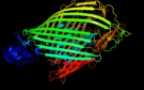
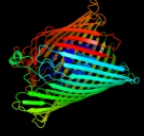
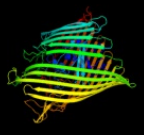
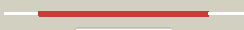
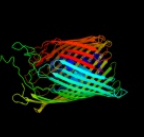
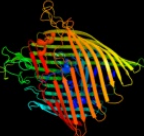
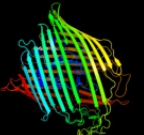
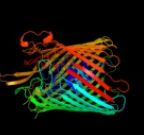
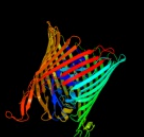
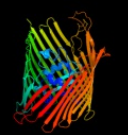
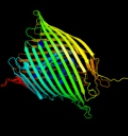
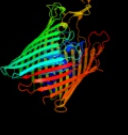
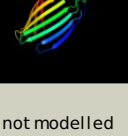


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iahA_	 Alignment		100.0	15	PDB header: membrane protein Chain: A: PDB Molecule: ferripyoverdine receptor; PDBTitle: crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
2	d1kmoa_	 Alignment		100.0	99	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
3	c1po3A_	 Alignment		100.0	100	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
4	d1by5a_	 Alignment		100.0	16	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
5	c2grxB_	 Alignment		100.0	16	PDB header: metal transport Chain: B: PDB Molecule: ferrichrome-iron receptor; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
6	c3qlbA_	 Alignment		100.0	16	PDB header: metal transport Chain: A: PDB Molecule: enantio-pyochelin receptor; PDBTitle: enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
7	c1xkhC_	 Alignment		100.0	13	PDB header: membrane protein Chain: C: PDB Molecule: ferripyoverdine receptor; PDBTitle: pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
8	c1xkWA_	 Alignment		100.0	14	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
9	c3fhhA_	 Alignment		100.0	16	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane heme receptor shua; PDBTitle: crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae
10	d2gufa1	 Alignment		100.0	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
11	d1fepa_	 Alignment		100.0	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel

12	c3efmA_	Alignment		100.0	17	PDB header: membrane protein Chain: A: PDB Molecule: ferric alcaligin siderophore receptor; PDBTitle: structure of the alcaligin outer membrane recepteur fau from2 bordetella pertussis
13	c3cslB_	Alignment		100.0	13	PDB header: membrane protein/heme binding protein Chain: B: PDB Molecule: hasr protein; PDBTitle: structure of the serratia marcescens hemophore receptor hasr in2 complex with its hemophore hasa and heme
14	c2hdiA_	Alignment		100.0	16	PDB header: protein transport,antimicrobial protein Chain: A: PDB Molecule: colicin i receptor; PDBTitle: crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
15	c2dluA_	Alignment		99.8	98	PDB header: metal transport Chain: A: PDB Molecule: iron(iii) dicitrate transport protein feca; PDBTitle: solution strcture of the periplasmic signaling domain of2 feca from escherichia coli
16	c1zzvA_	Alignment		99.8	100	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.
17	c2a02A_	Alignment		99.4	27	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.
18	d1tl6a_	Alignment		99.2	17	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
19	c3dwoX_	Alignment		98.9	16	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
20	c3brzA_	Alignment		97.6	15	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
21	c2y9kG_	Alignment	not modelled	96.7	18	PDB header: protein transport Chain: G: PDB Molecule: protein invg; PDBTitle: three-dimensional model of salmonella's needle complex at2 subnanometer resolution
22	c3gr5A_	Alignment	not modelled	95.8	14	PDB header: membrane protein Chain: A: PDB Molecule: escs; PDBTitle: periplasmic domain of the outer membrane secretin escs from2 enteropathogenic e.coli (epec)
23	c3ezjA_	Alignment	not modelled	91.8	18	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
24	c3ossD_	Alignment	not modelled	89.1	18	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
25	c3bryB_	Alignment	not modelled	87.4	16	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
26	c2k0lA_	Alignment	not modelled	81.8	8	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.
27	d1g90a_	Alignment	not modelled	79.7	20	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
28	c2y3mA_	Alignment	not modelled	79.4	11	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

