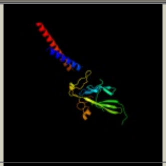
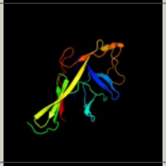
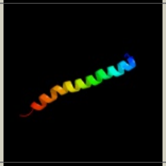
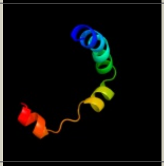
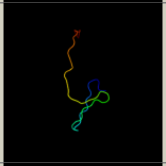
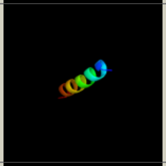
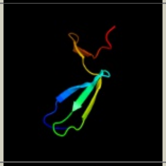
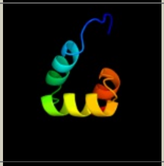
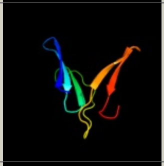
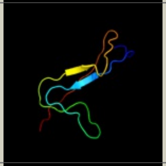
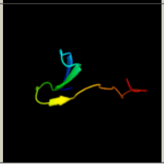
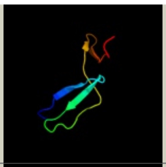
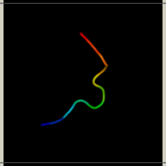
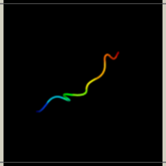
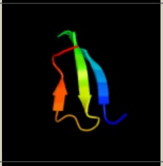
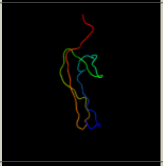
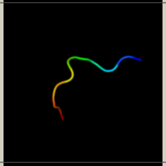
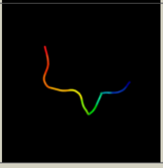
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P75938
Date	Thu Jan 5 12:16:12 GMT 2012
Unique Job ID	81d82c895378527b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a69A_	Alignment		100.0	26	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar hook protein flge; **PDBTitle:** atomic model of the bacterial flagellar hook based on2 docking an x-ray derived structure and terminal two alpha-3 helices into an 7.1 angstrom resolution cryoem map
2	d1wlga_	Alignment		99.9	28	**Fold:**Flagellar hook protein flgE **Superfamily:**Flagellar hook protein flgE **Family:**Flagellar hook protein flgE
3	d1ucua_	Alignment		91.7	13	**Fold:**Phase 1 flagellin **Superfamily:**Phase 1 flagellin **Family:**Phase 1 flagellin
4	c1oryB_	Alignment		65.5	18	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**flagellin; **PDBTitle:** flagellar export chaperone in complex with its cognate binding partner
5	d2czra1	Alignment		34.6	26	**Fold:**Restriction endonuclease-like **Superfamily:**TBP-interacting protein-like **Family:**TBP-interacting protein-like
6	c3k8vB_	Alignment		31.6	0	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin n20c20
7	d1b2pa_	Alignment		25.3	23	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
8	c2d9sA_	Alignment		22.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
9	d1kj1d_	Alignment		20.8	12	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
10	d2axwa1	Alignment		18.3	22	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
11	d1eeja2	Alignment		14.5	22	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like

12	c3mezB_	Alignment		12.9	15	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**mannose-specific lectin 3 chain 2; **PDBTitle:** x-ray structural analysis of a mannose specific lectin from dutch2 crocus (crocus vernus)
13	d1lvoa_	Alignment		12.3	36	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
14	c3afoB_	Alignment		12.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
15	c2q6fB_	Alignment		11.9	45	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**infectious bronchitis virus (ibv) main protease; **PDBTitle:** crystal structure of infectious bronchitis virus (ibv) main2 protease in complex with a michael acceptor inhibitor n3
16	d1t3ba2	Alignment		11.8	15	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
17	c2fvnA_	Alignment		11.0	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein afad; **PDBTitle:** the fibrillar tip complex of the afa/dr adhesins from2 pathogen e. coli displays synergistic binding to 5 1 and v3 3 integrins
18	c2oqkA_	Alignment		10.1	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
19	d2duca1	Alignment		10.1	27	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
20	c3d23A_	Alignment		9.5	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c-like proteinase; **PDBTitle:** main protease of hcov-hku1
21	d1g73a_	Alignment	not modelled	9.1	11	**Fold:**Spectrin repeat-like **Superfamily:**Smac/diablo **Family:**Smac/diablo
22	c2cazF_	Alignment	not modelled	9.0	17	**PDB header:**protein transport **Chain:** F: **PDB Molecule:**protein srn2; **PDBTitle:** escrt-i core
23	c2iyjA_	Alignment	not modelled	8.8	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol disulfide interchange protein dsbc; **PDBTitle:** crystal structure of the n-terminal dimer domain of e.coli2 dsbc
24	c3ec1A_	Alignment	not modelled	8.5	15	**PDB header:**hydrolase, signaling protein **Chain:** A: **PDB Molecule:**yqeh gtpase; **PDBTitle:** structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnos1 / atnoa1 ortholog)
25	d1p9sa_	Alignment	not modelled	8.1	27	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
26	c3h2yA_	Alignment	not modelled	8.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtpase family protein; **PDBTitle:** crystal structure of yqeh gtpase from bacillus anthracis with dgdp2 bound
27	c3lyvF_	Alignment	not modelled	8.0	19	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
28	d1niga_	Alignment	not modelled	8.0	29	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Hypothetical protein Ta1238

29	c1jzdA_	Alignment	not modelled	7.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
30	c2dk7A_	Alignment	not modelled	7.3	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation regulator 1; **PDBTitle:** solution structure of ww domain in transcription elongation2 regulator 1
31	d1vhoa1	Alignment	not modelled	7.1	21	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
32	c2dgyA_	Alignment	not modelled	7.1	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
33	c3r0eD_	Alignment	not modelled	6.9	9	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
34	c2kjzA_	Alignment	not modelled	6.9	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**atc0852; **PDBTitle:** solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2.
35	d1fewa_	Alignment	not modelled	6.9	11	**Fold:**Spectrin repeat-like **Superfamily:**Smac/diablo **Family:**Smac/diablo
36	c3bqxA_	Alignment	not modelled	6.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase-related enzyme; **PDBTitle:** high resolution crystal structure of a glyoxalase-related enzyme from2 fulvimarina pelagi
37	d1pn0a1	Alignment	not modelled	6.6	27	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
38	c2jnhA_	Alignment	not modelled	6.5	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
39	c1yt5A_	Alignment	not modelled	6.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of nad kinase from thermotoga maritima
40	c3ohgA_	Alignment	not modelled	6.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein from duf2233 family; **PDBTitle:** crystal structure of a protein with unknown function from duf22332 family (bacova_00430) from bacteroides ovatus at 1.80 a resolution
41	c2an1D_	Alignment	not modelled	5.9	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
42	d1o6wa2	Alignment	not modelled	5.7	39	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
43	c3jr0B_	Alignment	not modelled	5.7	38	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**gene 9 protein; **PDBTitle:** crystal structure of phage sf6 gp26 c-terminal knob domain
44	d1nrja_	Alignment	not modelled	5.5	67	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**SRP alpha N-terminal domain-like
45	d1jt8a_	Alignment	not modelled	5.5	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	d1m9sa4	Alignment	not modelled	5.5	16	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**GW domain
47	c3bk2A_	Alignment	not modelled	5.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
48	c3kglB_	Alignment	not modelled	5.2	13	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
49	c2dbhA_	Alignment	not modelled	5.1	43	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily **PDBTitle:** solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
50	c2gq1A_	Alignment	not modelled	5.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructose-1,6-bisphosphatase; **PDBTitle:** crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
51	d1d7qa_	Alignment	not modelled	5.1	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like