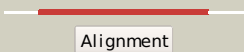
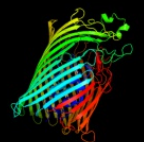
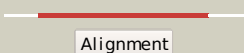
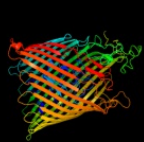
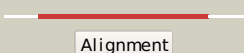
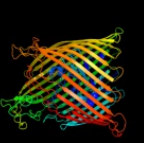
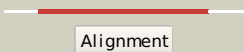
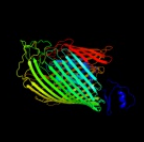

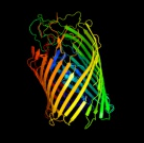
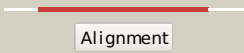
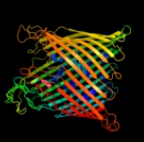
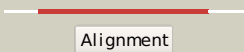
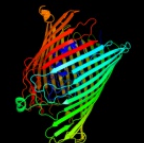
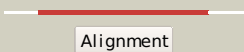
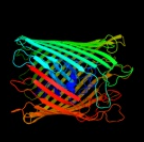
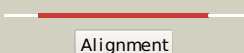
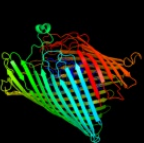


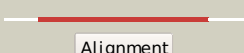

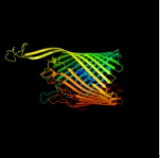
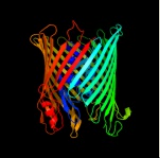
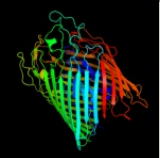
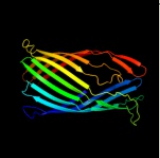

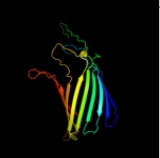
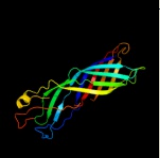
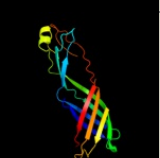



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1by5a_	 Alignment		100.0	100	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
2	c2grxB_	 Alignment		100.0	100	PDB header: metal transport Chain: B: PDB Molecule: ferrichrome-iron receptor; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
3	c3qlbA_	 Alignment		100.0	35	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
4	c2iahA_	 Alignment		100.0	19	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.
5	c1xkhC_	 Alignment		100.0	19	PDB header: membrane protein Chain: C: PDB Molecule: ferripyoverdine receptor; PDBTitle: pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
6	c1xkwA_	 Alignment		100.0	20	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
7	d1kmoa_	 Alignment		100.0	17	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
8	c3fhhA_	 Alignment		100.0	18	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
9	c1po3A_	 Alignment		100.0	16	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
10	c3efmA_	 Alignment		100.0	20	PDB header: membrane protein Chain: A: PDB Molecule: ferric alcaligin siderophore receptor; PDBTitle: structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
11	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.

12	c3cslB_	Alignment		100.0	16	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
13	d2gufa1	Alignment		100.0	19	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
14	d1fepa_	Alignment		100.0	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
15	d1t16a_	Alignment		99.5	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
16	c3dwoX_	Alignment		98.8	11	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
17	c3brzA_	Alignment		96.9	11	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
18	c2x27X_	Alignment		95.6	13	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	c2f1tB_	Alignment		95.3	15	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
20	c3qraA_	Alignment		91.9	14	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
21	d1qj8a_	Alignment	not modelled	84.0	11	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
22	c2k0lA_	Alignment	not modelled	83.6	11	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.
23	c3kvnA_	Alignment	not modelled	83.0	10	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
24	c3nb3C_	Alignment	not modelled	82.2	10	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
25	d1g90a_	Alignment	not modelled	80.8	8	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
26	d1qjpa_	Alignment	not modelled	79.4	14	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
27	c2wjqa_	Alignment	not modelled	79.4	19	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
28	c2jmmA_	Alignment	not modelled	77.0	15	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

29	d1p4ta_	Alignment	not modelled	68.6	18	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
30	d1uynx_	Alignment	not modelled	67.9	9	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
31	c2lhfA_	Alignment	not modelled	67.4	27	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
32	c3bryB_	Alignment	not modelled	60.1	12	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
33	d2fgqx1	Alignment	not modelled	55.9	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
34	c2y0kA_	Alignment	not modelled	47.0	15	PDB header: transport protein Chain: A: PDB Molecule: pyroglutamate porin opdo; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
35	c3k07A_	Alignment	not modelled	42.9	10	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
36	d1osma_	Alignment	not modelled	42.3	11	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
37	c3jtyB_	Alignment	not modelled	42.1	12	PDB header: transport protein Chain: B: PDB Molecule: benf-like porin; PDBTitle: crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
38	c3fcgB_	Alignment	not modelled	39.6	11	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: f1 capsule-anchoring protein; PDBTitle: crystal structure analysis of the middle domain of the2 caf1a usher
39	d1phoa_	Alignment	not modelled	35.8	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
40	d1w0na_	Alignment	not modelled	22.8	10	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 36 carbohydrate binding module, CBM36
41	d2a1ja1	Alignment	not modelled	17.0	40	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
42	c2vqiA_	Alignment	not modelled	15.7	16	PDB header: transport Chain: A: PDB Molecule: outer membrane usher protein papc; PDBTitle: structure of the p pilus usher (papc) translocation pore
43	c3ohnA_	Alignment	not modelled	14.2	15	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane usher protein fimd; PDBTitle: crystal structure of the fimd translocation domain
44	c2y0hA_	Alignment	not modelled	14.0	13	PDB header: transport protein Chain: A: PDB Molecule: probable porin; PDBTitle: crystal structure of pseudomonas aeruginosa opd1
45	d2zfga1	Alignment	not modelled	10.5	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
46	c2iwvD_	Alignment	not modelled	9.9	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
47	d1iwga6	Alignment	not modelled	9.7	9	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
48	c3sljA_	Alignment	not modelled	7.7	9	PDB header: protein transport Chain: A: PDB Molecule: serine protease espp; PDBTitle: pre-cleavage structure of the autotransporter espp - n1023a mutant
49	c3nsgA_	Alignment	not modelled	6.0	12	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
50	c2odjA_	Alignment	not modelled	5.4	10	PDB header: membrane protein Chain: A: PDB Molecule: porin d; PDBTitle: crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
51	d1gm5a2	Alignment	not modelled	5.4	10	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain