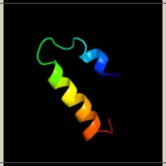
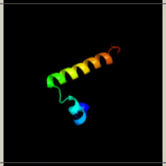
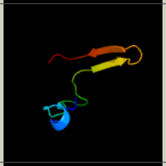
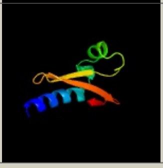
Unique Job ID	b288dce8d8a431e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wmia1	Alignment		98.7	18	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
2	c2kheA_	Alignment		98.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**toxin-like protein; **PDBTitle:** solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
3	c3bpqD_	Alignment		98.5	9	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
4	c3kixy_	Alignment		98.2	10	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:** **PDBTitle:** structure of rele nuclease bound to the 70s ribosome (postcleavage2 state; part 3 of 4)
5	c3g5oC_	Alignment		98.0	19	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**uncharacterized protein rv2866; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
6	d2a6sa1	Alignment		97.7	10	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**YoeB/Txe-like
7	c3oeiH_	Alignment		97.5	15	**PDB header:**toxin, protein binding **Chain:** H: **PDB Molecule:**relk (toxin rv3358); **PDBTitle:** crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
8	c5ja9D_	Alignment		96.8	21	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin higb-2; **PDBTitle:** crystal structure of the higb2 toxin in complex with nb6
9	c2otrA_	Alignment		95.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hp0892; **PDBTitle:** solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
10	d1z8ma1	Alignment		90.8	20	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
11	c5cw7H_	Alignment		84.6	16	**PDB header:**toxin **Chain:** H: **PDB Molecule:**plasmid stabilization protein pare; **PDBTitle:** crystal structure of the paaa2-pare2 antitoxin-toxin complex

12	c4q2uH_	Alignment		83.3	8	**PDB header:**toxin/toxin repressor **Chain:** H: **PDB Molecule:**mrna interferase yafq; **PDBTitle:** crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
13	c4mctD_	Alignment		77.8	10	**PDB header:**toxin **Chain:** D: **PDB Molecule:**killer protein; **PDBTitle:** p. vulgaris higba structure, crystal form 1
14	c5cegB_	Alignment		47.9	11	**PDB header:**toxin **Chain:** B: **PDB Molecule:**plasmid stabilization system; **PDBTitle:** x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
15	c6f8sD_	Alignment		18.1	11	**PDB header:**toxin **Chain:** D: **PDB Molecule:**putative killer protein; **PDBTitle:** toxin-antitoxin complex grata
16	c2kl4A_	Alignment		17.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2032 protein; **PDBTitle:** nmr structure of the protein nb7804a
17	c2ogfD_	Alignment		15.3	26	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0408; **PDBTitle:** crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
18	d2oc6a1	Alignment		12.4	10	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
19	d1kfia4	Alignment		8.6	32	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
20	c3kxeB_	Alignment		7.9	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**toxin protein pare-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
21	c4jenB_	Alignment	not modelled	7.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cmp n-glycosidase; **PDBTitle:** structure of clostridium botulinum cmp n-glycosidase, bcmb
22	c3bdiA_	Alignment	not modelled	7.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ta0194; **PDBTitle:** crystal structure of predicted cib-like hydrolase (np_393672.1) from2 thermoplasma acidophilum at 1.45 a resolution
23	c3kxeD_	Alignment	not modelled	7.1	13	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
24	c5cegC_	Alignment	not modelled	7.0	19	**PDB header:**toxin **Chain:** C: **PDB Molecule:**addiction module antidote protein, copg/arc/metj family; **PDBTitle:** x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
25	c5frdA_	Alignment	not modelled	6.5	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase (est-2); **PDBTitle:** structure of a thermophilic esterase
26	c4qwoA_	Alignment	not modelled	6.0	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**profilin; **PDBTitle:** 1.52 angstrom crystal structure of a42r profilin-like protein from2 monkeypox virus zaire-96-i-16
27	d1eiwa_	Alignment	not modelled	6.0	16	**Fold:**Flavodoxin-like **Superfamily:**Hypothetical protein MTH538 **Family:**Hypothetical protein MTH538
28	c4lgdF_	Alignment	not modelled	5.9	10	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**ras association domain family member 5, rassf5; **PDBTitle:** structural basis for autoactivation of human mst2 kinase

						and its2 regulation by rassf5
29	c1u2eA_	Alignment	not modelled	5.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-hydroxy-6-ketonona-2,4-dienedioic acid **PDBTitle:** crystal structure of the c-c bond hydrolase mhpc
30	c2fu4B_	Alignment	not modelled	5.8	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
31	c1fi4A_	Alignment	not modelled	5.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate 5-diphosphate decarboxylase; **PDBTitle:** the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
32	d3pmga4	Alignment	not modelled	5.6	18	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
33	c2p90B_	Alignment	not modelled	5.5	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
34	c1psvA_	Alignment	not modelled	5.4	42	**PDB header:**designed peptide **Chain:** A: **PDB Molecule:**pda8d; **PDBTitle:** computationally designed peptide with a beta-beta-alpha2 fold selection, nmr, 32 structures
35	d1ss4a_	Alignment	not modelled	5.3	19	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein BC1747