Phyre^2

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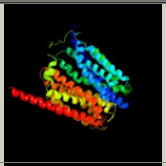
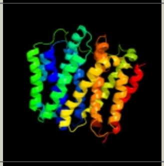
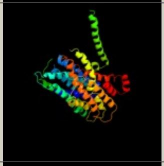
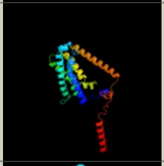
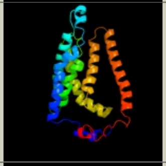
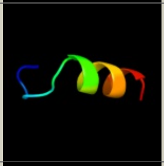
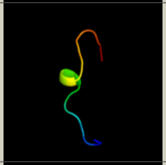
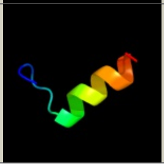
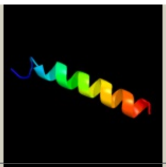
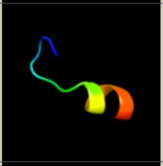
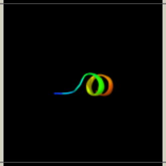
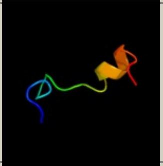
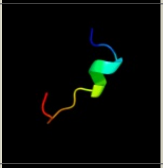
Description	P31679
Date	Thu Jan 5 11:48:36 GMT 2012
Unique Job ID	d6ed72eed497b8c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	Alignment		100.0	14	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
2	d1pv7a_	Alignment		100.0	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
3	c3o7pA_	Alignment		99.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
4	c2gfpA_	Alignment		99.9	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
5	c2xutC_	Alignment		99.9	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	c3b9yA_	Alignment		44.8	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
7	c3hd6A_	Alignment		42.6	10	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
8	c3ff5B_	Alignment		30.1	6	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 14; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
9	c2f9jP_	Alignment		27.0	22	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
10	d1fs1b1	Alignment		26.3	8	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
11	c2w85A_	Alignment		25.4	5	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19

12	d2fx0a2	Alignment		24.8	17	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
13	c3c9pA_	Alignment		21.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
14	c2wwaA_	Alignment		17.2	17	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**sec sixty-one protein homolog; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
15	d1fs2b1	Alignment		16.8	8	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
16	c3mmyF_	Alignment		15.4	14	**PDB header:**nuclear protein **Chain:** F: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
17	d1miua4	Alignment		15.0	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
18	d1ofcx1	Alignment		12.9	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
19	c2g9pA_	Alignment		12.8	43	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
20	d1nexa1	Alignment		12.6	25	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
21	d1xeqa1	Alignment	not modelled	12.5	24	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**N-terminal, RNA-binding domain of nonstructural protein NS1
22	c1by0A_	Alignment	not modelled	11.4	6	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
23	c3r66A_	Alignment	not modelled	11.4	24	**PDB header:**viral protein/antiviral protein **Chain:** A: **PDB Molecule:**non-structural protein 1; **PDBTitle:** crystal structure of human isg15 in complex with ns1 n-terminal region2 from influenza virus b, northeast structural genomics consortium3 target ids hx6481, hr2873, and or2
24	d2ovra1	Alignment	not modelled	11.2	8	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
25	d2csba1	Alignment	not modelled	11.2	15	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
26	d2j85a1	Alignment	not modelled	10.7	15	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
27	d1xjsa_	Alignment	not modelled	9.7	9	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
28	d1xpja_	Alignment	not modelled	9.2	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
						Fold: Heme-binding four-helical bundle

