
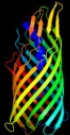
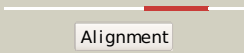
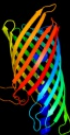

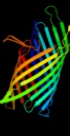

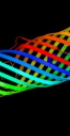

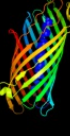
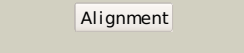
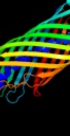
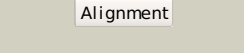
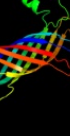
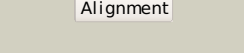
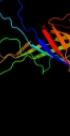


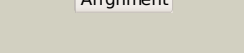

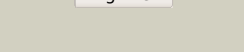

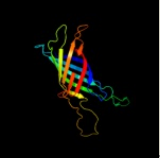

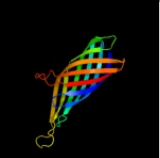
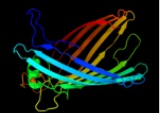

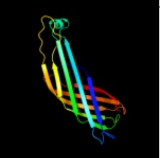

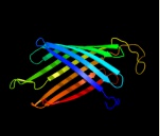
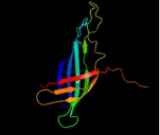





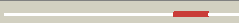

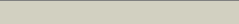


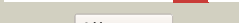



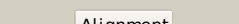
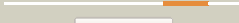




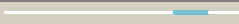



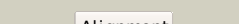
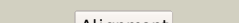
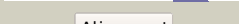


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sljA_	 Alignment		100.0	20	PDB header: protein transport Chain: A: PDB Molecule: serine protease espp; PDBTitle: pre-cleavage structure of the autotransporter espp - n1023a mutant
2	c3aehB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
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	21	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	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
7	d1g90a_	 Alignment		99.3	18	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
8	c2k0lA_	 Alignment		99.3	16	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.
9	d1qjpa_	 Alignment		99.2	16	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
10	d1p4ta_	 Alignment		99.1	19	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
11	c2x27X_	 Alignment		99.1	15	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein oprg; PDBTitle: crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa

12	c2jmmA_	Alignment		99.1	17	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
13	c3qraA_	Alignment		99.1	18	PDB header: cell invasion Chain: A: PDB Molecule: attachment invasion locus protein; PDBTitle: the crystal structure of ail, the attachment invasion locus protein of yersinia pestis
14	c3nb3C_	Alignment		99.0	17	PDB header: virus Chain: C: PDB Molecule: outer membrane protein a; PDBTitle: the host outer membrane proteins ompa and ompc are packed at specific sites in the shigella phage sf6 virion as structural components
15	c2iwwD_	Alignment		99.0	17	PDB header: ion channel Chain: D: PDB Molecule: outer membrane protein g; PDBTitle: structure of the monomeric outer membrane porin ompg in the open and closed conformation
16	c2f1tB_	Alignment		98.9	13	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
17	d1qj8a_	Alignment		98.7	17	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
18	c2x4mD_	Alignment		98.5	20	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
19	c2wjqA_	Alignment		98.5	16	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
20	c2lhfa_	Alignment		98.2	16	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	d1i78a_	Alignment	not modelled	98.1	20	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
22	d1t16a_	Alignment	not modelled	97.3	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
23	c3brzA_	Alignment	not modelled	97.0	15	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
24	d2vdfa1	Alignment	not modelled	96.8	18	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane adhesin/invasin OpcA
25	d3prna_	Alignment	not modelled	96.7	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
26	c3dwoX_	Alignment	not modelled	96.6	10	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadI homologue
27	d2pora_	Alignment	not modelled	96.6	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
28	c2iahA_	Alignment	not modelled	96.5	13	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.

29	c3ml3A		Alignment		not modelled	96.2	17	PDB header: protein transport Chain: A: PDB Molecule: outer membrane protein icsa autotransporter; PDBTitle: crystal structure of the icsa autochaperone region
30	c3bryB		Alignment		not modelled	95.7	13	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
31	c3a2rX		Alignment		not modelled	95.1	13	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein ii; PDBTitle: crystal structure of outer membrane protein porb from neisseria2 meningitidis
32	c1xkhC		Alignment		not modelled	93.3	11	PDB header: membrane protein Chain: C: PDB Molecule: ferripyoverdine receptor; PDBTitle: pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
33	c2hdiA		Alignment		not modelled	93.1	17	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.
34	d1osma		Alignment		not modelled	93.1	26	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
35	d1daba		Alignment			92.9	10	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Virulence factor P.69 pertactin
36	d2zfga1		Alignment		not modelled	92.5	16	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
37	c3nsgA		Alignment		not modelled	91.6	13	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
38	d2fgqx1		Alignment		not modelled	91.2	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
39	c2grxB		Alignment		not modelled	91.1	11	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
40	d1by5a		Alignment		not modelled	86.0	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
41	d1phoa		Alignment		not modelled	85.0	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
42	c3qlbA		Alignment		not modelled	83.4	13	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
43	c2ervA		Alignment		not modelled	81.3	13	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein paer03002360; PDBTitle: crystal structure of the outer membrane enzyme pagl
44	c1xkwA		Alignment		not modelled	79.6	10	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
45	c1po3A		Alignment		not modelled	50.1	10	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
46	d1kmoa		Alignment		not modelled	40.5	11	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
47	d2gr8a1		Alignment		not modelled	38.9	16	Fold: Pili subunits Superfamily: Pili subunits Family: YadA C-terminal domain-like
48	d2gufa1		Alignment		not modelled	38.8	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
49	c2gr7C		Alignment		not modelled	35.4	16	PDB header: membrane protein Chain: C: PDB Molecule: adhesin; PDBTitle: hia 992-1098
50	d2gr7a1		Alignment		not modelled	35.4	16	Fold: Pili subunits Superfamily: Pili subunits Family: YadA C-terminal domain-like
51	c3emoA		Alignment		not modelled	17.6	14	PDB header: membrane protein/cell adhesion Chain: A: PDB Molecule: hia (adhesin); PDBTitle: crystal structure of transmembrane hia 973-1098
52	c2o4vA		Alignment		not modelled	17.5	15	PDB header: membrane protein Chain: A: PDB Molecule: porin p; PDBTitle: an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
53	c1ad6C		Alignment		not modelled	13.4	22	PDB header: membrane protein Chain: C: PDB Molecule: protein (outer membrane phospholipase

53	c1q00C_	Alignment	not modelled	13.4	42	(ompla)); PDBTitle: outer membrane phospholipase a from escherichia coli PDB header: membrane protein
54	c3fhA_	Alignment	not modelled	13.0	7	Chain: A: PDB Molecule: outer membrane heme receptor shua; PDBTitle: crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae
55	d2f0ca1	Alignment	not modelled	12.8	29	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Lactophage receptor-binding protein head domain
56	c2y0hA_	Alignment	not modelled	12.7	13	PDB header: transport protein Chain: A: PDB Molecule: probable porin; PDBTitle: crystal structure of pseudomonas aeruginosa opd1
57	c3syjA_	Alignment	not modelled	10.2	10	PDB header: cell adhesion Chain: A: PDB Molecule: adhesion and penetration protein autotransporter; PDBTitle: crystal structure of the haemophilus influenzae hap adhesin
58	c3rbhC_	Alignment	not modelled	10.0	12	PDB header: transport protein Chain: C: PDB Molecule: alginate production protein alge; PDBTitle: structure of alginate export protein alge from pseudomonas aeruginosa
59	d1nrja_	Alignment	not modelled	8.1	33	Fold: Profilin-like Superfamily: SNARE-like Family: SRP alpha N-terminal domain-like
60	d1g5aa1	Alignment	not modelled	7.8	27	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
61	c3jtyB_	Alignment	not modelled	7.2	8	PDB header: transport protein Chain: B: PDB Molecule: benf-like porin; PDBTitle: crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
62	c3csIB_	Alignment	not modelled	6.6	9	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
63	d1fepa_	Alignment	not modelled	6.5	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
64	c3dzmB_	Alignment	not modelled	5.5	19	PDB header: unknown function Chain: B: PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of a major outer membrane protein from thermus2 thermophilus hb27