Phyre2

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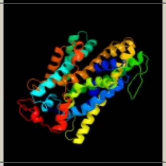
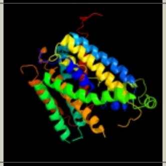
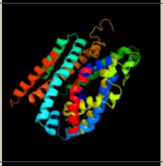
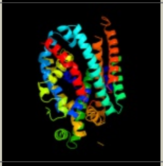
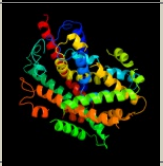
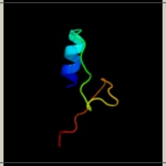
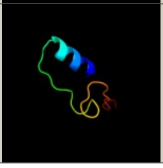
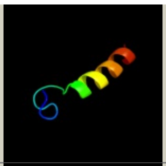
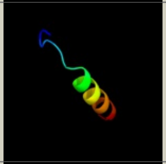
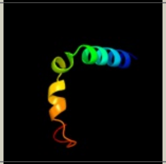
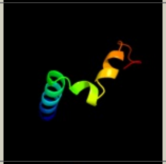
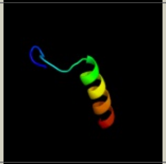
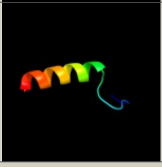
Description	P30143
Date	Thu Jan 5 11:46:07 GMT 2012
Unique Job ID	ad74ab9e09d57c49

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3giaA_	Alignment		99.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
2	c2jlnA_	Alignment		99.8	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
3	c3lrcC_	Alignment		99.6	15	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
4	c3dh4A_	Alignment		99.0	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
5	c2xq2A_	Alignment		99.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
6	d2a65a1	Alignment		98.7	15	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
7	c2w8aC_	Alignment		96.0	14	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
8	c3hfxA_	Alignment		94.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
9	d1c8za_	Alignment		48.2	23	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**Transcriptional factor tubby, C-terminal domain
10	c2h2wA_	Alignment		30.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
11	d2ghra1	Alignment		28.3	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like

12	d1ml8a_	Alignment		26.9	0	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**YhfA-like
13	d1vlaa_	Alignment		22.7	14	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**YhfA-like
14	d1htjf_	Alignment		22.4	19	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
15	c1htjF_	Alignment		22.4	19	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**kiaa0380; **PDBTitle:** structure of the rgs-like domain from pdz-rhogef
16	c2kncB_	Alignment		19.2	13	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
17	d2hxva2	Alignment		18.4	10	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
18	d1fftb2	Alignment		17.5	8	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
19	c1lqlE_	Alignment		16.8	22	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**osmotical inducible protein c like family; **PDBTitle:** crystal structure of osmc like protein from mycoplasma2 pneumoniae
20	d1lqla_	Alignment		16.8	22	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
21	c2lkgA_	Alignment	not modelled	16.8	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acetylcholine receptor; **PDBTitle:** wsa major conformation
22	c2k21A_	Alignment	not modelled	16.6	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
23	d1z3aa1	Alignment	not modelled	15.4	23	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
24	d1qwia_	Alignment	not modelled	15.3	14	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
25	c2egtA_	Alignment	not modelled	14.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein aq_1549; **PDBTitle:** crystal structure of hypothetical protein (aq1549) from aquifex2 aeolicus
26	d2pn2a1	Alignment	not modelled	13.5	20	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
27	d2b3ja1	Alignment	not modelled	12.9	11	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
28	c2be6F_	Alignment	not modelled	12.3	19	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex

29	c2bjoA_	Alignment	not modelled	11.5	23	**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
30	c3m4wH_	Alignment	not modelled	10.6	44	**PDB header:**signaling protein/signaling protein **Chain:** H: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** structural basis for the negative regulation of bacterial stress2 response by rseb
31	c1shzF_	Alignment	not modelled	8.7	15	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**rho guanine nucleotide exchange factor 1; **PDBTitle:** crystal structure of the p115rhogef rgrgs domain in a2 complex with galpha(13):galpha(i1) chimera
32	c3eerA_	Alignment	not modelled	8.4	14	**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
33	d2b3za2	Alignment	not modelled	8.2	15	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
34	d2onfa1	Alignment	not modelled	8.1	17	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
35	c2kncA_	Alignment	not modelled	7.9	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
36	d2opla1	Alignment	not modelled	7.7	13	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
37	c2latA_	Alignment	not modelled	7.4	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** solution structure of a human minimembrane protein ost4
38	d2d7va1	Alignment	not modelled	7.4	4	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
39	c2pjwH_	Alignment	not modelled	7.0	24	**PDB header:**endocytosis/exocytosis **Chain:** H: **PDB Molecule:**uncharacterized protein yhl002w; **PDBTitle:** the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
40	d2fika2	Alignment	not modelled	6.9	20	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
41	c1k8vA_	Alignment	not modelled	6.9	45	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**neuropeptide f; **PDBTitle:** the nmr-derived conformation of neuropeptide f from2 moniezia expansa
42	d2o34a1	Alignment	not modelled	6.8	16	**Fold:**T-fold **Superfamily:**ApbE-like **Family:**DVU1097-like
43	c1iflA_	Alignment	not modelled	6.6	16	**PDB header:**virus **Chain:** A: **PDB Molecule:**inovirus; **PDBTitle:** molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13),3 if1 and ike
44	c2ql8A_	Alignment	not modelled	6.6	22	**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
45	c2qy6A_	Alignment	not modelled	6.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0209 protein yfck; **PDBTitle:** crystal structure of the n-terminal domain of upf0209 protein yfck2 from escherichia coli o157:h7
46	c2kluA_	Alignment	not modelled	6.3	30	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
47	c3mk7F_	Alignment	not modelled	6.1	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
48	c3cjeA_	Alignment	not modelled	6.1	9	**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
49	d1p6oa_	Alignment	not modelled	6.1	11	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
50	d1iapa_	Alignment	not modelled	6.0	13	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
51	c3lm3A_	Alignment	not modelled	5.9	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase/deacetylase2 (bdi_3119) from parabacteroides distasonis at 1.44 a resolution
52	d1uspa_	Alignment	not modelled	5.8	18	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins

53	d2a6aa1	Alignment	not modelled	5.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
54	c2nx8A_	Alignment	not modelled	5.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna-specific adenosine deaminase; **PDBTitle:** the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
55	d2po6a2	Alignment	not modelled	5.4	15	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
56	d1onqa2	Alignment	not modelled	5.3	15	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
57	c2x58B_	Alignment	not modelled	5.2	42	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa