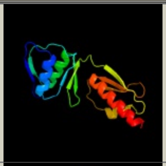
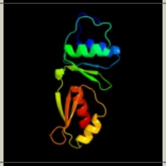
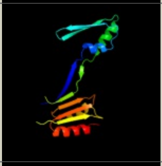
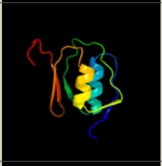
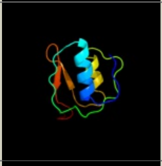
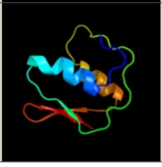
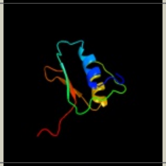
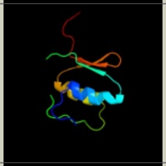
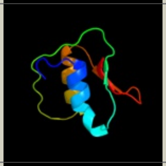
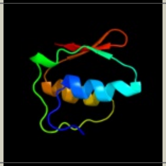
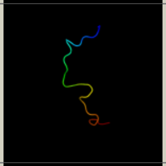
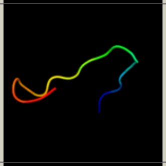
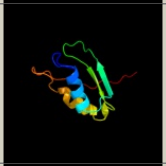
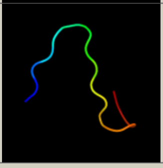
Email	l.a.kelley@imperial.ac.uk
Description	P34749
Date	Thu Jan 5 11:53:09 GMT 2012
Unique Job ID	a510de9620fac5ae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gr5A_	Alignment		99.9	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**escc; **PDBTitle:** periplasmic domain of the outer membrane secretin escc from2 enteropathogenic e.coli (epec)
2	c2y9kG_	Alignment		99.9	17	**PDB header:**protein transport **Chain:** G: **PDB Molecule:**protein invg; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
3	c3ossD_	Alignment		99.8	12	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**type 2 secretion system, secretin gspd; **PDBTitle:** the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
4	c2y3mA_	Alignment		99.8	31	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein hofq; **PDBTitle:** structure of the extra-membranous domain of the secretin2 hofq from actinobacillus actinomycetemcomitans
5	c3ezjA_	Alignment		99.7	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**general secretion pathway protein gspd; **PDBTitle:** crystal structure of the n-terminal domain of the secretin gspd from2 etec determined with the assistance of a nanobody
6	c2a02A_	Alignment		98.9	25	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**ferric-pseudobactin 358 receptor; **PDBTitle:** solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter pupa from3 pseudomonas putida.
7	c2iahA_	Alignment		97.5	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
8	c1zzvA_	Alignment		97.3	16	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca; **PDBTitle:** solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter feca from3 escherichia coli.
9	c2d1uA_	Alignment		97.1	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca; **PDBTitle:** solution strcuture of the periplasmic signaling domain of2 feca from escherichia coli
10	c3adyA_	Alignment		95.1	16	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**dotd; **PDBTitle:** crystal structure of dotd from legionella
11	d3cdda2	Alignment		93.9	12	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like

12	c3cddD_	Alignment		93.5	12	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**prophage muso2, 43 kda tail protein; **PDBTitle:** crystal structure of prophage muso2, 43 kda tail protein from2 shewanella oneidensis
13	c3d37A_	Alignment		85.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tail protein, 43 kda; **PDBTitle:** the crystal structure of the tail protein from neisseria meningitidis2 mc58
14	c1wruA_	Alignment		75.4	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**43 kda tail protein; **PDBTitle:** structure of central hub elucidated by x-ray analysis of gene product2 44; baseplate component of bacteriophage mu
15	d3d37a1	Alignment		75.0	22	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
16	d1wrua2	Alignment		69.9	12	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
17	c1b35D_	Alignment		21.1	20	**PDB header:**virus **Chain:** D: **PDB Molecule:**protein (cricket paralysis virus, vp4); **PDBTitle:** cricket paralysis virus (crpv)
18	c3ec1A_	Alignment		13.8	29	**PDB header:**hydrolase, signaling protein **Chain:** A: **PDB Molecule:**yqeh gtpase; **PDBTitle:** structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnos1 / atnoa1 ortholog)
19	c2e44A_	Alignment		13.6	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**insulin-like growth factor 2 mrna binding **PDBTitle:** solution structure of rna binding domain in insulin-like2 growth factor 2 mrna binding protein 3
20	c3h2yA_	Alignment		13.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtpase family protein; **PDBTitle:** crystal structure of yqeh gtpase from bacillus anthracis with dgdp2 bound
21	d1v95a_	Alignment	not modelled	10.0	14	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
22	d1k25a2	Alignment	not modelled	8.5	14	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
23	c2j8aA_	Alignment	not modelled	8.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-4 **PDBTitle:** x-ray structure of the n-terminus rrm domain of set1
24	d1jqga2	Alignment	not modelled	7.8	6	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
25	d1ueba3	Alignment	not modelled	7.2	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	c3gs9A_	Alignment	not modelled	7.0	5	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein gp18; **PDBTitle:** crystal structure of prophage tail protein gp18 (np_465809.1) from2 listeria monocytogenes egd-e at 1.70 a resolution
27	c3ov5A_	Alignment	not modelled	6.7	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** atomic structure of the xanthomonas citri virb7 globular domain.
28	d1pyya2	Alignment	not modelled	6.0	11	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain

29	d1rp5a2	Alignment	not modelled	5.3	14	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain