Phyre^2

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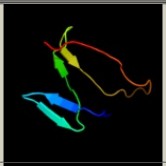
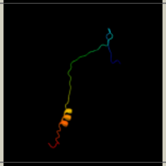
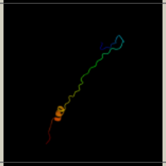
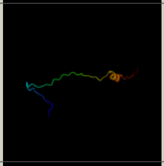
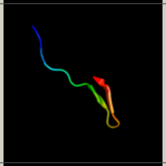
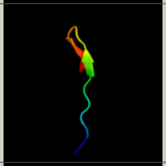
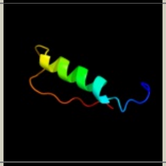
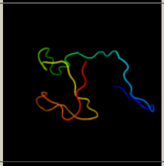
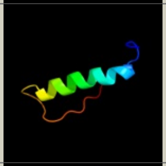
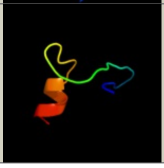
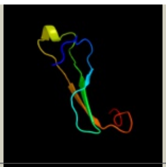
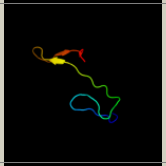
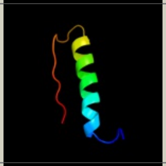
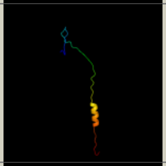
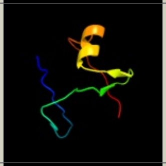
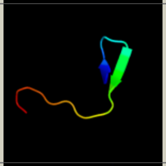
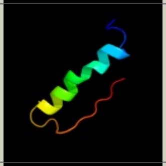
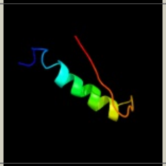
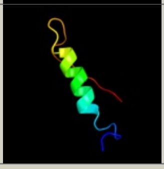
Description	P76498
Date	Thu Jan 5 12:23:34 GMT 2012
Unique Job ID	aec17e4e8f8d947f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1aqta2	Alignment		37.3	21	**Fold:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Superfamily:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Family:**Epsilon subunit of F1F0-ATP synthase N-terminal domain
2	c1s3rA_	Alignment		35.3	27	**PDB header:**toxin **Chain:** A: **PDB Molecule:**intermedilysin; **PDBTitle:** crystal structure of the human-specific toxin intermedilysin
3	c1pfoA_	Alignment		33.1	20	**PDB header:**toxin **Chain:** A: **PDB Molecule:**perfringolysin o; **PDBTitle:** perfringolysin o
4	d1pfoa_	Alignment		33.1	20	**Fold:**Perfringolysin **Superfamily:**Perfringolysin **Family:**Perfringolysin
5	c1fs0E_	Alignment		30.3	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**atp synthase epsilon subunit; **PDBTitle:** complex of gamma/epsilon atp synthase from e.coli
6	c2rq7A_	Alignment		29.8	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase epsilon chain; **PDBTitle:** solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
7	d2p02a3	Alignment		29.2	30	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
8	d1g94a1	Alignment		28.2	20	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
9	d1qm4a3	Alignment		27.6	30	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
10	d3dhpa1	Alignment		27.2	24	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
11	c3b5wE_	Alignment		25.2	19	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba

12	c2xu8B_	Alignment		22.5	27	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**pa1645; **PDBTitle:** structure of pa1645
13	d2e74d1	Alignment		22.5	23	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
14	c3so4C_	Alignment		21.0	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
15	c3hvnA_	Alignment		20.2	20	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of cytotoxin protein suilysin from2 streptococcus suis
16	c2e5yA_	Alignment		19.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase epsilon chain; **PDBTitle:** epsilon subunit and atp complex of f1f0-atp synthase from2 the thermophilic bacillus ps3
17	d1v58a2	Alignment		19.8	44	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
18	c2obvA_	Alignment		19.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine synthetase isoform type-1; **PDBTitle:** crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
19	c1rg9D_	Alignment		19.2	34	**PDB header:**transferase **Chain:** D: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** s-adenosylmethionine synthetase complexed with sam and ppnp
20	c3imlB_	Alignment		18.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
21	c3rv2B_	Alignment	not modelled	17.6	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
22	c2wanA_	Alignment	not modelled	16.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
23	c2l92A_	Alignment	not modelled	13.6	50	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**histone family protein nucleoid-structuring protein h-ns; **PDBTitle:** solution structure of the c-terminal domain of h-ns like protein bv3f
24	c1h8eH_	Alignment	not modelled	13.3	14	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**bovine mitochondrial f1-atpase; **PDBTitle:** (adp.alf4)2(adp.so4) bovine f1-atpase2 (all three catalytic sites occupied)
25	c3ebeA_	Alignment	not modelled	11.8	24	**PDB header:**replication **Chain:** A: **PDB Molecule:**protein mcm10 homolog; **PDBTitle:** crystal structure of xenopus laevis replication initiation factor2 mcm10 internal domain
26	d2j07a1	Alignment	not modelled	11.8	23	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
27	d1ig4a_	Alignment	not modelled	10.6	50	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
28	d1e6vb2	Alignment	not modelled	10.5	18	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain

29	c2qe7H_	Alignment	not modelled	10.3	27	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**atp synthase subunit epsilon; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
30	d1ik0a_	Alignment	not modelled	9.9	35	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
31	d1hbnb2	Alignment	not modelled	9.4	45	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
32	d1mxaa3	Alignment	not modelled	9.2	30	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
33	d1jaea1	Alignment	not modelled	9.1	26	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
34	c1dvaY_	Alignment	not modelled	8.9	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** Y: **PDB Molecule:**peptide e-76; **PDBTitle:** crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
35	c1dvaX_	Alignment	not modelled	8.9	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** X: **PDB Molecule:**peptide e-76; **PDBTitle:** crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
36	d1r44a_	Alignment	not modelled	8.8	20	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**VanX-like
37	d2j2ja1	Alignment	not modelled	8.6	33	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Adenovirus fiber protein "knob" domain
38	c2e76D_	Alignment	not modelled	8.6	25	**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
39	c3ideD_	Alignment	not modelled	8.5	21	**PDB header:**virus like particle **Chain:** D: **PDB Molecule:**capsid protein vp2; **PDBTitle:** structure of ipnv subviral particle
40	c2df7H_	Alignment	not modelled	8.5	43	**PDB header:**virus like particle **Chain:** H: **PDB Molecule:**structural polyprotein vp2; **PDBTitle:** crystal structure of infectious bursal disease virus vp2 subviral2 particle
41	c2wstE_	Alignment	not modelled	8.4	50	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**putative fiber protein; **PDBTitle:** head domain of porcine adenovirus type 4 nadc-1 isolate2 fibre
42	d2df7a1	Alignment	not modelled	8.3	43	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Birnaviridae-like VP
43	c2rkcA_	Alignment	not modelled	8.2	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the measles virus hemagglutinin
44	c3m05A_	Alignment	not modelled	8.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480; **PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
45	c2ky8A_	Alignment	not modelled	7.7	60	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 2; **PDBTitle:** solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
46	d1v1ha1	Alignment	not modelled	7.6	25	**Fold:**Triple beta-spiral **Superfamily:**Fibre shaft of virus attachment proteins **Family:**Adenovirus
47	c2yxhB_	Alignment	not modelled	7.4	75	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mazg-related protein; **PDBTitle:** crystal structure of mazg-related protein from thermotoga maritima
48	d1ua7a1	Alignment	not modelled	7.4	17	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
49	d1wi9a_	Alignment	not modelled	7.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
50	c3oqcB_	Alignment	not modelled	7.3	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ufm1-specific protease 2; **PDBTitle:** ubiquitin-fold modifier 1 specific protease, ufsp2
51	c1z8rA_	Alignment	not modelled	7.3	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coxsackievirus b4 polyprotein; **PDBTitle:** 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschoten / new york / 51)
52	c2z84A_	Alignment	not modelled	7.2	67	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ufm1-specific protease 1; **PDBTitle:** insights from crystal and solution structures of mouse ufsp1
53	c3crcB_	Alignment	not modelled	7.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein mazg; **PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
54	d2j4wd1	Alignment	not modelled	6.7	80	**Fold:**Apical membrane antigen 1 **Superfamily:**Apical membrane antigen 1 **Family:**Apical membrane antigen 1
55	c2j4wD	Alignment	not modelled	6.7	80	**PDB header:**immune system **Chain:** D: **PDB Molecule:**apical membrane antigen 1;

55	c2j4wD_	Alignment	not modelled	6.7	80	**PDBTitle:** structure of a plasmodium vivax apical membrane antigen 1-2 fab f8.12.19 complex
56	d2ysca1	Alignment	not modelled	6.0	71	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
57	c2i5pO_	Alignment	not modelled	5.9	21	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
58	c2l1qA_	Alignment	not modelled	5.9	42	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**liver-expressed antimicrobial peptide 2; **PDBTitle:** solution structure of human liver expressed antimicrobial peptide 2
59	c3obhA_	Alignment	not modelled	5.9	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
60	c2pbdV_	Alignment	not modelled	5.9	75	**PDB header:**structural protein **Chain:** V: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** ternary complex of profilin-actin with the poly-pro-gab2 domain of vasp*
61	c2yyyB_	Alignment	not modelled	5.9	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
62	c2j5lA_	Alignment	not modelled	5.7	100	**PDB header:**immune system **Chain:** A: **PDB Molecule:**apical membrane antigen 1; **PDBTitle:** structure of a plasmodium falciparum apical membrane2 antigen 1-fab f8.12.19 complex
63	d2j5la1	Alignment	not modelled	5.7	100	**Fold:**Apical membrane antigen 1 **Superfamily:**Apical membrane antigen 1 **Family:**Apical membrane antigen 1
64	d1obfo2	Alignment	not modelled	5.7	21	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
65	d1rm4a2	Alignment	not modelled	5.2	27	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like