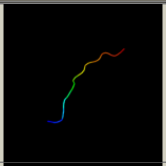
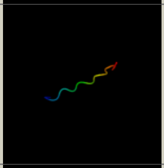
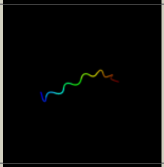
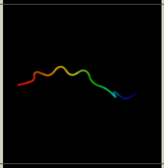
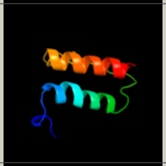
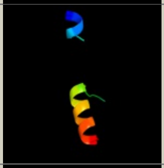
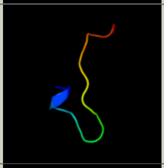
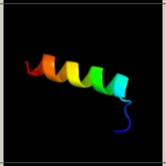
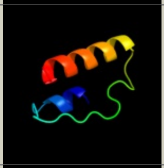
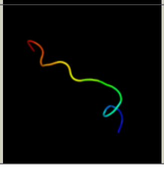
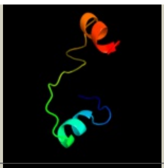
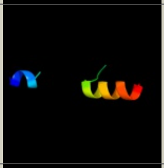
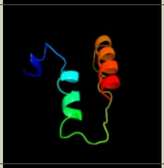
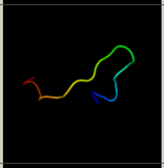
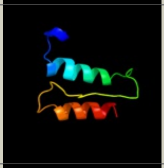
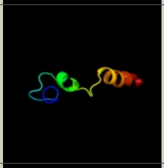
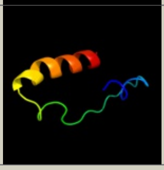
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q9JMS6
Date	Thu Jan 5 12:38:02 GMT 2012
Unique Job ID	facdcc9597abd74e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nm7C_	Alignment		12.5	31	**PDB header:**nucleic acid binding protein **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
2	c3nm7D_	Alignment		12.0	31	**PDB header:**nucleic acid binding protein **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
3	c3n8bA_	Alignment		12.0	31	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
4	c3n8bB_	Alignment		11.8	31	**PDB header:**nucleic acid binding protein **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
5	c2pcjB_	Alignment		11.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipoprotein-releasing system atp-binding protein lold; **PDBTitle:** crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
6	c1bjtA_	Alignment		11.2	35	**PDB header:**topoisomerase **Chain:** A: **PDB Molecule:**topoisomerase ii; **PDBTitle:** topoisomerase ii residues 409-1201
7	d1bjta_	Alignment		11.2	35	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
8	d1l4db_	Alignment		11.1	38	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
9	d1uw0a_	Alignment		11.0	35	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**PARP-type zinc finger
10	d1l2ta_	Alignment		10.1	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
11	d1bmlc1	Alignment		10.0	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase

12	c3gkxB_	Alignment		10.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
13	c3qx3B_	Alignment		10.0	30	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide
14	d1v43a3	Alignment		9.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
15	d1l4zb_	Alignment		9.5	38	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
16	d2foka4	Alignment		8.7	19	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease FokI, C-terminal (catalytic) domain
17	d1sgwa_	Alignment		8.6	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
18	c3nymA_	Alignment		8.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of functionally unknown protein from neisseria2 meningitidis mc58
19	c2wshC_	Alignment		8.0	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
20	d3d31a2	Alignment		7.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
21	c2cs2A_	Alignment	not modelled	6.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of the second zn-finger domain of2 poly(adp-ribose) polymerase-1
22	c1s2xA_	Alignment	not modelled	6.5	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cag-z; **PDBTitle:** crystal structure of cag-z from helicobacter pylori
23	d1s2xa_	Alignment	not modelled	6.5	35	**Fold:**STAT-like **Superfamily:**Cag-Z **Family:**Cag-Z
24	d1vpla_	Alignment	not modelled	6.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
25	d1o8ba1	Alignment	not modelled	6.3	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
26	d1ueba2	Alignment	not modelled	6.0	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
27	c3rnvA_	Alignment	not modelled	5.6	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
28	d1uura1	Alignment	not modelled	5.5	17	**Fold:**STAT-like **Superfamily:**STAT **Family:**STAT