Phyre²

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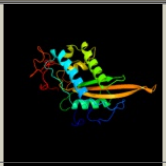
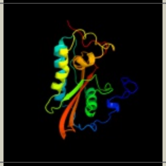
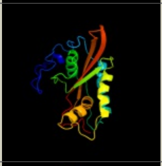
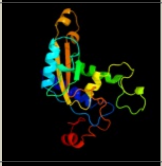
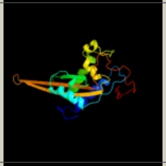
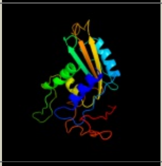
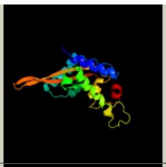
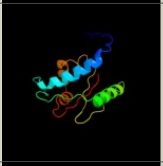
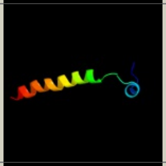
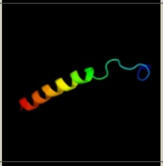
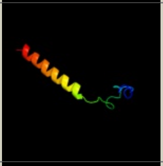
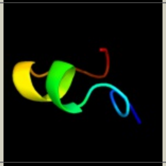
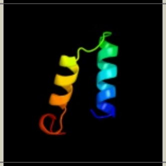
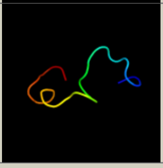
Description	A2A5I3
Date	Tue Jul 30 13:02:03 BST 2013
Unique Job ID	fa958de14c9bd80b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3u3uC_	Alignment		100.0	16	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**tablysin 15; **PDBTitle:** crystal structure of the tablysin-15-leukotriene e4 complex
2	c3nt8A_	Alignment		100.0	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ancylostoma secreted protein 1; **PDBTitle:** crystal structure of na-asp-1
3	c2vznA_	Alignment		100.0	28	**PDB header:**allergen **Chain:** A: **PDB Molecule:**venom allergen 3; **PDBTitle:** crystal structure of the major allergen from fire ant2 venom, sol i 3
4	d1qnxa_	Alignment		100.0	29	**Fold:**PR-1-like **Superfamily:**PR-1-like **Family:**PR-1-like
5	c1xx5B_	Alignment		100.0	33	**PDB header:**toxin **Chain:** B: **PDB Molecule:**natrin 1; **PDBTitle:** crystal structure of natrin from naja atra snake venom
6	c1u53A_	Alignment		100.0	28	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**secreted protein asp-2; **PDBTitle:** novel x-ray structure of na-asp-2, a pr-1 protein from the2 nematode parasite necator americanus and a vaccine antigen3 for human hookworm infection
7	c4g2uA_	Alignment		100.0	22	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ancylostoma-secreted protein-like protein; **PDBTitle:** crystal structure analysis of ostertagia ostertagi asp-1
8	c2epfD_	Alignment		100.0	34	**PDB header:**toxin **Chain:** D: **PDB Molecule:**pseudecin; **PDBTitle:** crystal structure of zinc-bound pseudecin from pseudechis porphyriacus
9	c3s6sB_	Alignment		100.0	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ac-asp-7; **PDBTitle:** ancylostoma-secreted protein ac-asp-7
10	d1rc9a1	Alignment		100.0	31	**Fold:**PR-1-like **Superfamily:**PR-1-like **Family:**PR-1-like
11	d1cfea_	Alignment		100.0	36	**Fold:**PR-1-like **Superfamily:**PR-1-like **Family:**PR-1-like

12	d1smba_	Alignment		100.0	21	**Fold:**PR-1-like **Superfamily:**PR-1-like **Family:**PR-1-like
13	c4h0aB_	Alignment		98.8	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein (sav1118) from2 staphylococcus aureus subsp. aureus mu50 at 1.90 a resolution
14	c4ifaA_	Alignment		98.6	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**extracellular protein containing a scp domain; **PDBTitle:** 1.5 angstrom resolution crystal structure of an extracellular protein2 containing a scp domain from bacillus anthracis str. ames
15	c3ghgD_	Alignment		55.0	8	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
16	c2a45J_	Alignment		55.0	9	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** J: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
17	c1m1jA_	Alignment		49.7	11	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
18	d1rc9a2	Alignment		37.3	40	**Fold:**Crisp domain-like **Superfamily:**Crisp domain-like **Family:**Crisp domain
19	d1t3ta1	Alignment		36.1	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**FGAM synthase PurL, linker domain **Family:**FGAM synthase PurL, linker domain
20	d1ha8a_	Alignment		31.2	30	**Fold:**Pheromone ER-23 **Superfamily:**Pheromone ER-23 **Family:**Pheromone ER-23
21	c1decA_	Alignment	not modelled	17.9	28	**PDB header:**blood coagulation **Chain:** A: **PDB Molecule:**decorsin; **PDBTitle:** structure of the rgd protein decorsin: conserved motif and2 distinct function in leech proteins that affect blood3 clotting
22	d1deca_	Alignment	not modelled	17.9	28	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
23	d1l6pa_	Alignment	not modelled	17.3	45	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha) **Family:**Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha)
24	d1uzka3	Alignment	not modelled	16.2	38	**Fold:**TB module/8-cys domain **Superfamily:**TB module/8-cys domain **Family:**TB module/8-cys domain
25	c2k0rA_	Alignment	not modelled	16.1	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbd; **PDBTitle:** solution structure of the c103s mutant of the n-terminal2 domain of dsbd from neisseria meningitidis
26	d1tdza3	Alignment	not modelled	15.9	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
27	c2a05A_	Alignment	not modelled	15.4	46	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cysteine-rich secretory protein-2; **PDBTitle:** the cysteine-rich secretory protein domain of tpx-1 is2 related to ion channel toxins and regulates ryanodine3 receptor ca2+ signaling
28	c2knnA_	Alignment	not modelled	14.9	35	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cycloviolacin-o2; **PDBTitle:** solution structure of the cyclotide cycloviolacin o2 with2

						glu6 methylated (cyo2me)
29	c3rv2B_	Alignment	not modelled	14.6	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
30	d1sg1x1	Alignment	not modelled	9.8	33	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
31	c3vgxD_	Alignment	not modelled	9.3	29	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** structure of gp41 t21/cp621-652
32	d1vk3a1	Alignment	not modelled	9.1	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
33	c3imlB_	Alignment	not modelled	8.9	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
34	c1jpeA_	Alignment	not modelled	8.7	45	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dsbd-alpha; **PDBTitle:** crystal structure of dsbd-alpha; the n-terminal domain of2 dsbd
35	c3so4C_	Alignment	not modelled	8.6	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
36	d1hpia_	Alignment	not modelled	8.2	22	**Fold:**HIPIP (high potential iron protein) **Superfamily:**HIPIP (high potential iron protein) **Family:**HIPIP (high potential iron protein)
37	d1l1ta3	Alignment	not modelled	6.7	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
38	c2hs0A_	Alignment	not modelled	6.2	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** t. maritima purl complexed with atp
39	d1i25a_	Alignment	not modelled	5.8	28	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
40	c1i25A_	Alignment	not modelled	5.8	28	**PDB header:**toxin **Chain:** A: **PDB Molecule:**huwentoxin-ii; **PDBTitle:** three dimensional solution structure of huwentoxin-ii by 2d2 1h-nmr
41	c1t3tA_	Alignment	not modelled	5.5	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
42	d1sg1x3	Alignment	not modelled	5.3	33	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
43	d1k3xa3	Alignment	not modelled	5.3	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
44	d1apja_	Alignment	not modelled	5.3	27	**Fold:**TB module/8-cys domain **Superfamily:**TB module/8-cys domain **Family:**TB module/8-cys domain
45	c1iqrA_	Alignment	not modelled	5.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**photolyase; **PDBTitle:** crystal structure of dna photolyase from thermus2 thermophilus