Phyre^{2}

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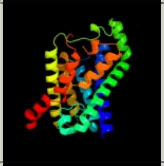
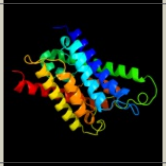
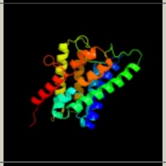
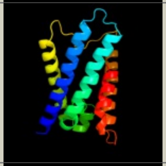
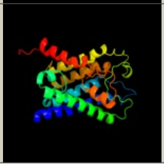
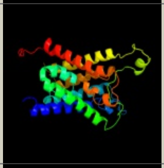
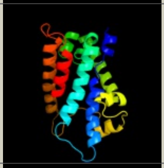
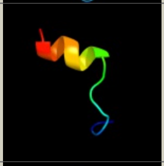
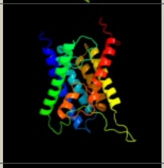
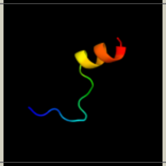
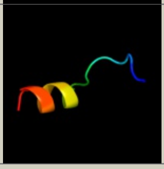
Description	P0AC23
Date	Thu Jan 5 11:16:57 GMT 2012
Unique Job ID	f5431b30df416b7a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3klzE_	Alignment		100.0	55	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**putative formate transporter 1; **PDBTitle:** pentameric formate channel with formate bound
2	c3kcvG_	Alignment		100.0	100	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**probable formate transporter 1; **PDBTitle:** structure of formate channel
3	c1ldaA_	Alignment		95.6	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
4	d1fx8a_	Alignment		95.6	14	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
5	c3llqB_	Alignment		93.6	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin z 2; **PDBTitle:** aquaporin structure from plant pathogen agrobacterium tumerfaciens
6	c2b5fD_	Alignment		91.0	11	**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
7	d1rc2a_	Alignment		88.9	11	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
8	c3iyzA_	Alignment		88.4	16	**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
9	c3gd8A_	Alignment		84.6	17	**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
10	c2w2eA_	Alignment		79.5	12	**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
11	d1j4na_	Alignment		77.9	12	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like

12	c2d57A_	Alignment		77.6	15	**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
13	c3c02A_	Alignment		73.3	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaglyceroporin; **PDBTitle:** x-ray structure of the aquaglyceroporin from plasmodium falciparum
14	c3d9sB_	Alignment		50.3	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
15	c2f2bA_	Alignment		48.5	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin aqpm; **PDBTitle:** crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
16	d1w2za2	Alignment		46.4	25	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
17	c1ymgA_	Alignment		46.0	14	**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
18	d1ymga1	Alignment		46.0	14	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
19	d1d6za2	Alignment		41.9	21	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
20	d2oqea2	Alignment		41.3	25	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
21	d1w6ga2	Alignment	not modelled	40.6	25	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
22	d1h6ia_	Alignment	not modelled	21.0	9	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
23	c3e49A_	Alignment	not modelled	16.1	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849 with a tim barrel fold; **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bxe_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
24	c3lotC_	Alignment	not modelled	15.5	18	**PDB header:**structure genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
25	c3c6cA_	Alignment	not modelled	15.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
26	c2y7eA_	Alignment	not modelled	13.6	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
27	d1c17m_	Alignment	not modelled	13.6	31	**Fold:**F1F0 ATP synthase subunit A **Superfamily:**F1F0 ATP synthase subunit A **Family:**F1F0 ATP synthase subunit A

28	c1ksiA_	Alignment	not modelled	12.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a eukaryotic (pea seedling) copper-containing2 amine oxidase at 2.2a resolution
29	c3loyB_	Alignment	not modelled	12.5	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a copper-containing benzylamine oxidase from2 hansenula polymorpha
30	c3no5C_	Alignment	not modelled	12.1	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
31	c3chvA_	Alignment	not modelled	11.9	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
32	c1d6uB_	Alignment	not modelled	11.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
33	c1ui7A_	Alignment	not modelled	11.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenylethylamine oxidase; **PDBTitle:** site-directed mutagenesis of his433 involved in binding of2 copper ion in arthrobacter globiformis amine oxidase
34	c1ekmC_	Alignment	not modelled	10.5	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure at 2.5 a resolution of zinc-substituted2 copper amine oxidase of hansenula polymorpha expressed in3 escherichia coli
35	c3nbbC_	Alignment	not modelled	10.1	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxisomal primary amine oxidase; **PDBTitle:** crystal structure of mutant y305f expressed in e. coli in the copper2 amine oxidase from hansenula polymorpha
36	c3e02A_	Alignment	not modelled	9.3	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849; **PDBTitle:** crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
37	c2jy0A_	Alignment	not modelled	8.5	50	**PDB header:**membrane protein, viral protein **Chain:** A: **PDB Molecule:**protease ns2-3; **PDBTitle:** solution nmr structure of hcv ns2 protein, membrane segment2 (1-27)
38	d2c1wa1	Alignment	not modelled	8.2	67	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Eukaryotic EndoU ribonuclease
39	d1rm6b2	Alignment	not modelled	7.7	25	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
40	d2foka2	Alignment	not modelled	7.0	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Restriction endonuclease FokI, N-terminal (recognition) domain
41	c1rm6E_	Alignment	not modelled	6.9	25	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**4-hydroxybenzoyl-coa reductase beta subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
42	c2voyG_	Alignment	not modelled	5.5	39	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus