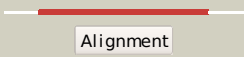
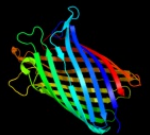
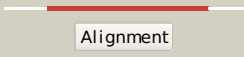

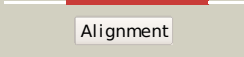

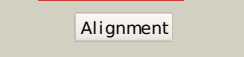

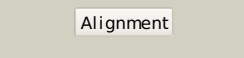
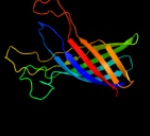
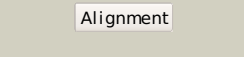

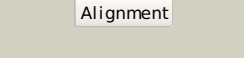
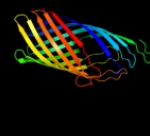
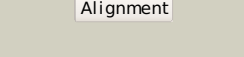



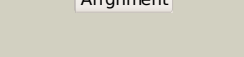

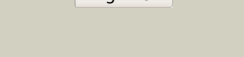
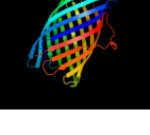

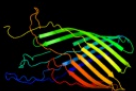


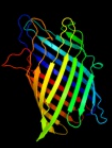
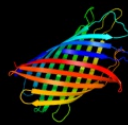

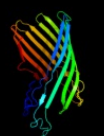

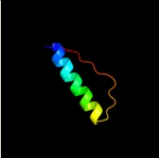


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iwwD_	 Alignment		100.0	100	PDB header: ion channel Chain: D: PDB Molecule: outer membrane protein g; PDBTitle: structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
2	dluynx_	 Alignment		98.5	18	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
3	c3dwoX_	 Alignment		98.4	12	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadI homologue
4	c2wjgA_	 Alignment		98.3	15	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
5	dlg90a_	 Alignment		98.2	18	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
6	c3aehB_	 Alignment		98.2	12	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
7	c3sljA_	 Alignment		98.2	13	PDB header: protein transport Chain: A: PDB Molecule: serine protease espp; PDBTitle: pre-cleavage structure of the autotransporter espp - n1023a mutant
8	dlp4ta_	 Alignment		98.1	13	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
9	dlqjpa_	 Alignment		98.0	19	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
10	c2k0lA_	 Alignment		98.0	17	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.
11	c2qomB_	 Alignment		97.7	10	PDB header: hydrolase Chain: B: PDB Molecule: serine protease espp; PDBTitle: the crystal structure of the e.coli espp autotransporter beta-domain.

12	c2f1tB_	Alignment		97.6	8	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
13	d1t16a_	Alignment		97.6	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
14	c3nb3C_	Alignment		97.5	21	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
15	c2jmmA_	Alignment		97.5	16	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
16	c3qq2C_	Alignment		97.4	14	PDB header: membrane protein/protein transport Chain: C: PDB Molecule: brka autotransporter; PDBTitle: crystal structure of the beta domain of the bordetella autotransporter2 brka
17	c3kvnA_	Alignment		97.2	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
18	c3qraA_	Alignment		97.2	15	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
19	c3bryB_	Alignment		96.9	15	PDB header: transport protein Chain: B: PDB Molecule: tbox; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbox
20	c2lhfa_	Alignment		96.6	12	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	c3brzA_	Alignment	not modelled	96.6	15	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
22	c2x4mD_	Alignment	not modelled	96.2	18	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
23	c2x27X_	Alignment	not modelled	95.7	12	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein oprg; PDBTitle: crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
24	c3dzmB_	Alignment	not modelled	94.9	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
25	d1qj8a_	Alignment	not modelled	94.8	10	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
26	c3a2rX_	Alignment	not modelled	94.7	15	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein ii; PDBTitle: crystal structure of outer membrane protein porb from neisseria2 meningitidis
27	d2fgqx1	Alignment	not modelled	92.9	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
28	d1phoa_	Alignment	not modelled	92.2	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
						Fold: Transmembrane beta-barrels

