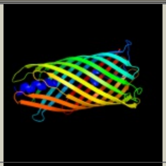
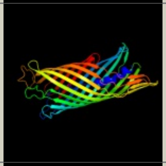
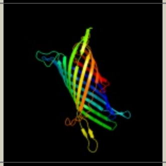
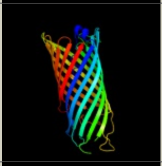
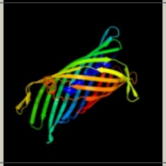
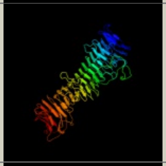
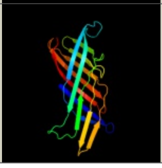
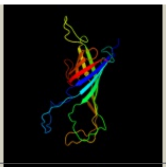
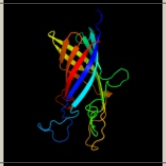
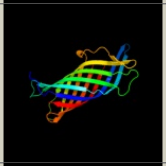
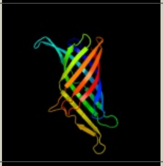
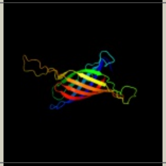
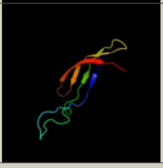
Email	l.a.kelley@imperial.ac.uk
Description	Q9JMS5
Date	Wed Jan 25 15:21:16 GMT 2012
Unique Job ID	8f820e0254565e26

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3aehB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
2	c3sljA_	Alignment		100.0	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
3	c3qq2C_	Alignment		100.0	22	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
4	c2qomB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
5	d1uynx_	Alignment		100.0	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
6	c3kvnA_	Alignment		100.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
7	d1daba_	Alignment		99.9	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Virulence factor P.69 pertactin
8	c3ml3A_	Alignment		99.9	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**outer membrane protein icsa autotransporter; **PDBTitle:** crystal structure of the icsa autochaperone region
9	c3h09B_	Alignment		99.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**immunoglobulin a1 protease; **PDBTitle:** the structure of haemophilus influenzae iga1 protease
10	c3syjA_	Alignment		99.6	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesion and penetration protein autotransporter; **PDBTitle:** crystal structure of the haemophilus influenzae hap adhesin
11	c3qraA_	Alignment		98.3	16	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**attachment invasion locus protein; **PDBTitle:** the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis

12	c2k0lA_	Alignment		98.2	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
13	d1g90a_	Alignment		98.2	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
14	d1p4ta_	Alignment		98.1	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
15	d1qjpa_	Alignment		98.0	16	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
16	c3nb3C_	Alignment		97.9	15	**PDB header:**virus **Chain:** C: **PDB Molecule:**outer membrane protein a; **PDBTitle:** the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
17	c2jmmA_	Alignment		97.7	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein
18	c2x27X_	Alignment		97.4	18	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
19	d1qj8a_	Alignment		96.8	10	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
20	c2lhfA_	Alignment		96.0	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein h1; **PDBTitle:** solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles
21	d2pora_	Alignment	not modelled	95.7	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
22	c2wjqA_	Alignment	not modelled	95.3	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
23	d2zfga1	Alignment	not modelled	94.9	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
24	c3a2rX_	Alignment	not modelled	94.4	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
25	c2iwvD_	Alignment	not modelled	93.6	15	**PDB header:**ion channel **Chain:** D: **PDB Molecule:**outer membrane protein g; **PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
26	d3prna_	Alignment	not modelled	93.1	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
27	d1osma_	Alignment	not modelled	92.1	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
28	d2fgqx1	Alignment	not modelled	90.6	13	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
						PDB header:membrane protein

29	c2f1tB_	Alignment	not modelled	90.6	14	**Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
30	d2vdfa1	Alignment	not modelled	87.9	14	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
31	c3brzA_	Alignment	not modelled	83.8	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
32	d1phoa_	Alignment	not modelled	81.2	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
33	c3nsgA_	Alignment	not modelled	68.5	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
34	d1w0pa2	Alignment	not modelled	38.4	12	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Vibrio cholerae sialidase, N-terminal and insertion domains
35	c3ak5B_	Alignment	not modelled	28.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp; **PDBTitle:** hemoglobin protease (hbp) passenger missing domain-2
36	c3rbhC_	Alignment	not modelled	26.7	21	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**alginate production protein alge; **PDBTitle:** structure of alginate export protein alge from pseudomonas aeruginosa
37	d1t16a_	Alignment	not modelled	26.6	16	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
38	d1pm6a_	Alignment	not modelled	21.6	0	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
39	c2lfeA_	Alignment	not modelled	18.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw2; **PDBTitle:** solution nmr structure of n-terminal domain of human e3 ubiquitin-2 protein ligase hecw2, northeast structural genomics consortium (nesg)3 target ht6306a
40	c1yo8A_	Alignment	not modelled	17.8	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-2; **PDBTitle:** structure of the c-terminal domain of human thrombospondin-2
41	d1txka2	Alignment	not modelled	16.1	12	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
42	d2mpra_	Alignment	not modelled	15.7	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Maltoporin-like
43	c2x4mD_	Alignment	not modelled	15.6	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
44	c1txkA_	Alignment	not modelled	13.4	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
45	d1tywa_	Alignment	not modelled	12.9	11	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**P22 tailspike protein
46	d1vpra1	Alignment	not modelled	12.3	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Dinoflagellate luciferase repeat
47	d2evra2	Alignment	not modelled	11.6	20	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
48	c3fbyC_	Alignment	not modelled	11.2	15	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**cartilage oligomeric matrix protein; **PDBTitle:** the crystal structure of the signature domain of cartilage oligomeric2 matrix protein.
49	d1upsa2	Alignment	not modelled	10.9	11	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**GlcNAc-alpha-1,4-Gal-releasing endo-beta-galactosidase, GngC, C-terminal domain
50	c2r5xA_	Alignment	not modelled	10.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein yugn from2 geobacillus kaustophilus hta426
51	c2xc1A_	Alignment	not modelled	10.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bifunctional tail protein; **PDBTitle:** full-length tailspike protein mutant y108w of bacteriophage2 p22
52	c2fg0B_	Alignment	not modelled	10.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
53	c1q40C_	Alignment	not modelled	10.3	13	**PDB header:**translation **Chain:** C: **PDB Molecule:**mrna transport regulator mtr2; **PDBTitle:** crystal structure of the c. albicans mtr2-mex67 m domain complex
54	d1rh6a_	Alignment	not modelled	9.5	0	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
						Fold:TBP-like

