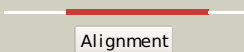

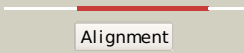



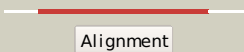
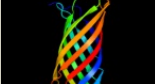
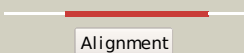

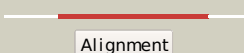

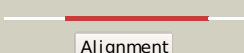

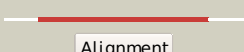

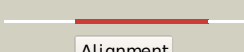

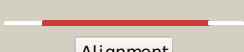

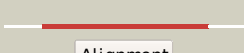







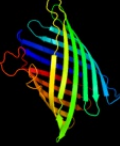

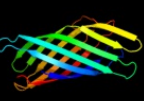


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2iwyD_</a>	 Alignment		97.9	16	<b>PDB header:</b> ion channel <b>Chain:</b> D: <b>PDB Molecule:</b> outer membrane protein g; <b>PDBTitle:</b> structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
2	<a href="#">c3qraA_</a>	 Alignment		96.9	11	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> attachment invasion locus protein; <b>PDBTitle:</b> the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis
3	<a href="#">c3nb3C_</a>	 Alignment		96.8	16	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> outer membrane protein a; <b>PDBTitle:</b> the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
4	<a href="#">d1p4ta_</a>	 Alignment		96.8	10	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
5	<a href="#">c2f1tB_</a>	 Alignment		96.7	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer membrane protein w; <b>PDBTitle:</b> outer membrane protein ompw
6	<a href="#">c2wjgA_</a>	 Alignment		96.6	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable n-acetylneuraminic acid outer membrane channel <b>PDBTitle:</b> nanc porin structure in hexagonal crystal form.
7	<a href="#">d1qjpa_</a>	 Alignment		96.6	16	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
8	<a href="#">c2k0lA_</a>	 Alignment		96.5	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein a; <b>PDBTitle:</b> nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
9	<a href="#">d1g90a_</a>	 Alignment		95.9	12	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
10	<a href="#">c3aehB_</a>	 Alignment		95.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hemoglobin-binding protease hbp autotransporter; <b>PDBTitle:</b> integral membrane domain of autotransporter hbp
11	<a href="#">c3sljA_</a>	 Alignment		95.3	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease esp; <b>PDBTitle:</b> pre-cleavage structure of the autotransporter esp - n1023a mutant

12	<a href="#">d2vdfa1</a>	Alignment		94.7	19	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPT-like <b>Family:</b> Outer membrane adhesin/invasin OpcA
13	<a href="#">c2jmmA_</a>	Alignment		94.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein a; <b>PDBTitle:</b> nmr solution structure of a minimal transmembrane beta-2 barrel platform protein
14	<a href="#">c3kvnA_</a>	Alignment		93.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase esta; <b>PDBTitle:</b> crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
15	<a href="#">c2odjA_</a>	Alignment		92.7	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> porin d; <b>PDBTitle:</b> crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
16	<a href="#">c3dwoX_</a>	Alignment		92.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> probable outer membrane protein; <b>PDBTitle:</b> crystal structure of a pseudomonas aeruginosa fadl homologue
17	<a href="#">c2qomB_</a>	Alignment		90.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> serine protease espp; <b>PDBTitle:</b> the crystal structure of the e.coli espp autotransporter beta-domain.
18	<a href="#">c3qq2C_</a>	Alignment		90.1	12	<b>PDB header:</b> membrane protein/protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> brka autotransporter; <b>PDBTitle:</b> crystal structure of the beta domain of the bordetella autotransporter2 brka
19	<a href="#">c2x27X_</a>	Alignment		85.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> outer membrane protein oprg; <b>PDBTitle:</b> crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
20	<a href="#">d1qi8a_</a>	Alignment		85.0	12	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
21	<a href="#">c2x4mD_</a>	Alignment	not modelled	78.6	9	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> coagulase/fibrinolysin; <b>PDBTitle:</b> yersinia pestis plasminogen activator pla
22	<a href="#">c3a2rX_</a>	Alignment	not modelled	70.2	10	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> outer membrane protein ii; <b>PDBTitle:</b> crystal structure of outer membrane protein porb from neisseria2 meningitidis
23	<a href="#">c2hdiA_</a>	Alignment	not modelled	69.8	12	<b>PDB header:</b> protein transport, antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin i receptor; <b>PDBTitle:</b> crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
24	<a href="#">d1uynX_</a>	Alignment	not modelled	64.3	15	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Autotransporter <b>Family:</b> Autotransporter
25	<a href="#">d1i78a_</a>	Alignment	not modelled	62.4	10	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPT-like <b>Family:</b> Outer membrane protease OMPT
26	<a href="#">c2lhfA_</a>	Alignment	not modelled	61.2	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein h1; <b>PDBTitle:</b> solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles
27	<a href="#">d1by5a_</a>	Alignment	not modelled	53.4	11	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Ligand-gated protein channel
28	<a href="#">c3brzA_</a>	Alignment	not modelled	51.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> todx; <b>PDBTitle:</b> crystal structure of the pseudomonas putida toluene2 transporter todx
						<b>PDB header:</b> metal transport

29	<a href="#">c2grxB</a>	Alignment	not modelled	40.9	9	<b>Chain:</b> B: <b>PDB Molecule:</b> ferrichrome-iron receptor; <b>PDBTitle:</b> crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
30	<a href="#">c2y0kA</a>	Alignment	not modelled	37.2	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> pyroglutamate porin opdo; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa opdo
31	<a href="#">c3qlbA</a>	Alignment	not modelled	36.8	10	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> enantio-pyochelin receptor; <b>PDBTitle:</b> enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
32	<a href="#">d2fgqx1</a>	Alignment	not modelled	33.9	8	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
33	<a href="#">d2pora</a>	Alignment	not modelled	32.8	8	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
34	<a href="#">c2y0hA</a>	Alignment	not modelled	32.5	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable porin; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa opdl
35	<a href="#">c2qdZA</a>	Alignment	not modelled	30.4	10	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> tpsb transporter fhac; <b>PDBTitle:</b> structure of the membrane protein fhac: a member of the2 omp85/tpsb transporter family
36	<a href="#">d1t16a</a>	Alignment	not modelled	29.4	15	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Outer membrane protein transport protein
37	<a href="#">d1v54g</a>	Alignment	not modelled	28.1	13	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIa <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIa
38	<a href="#">d2zfga1</a>	Alignment	not modelled	17.3	7	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
39	<a href="#">d1af6a</a>	Alignment	not modelled	16.6	18	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Maltoporin-like
40	<a href="#">c2iahA</a>	Alignment	not modelled	11.7	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferripyoverdine receptor; <b>PDBTitle:</b> crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
41	<a href="#">c3bryB</a>	Alignment	not modelled	7.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> tbux; <b>PDBTitle:</b> crystal structure of the ralstonia pickettii toluene2 transporter tbux
42	<a href="#">d2f0ca1</a>	Alignment	not modelled	7.5	26	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Lactophage receptor-binding protein head domain
43	<a href="#">c1xkwA</a>	Alignment	not modelled	7.2	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> fe(iii)-pyochelin receptor; <b>PDBTitle:</b> pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
44	<a href="#">c1xkhC</a>	Alignment	not modelled	6.6	9	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> ferripyoverdine receptor; <b>PDBTitle:</b> pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
45	<a href="#">d1a0tp</a>	Alignment	not modelled	6.1	8	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Maltoporin-like