Phyre2

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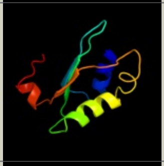
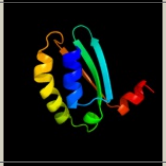
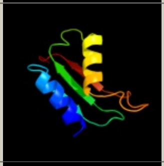
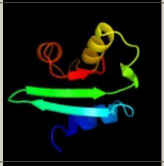
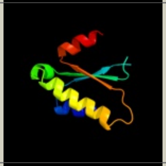
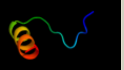
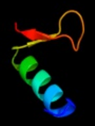
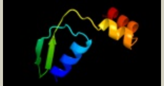
Description	P0A9W6
Date	Thu Jan 5 11:11:35 GMT 2012
Unique Job ID	df7a025fc286cbdd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ny8a_	Alignment		100.0	100	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
2	c3tr3A_	Alignment		100.0	32	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola; **PDBTitle:** structure of a bola protein homologue from coxiella burnetii
3	c3o2eA_	Alignment		100.0	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola-like protein; **PDBTitle:** crystal structure of a bol-like protein from babesia bovis
4	d1v9ja_	Alignment		100.0	27	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
5	c2dhmA_	Alignment		100.0	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bola; **PDBTitle:** solution structure of the bola protein from escherichia coli
6	c1v60A_	Alignment		100.0	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**riken cdna 1810037g04; **PDBTitle:** solution structure of bola1 protein from mus musculus
7	c2kdnA_	Alignment		100.0	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein pfe0790c; **PDBTitle:** solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
8	c1xs3A_	Alignment		100.0	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein xc975; **PDBTitle:** solution structure analysis of the xc975 protein
9	c2kz0A_	Alignment		99.9	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bola family protein; **PDBTitle:** solution structure of a bola protein (ech_0303) from ehrlichia2 chaffeensis. seattle structural genomics center for infectious3 disease target ehcha.10365.a
10	d1ylqa1	Alignment		97.4	21	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
11	c2rffA_	Alignment		58.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotidyltransferase; **PDBTitle:** crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from sulfolobus solfataricus at 1.40 a3 resolution

12	c2jsoA_	Alignment		30.2	35	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin resistance protein pmrd; **PDBTitle:** antimicrobial resistance protein
13	c1dpuA_	Alignment		19.0	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
14	d1dpua_	Alignment		19.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
15	d1ubdc2	Alignment		17.8	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
16	d2hjja1	Alignment		15.2	36	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YkfF-like
17	c2hjjA_	Alignment		15.2	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ykff; **PDBTitle:** solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
18	d2pzza1	Alignment		12.9	5	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**SSO1042-like
19	d1znfa_	Alignment		12.0	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
20	c1znfA_	Alignment		12.0	29	**PDB header:**zinc finger dna binding domain **Chain:** A: **PDB Molecule:**31st zinc finger from xfin; **PDBTitle:** three-dimensional solution structure of a single zinc2 finger dna-binding domain
21	c3c9gB_	Alignment	not modelled	11.5	12	**PDB header:**nucleotide binding protein **Chain:** B: **PDB Molecule:**upf0200/upf0201 protein af_1395; **PDBTitle:** crystal structure of uncharacterized upf0201 protein af_135
22	d1flma_	Alignment	not modelled	10.1	21	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
23	c1cirA_	Alignment	not modelled	10.0	15	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** complex of two fragments of ci2 [(1-40)(dot)(41-64)]
24	c1xb4C_	Alignment	not modelled	9.3	22	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**hypothetical 23.6 kda protein in yuh1-ura8 **PDBTitle:** crystal structure of subunit vps25 of the endosomal2 trafficking complex escrt-ii
25	d1ijwc_	Alignment	not modelled	8.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
26	d1x7fa2	Alignment	not modelled	8.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
27	c2kwhA_	Alignment	not modelled	8.1	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**rala-binding protein 1; **PDBTitle:** ral binding domain of rlip76 (ralbp1)
28	c2p0oA_	Alignment	not modelled	7.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf871; **PDBTitle:** crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function

29	d1ccwb_	Alignment	not modelled	7.5	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Glutamate mutase, large subunit
30	d1hcra_	Alignment	not modelled	7.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
31	d2g7oa1	Alignment	not modelled	7.0	16	**Fold:**TraM-like **Superfamily:**TraM-like **Family:**TraM-like
32	d1hh2p3	Alignment	not modelled	6.7	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
33	d1ur3m_	Alignment	not modelled	6.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
34	c2kneB_	Alignment	not modelled	6.6	28	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**atpase, ca++ transporting, plasma membrane 4; **PDBTitle:** calmodulin wraps around its binding domain in the plasma2 membrane ca2+ pump anchored by a novel 18-1 motif
35	d1cf7b_	Alignment	not modelled	6.2	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
36	d1pbya2	Alignment	not modelled	5.9	38	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
37	c1x7fA_	Alignment	not modelled	5.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
38	c3qfiA_	Alignment	not modelled	5.6	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** x-ray crystal structure of transcriptional regulator (ef0465) from2 enterococcus faecalis, northeast structural genomics consortium3 target efr190