Phyre^2

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Description	P39321
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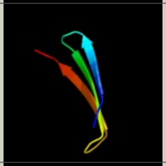
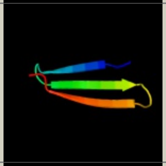
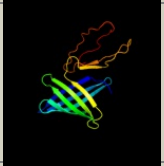
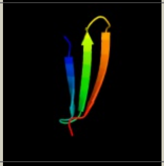
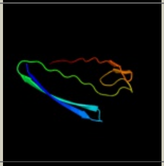
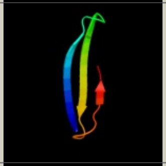
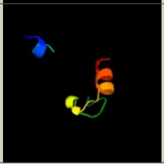
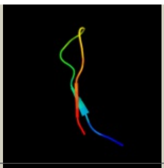
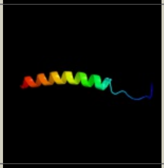
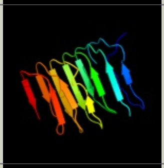
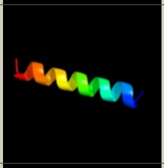
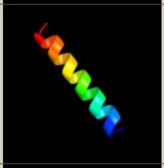
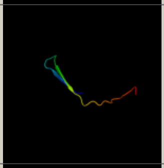
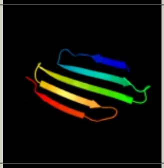
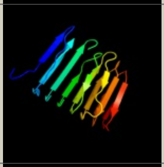
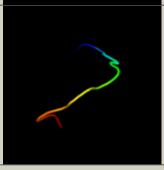
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v54g_	Alignment		72.3	16	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa
2	c3nb3C_	Alignment		68.0	17	**PDB header:**virus **Chain:** C: **PDB Molecule:**outer membrane protein a; **PDBTitle:** the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
3	d1qjpa_	Alignment		67.7	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
4	c1pbyA_	Alignment		38.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda **PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
5	d1p4ta_	Alignment		30.8	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
6	d1g90a_	Alignment		25.8	21	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
7	d1wuba_	Alignment		20.3	14	**Fold:**Streptavidin-like **Superfamily:**YceI-like **Family:**YceI-like
8	c2wjqA_	Alignment		18.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
9	d2olua1	Alignment		12.3	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
10	c2jmmA_	Alignment		11.4	15	**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
11	d2oqoa1	Alignment		11.0	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like

12	c2lhfA_	Alignment		10.2	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
13	d1xrda1	Alignment		9.8	14	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
14	c3petA_	Alignment		9.4	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**putative adhesin; **PDBTitle:** crystal structure of a putative adhesin (bf0245) from bacteroides2 fragilis nctc 9343 at 2.07 a resolution
15	c2y69Q_	Alignment		9.1	14	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
16	d1v54d_	Alignment		8.8	14	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
17	c2x27X_	Alignment		8.7	19	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
18	d1osma_	Alignment		8.1	18	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
19	c3lycL_	Alignment		7.9	14	**PDB header:**cell adhesion **Chain:** L: **PDB Molecule:**putative pectinase; **PDBTitle:** crystal structure of putative pectinase (yp_001304412.1) from2 parabacteroides distasonis atcc 8503 at 2.30 a resolution
20	d1efva2	Alignment		7.7	27	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
21	c2olvA_	Alignment	not modelled	7.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
22	d2guka1	Alignment	not modelled	7.5	18	**Fold:**PG1857-like **Superfamily:**PG1857-like **Family:**PG1857-like
23	c3dwkC_	Alignment	not modelled	7.5	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
24	c3o0rC_	Alignment	not modelled	7.2	17	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
25	d1m56d_	Alignment	not modelled	7.1	10	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
26	c2x4mD_	Alignment	not modelled	7.1	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
27	d1efpa2	Alignment	not modelled	7.1	33	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
28	c3uc0B_	Alignment	not modelled	6.8	18	**PDB header:**viral protein/immune system **Chain:** B: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2

29	c3bryB_	Alignment	not modelled	6.5	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
30	d1pbya3	Alignment	not modelled	6.5	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
31	c2f1tB_	Alignment	not modelled	6.4	14	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
32	c3hd7A_	Alignment	not modelled	6.2	12	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
33	c2k4tA_	Alignment	not modelled	6.2	13	**PDB header:**membrane protein,apoptosis **Chain:** A: **PDB Molecule:**voltage-dependent anion-selective channel **PDBTitle:** solution structure of human vdac-1 in ldao micelles
34	d1fsea_	Alignment	not modelled	6.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
35	c1efpC_	Alignment	not modelled	5.7	33	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**protein (electron transfer flavoprotein); **PDBTitle:** electron transfer flavoprotein (etf) from paracoccus2 denitrificans
36	d1bvp11	Alignment	not modelled	5.7	24	**Fold:**A virus capsid protein alpha-helical domain **Superfamily:**A virus capsid protein alpha-helical domain **Family:**Orbivirus capsid
37	d3clsd2	Alignment	not modelled	5.5	27	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
38	c1bvp5_	Alignment	not modelled	5.4	24	**PDB header:**viral protein **Chain:** 5: **PDB Molecule:**bluetongue virus coat protein vp7; **PDBTitle:** the crystal structure of bluetongue virus vp7
39	d2p5zx1	Alignment	not modelled	5.4	50	**Fold:**OB-fold **Superfamily:**gp5 N-terminal domain-like **Family:**gp4 N-terminal domain-like
40	d1ihma_	Alignment	not modelled	5.4	27	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Caliciviridae-like VP
41	c1ljzB_	Alignment	not modelled	5.4	67	**PDB header:**receptor, toxin **Chain:** B: **PDB Molecule:**acetylcholine receptor protein; **PDBTitle:** nmr structure of an achr-peptide (torpedo californica,2 alpha-subunit residues 182-202) in complex with alpha-3 bungarotoxin
42	c1ihmC_	Alignment	not modelled	5.4	27	**PDB header:**virus **Chain:** C: **PDB Molecule:**capsid protein; **PDBTitle:** crystal structure analysis of norwalk virus capsid
43	c3ltgA_	Alignment	not modelled	5.3	20	**PDB header:**transferase/transferase regulator **Chain:** A: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** crystal structure of the drosophila epidermal growth factor receptor2 ectodomain complexed with a low affinity spitz mutant
44	c1qiuC_	Alignment	not modelled	5.2	16	**PDB header:**fibre protein **Chain:** C: **PDB Molecule:**adenovirus fibre; **PDBTitle:** a triple beta-spiral in the adenovirus fibre shaft reveals2 a new structural motif for biological fibres