29	d2bs2c1	Alignment	not modelled	9.0	19	**Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Fumarate reductase respiratory complex cytochrome b subunit, FrdC
30	c3dinF_	Alignment	not modelled	8.6	15	**PDB header:**membrane protein, protein transport **Chain:** F: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
31	d1iyjb4	Alignment	not modelled	8.5	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
32	c3qnqD_	Alignment	not modelled	8.4	8	**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
33	d2a26a1	Alignment	not modelled	8.3	16	**Fold:**Long alpha-hairpin **Superfamily:**Calcyclin-binding protein-like **Family:**Siah interacting protein N terminal domain-like
34	c2vpzG_	Alignment	not modelled	8.0	16	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**hypothetical membrane spanning protein; **PDBTitle:** polysulfide reductase native structure
35	d1y7oa1	Alignment	not modelled	8.0	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
36	d1ee8a1	Alignment	not modelled	7.8	14	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
37	c2a7wF_	Alignment	not modelled	7.8	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**phosphoribosyl-atp pyrophosphatase; **PDBTitle:** crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
38	d2a7wa1	Alignment	not modelled	7.8	14	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
39	d1agxa_	Alignment	not modelled	7.4	20	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
40	c1egpA_	Alignment	not modelled	7.3	27	**PDB header:**proteinase inhibitor **Chain:** A: **PDB Molecule:**eglin-c; **PDBTitle:** proteinase inhibitor eglin c with hydrolysed reactive center
41	c3ig4E_	Alignment	not modelled	7.3	0	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** structure of a putative aminopeptidase p from bacillus anthracis
42	c3nxkE_	Alignment	not modelled	7.1	0	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
43	d1gu7a2	Alignment	not modelled	7.1	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
44	d1pyya2	Alignment	not modelled	7.0	11	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
45	c2ht2B_	Alignment	not modelled	7.0	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
46	c2zqpY_	Alignment	not modelled	7.0	9	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** crystal structure of secye translocon from thermus2 thermophilus
47	d1su0b_	Alignment	not modelled	7.0	12	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
48	c3m0zD_	Alignment	not modelled	6.9	5	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of putative aldolase from klebsiella2 pneumoniae.
49	d1rp5a2	Alignment	not modelled	6.9	11	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
50	c3pvpA_	Alignment	not modelled	6.8	22	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
51	d1ysma1	Alignment	not modelled	6.7	16	**Fold:**Long alpha-hairpin **Superfamily:**Calcyclin-binding protein-like **Family:**Siah interacting protein N terminal domain-like
52	c1ysmA_	Alignment	not modelled	6.7	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** nmr structure of n-terminal domain (residues 1-77) of siah-2 interacting protein.
53	c2kdcC_	Alignment	not modelled	6.5	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
						Fold:H-NS histone-like proteins

54	d1ov9a_	Alignment	not modelled	6.4	13	**Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
55	d1k25a2	Alignment	not modelled	6.3	11	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
56	c3cvfA_	Alignment	not modelled	6.2	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
57	c1y7oE_	Alignment	not modelled	6.1	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** the structure of streptococcus pneumoniae a153p clpp
58	d1tdza1	Alignment	not modelled	6.1	14	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
59	d1wfza_	Alignment	not modelled	6.1	8	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
60	c2yxhB_	Alignment	not modelled	6.1	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mazg-related protein; **PDBTitle:** crystal structure of mazg-related protein from thermotoga maritima
61	d1ymga1	Alignment	not modelled	6.1	13	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
62	c1ymgA_	Alignment	not modelled	6.1	13	**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
63	d1nh2d1	Alignment	not modelled	5.9	23	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
64	c3bzjA_	Alignment	not modelled	5.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
65	c2p1nD_	Alignment	not modelled	5.8	8	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
66	d1ni8a_	Alignment	not modelled	5.8	21	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
67	c2wltA_	Alignment	not modelled	5.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution
68	c2zkrv_	Alignment	not modelled	5.7	11	**PDB header:**ribosomal protein/rna **Chain:** V: **PDB Molecule:**rna expansion segment es9 part2; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
69	c3q7hM_	Alignment	not modelled	5.7	17	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** structure of the clpp subunit of the atp-dependent clp protease from2 coxiella burnetii
70	d1nvpd1	Alignment	not modelled	5.7	23	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
71	c3hd7A_	Alignment	not modelled	5.6	16	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
72	c3cveC_	Alignment	not modelled	5.4	32	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**homer protein homolog 1; **PDBTitle:** crystal structure of the carboxy terminus of homer1
73	c1yewC_	Alignment	not modelled	5.4	14	**PDB header:**oxidoreductase, membrane protein **Chain:** C: **PDB Molecule:**particulate methane monooxygenase subunit c2; **PDBTitle:** crystal structure of particulate methane monooxygenase
74	c3hm5A_	Alignment	not modelled	5.3	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna methyltransferase 1-associated protein 1; **PDBTitle:** sant domain of human dna methyltransferase 1 associated2 protein 1
75	c3rkoK_	Alignment	not modelled	5.3	14	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
76	d1v54i_	Alignment	not modelled	5.2	15	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIc **Family:**Mitochondrial cytochrome c oxidase subunit VIc
77	d1vqov1	Alignment	not modelled	5.2	21	**Fold:**Long alpha-hairpin **Superfamily:**Ribosomal protein L29 (L29p) **Family:**Ribosomal protein L29 (L29p)
78	d4pgaa_	Alignment	not modelled	5.2	7	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
79	d1j1va_	Alignment	not modelled	5.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
						Fold:HAD-like

80	d1o08a_	Alignment	not modelled	5.2	19	**Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
81	c3u4gA_	Alignment	not modelled	5.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**namn:dmb phosphoribosyltransferase; **PDBTitle:** the structure of cobt from pyrococcus horikoshii
82	d1nnsa_	Alignment	not modelled	5.1	13	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
83	c3bboZ_	Alignment	not modelled	5.1	14	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**ribosomal protein l29; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
84	d2p8ta1	Alignment	not modelled	5.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PH0730 N-terminal domain-like