29	d2vdfa1	Alignment	not modelled	92.1	20	Superfamily: OMPT-like Family: Outer membrane adhesin/invasin OpcA
30	d2zfga1	Alignment	not modelled	91.5	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
31	c3nsgA	Alignment	not modelled	88.5	14	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
32	d3prna	Alignment	not modelled	87.3	16	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
33	d1osma	Alignment	not modelled	85.6	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
34	c2hdiA	Alignment	not modelled	84.7	15	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.
35	d1i78a	Alignment	not modelled	80.2	14	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
36	d1ml8a	Alignment		66.6	6	Fold: OsmC-like Superfamily: OsmC-like Family: YhfA-like
37	d2pora	Alignment	not modelled	65.0	17	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
38	c1fw3A	Alignment	not modelled	60.4	15	PDB header: hydrolase, membrane protein Chain: A: PDB Molecule: outer membrane phospholipase a; PDBTitle: outer membrane phospholipase a from escherichia coli
39	d1nyed	Alignment	not modelled	49.3	18	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
40	c2ql8A	Alignment	not modelled	46.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative redox protein; PDBTitle: crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
41	c2grxB	Alignment	not modelled	41.2	13	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
42	d1vlaa	Alignment	not modelled	38.9	19	Fold: OsmC-like Superfamily: OsmC-like Family: YhfA-like
43	c1qd6C	Alignment	not modelled	38.6	13	PDB header: membrane protein Chain: C: PDB Molecule: protein (outer membrane phospholipase (ompla)); PDBTitle: outer membrane phospholipase a from escherichia coli
44	d1af6a	Alignment	not modelled	36.2	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
45	c3qlbA	Alignment	not modelled	34.7	11	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
46	c2iahA	Alignment	not modelled	34.4	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.
47	d2pn2a1	Alignment	not modelled	34.3	18	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
48	d1uspa	Alignment	not modelled	34.1	12	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
49	d1a0tp	Alignment	not modelled	32.0	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
50	c3eerA	Alignment	not modelled	31.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein, putative; PDBTitle: high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961
51	c2egtA	Alignment	not modelled	30.3	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein aq_1549; PDBTitle: crystal structure of hypothetical protein (aq1549) from aquifex2 aeolicus
52	c2o4vA	Alignment	not modelled	28.9	10	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	c2bjoA	Alignment	not modelled	28.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein ohrb; PDBTitle: crystal structure of the organic hydroperoxide

						resistance2 protein ohrb of bacillus subtilis
54	d2d7va1	Alignment	not modelled	27.7	12	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
55	c1xkhC	Alignment	not modelled	27.7	12	PDB header: membrane protein Chain: C: PDB Molecule: ferripyoverdine receptor; PDBTitle: pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
56	c1xkwA	Alignment	not modelled	27.6	12	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
57	d1by5a	Alignment	not modelled	24.4	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
58	c1lqlE	Alignment	not modelled	23.6	6	PDB header: unknown function Chain: E: PDB Molecule: osmotic inducible protein c like family; PDBTitle: crystal structure of osmc like protein from mycoplasma2 pneumoniae
59	d1qla	Alignment	not modelled	23.6	6	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
60	d2opla1	Alignment	not modelled	23.1	15	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
61	d2onfa1	Alignment	not modelled	17.9	18	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
62	d1n2fa	Alignment	not modelled	17.1	12	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
63	d1t1ya	Alignment	not modelled	17.0	15	Fold: Transmembrane beta-barrels Superfamily: Tsx-like channel Family: Tsx-like channel
64	c3gpiA	Alignment	not modelled	13.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
65	d1qwia	Alignment	not modelled	13.6	16	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
66	c3cjeA	Alignment	not modelled	12.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
67	c3dhnA	Alignment	not modelled	12.4	16	PDB header: isomerase, lyase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
68	c3k6gA	Alignment	not modelled	11.5	20	PDB header: protein binding Chain: A: PDB Molecule: telomeric repeat-binding factor 2-interacting protein 1; PDBTitle: crystal structure of rap1 and trf2 complex
69	c3efmA	Alignment	not modelled	10.6	13	PDB header: membrane protein Chain: A: PDB Molecule: ferric alcaligin siderophore receptor; PDBTitle: structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
70	c2ervA	Alignment	not modelled	9.8	11	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein paer03002360; PDBTitle: crystal structure of the outer membrane enzyme pagl
71	d2c7pa1	Alignment	not modelled	8.7	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: C5 cytosine-specific DNA methylase, DCM
72	c2q5xA	Alignment	not modelled	8.6	10	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore complex protein nup98; PDBTitle: crystal structure of the c-terminal domain of hnup98
73	d1i5pa1	Alignment	not modelled	7.9	23	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
74	c2konA	Alignment	not modelled	6.7	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of cv_2116 from chromobacterium2 violaceum. northeast structural genomics consortium target3 cvt4(1-82)
75	c2k4tA	Alignment	not modelled	6.4	15	PDB header: membrane protein,apoptosis Chain: A: PDB Molecule: voltage-dependent anion-selective channel PDBTitle: solution structure of human vdac-1 in ldao micelles
76	d1prtc2	Alignment	not modelled	6.1	20	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Aerolysin/Pertussis toxin (APT) domain