Phyre^2

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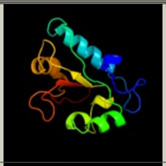
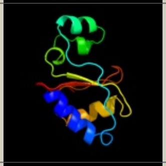
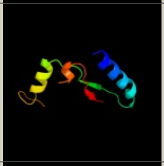
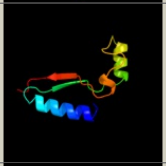
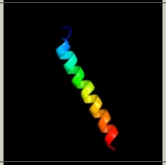
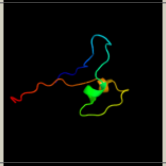
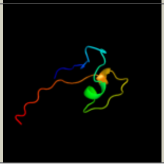
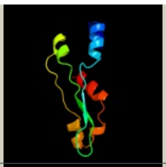
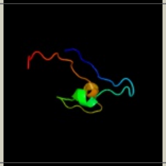
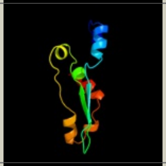
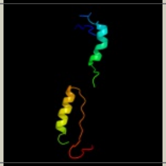
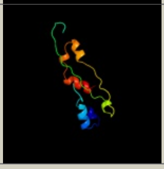
Description	P0AB06
Date	Thu Jan 5 11:14:17 GMT 2012
Unique Job ID	cb9bc0cc529f56ee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lbua2	 Alignment		100.0	26	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**Muramoyl-pentapeptide carboxypeptidase
2	c1lbuA_	 Alignment		99.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**muramoyl-pentapeptide carboxypeptidase; **PDBTitle:** hydrolase metallo (zn) dd-peptidase
3	c2vo9C_	 Alignment		98.2	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**l-alanyl-d-glutamate peptidase; **PDBTitle:** crystal structure of the enzymatically active domain of the2 listeria monocytogenes bacteriophage 500 endolysin ply500
4	d2vo9a1	 Alignment		98.1	25	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**VanY-like
5	d2ibge1	 Alignment		97.2	16	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**Hedgehog (development protein), N-terminal signaling domain
6	c3m1nB_	 Alignment		97.2	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**sonic hedgehog protein; **PDBTitle:** crystal structure of human sonic hedgehog n-terminal domain
7	d3d1ma1	 Alignment		97.1	20	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**Hedgehog (development protein), N-terminal signaling domain
8	d1r44a_	 Alignment		96.0	27	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**VanX-like
9	c2e76D_	 Alignment		59.7	17	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
10	c2f2fC_	 Alignment		53.4	23	**PDB header:**toxin **Chain:** C: **PDB Molecule:**cytolethal distending toxin c; **PDBTitle:** crystal structure of cytolethal distending toxin (cdt) from2 actinobacillus actinomycetemcomitans
11	d2f2fc1	 Alignment		53.4	23	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like

12	d1gtma2	Alignment		43.3	29	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
13	c1p84E_	Alignment		39.2	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
14	d1sr4c_	Alignment		36.1	21	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
15	c3g7kD_	Alignment		30.3	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**3-methylitaconate isomerase; **PDBTitle:** crystal structure of methylitaconate-delta-isomerase
16	d1bvua2	Alignment		29.7	28	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
17	c2h31A_	Alignment		29.1	9	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
18	c3k8zD_	Alignment		28.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
19	d1am7a_	Alignment		26.8	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Lambda lysozyme
20	d1euza2	Alignment		23.8	25	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
21	d1m0wa1	Alignment	not modelled	22.5	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Eukaryotic glutathione synthetase, substrate-binding domain
22	c2fynO_	Alignment	not modelled	21.5	21	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
23	d2hgsa1	Alignment	not modelled	20.6	26	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Eukaryotic glutathione synthetase, substrate-binding domain
24	c2fyuE_	Alignment	not modelled	19.5	7	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
25	c3kalB_	Alignment	not modelled	18.4	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**homoglutathione synthetase; **PDBTitle:** structure of homoglutathione synthetase from glycine max in2 closed conformation with homoglutathione, adp, a sulfate3 ion, and three magnesium ions bound
26	c3a7kD_	Alignment	not modelled	14.3	11	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**halorhodopsin; **PDBTitle:** crystal structure of halorhodopsin from natronomonas2 pharaonis
27	c3aoeC_	Alignment	not modelled	14.3	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
						PDB header:unknown function

