Phyre^2

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Description	P0AER8
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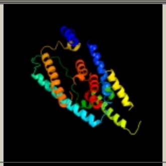
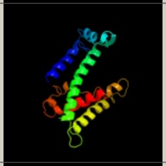
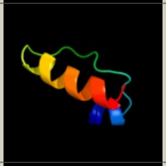
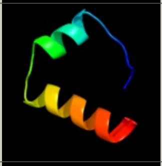
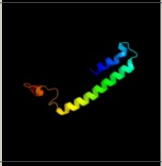
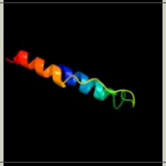
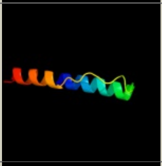
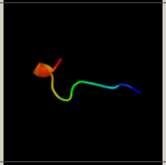
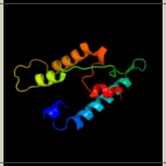
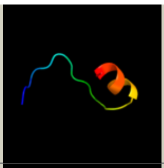
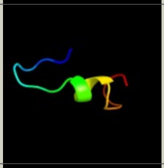
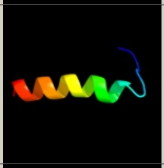
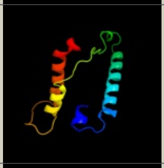
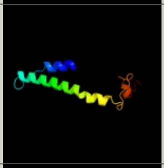
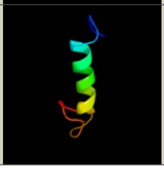
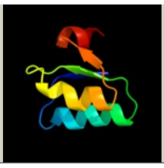
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2nwwa1	Alignment		93.7	17	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
2	c1zcdA_	Alignment		28.7	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na(+)/h(+) antiporter 1; **PDBTitle:** crystal structure of the na+/h+ antiporter nhaa
3	d1e9yb2	Alignment		24.9	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
4	d1ejxc2	Alignment		23.4	37	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
5	c3b9yA_	Alignment		18.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
6	c3chxF_	Alignment		8.7	19	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**pmoa; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
7	d3bl2a1	Alignment		8.4	19	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
8	c1yewF_	Alignment		7.9	24	**PDB header:**oxidoreductase, membrane protein **Chain:** F: **PDB Molecule:**particulate methane monooxygenase, a subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
9	d2fnaa1	Alignment		7.2	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
10	c3gd8A_	Alignment		7.1	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
11	d2pv7a2	Alignment		6.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain

12	c3cpiH_	Alignment		6.9	29	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**rab gdp-dissociation inhibitor; **PDBTitle:** crystal structure of yeast rab-gdi
13	d1ivya_	Alignment		6.4	39	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Serine carboxypeptidase-like
14	c3czcA_	Alignment		6.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
15	c2d57A_	Alignment		6.1	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
16	c3hd6A_	Alignment		5.9	12	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
17	d1ohea2	Alignment		5.5	33	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like

18	c3pduF_	Alignment		5.3	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase family protein; **PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+