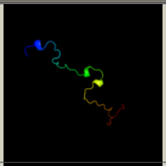
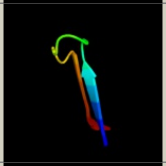
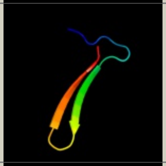
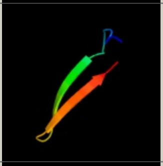
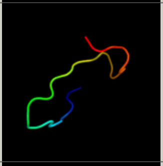
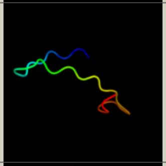
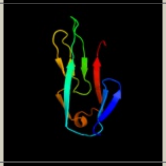
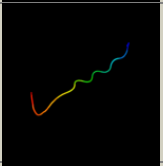
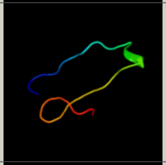
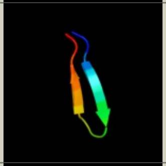
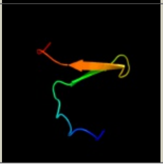
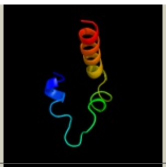
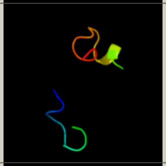
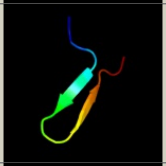
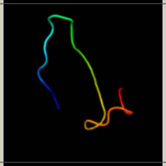
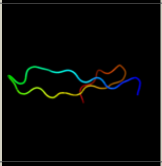
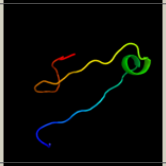
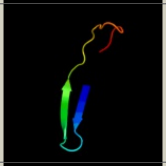
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P28911
Date	Thu Jan 5 11:45:22 GMT 2012
Unique Job ID	eb85fd122e621475

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kk7B_	Alignment		51.3	23	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**putative cell invasion protein with mac/perforin domain; **PDBTitle:** crystal structure of putative cell invasion protein with mac/perforin2 domain (np_812351.1) from bacteriodes thetaiotaomicron vpi-5482 at3 2.46 a resolution
2	c1f0cB_	Alignment		25.0	44	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**ice inhibitor; **PDBTitle:** structure of the viral serpin crma
3	c2epgB_	Alignment		24.3	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha1785; **PDBTitle:** crystal structure of ttha1785
4	d1uc2a_	Alignment		21.9	24	**Fold:**Hypothetical protein PH1602 **Superfamily:**Hypothetical protein PH1602 **Family:**Hypothetical protein PH1602
5	c2obkE_	Alignment		18.7	32	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**selt/selw/selh selenoprotein domain; **PDBTitle:** x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
6	d2fa8a1	Alignment		18.2	37	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
7	c2r32A_	Alignment		15.0	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
8	d1ibxa_	Alignment		12.4	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
9	c3dexA_	Alignment		11.6	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sav_2001; **PDBTitle:** crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
10	d3c0na1	Alignment		11.3	33	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Aerolysin/Pertussis toxin (APT) domain
11	c1eptA_	Alignment		11.3	23	**PDB header:**hydrolase (serine protease) **Chain:** A: **PDB Molecule:**porcine e-trypsin; **PDBTitle:** refined 1.8 angstroms resolution crystal structure of2 porcine epsilon-trypsin

12	d1tm9a_	Alignment		10.8	28	**Fold:**Hypothetical protein MG354 **Superfamily:**Hypothetical protein MG354 **Family:**Hypothetical protein MG354
13	c2gvsA_	Alignment		10.8	52	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**chemosensory protein csp-sg4; **PDBTitle:** nmr solution structure of cspsg4
14	d2oaia1	Alignment		10.1	28	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
15	c2ojlB_	Alignment		9.6	37	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
16	c2p0gB_	Alignment		9.4	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**selenoprotein w-related protein; **PDBTitle:** crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75
17	c2npbA_	Alignment		8.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw
18	c3lznA_	Alignment		8.3	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**p19 protein; **PDBTitle:** crystal structure analysis of the apo p19 protein from campylobacter2 jejuni at 1.59 a at ph 9
19	c2v31A_	Alignment		7.6	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-activating enzyme e1 x; **PDBTitle:** structure of first catalytic cysteine half-domain of mouse2 ubiquitin-activating enzyme
20	c3bq9A_	Alignment		7.5	60	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
21	c2latA_	Alignment	not modelled	6.6	46	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** solution structure of a human minimembrane protein ost4
22	d2p13a1	Alignment	not modelled	6.4	22	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
23	c2hgoA_	Alignment	not modelled	5.2	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cassiicolin; **PDBTitle:** nmr structure of cassiicolin
24	c2o62A_	Alignment	not modelled	5.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein with unknown function from duf35982 family (npun_r4044) from nostoc punctiforme pcc 73102 at 1.75 a3 resolution
25	c3iufA_	Alignment	not modelled	5.0	43	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**zinc finger protein ubi-d4; **PDBTitle:** crystal structure of the c2h2-type zinc finger domain of2 human ubi-d4