28	c2pw0A_	Alignment	not modelled	12.7	9	**Chain:** A: **PDB Molecule:**prpf methylaconitate isomerase; **PDBTitle:** crystal structure of trans-aconitate bound to methylaconitate2 isomerase prpf from shewanella oneidensis
29	c2pq4B_	Alignment	not modelled	12.4	29	**PDB header:**chaperone/oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-352 signal peptide
30	c2c7hA_	Alignment	not modelled	12.4	33	**PDB header:**ubiquitin-like protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6, isoform 3; **PDBTitle:** solution nmr structure of the dwnn domain from human rbbp6
31	c3n6jA_	Alignment	not modelled	11.2	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from actinobacillus succinogenes 130z
32	c3mfnD_	Alignment	not modelled	11.2	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** dfer_2879 protein of unknown function from dyadobacter fermentans
33	d2h9fa1	Alignment	not modelled	10.0	18	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
34	d1b26a2	Alignment	not modelled	10.0	34	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
35	c2hgsA_	Alignment	not modelled	9.9	26	**PDB header:**amine/carboxylate ligase **Chain:** A: **PDB Molecule:**protein (glutathione synthetase); **PDBTitle:** human glutathione synthetase
36	d2hrkb1	Alignment	not modelled	9.9	47	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Arc1p N-terminal domain-like
37	c3bbnP_	Alignment	not modelled	9.7	20	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**ribosomal protein s16; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
38	d1u02a_	Alignment	not modelled	9.5	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
39	d2r25b1	Alignment	not modelled	9.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
40	c1bvuF_	Alignment	not modelled	9.3	29	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** glutamate dehydrogenase from thermococcus litoralis
41	c1nr1A_	Alignment	not modelled	9.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase 1; **PDBTitle:** crystal structure of the r463a mutant of human glutamate2 dehydrogenase
42	d1okga3	Alignment	not modelled	8.6	44	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**3-mercaptopyruvate sulfurtransferase, C-terminal domain
43	d1qw1a1	Alignment	not modelled	8.6	18	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
44	d1v9la2	Alignment	not modelled	8.4	25	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
45	c1xf7A_	Alignment	not modelled	8.4	57	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wilms' tumor protein; **PDBTitle:** high resolution nmr structure of the wilms' tumor2 suppressor protein (wt1) finger 3
46	d1xf7a_	Alignment	not modelled	8.4	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
47	c1m0tB_	Alignment	not modelled	7.7	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutathione synthetase; **PDBTitle:** yeast glutathione synthase
48	c3s2xB_	Alignment	not modelled	7.7	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
49	c3hdvB_	Alignment	not modelled	7.0	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
50	d1bgva2	Alignment	not modelled	7.0	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
51	c2wyoC_	Alignment	not modelled	7.0	19	**PDB header:**ligase **Chain:** C: **PDB Molecule:**glutathione synthetase; **PDBTitle:** trypanosoma brucei glutathione synthetase
52	d1sp2a_	Alignment	not modelled	6.6	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
53	d1dz3a_	Alignment	not modelled	6.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
54	d1qcza_	Alignment	not modelled	6.5	19	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)

						Family:N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
55	c2jx5A_	Alignment	not modelled	6.5	35	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**glub(s27a); **PDBTitle:** solution structure of the ubiquitin domain n-terminal to2 the s27a ribosomal subunit of giardia lamblia
56	c1arfA_	Alignment	not modelled	6.1	43	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**yeast transcription factor adr1; **PDBTitle:** structures of dna-binding mutant zinc finger domains:2 implications for dna binding
57	d2adra1	Alignment	not modelled	5.8	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
58	c3dclC_	Alignment	not modelled	5.8	40	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**tm1086; **PDBTitle:** crystal structure of tm1086
59	d1x6ha2	Alignment	not modelled	5.7	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
60	c1areA_	Alignment	not modelled	5.7	43	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**yeast transcription factor adr1; **PDBTitle:** structures of dna-binding mutant zinc finger domains:2 implications for dna binding
61	d1ynja1	Alignment	not modelled	5.5	7	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain
62	c3rggD_	Alignment	not modelled	5.3	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
63	c3thaB_	Alignment	not modelled	5.3	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
64	c3lk2B_	Alignment	not modelled	5.3	44	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**f-actin-capping protein subunit beta isoforms 1 and 2; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil
65	c2g9mB_	Alignment	not modelled	5.1	11	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**phycoerythrin; **PDBTitle:** crystal structure of the pigment protein phycoerythrin from2 cyanobacterium at 2.6a resolution