Phyre2

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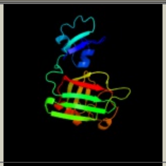
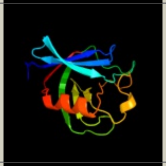
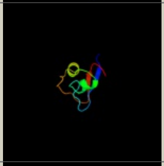
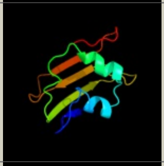
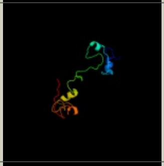
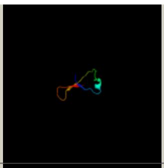
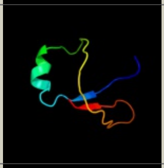
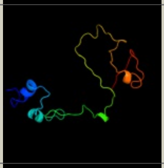
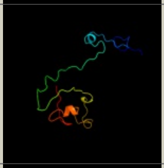
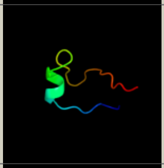
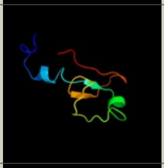
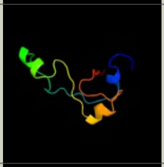
Description	P0AAX8
Date	Thu Jan 5 11:14:05 GMT 2012
Unique Job ID	a9a677dac9d3dd3c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y7mB_	Alignment		100.0	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
2	d1y7ma1	Alignment		100.0	32	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
3	c2hklB_	Alignment		100.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l,d-transpeptidase; **PDBTitle:** crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
4	d1zata1	Alignment		100.0	26	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
5	c2l9yA_	Alignment		97.9	22	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
6	d1y7ma2	Alignment		97.4	24	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
7	c2djpA_	Alignment		97.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
8	d1e0ga_	Alignment		97.2	16	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
9	c2gu1A_	Alignment		90.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
10	c1h5nC_	Alignment		70.6	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
11	c3mcaB_	Alignment		57.5	25	**PDB header:**translation regulation/hydrolase **Chain:** B: **PDB Molecule:**protein dom34; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay

12	d1wjja_	Alignment		41.6	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
13	c2kkeA_	Alignment		25.7	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
14	c2k50A_	Alignment		21.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
15	c1eu1A_	Alignment		20.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dimethyl sulfoxide reductase; **PDBTitle:** the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
16	c1y5iA_	Alignment		18.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
17	d1ogya1	Alignment		17.6	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
18	c2ki8A_	Alignment		15.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase, **PDBTitle:** solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
19	d1y5ia1	Alignment		14.9	21	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
20	d1t3la1	Alignment		13.3	25	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
21	d2iv2x1	Alignment	not modelled	11.3	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
22	d2vgna1	Alignment	not modelled	10.9	19	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
23	c1tmoA_	Alignment	not modelled	10.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
24	d1k78a1	Alignment	not modelled	10.4	100	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
25	d2hthb1	Alignment	not modelled	10.4	16	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**VPS36 N-terminal domain-like
26	d2jioa1	Alignment	not modelled	9.2	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
27	d2qi2a1	Alignment	not modelled	9.1	19	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
28	c3rf1B_	Alignment	not modelled	9.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glycyl-trna synthetase alpha subunit; **PDBTitle:** the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
						Fold: Double psi beta-barrel

29	d1eu1a1	Alignment	not modelled	9.0	12	**Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
30	d6paxa1	Alignment	not modelled	8.8	71	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
31	c3d12A_	Alignment	not modelled	8.6	25	**PDB header:**hydrolase/membrane protein **Chain:** A: **PDB Molecule:**hemagglutinin-neuraminidase; **PDBTitle:** crystal structures of nipah virus g attachment glycoprotein in complex2 with its receptor ephrin-b3
32	c2iheA_	Alignment	not modelled	8.2	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
33	d2c42a3	Alignment	not modelled	8.1	24	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
34	c1r1gB_	Alignment	not modelled	8.0	27	**PDB header:**toxin **Chain:** B: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** crystal structure of the scorpion toxin bmbkttx1
35	c1r1gA_	Alignment	not modelled	8.0	27	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** crystal structure of the scorpion toxin bmbkttx1
36	d1r1ga_	Alignment	not modelled	8.0	27	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
37	d1h0ha1	Alignment	not modelled	7.7	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d2gp4a1	Alignment	not modelled	7.3	29	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
39	c2vw9B_	Alignment	not modelled	7.0	12	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**single-stranded dna binding protein; **PDBTitle:** single stranded dna binding protein complex from2 helicobacter pylori
40	d1cz5a1	Alignment	not modelled	6.9	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
41	c3bbnD_	Alignment	not modelled	6.6	13	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
42	c1eqqD_	Alignment	not modelled	6.5	15	**PDB header:**replication/rna **Chain:** D: **PDB Molecule:**single stranded dna binding protein; **PDBTitle:** single stranded dna binding protein and ssdna complex
43	c2k27A_	Alignment	not modelled	6.4	88	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
44	d2hh8a1	Alignment	not modelled	6.3	29	**Fold:**YdfO-like **Superfamily:**YdfO-like **Family:**YdfO-like
45	c2pjhB_	Alignment	not modelled	6.0	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
46	d1usra_	Alignment	not modelled	6.0	38	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
47	c3nfgG_	Alignment	not modelled	5.8	17	**PDB header:**transcription **Chain:** G: **PDB Molecule:**dna-directed rna polymerase i subunit rpa49; **PDBTitle:** crystal structure of dimerization module of rna polymerase i2 subcomplex a49/a34.5
48	c3agjB_	Alignment	not modelled	5.3	31	**PDB header:**translation/hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
49	c3agjD_	Alignment	not modelled	5.3	31	**PDB header:**translation/hydrolase **Chain:** D: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
50	c1z4xA_	Alignment	not modelled	5.3	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hemagglutinin-neuraminidase; **PDBTitle:** parainfluenza virus 5 (sv5) hemagglutinin-neuraminidase (hn) with2 ligand sialyllactose (soaked with sialyllactose, ph8.0)
51	c3obyB_	Alignment	not modelled	5.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
52	c2yx0A_	Alignment	not modelled	5.1	43	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1