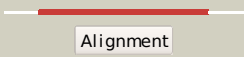

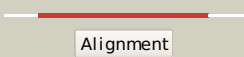

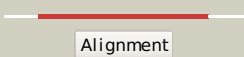

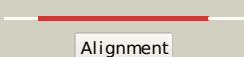

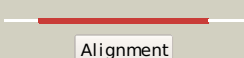
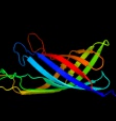
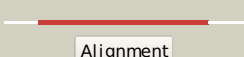

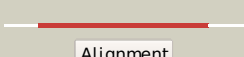

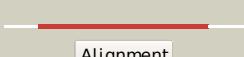

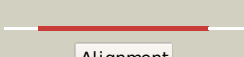

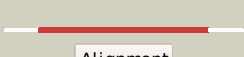








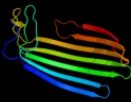





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1qj8a_</a>	 Alignment		100.0	99	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
2	<a href="#">c3qraA_</a>	 Alignment		100.0	45	<b>PDB header:</b> cell 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 of <i>Yersinia pestis</i>
3	<a href="#">d1qjpa_</a>	 Alignment		99.9	19	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
4	<a href="#">c3nb3C_</a>	 Alignment		99.9	20	<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 specific sites in the shigella phage sf6 virion as structural components
5	<a href="#">d1g90a_</a>	 Alignment		99.9	20	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
6	<a href="#">d1p4ta_</a>	 Alignment		99.9	17	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPA-like <b>Family:</b> Outer membrane protein
7	<a href="#">c2k0lA_</a>	 Alignment		99.9	20	<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 <i>Klebsiella pneumoniae</i> in dhpc3 micelles.
8	<a href="#">c2f1tB_</a>	 Alignment		99.9	17	<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
9	<a href="#">c2x27X_</a>	 Alignment		99.9	19	<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 from <i>Pseudomonas aeruginosa</i>
10	<a href="#">c2jmmA_</a>	 Alignment		99.9	17	<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
11	<a href="#">c2lhfa_</a>	 Alignment		99.7	16	<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 <i>P. aeruginosa</i> in dhpc micelles

12	<a href="#">d1uynx_</a>	Alignment		99.1	18	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Autotransporter <b>Family:</b> Autotransporter
13	<a href="#">c3dwoX_</a>	Alignment		98.9	20	<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 fadI homologue
14	<a href="#">c3aehB_</a>	Alignment		98.9	20	<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
15	<a href="#">d1phoa_</a>	Alignment		98.9	17	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
16	<a href="#">d1t16a_</a>	Alignment		98.9	15	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Outer membrane protein transport protein
17	<a href="#">d2zfqa1</a>	Alignment		98.8	15	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
18	<a href="#">d1osma_</a>	Alignment		98.7	13	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
19	<a href="#">c3kvnA_</a>	Alignment		98.6	15	<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
20	<a href="#">c3sljA_</a>	Alignment		98.5	16	<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
21	<a href="#">d2fgqx1</a>	Alignment	not modelled	98.5	12	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
22	<a href="#">c3a2rX_</a>	Alignment	not modelled	98.5	13	<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="#">c3nsgA_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein f; <b>PDBTitle:</b> crystal structure of ompf, an outer membrane protein from salmonella2 typhi
24	<a href="#">c3qq2C_</a>	Alignment	not modelled	98.4	19	<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
25	<a href="#">c2qomB_</a>	Alignment	not modelled	98.2	18	<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.
26	<a href="#">c3brzA_</a>	Alignment	not modelled	98.1	7	<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
27	<a href="#">c3bryB_</a>	Alignment	not modelled	98.1	12	<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
28	<a href="#">c2x4mD_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> coagulase/fibrinolysin; <b>PDBTitle:</b> yersinia pestis plasminogen activator pla
						<b>PDB header:</b> ion channel

