Phyre^2

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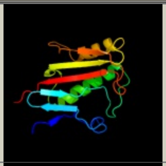
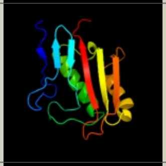
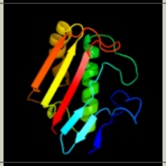
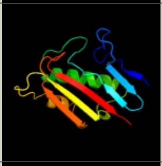
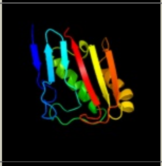
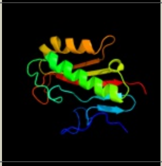
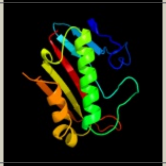
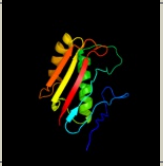
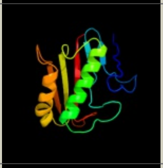
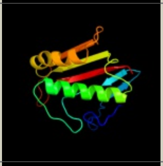
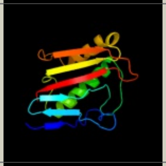
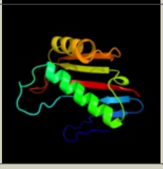
Description	P39332
Date	Thu Jan 5 11:59:23 GMT 2012
Unique Job ID	89314ab7b8384782

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pf5a_	Alignment		100.0	100	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
2	d1onia_	Alignment		100.0	23	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
3	c3k0tA_	Alignment		100.0	30	**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
4	d2b33a1	Alignment		100.0	26	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
5	d1nq3a_	Alignment		100.0	25	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
6	c3lmeE_	Alignment		100.0	28	**PDB header:**translation **Chain:** E: **PDB Molecule:**possible translation initiation inhibitor; **PDBTitle:** structure of probable translation initiation inhibitor from2 (rpa2473) from rhodopseudomonas palustris
7	c3r0pB_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-psp putative endoribonuclease; **PDBTitle:** crystal structure of l-psp putative endoribonuclease from uncultured2 organism
8	d1qaha_	Alignment		100.0	25	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
9	c3v4dC_	Alignment		100.0	21	**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
10	d2cvla1	Alignment		100.0	32	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
11	c2ig8C_	Alignment		100.0	23	**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

12	c3l7qD_	Alignment		100.0	28	**PDB header:**translation **Chain:** D: **PDB Molecule:**putative translation initiation inhibitor, aldr regulator- **PDBTitle:** crystal structure of aldr from streptococcus mutans
13	d1j7ha_	Alignment		100.0	26	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
14	c1xrgB_	Alignment		100.0	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative translation initiation inhibitor, yjgf **PDBTitle:** conserved hypothetical protein from clostridium2 thermocellum cth-2968
15	c2dyyG_	Alignment		100.0	31	**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
16	c3quwA_	Alignment		100.0	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein mmf1; **PDBTitle:** crystal structure of yeast mmf1
17	d1qd9a_	Alignment		100.0	30	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
18	d1jd1a_	Alignment		100.0	26	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
19	c3m4sC_	Alignment		100.0	23	**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	d2ewca1	Alignment		100.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
21	d1xrga_	Alignment	not modelled	100.0	28	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
22	c3gtzA_	Alignment	not modelled	100.0	21	**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
23	c3i7tA_	Alignment	not modelled	100.0	31	**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
24	d1x25a1	Alignment	not modelled	100.0	30	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
25	c3kjjL_	Alignment	not modelled	100.0	21	**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	c3k12F_	Alignment	not modelled	100.0	19	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein a6v7t0; **PDBTitle:** crystal structure of an uncharacterized protein a6v7t0 from2 pseudomonas aeruginosa
27	c3i3fB_	Alignment	not modelled	100.0	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from giardia lamblia gl50803_14299
28	d1qu9a_	Alignment	not modelled	100.0	23	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP

29	d2cwja1	Alignment	not modelled	100.0	37	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
30	d2otma1	Alignment	not modelled	100.0	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
31	c3d01G_	Alignment	not modelled	99.9	23	**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
32	c3lybC_	Alignment	not modelled	99.9	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative endoribonuclease; **PDBTitle:** structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae
33	c2wknE_	Alignment	not modelled	28.4	16	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**formamidase; **PDBTitle:** gamma lactamase from delftia acidovorans
34	d1aisa1	Alignment	not modelled	15.8	26	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
35	d1qnaa1	Alignment	not modelled	13.6	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
36	c2yh5A_	Alignment	not modelled	12.1	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
37	c3a1yF_	Alignment	not modelled	11.8	44	**PDB header:**ribosomal protein **Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p); **PDBTitle:** the structure of protein complex
38	c3tixB_	Alignment	not modelled	11.2	14	**PDB header:**gene regulation/protein binding **Chain:** B: **PDB Molecule:**chromo domain-containing protein 1; **PDBTitle:** crystal structure of the chp1-tas3 complex core
39	d1cdwa1	Alignment	not modelled	9.8	22	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
40	d1nh2a1	Alignment	not modelled	9.7	19	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
41	d1mp9a1	Alignment	not modelled	9.7	23	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
42	d1xb2b1	Alignment	not modelled	9.2	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
43	d1ox0a2	Alignment	not modelled	8.9	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
44	d1r5pa_	Alignment	not modelled	8.9	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
45	d1u0ua1	Alignment	not modelled	8.4	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
46	c2d3mA_	Alignment	not modelled	7.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pentaketide chromone synthase; **PDBTitle:** pentaketide chromone synthase complexed with coenzyme a
47	c2wuaA_	Alignment	not modelled	7.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetoacetyl coa thiolase; **PDBTitle:** structure of the peroxisomal 3-ketoacyl-coa thiolase from2 sunflower
48	c1tqyD_	Alignment	not modelled	7.2	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**actinorhodin polyketide putative beta-ketoacyl synthase 2; **PDBTitle:** the actinorhodin ketosynthase/chain length factor
49	d1xhja_	Alignment	not modelled	7.2	23	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
50	c3fqmA_	Alignment	not modelled	7.0	33	**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
51	d1mp9a2	Alignment	not modelled	6.8	23	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
52	c3iz5a_	Alignment	not modelled	6.6	19	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**60s ribosomal protein l1 (l1p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
53	d2ns9a1	Alignment	not modelled	6.6	14	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**CoxG-like
54	c3cqrB_	Alignment	not modelled	6.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**violaxanthin de-epoxidase, chloroplast; **PDBTitle:** crystal structure of the lipocalin domain of violaxanthin2 de-epoxidase (vde) at ph5
55	c2dvzA_	Alignment	not modelled	5.9	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
						Fold: RuvA C-terminal domain-like

56	d1efub3	Alignment	not modelled	5.9	8	**Superfamily:**UBA-like **Family:**TS-N domain
57	c2gqdB_	Alignment	not modelled	5.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 2; **PDBTitle:** the crystal structure of b-ketoacyl-acp synthase ii (fabf)2 from staphylococcus aureus
58	c2kjwA_	Alignment	not modelled	5.5	20	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55
59	d2d6fa1	Alignment	not modelled	5.5	19	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
60	d2cp9a1	Alignment	not modelled	5.5	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
61	d1un7a2	Alignment	not modelled	5.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
62	d1nfpa_	Alignment	not modelled	5.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
63	c2qbbF_	Alignment	not modelled	5.2	21	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** crystal structure of the bacterial ribosome from2 escherichia coli in complex with gentamicin. this file3 contains the 30s subunit of the second 70s ribosome, with4 gentamicin bound. the entire crystal structure contains5 two 70s ribosomes and is described in remark 400.
64	d2qalf1	Alignment	not modelled	5.2	21	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S6 **Family:**Ribosomal protein S6
65	d2ofya1	Alignment	not modelled	5.2	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like