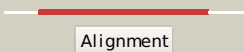
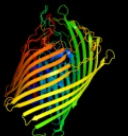
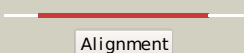
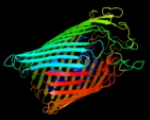
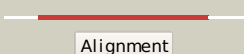
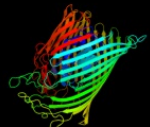
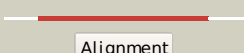
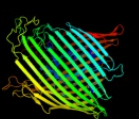
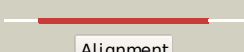
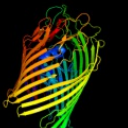
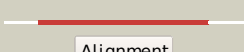
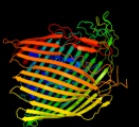
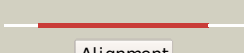
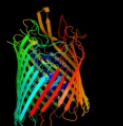
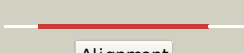
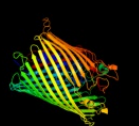
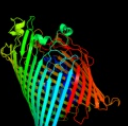
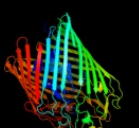
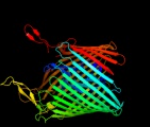
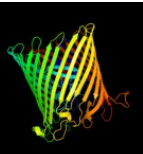
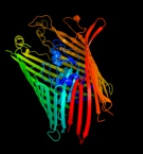
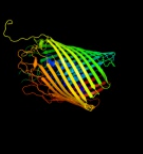
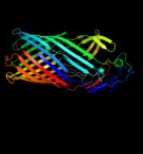
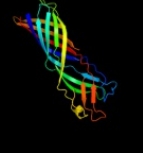


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qlbA_	 Alignment		100.0	17	PDB header: metal transport Chain: A: PDB Molecule: enantio-pyochelin receptor; PDBTitle: enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
2	c2grxB_	 Alignment		100.0	18	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	d1by5a_	 Alignment		100.0	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
4	c2iahA_	 Alignment		100.0	17	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	17	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	17	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
7	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
8	d1kmoa_	 Alignment		100.0	20	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
9	c1po3A_	 Alignment		100.0	19	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	d1fepa_	 Alignment		100.0	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
11	c2hdiA_	 Alignment		100.0	21	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	d2gufa1	Alignment		100.0	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
13	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
14	c3cslB	Alignment		100.0	18	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
15	d1t16a	Alignment		99.2	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
16	c3dwoX	Alignment		97.6	12	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
17	c2x27X	Alignment		96.1	14	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein oprg; PDBTitle: crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
18	c3brzA	Alignment		95.7	9	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
19	d1g90a	Alignment		91.1	7	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
20	c2f1tB	Alignment		88.3	11	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
21	c3qraA	Alignment	not modelled	88.1	11	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
22	c2wjqa	Alignment	not modelled	87.4	10	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
23	c2lhfa	Alignment	not modelled	83.3	7	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
24	d1osma	Alignment	not modelled	81.8	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
25	d1qj8a	Alignment	not modelled	78.7	13	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
26	d1p4ta	Alignment	not modelled	66.9	13	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
27	c3nb3C	Alignment	not modelled	66.8	7	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
28	d1phoa	Alignment	not modelled	57.3	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin

29	d1qjpa_	Alignment	not modelled	56.9	7	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
30	c2iwwD_	Alignment	not modelled	55.4	14	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
31	d2zfga1	Alignment	not modelled	54.3	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
32	d2fgqx1	Alignment	not modelled	52.3	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
33	d1uynx_	Alignment	not modelled	40.0	13	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
34	c2k0lA_	Alignment	not modelled	38.2	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.
35	c3bryB_	Alignment	not modelled	35.7	9	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
36	c3kvnA_	Alignment	not modelled	34.6	12	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
37	d2a1ja1	Alignment	not modelled	19.1	30	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
38	c3nsgA_	Alignment	not modelled	15.6	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
39	c2jmmA_	Alignment	not modelled	14.4	6	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
40	c2odja_	Alignment	not modelled	13.3	9	PDB header: membrane protein Chain: A: PDB Molecule: porin d; PDBTitle: crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
41	d1w0na_	Alignment	not modelled	11.0	28	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 36 carbohydrate binding module, CBM36
42	c1wx4B_	Alignment	not modelled	8.6	33	PDB header: oxidoreductase/metal transport Chain: B: PDB Molecule: melc; PDBTitle: crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of dithiothreitol
43	c2e0kA_	Alignment	not modelled	7.4	8	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
44	c3eo6B_	Alignment	not modelled	7.4	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of unknown function (duf1255); PDBTitle: crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution
45	d1pjqa2	Alignment	not modelled	6.1	16	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
46	c1n0wB_	Alignment	not modelled	6.0	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
47	d1okja1	Alignment	not modelled	5.7	32	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
48	c3k07A_	Alignment	not modelled	5.7	13	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
49	d2aq0a1	Alignment	not modelled	5.4	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
50	d1isia_	Alignment	not modelled	5.3	13	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: ADP ribosyl cyclase-like
51	c2gefA_	Alignment	not modelled	5.1	17	PDB header: hydrolase Chain: A: PDB Molecule: protease vp4; PDBTitle: crystal structure of a novel viral protease with a2 serine/lysine catalytic dyad mechanism