
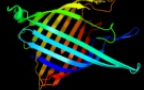

















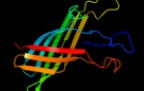





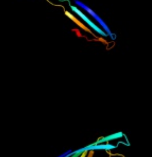
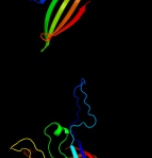

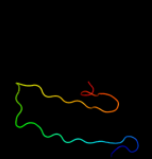

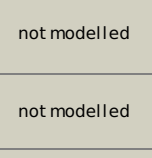


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1t1ya_</a>	 Alignment		100.0	14	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Tsx-like channel <b>Family:</b> Tsx-like channel
2	<a href="#">d1qjpa_</a>	 Alignment		95.9	13	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
3	<a href="#">c3nb3C_</a>	 Alignment		95.7	11	<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="#">d1qj8a_</a>	 Alignment		94.8	12	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
5	<a href="#">c3aehB_</a>	 Alignment		93.9	18	<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
6	<a href="#">d1uynx_</a>	 Alignment		92.7	14	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Autotransporter <b>Family:</b> Autotransporter
7	<a href="#">c3qraA_</a>	 Alignment		92.2	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
8	<a href="#">c2k0IA_</a>	 Alignment		91.4	13	<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="#">d1p4ta_</a>	 Alignment		90.0	13	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
10	<a href="#">d1g90a_</a>	 Alignment		83.8	13	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
11	<a href="#">c2x27X_</a>	 Alignment		73.6	20	<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

12	<a href="#">c3sljA_</a>	Alignment		62.2	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease espp; <b>PDBTitle:</b> pre-cleavage structure of the autotransporter espp - n1023a mutant
13	<a href="#">c2iwwD_</a>	Alignment		58.2	9	<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
14	<a href="#">c2f1tB_</a>	Alignment		58.1	16	<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
15	<a href="#">c3brzA_</a>	Alignment		54.7	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
16	<a href="#">c2wjgA_</a>	Alignment		49.2	20	<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.
17	<a href="#">c2lhfA_</a>	Alignment		36.7	9	<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
18	<a href="#">c3qq2C_</a>	Alignment		23.9	15	<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="#">c2eefA_</a>	Alignment		21.3	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein phosphatase 1, regulatory (inhibitor) <b>PDBTitle:</b> solution structure of the cbm_21 domain from human protein2 phosphatase 1, regulatory (inhibitor) subunit 3b
20	<a href="#">d1phoa_</a>	Alignment		12.9	8	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
21	<a href="#">c2jmmA_</a>	Alignment	not modelled	10.7	12	<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
22	<a href="#">d1u4ga_</a>	Alignment	not modelled	10.0	11	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Thermolysin-like
23	<a href="#">c2qomB_</a>	Alignment	not modelled	8.7	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.
24	<a href="#">c2vqxX_</a>	Alignment	not modelled	7.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metalloproteinase; <b>PDBTitle:</b> precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
25	<a href="#">d1osma_</a>	Alignment	not modelled	6.1	9	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
26	<a href="#">c3dwoX_</a>	Alignment	not modelled	6.0	11	<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
27	<a href="#">d1tdja3</a>	Alignment	not modelled	5.5	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Allosteric threonine deaminase C-terminal domain