29	<a href="#">c2iwwD_</a>	Alignment	not modelled	97.2	11	<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
30	<a href="#">d3prna_</a>	Alignment	not modelled	97.2	16	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
31	<a href="#">d1i78a_</a>	Alignment	not modelled	96.4	19	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPT-like <b>Family:</b> Outer membrane protease OMPT
32	<a href="#">c2wjgA_</a>	Alignment	not modelled	96.4	12	<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.
33	<a href="#">d2pora_</a>	Alignment	not modelled	95.8	16	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Porin
34	<a href="#">c2ervA_</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein paer03002360; <b>PDBTitle:</b> crystal structure of the outer membrane enzyme pagl
35	<a href="#">d2gufa1</a>	Alignment	not modelled	94.6	7	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Ligand-gated protein channel
36	<a href="#">c3dzmb_</a>	Alignment	not modelled	94.5	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical conserved protein; <b>PDBTitle:</b> crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
37	<a href="#">c2o4vA_</a>	Alignment	not modelled	93.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> porin p; <b>PDBTitle:</b> an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
38	<a href="#">c2iahA_</a>	Alignment	not modelled	93.7	8	<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.
39	<a href="#">c2hdiA_</a>	Alignment	not modelled	93.5	13	<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.
40	<a href="#">c2grxB_</a>	Alignment	not modelled	89.6	12	<b>PDB header:</b> metal transport <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
41	<a href="#">d1af6a_</a>	Alignment	not modelled	84.3	12	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Maltoporin-like
42	<a href="#">d1a0tp_</a>	Alignment	not modelled	83.7	13	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Maltoporin-like
43	<a href="#">d1by5a_</a>	Alignment	not modelled	82.2	12	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Ligand-gated protein channel
44	<a href="#">c3efmA_</a>	Alignment	not modelled	79.0	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferric alcaligin siderophore receptor; <b>PDBTitle:</b> structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
45	<a href="#">d2vdfa1</a>	Alignment	not modelled	78.7	14	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> OMPT-like <b>Family:</b> Outer membrane adhesin/invasin OpcA
46	<a href="#">d2mpa_</a>	Alignment	not modelled	74.0	15	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Maltoporin-like
47	<a href="#">d1fepa_</a>	Alignment	not modelled	72.6	12	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Ligand-gated protein channel
48	<a href="#">d2gr7a1</a>	Alignment	not modelled	51.0	23	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> YadA C-terminal domain-like
49	<a href="#">c2gr7C_</a>	Alignment	not modelled	51.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> adhesin; <b>PDBTitle:</b> hia 992-1098
50	<a href="#">d2jnaa1</a>	Alignment	not modelled	49.5	29	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> YdgH-like <b>Family:</b> YdgH-like
51	<a href="#">c1xkhC_</a>	Alignment	not modelled	45.9	11	<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
52	<a href="#">d2gr8a1</a>	Alignment	not modelled	36.6	24	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> YadA C-terminal domain-like
53	<a href="#">c3emoA_</a>	Alignment	not modelled	33.6	24	<b>PDB header:</b> membrane protein/cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> hia (adhesin); <b>PDBTitle:</b> crystal structure of transmembrane hia 973-1098
54	<a href="#">c3qlbA_</a>	Alignment	not modelled	33.3	11	<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
55	<a href="#">c1xkwA_</a>	Alignment	not modelled	31.3	9	<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
56	<a href="#">c2y0hA_</a>	Alignment	not modelled	31.0	8 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable porin; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa opd1
57	<a href="#">c2k3aA_</a>	Alignment	not modelled	13.6	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chap domain protein; <b>PDBTitle:</b> nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
58	<a href="#">c3fhhA_</a>	Alignment	not modelled	13.1	13 <b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane heme receptor shua; <b>PDBTitle:</b> crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae
59	<a href="#">c2qdzA_</a>	Alignment	not modelled	12.8	13 <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
60	<a href="#">c2kerA_</a>	Alignment	not modelled	11.8	15 <b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase inhibitor z-2685; <b>PDBTitle:</b> alpha-amylase inhibitor parvulostat (z-2685) from2 streptomyces parvulus
61	<a href="#">d1ok0a_</a>	Alignment	not modelled	10.5	26 <b>Fold:</b> alpha-Amylase inhibitor tendamistat <b>Superfamily:</b> alpha-Amylase inhibitor tendamistat <b>Family:</b> alpha-Amylase inhibitor tendamistat
62	<a href="#">c3egbA_</a>	Alignment	not modelled	9.6	15 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein pellino homolog 2; <b>PDBTitle:</b> structure of pellino2 fha domain at 3.3 angstroms2 resolution.
63	<a href="#">c2y0kA_</a>	Alignment	not modelled	7.8	9 <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
64	<a href="#">c2odjA_</a>	Alignment	not modelled	7.1	11 <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
65	<a href="#">d1kmoa_</a>	Alignment	not modelled	6.7	15 <b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Ligand-gated protein channel
66	<a href="#">c2k4tA_</a>	Alignment	not modelled	6.6	18 <b>PDB header:</b> membrane protein,apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> voltage-dependent anion-selective channel <b>PDBTitle:</b> solution structure of human vdac-1 in ldao micelles