Phyre^2

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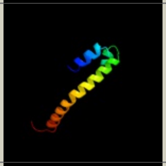
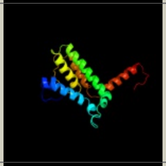
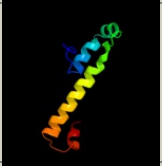
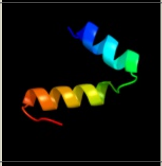
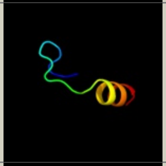
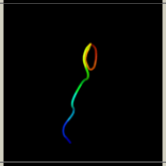
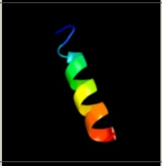
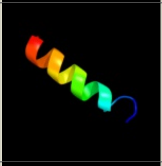
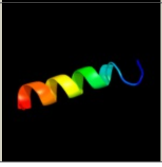
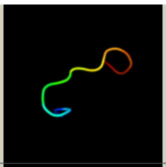
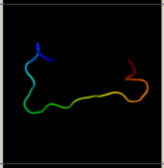
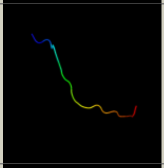
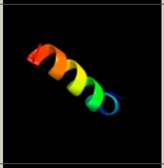
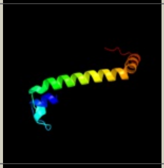
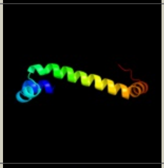
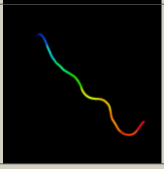
Description	P76552
Date	Wed Jan 25 15:21:09 GMT 2012
Unique Job ID	4d33e6cdac4bab53

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hlya1	Alignment		35.4	33	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Atu2299-like
2	c3qnqD_	Alignment		35.0	14	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
3	c3pjzA_	Alignment		34.3	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**potassium uptake protein trkh; **PDBTitle:** crystal structure of the potassium transporter trkh from vibrio2 parahaemolyticus
4	d1j4na_	Alignment		21.8	22	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
5	c3ajvA_	Alignment		17.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** splicing endonuclease from aeropyrum pernix
6	c2ntxB_	Alignment		16.3	29	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**emb cab41934.1;
7	c3ai9X_	Alignment		16.0	42	**PDB header:**transferase **Chain:** X: **PDB Molecule:**upf0217 protein mj1640; **PDBTitle:** crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
8	c2ka2A_	Alignment		15.2	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
9	c2ka2B_	Alignment		15.2	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
10	c2ka1B_	Alignment		15.2	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
11	c2ka1A_	Alignment		15.2	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles

12	d2qwva1	Alignment		15.0	25	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
13	d2qmma1	Alignment		13.6	27	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
14	d1acca_	Alignment		13.1	16	**Fold:**Anthrax protective antigen **Superfamily:**Anthrax protective antigen **Family:**Anthrax protective antigen
15	d1ig8a1	Alignment		11.7	60	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
16	c2j5dA_	Alignment		11.2	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
17	d1fx8a_	Alignment		11.1	20	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
18	c1ldaA_	Alignment		11.1	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycerol uptake facilitator protein; **PDBTitle:** crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
19	c3zy6A_	Alignment		11.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative gdp-fucose protein o-fucosyltransferase 1; **PDBTitle:** crystal structure of pofut1 in complex with gdp-fucose2 (crystal-form-ii)
20	d1czan1	Alignment		10.8	50	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
21	c2b2hA_	Alignment	not modelled	10.2	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
22	c3op9A_	Alignment	not modelled	10.0	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
23	d1czan3	Alignment	not modelled	9.9	60	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
24	d1bdga1	Alignment	not modelled	9.3	60	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
25	d1bg3a3	Alignment	not modelled	9.2	60	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
26	d1bg3a1	Alignment	not modelled	9.1	50	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
27	c2k3uA_	Alignment	not modelled	8.8	37	**PDB header:**immune system **Chain:** A: **PDB Molecule:**chemotaxis inhibitory protein; **PDBTitle:** structure of the tyrosine-sulfated c5a receptor n-terminus2 in complex with the immune evasion protein chips.
28	c3llqB_	Alignment	not modelled	8.8	19	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin z 2; **PDBTitle:** aquaporin structure from plant pathogen agrobacterium tumerfaciens
						Fold: Ribonuclease H-like motif

29	d1v4sa1	Alignment	not modelled	8.4	50	**Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
30	c2lmfA_	Alignment	not modelled	7.2	43	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antibacterial protein ll-37; **PDBTitle:** solution structure of human ll-23 bound to membrane-mimetic micelles
31	c3hm8D_	Alignment	not modelled	7.0	60	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hexokinase-3; **PDBTitle:** crystal structure of the c-terminal hexokinase domain of human hk3
32	c2w2eA_	Alignment	not modelled	6.9	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin; **PDBTitle:** 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
33	d1rc2a_	Alignment	not modelled	6.9	13	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
34	c3p04B_	Alignment	not modelled	6.6	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
35	c2magA_	Alignment	not modelled	6.4	35	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**magainin 2; **PDBTitle:** nmr structure of magainin 2 in dpc micelles, 10 structures
36	c3c9jD_	Alignment	not modelled	6.2	21	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
37	c3c9jA_	Alignment	not modelled	6.2	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
38	c3c9jB_	Alignment	not modelled	6.2	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
39	c3c9jC_	Alignment	not modelled	6.2	21	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**proton channel protein m2, transmembrane segment; **PDBTitle:** the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
40	c3ct5A_	Alignment	not modelled	6.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
41	d1u9ya2	Alignment	not modelled	6.0	38	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
42	d1u7ga_	Alignment	not modelled	5.9	16	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter
43	d1wi9a_	Alignment	not modelled	5.7	63	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
44	c1ymgA_	Alignment	not modelled	5.7	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
45	d1ymga1	Alignment	not modelled	5.7	26	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
46	d1l8wd_	Alignment	not modelled	5.6	35	**Fold:**Variable surface antigen VlsE **Superfamily:**Variable surface antigen VlsE **Family:**Variable surface antigen VlsE
47	c3c1iA_	Alignment	not modelled	5.5	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonia channel; **PDBTitle:** substrate binding, deprotonation and selectivity at the2 periplasmic entrance of the e. coli ammonia channel amtb
48	c1iyjC_	Alignment	not modelled	5.5	55	**PDB header:**gene regulation/antitumor protein **Chain:** C: **PDB Molecule:**deleted in split hand/split foot protein 1; **PDBTitle:** structure of a brca2-dss1 complex
49	c1bdgA_	Alignment	not modelled	5.5	60	**PDB header:**hexokinase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** hexokinase from schistosoma mansoni complexed with glucose
50	c1v4sA_	Alignment	not modelled	5.5	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase isoform 2; **PDBTitle:** crystal structure of human glucokinase
51	c1ig8A_	Alignment	not modelled	5.4	60	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase pii; **PDBTitle:** crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
52	c2oarA_	Alignment	not modelled	5.3	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
53	c3hzqA_	Alignment	not modelled	5.3	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state
						PDB header:dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein

54	c3pvpA_	Alignment	not modelled	5.1	10	dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna