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Description	P0AFQ5
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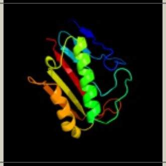
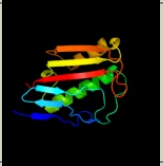
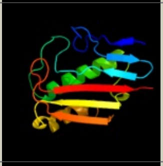
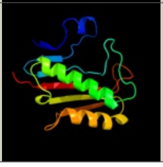
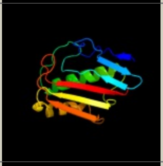
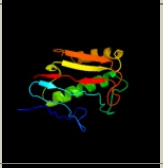
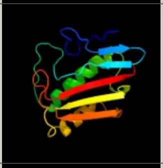
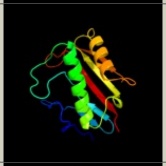
Unique Job ID	3ccc700913d1897c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1onia_	Alignment		100.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
2	d1nq3a_	Alignment		100.0	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
3	c3r0pB_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-psp putative endoribonuclease; **PDBTitle:** crystal structure of l-psp putative endoribonuclease from uncultured2 organism
4	d1qaha_	Alignment		100.0	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
5	d2b33a1	Alignment		100.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
6	c3k0tA_	Alignment		100.0	32	**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
7	c3l7qD_	Alignment		100.0	25	**PDB header:**translation **Chain:** D: **PDB Molecule:**putative translation initiation inhibitor, aldr regulator- **PDBTitle:** crystal structure of aldr from streptococcus mutans
8	c3m4sC_	Alignment		100.0	27	**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
9	c1xrgB_	Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative translation initiation inhibitor, yjgf **PDBTitle:** conserved hypothetical protein from clostridium2 thermocellum cth-2968
10	d1x25a1	Alignment		100.0	30	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
11	c3v4dC_	Alignment		100.0	97	**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

12	d2cvla1	Alignment		100.0	26	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
13	c2dyyG_	Alignment		100.0	32	**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
14	d1xrga_	Alignment		100.0	26	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
15	c3quwA_	Alignment		100.0	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein mmf1; **PDBTitle:** crystal structure of yeast mmf1
16	d1jd1a_	Alignment		100.0	23	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
17	d1j7ha_	Alignment		100.0	30	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
18	d1qd9a_	Alignment		100.0	30	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
19	c3lmeE_	Alignment		100.0	22	**PDB header:**translation **Chain:** E: **PDB Molecule:**possible translation initiation inhibitor; **PDBTitle:** structure of probable translation initiation inhibitor from2 (rpa2473) from rhodopseudomonas palustris
20	d2cwja1	Alignment		100.0	23	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
21	d1qu9a_	Alignment	not modelled	100.0	23	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
22	d1pf5a_	Alignment	not modelled	100.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
23	c2ig8C_	Alignment	not modelled	100.0	27	**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
24	c3i7tA_	Alignment	not modelled	100.0	26	**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
25	d2otma1	Alignment	not modelled	100.0	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
26	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
27	d2ewca1	Alignment	not modelled	100.0	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
28	c3kjjL_	Alignment	not modelled	100.0	28	**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)

29	c3k12F_	Alignment	not modelled	100.0	28	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein a6v7t0; **PDBTitle:** crystal structure of an uncharacterized protein a6v7t0 from2 pseudomonas aeruginosa
30	c3d01G_	Alignment	not modelled	100.0	21	**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	26	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from giardia lamblia gl50803_14299
32	c3lybC_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative endoribonuclease; **PDBTitle:** structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae
33	d1g0wa1	Alignment	not modelled	20.6	24	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
34	d1qh4a1	Alignment	not modelled	19.9	24	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
35	d1crka1	Alignment	not modelled	14.5	16	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
36	d1u6ra1	Alignment	not modelled	14.2	25	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
37	d1vrpa1	Alignment	not modelled	13.4	22	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
38	d1qk1a1	Alignment	not modelled	12.7	19	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
39	d1aisa1	Alignment	not modelled	10.6	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
40	d1twfc2	Alignment	not modelled	9.7	5	**Fold:**Insert subdomain of RNA polymerase alpha subunit **Superfamily:**Insert subdomain of RNA polymerase alpha subunit **Family:**Insert subdomain of RNA polymerase alpha subunit
41	d1qnaa1	Alignment	not modelled	8.6	8	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
42	c3n2lA_	Alignment	not modelled	8.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
43	d1i0ea1	Alignment	not modelled	7.5	21	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
44	c2x47A_	Alignment	not modelled	7.4	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**macro domain-containing protein 1; **PDBTitle:** crystal structure of human macrod1
45	d1cdwa1	Alignment	not modelled	7.0	14	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
46	d2oo3a1	Alignment	not modelled	6.8	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**LPG1296-like
47	d1ulqa1	Alignment	not modelled	6.7	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
48	d1xb2b1	Alignment	not modelled	6.4	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
49	c2wuaA_	Alignment	not modelled	6.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetoacetyl coa thiolase; **PDBTitle:** structure of the peroxisomal 3-ketoacyl-coa thiolase from2 sunflower
50	d1nh2a1	Alignment	not modelled	5.9	14	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
51	d1xhja_	Alignment	not modelled	5.5	23	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
52	c3fqmA_	Alignment	not modelled	5.4	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural protein 5a; **PDBTitle:** crystal structure of a novel dimeric form of hcv ns5a domain i protein
53	c2kjwA_	Alignment	not modelled	5.4	24	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55