29	d1qjpa_	Alignment	not modelled	70.0	18	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
30	c3qraA_	Alignment	not modelled	65.4	12	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
31	c2x27X_	Alignment	not modelled	63.4	12	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein oprg; PDBTitle: crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
32	d1p4ta_	Alignment	not modelled	61.0	13	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
33	c2iwvD_	Alignment	not modelled	58.0	13	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
34	d1qj8a_	Alignment	not modelled	55.0	17	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
35	c2f1tB_	Alignment	not modelled	52.4	12	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
36	c2lhfA_	Alignment	not modelled	51.5	9	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
37	c3nb3C_	Alignment	not modelled	42.6	18	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
38	c3kvnA_	Alignment	not modelled	42.1	11	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
39	d1osma_	Alignment	not modelled	36.3	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
40	d2fgqx1	Alignment	not modelled	31.5	16	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
41	d3cdda2	Alignment	not modelled	29.6	11	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
42	d1phoa_	Alignment	not modelled	25.6	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
43	d3d37a1	Alignment	not modelled	25.0	12	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
44	d2a1ja1	Alignment	not modelled	18.8	40	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
45	c2y0hA_	Alignment	not modelled	12.9	12	PDB header: transport protein Chain: A: PDB Molecule: probable porin; PDBTitle: crystal structure of pseudomonas aeruginosa opdl
46	c2qtkB_	Alignment	not modelled	12.3	12	PDB header: membrane protein Chain: B: PDB Molecule: probable porin; PDBTitle: crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
47	c3t7yB_	Alignment	not modelled	11.5	15	PDB header: protein transport Chain: B: PDB Molecule: yop proteins translocation protein u; PDBTitle: structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
48	c3jtyB_	Alignment	not modelled	11.4	13	PDB header: transport protein Chain: B: PDB Molecule: benf-like porin; PDBTitle: crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
49	d2zfga1	Alignment	not modelled	9.8	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
50	d1gm5a2	Alignment	not modelled	9.1	30	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
51	c3cddD_	Alignment	not modelled	9.0	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
52	d1viga_	Alignment	not modelled	8.5	17	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
53	c3c00B_	Alignment	not modelled	8.5	15	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: escu; PDBTitle: crystal structural of the mutated g247t escu/spas c-terminal domain
54	c1wruA_	Alignment	not modelled	8.5	16	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
						Fold: EscU C-terminal domain-like

55	d3bzra1	Alignment	not modelled	8.5	21	Superfamily: EscU C-terminal domain-like Family: EscU C-terminal domain-like
56	c3bzaA	Alignment	not modelled	8.5	21	PDB header: membrane protein, protein transport Chain: A: PDB Molecule: escu; PDBTitle: crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
57	c3adyA	Alignment	not modelled	8.3	20	PDB header: proton transport Chain: A: PDB Molecule: dotd; PDBTitle: crystal structure of dotd from legionella
58	c3sljA	Alignment	not modelled	8.0	13	PDB header: protein transport Chain: A: PDB Molecule: serine protease espp; PDBTitle: pre-cleavage structure of the autotransporter espp - n1023a mutant
59	c2vt1B	Alignment	not modelled	7.9	19	PDB header: membrane protein Chain: B: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structure of the cytoplasmic domain of spa40, the2 specificity switch for the shigella flexneri type iii3 secretion system
60	d1pyya2	Alignment	not modelled	7.3	12	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
61	c3cinA	Alignment	not modelled	7.1	20	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
62	c1pmdA	Alignment	not modelled	6.9	12	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x)
63	dli78a	Alignment	not modelled	6.6	8	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
64	d1wrua2	Alignment	not modelled	6.5	12	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
65	c3c01H	Alignment	not modelled	6.4	20	PDB header: membrane protein, protein transport Chain: H: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structural of native spas c-terminal domain
66	c1n0wB	Alignment	not modelled	6.4	63	PDB header: gene regulation/antitumor protein Chain: B: PDB Molecule: breast cancer type 2 susceptibility protein; PDBTitle: crystal structure of a rad51-brca2 brc repeat complex
67	d1rp5a2	Alignment	not modelled	6.3	9	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
68	c3ov5A	Alignment	not modelled	6.3	24	PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: atomic structure of the xanthomonas citri virb7 globular domain.
69	d2ctma1	Alignment	not modelled	6.2	16	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
70	d2aq0a1	Alignment	not modelled	6.1	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
71	c3nsgA	Alignment	not modelled	6.0	16	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
72	c3a2rX	Alignment	not modelled	6.0	10	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein ii; PDBTitle: crystal structure of outer membrane protein porb from neisseria2 meningitidis
73	c2qomB	Alignment	not modelled	5.9	11	PDB header: hydrolase Chain: B: PDB Molecule: serine protease espp; PDBTitle: the crystal structure of the e.coli espp autotransporter beta-domain.
74	c1zq1B	Alignment	not modelled	5.9	15	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
75	c2y0lA	Alignment	not modelled	5.9	11	PDB header: transport protein Chain: A: PDB Molecule: cis-aconitate porin opdh; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
76	d1okja1	Alignment	not modelled	5.7	32	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
77	d2b59b2	Alignment	not modelled	5.7	19	Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Pre-dockerin domain
78	d1k25a2	Alignment	not modelled	5.6	9	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