55	d2pwwa1	Alignment	not modelled	9.4	20	**Superfamily:**YugN-like **Family:**YugN-like
56	d3ejva1	Alignment	not modelled	9.4	23	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
57	c2bvbA_	Alignment	not modelled	9.1	19	**PDB header:**adhesion **Chain:** A: **PDB Molecule:**micronemal protein 1; **PDBTitle:** the c-terminal domain from micronemal protein 1 (mic1) from2 toxoplasma gondii
58	c3emoA_	Alignment	not modelled	9.0	16	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
59	c1lj2B_	Alignment	not modelled	8.8	45	**PDB header:**viral protein/ translation **Chain:** B: **PDB Molecule:**nonstructural rna-binding protein 34; **PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
60	c3dwoX_	Alignment	not modelled	8.7	12	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
61	c1po3A_	Alignment	not modelled	8.2	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca **PDBTitle:** crystal structure of ferric citrate transporter feca in2 complex with ferric citrate
62	c2k4tA_	Alignment	not modelled	7.8	13	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
63	c2gr7C_	Alignment	not modelled	7.4	16	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
64	d2gr7a1	Alignment	not modelled	7.4	16	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
65	c2npiD_	Alignment	not modelled	7.1	57	**PDB header:**transcription **Chain:** D: **PDB Molecule:**protein pcf11; **PDBTitle:** clp1-atp-pcf11 complex
66	d1zrua3	Alignment	not modelled	6.7	50	**Fold:**Pseudo beta-prism **Superfamily:**Bacteriophage trimeric proteins domain **Family:**Lactophage receptor-binding protein N-terminal domain
67	c2v5iA_	Alignment	not modelled	6.4	8	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**salmonella typhimurium db7155 bacteriophage det7 **PDBTitle:** structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
68	d1vjpa2	Alignment	not modelled	6.3	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
69	c2d4nA_	Alignment	not modelled	6.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**du; **PDBTitle:** crystal structure of m-pmv dutpase complexed with dupnpp, substrate2 analogue
70	d2gr8a1	Alignment	not modelled	6.2	16	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
71	d2h1ta1	Alignment	not modelled	6.0	19	**Fold:**Spiral beta-roll **Superfamily:**PA1994-like **Family:**PA1994-like
72	c2fhdA_	Alignment	not modelled	6.0	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
73	c3cinA_	Alignment	not modelled	6.0	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**myo-inositol-1-phosphate synthase-related protein; **PDBTitle:** crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
74	c2k1gA_	Alignment	not modelled	5.9	35	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**lipoprotein spr; **PDBTitle:** solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
75	d1jmxa4	Alignment	not modelled	5.9	39	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
76	d1p1ja2	Alignment	not modelled	5.9	25	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
77	d2h7za1	Alignment	not modelled	5.9	29	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
78	d1k1za_	Alignment	not modelled	5.8	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
79	d1zvca1	Alignment	not modelled	5.8	15	**Fold:**AOC barrel-like **Superfamily:**Allene oxide cyclase-like **Family:**Allene oxide cyclase-like
80	c2odlA_	Alignment	not modelled	5.8	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesin; **PDBTitle:** crystal structure of the hmw1 secretion domain from2 haemophilus influenzae

81	c1w0pA_	Alignment	not modelled	5.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sialidase; **PDBTitle:** vibrio cholerae sialidase with alpha-2,6-sialyllactose
82	c2o18A_	Alignment	not modelled	5.7	16	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**thiamine biosynthesis lipoprotein apbe; **PDBTitle:** crystal structure of a thiamine biosynthesis lipoprotein2 apbe, northeast strcutural genomics target er559
83	c1dfcB_	Alignment	not modelled	5.6	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**fascin; **PDBTitle:** crystal structure of human fascin, an actin-crosslinking protein
84	d1gcqc_	Alignment	not modelled	5.6	10	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
85	d1ylea1	Alignment	not modelled	5.6	9	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
86	d2g03a1	Alignment	not modelled	5.6	14	**Fold:**Fic-like **Superfamily:**Fic-like **Family:**Fic-like
87	d1sm3h2	Alignment	not modelled	5.6	4	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
88	c1xkwA_	Alignment	not modelled	5.4	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
89	d2ihoa2	Alignment	not modelled	5.3	17	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**MOA C-terminal domain-like
90	c3n0kA_	Alignment	not modelled	5.3	13	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine protease inhibitor 1; **PDBTitle:** proteinase inhibitor from coprinopsis cinerea