Phyre^2

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Description	P0AF93
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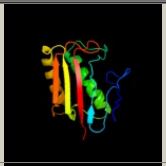
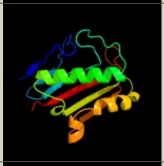
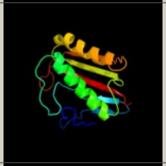
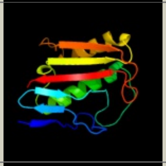
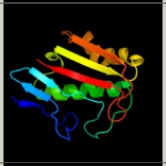
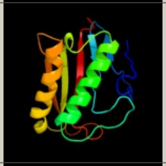
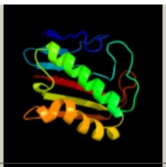
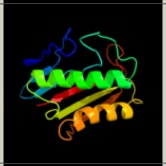
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1j7ha_	Alignment		100.0	77	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
2	d1qu9a_	Alignment		100.0	100	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
3	d1onia_	Alignment		100.0	46	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
4	d1nq3a_	Alignment		100.0	46	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
5	c3quwA_	Alignment		100.0	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein mmf1; **PDBTitle:** crystal structure of yeast mmf1
6	d2b33a1	Alignment		100.0	48	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
7	d1qaha_	Alignment		100.0	49	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
8	c3k0tA_	Alignment		100.0	42	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**endoribonuclease l-psp, putative; **PDBTitle:** crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
9	d1jd1a_	Alignment		100.0	41	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
10	d2cvla1	Alignment		100.0	39	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
11	d1qd9a_	Alignment		100.0	49	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP

12	c3r0pB_	Alignment		100.0	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-psp putative endoribonuclease; **PDBTitle:** crystal structure of l-psp putative endoribonuclease from uncultured2 organism
13	c1xrgB_	Alignment		100.0	51	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative translation initiation inhibitor, yjgf **PDBTitle:** conserved hypothetical protein from clostridium2 thermocellum cth-2968
14	c2dyyG_	Alignment		100.0	55	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**upf0076 protein ph0854; **PDBTitle:** crystal structure of putative translation initiation2 inhibitor ph0854 from pyrococcus horikoshii
15	d1x25a1	Alignment		100.0	48	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
16	c3l7qD_	Alignment		100.0	54	**PDB header:**translation **Chain:** D: **PDB Molecule:**putative translation initiation inhibitor, aldr regulator- **PDBTitle:** crystal structure of aldr from streptococcus mutans
17	d1xrga_	Alignment		100.0	51	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
18	c3lmeE_	Alignment		100.0	25	**PDB header:**translation **Chain:** E: **PDB Molecule:**possible translation initiation inhibitor; **PDBTitle:** structure of probable translation initiation inhibitor from2 (rpa2473) from rhodopseudomonas palustris
19	c3m4sC_	Alignment		100.0	37	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative endoribonuclease l-psp; **PDBTitle:** crystal structure of a putative endoribonuclease l-psp from entamoeba2 histolytica, orthorhombic form
20	c3v4dC_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aminoacrylate peracid reductase rutc; **PDBTitle:** crystal structure of rutc protein a member of the yjgf family from2 e.coli
21	d2cwja1	Alignment	not modelled	100.0	45	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
22	c2ig8C_	Alignment	not modelled	100.0	31	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein pa3499; **PDBTitle:** crystal structure of a protein of unknown function pa3499 from2 pseudomonas aeruginosa
23	d1pf5a_	Alignment	not modelled	100.0	25	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
24	d2otma1	Alignment	not modelled	100.0	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
25	c3kjjL_	Alignment	not modelled	100.0	25	**PDB header:**unknown function **Chain:** L: **PDB Molecule:**nmb1025 protein; **PDBTitle:** crystal structure of nmb1025, a member of yjgf protein family, from2 neisseria meningitidis (hexagonal crystal form)
26	c3i7tA_	Alignment	not modelled	100.0	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
27	d2ewca1	Alignment	not modelled	100.0	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
28	c3k12F_	Alignment	not modelled	100.0	21	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein a6v7t0; **PDBTitle:** crystal structure of an uncharacterized protein a6v7t0 from2 pseudomonas aeruginosa

29	c3gtzA_	Alignment	not modelled	100.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative translation initiation inhibitor; **PDBTitle:** crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
30	c3d01G_	Alignment	not modelled	100.0	28	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the protein atu1372 with unknown function from2 agrobacterium tumefaciens
31	c3i3fB_	Alignment	not modelled	100.0	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from giardia lamblia gl50803_14299
32	c3lybC_	Alignment	not modelled	99.9	32	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative endoribonuclease; **PDBTitle:** structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae
33	d1crka1	Alignment	not modelled	14.6	7	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
34	d1qh4a1	Alignment	not modelled	13.5	5	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
35	c2wknE_	Alignment	not modelled	13.3	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**formamidase; **PDBTitle:** gamma lactamase from delftia acidovorans
36	d1g0wa1	Alignment	not modelled	12.0	9	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
37	d1w5da1	Alignment	not modelled	10.7	27	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
38	d2ex2a1	Alignment	not modelled	10.1	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
39	c2jvfA_	Alignment	not modelled	10.1	9	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
40	c1qysA_	Alignment	not modelled	9.7	12	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
41	d1i0ea1	Alignment	not modelled	9.5	7	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
42	d1u6ra1	Alignment	not modelled	8.9	7	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
43	d1vrpa1	Alignment	not modelled	7.8	7	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
44	d1w79a1	Alignment	not modelled	7.4	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
45	d1qk1a1	Alignment	not modelled	6.0	9	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
46	d1vjta2	Alignment	not modelled	5.3	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
47	c2zxeB_	Alignment	not modelled	5.3	10	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**na+,k+-atpase beta subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
48	c3a3eB_	Alignment	not modelled	5.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**penicillin-binding protein 4; **PDBTitle:** crystal structure of penicillin binding protein 4 (dacb)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)