Phyre^2

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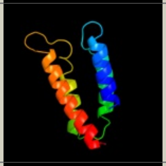
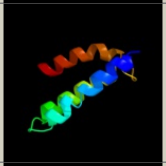
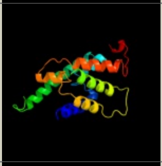
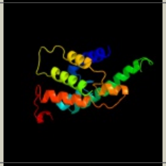
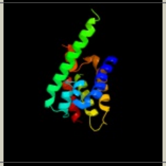
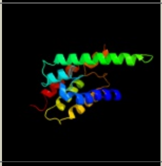
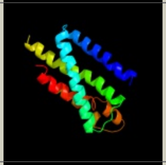
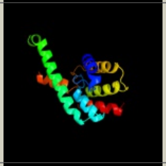
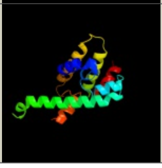
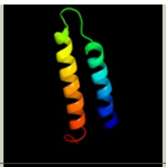
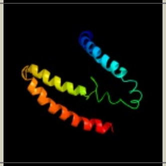
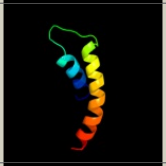
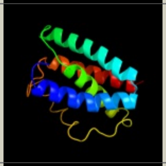
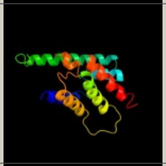
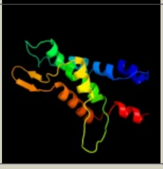
Description	P76186
Date	Thu Jan 5 12:20:15 GMT 2012
Unique Job ID	426a5911f7d96b95

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k3gA_	Alignment		85.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**urea transporter; **PDBTitle:** crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
2	c2ksfA_	Alignment		54.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein kdpd; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor kdpd, center for structures of3 membrane proteins (csmp) target 4312c
3	d2r6gf1	Alignment		36.2	11	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
4	d1ymga1	Alignment		34.6	13	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
5	c1ymgA_	Alignment		34.6	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
6	c3llqB_	Alignment		26.9	20	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin z 2; **PDBTitle:** aquaporin structure from plant pathogen agrobacterium tumerfaciens
7	c2b5fD_	Alignment		26.7	17	**PDB header:**transport protein,membrane protein **Chain:** D: **PDB Molecule:**aquaporin; **PDBTitle:** crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
8	d1rc2a_	Alignment		22.3	17	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
9	c3k07A_	Alignment		20.7	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
10	d1fx8a_	Alignment		13.6	14	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
11	c1ldaA_	Alignment		13.6	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycerol uptake facilitator protein; **PDBTitle:** crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol

12	d1iwga7	Alignment		13.2	17	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
13	c2yvxD_	Alignment		12.4	14	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
14	d1kpla_	Alignment		11.4	18	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
15	c3d9sB_	Alignment		10.8	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
16	c2kr6A_	Alignment		10.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**presenilin-1; **PDBTitle:** solution structure of presenilin-1 ctf subunit
17	d2nr9a1	Alignment		9.2	7	**Fold:**Rhomboid-like **Superfamily:**Rhomboid-like **Family:**Rhomboid-like
18	c2w2eA_	Alignment		8.9	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin; **PDBTitle:** 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
19	c2d57A_	Alignment		8.8	7	**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
20	c2ht2B_	Alignment		8.1	19	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
21	c2oarA_	Alignment	not modelled	7.8	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
22	d2oara1	Alignment	not modelled	7.6	20	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
23	c1oy8A_	Alignment	not modelled	7.0	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
24	d1h6ia_	Alignment	not modelled	6.8	14	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
25	c1ciiA_	Alignment	not modelled	6.7	14	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
26	c3dh4A_	Alignment	not modelled	6.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
27	c3mk7F_	Alignment	not modelled	6.5	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
28	c3nd0A_	Alignment	not modelled	6.5	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
						PDB header:membrane protein

29	c3hzqA_	Alignment	not modelled	6.5	17	**Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state
30	c2jo1A_	Alignment	not modelled	6.4	19	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
31	d2yvxa3	Alignment	not modelled	5.9	14	**Fold:**MgtE membrane domain-like **Superfamily:**MgtE membrane domain-like **Family:**MgtE membrane domain-like
32	c3iyzA_	Alignment	not modelled	5.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** structure of aquaporin-4 s180d mutant at 10.0 a resolution from2 electron micrograph
33	d1s7ba_	Alignment	not modelled	5.7	12	**Fold:**Multidrug resistance efflux transporter EmrE **Superfamily:**Multidrug resistance efflux transporter EmrE **Family:**Multidrug resistance efflux transporter EmrE
34	c2zxeG_	Alignment	not modelled	5.6	16	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
35	d2o7ta2	Alignment	not modelled	5.2	18	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
36	d1j4na_	Alignment	not modelled	5.2	13	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
37	d1k1fa_	Alignment	not modelled	5.1	20	**Fold:**Bcr-Abl oncoprotein oligomerization domain **Superfamily:**Bcr-Abl oncoprotein oligomerization domain **Family:**Bcr-Abl oncoprotein oligomerization domain