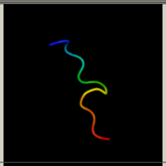
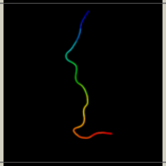
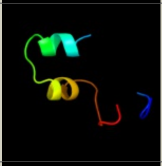
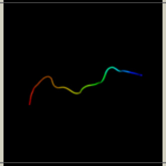
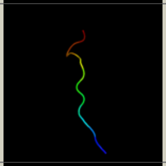
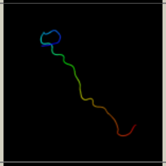
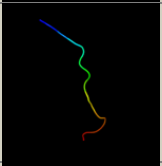
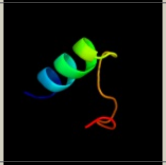
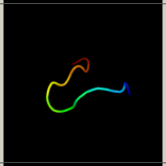
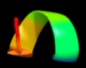
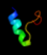
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P62066
Date	Thu Jan 5 12:07:28 GMT 2012
Unique Job ID	de2ed8fa44624280

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k2wA_	Alignment		33.7	50	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**recombination and dna repair protein; **PDBTitle:** second brct domain of nbs1
2	d1twfj_	Alignment		17.2	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
3	c3czbA_	Alignment		16.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transglycosylase; **PDBTitle:** crystal structure of putative transglycosylase from caulobacter2 crescentus
4	c2pmzN_	Alignment		13.0	41	**PDB header:**translation, transferase **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
5	d2pnwa1	Alignment		12.9	40	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
6	d2g5da1	Alignment		11.3	33	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
7	d2pi8a1	Alignment		10.7	26	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
8	d2ae0x1	Alignment		10.3	40	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
9	c3cqyA_	Alignment		8.9	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
10	d1niya_	Alignment		8.6	54	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
11	d1mb6a_	Alignment		8.3	46	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins

12	d1b8ta4	Alignment		7.5	71	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
13	d1b8ta2	Alignment		7.5	71	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
14	d2djfa1	Alignment		7.1	40	**Fold:**Streptavidin-like **Superfamily:**Dipeptidyl peptidase I (cathepsin C), exclusion domain **Family:**Dipeptidyl peptidase I (cathepsin C), exclusion domain
15	d1mwpa_	Alignment		7.0	25	**Fold:**SRCR-like **Superfamily:**A heparin-binding domain **Family:**A heparin-binding domain
16	c1n93X_	Alignment		6.8	50	**PDB header:**viral protein **Chain:** X: **PDB Molecule:**p40 nucleoprotein; **PDBTitle:** crystal structure of the borna disease virus nucleoprotein
17	d1n93x_	Alignment		6.8	50	**Fold:**P40 nucleoprotein **Superfamily:**P40 nucleoprotein **Family:**P40 nucleoprotein
18	d1jxca_	Alignment		6.7	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Plant defensins
19	d1jqpa1	Alignment		6.4	40	**Fold:**Streptavidin-like **Superfamily:**Dipeptidyl peptidase I (cathepsin C), exclusion domain **Family:**Dipeptidyl peptidase I (cathepsin C), exclusion domain
20	c3qbwA_	Alignment		6.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 actetylmuramic acid kinase (anmk) bound to adenosine diphosphate
21	c3eudE_	Alignment	not modelled	5.4	42	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**protein shq1; **PDBTitle:** structure of the cs domain of the essential h/aca rnp2 assembly protein shq1p
22	c2k8qA_	Alignment	not modelled	5.2	42	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein shq1; **PDBTitle:** nmr structure of shq1p n-terminal domain
23	d1x4ka1	Alignment	not modelled	5.2	71	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain