Phyre^{2}

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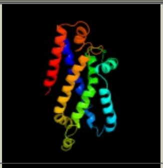
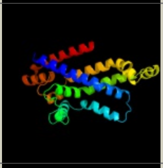
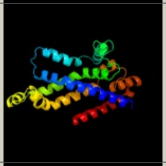
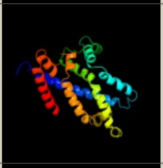
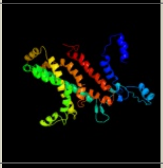
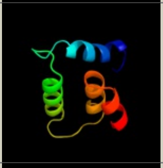
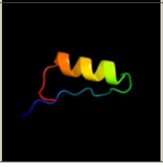
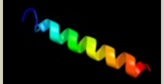
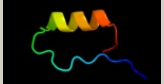
Description	P0AEF8
Date	Thu Jan 5 11:23:12 GMT 2012
Unique Job ID	36d28c511a3f81fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3dhwa1	Alignment		99.9	23	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
2	d2onkc1	Alignment		99.8	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
3	c2onkC_	Alignment		99.8	12	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
4	c3d31D_	Alignment		99.7	11	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
5	d3d31c1	Alignment		99.7	11	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
6	d2r6gf2	Alignment		99.6	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c3fh6F_	Alignment		99.6	15	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
8	c2r6gF_	Alignment		99.5	12	**PDB header:**hydrolase/transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** the crystal structure of the e. coli maltose transporter
9	d2r6gg1	Alignment		99.1	13	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c1ciiA_	Alignment		26.3	16	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
11	c3ednB_	Alignment		26.2	21	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**phenazine biosynthesis protein, phzf family; **PDBTitle:** crystal structure of the bacillus anthracis phenazine2 biosynthesis protein, phzf family

12	d1qy9a1	Alignment		26.2	17	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
13	c2ka1A_	Alignment		24.4	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
14	c2ka2B_	Alignment		24.4	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
15	c2ka2A_	Alignment		24.4	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
16	c2ka1B_	Alignment		24.4	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
17	d1xuba1	Alignment		23.5	21	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
18	c1u0kA_	Alignment		21.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gene product pa4716; **PDBTitle:** the structure of a predicted epimerase pa4716 from pseudomonas2 aeruginosa
19	d1u0ka1	Alignment		20.1	10	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
20	d1s7ja_	Alignment		19.6	17	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
21	c2j5dA_	Alignment	not modelled	19.5	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
22	c1u1wA_	Alignment	not modelled	19.4	21	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**phenazine biosynthesis protein phzf; **PDBTitle:** structure and function of phenazine-biosynthesis protein phzf from2 pseudomonas fluorescens 2-79
23	c1wz4A_	Alignment	not modelled	19.4	38	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**major surface antigen; **PDBTitle:** solution conformation of adr subtype hbv pre-s2 epitope
24	c1qy9B_	Alignment	not modelled	17.1	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ydde; **PDBTitle:** crystal structure of e. coli se-met protein ydde
25	d2d6fc1	Alignment	not modelled	16.9	15	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
26	c2cw1A_	Alignment	not modelled	16.1	32	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
27	c2iv1J_	Alignment	not modelled	16.0	22	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
28	c1y66D_	Alignment	not modelled	13.6	21	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**engrailed homeodomain; **PDBTitle:** dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3

						variant
29	c2hw2A_	Alignment	not modelled	13.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
30	d1a9xa1	Alignment	not modelled	12.9	19	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
31	c1ym5A_	Alignment	not modelled	10.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical 32.6 kda protein in dap2-slt2 **PDBTitle:** crystal structure of yhi9, the yeast member of the2 phenazine biosynthesis phzf enzyme superfamily.
32	c2v9kA_	Alignment	not modelled	9.6	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein flj32312; **PDBTitle:** crystal structure of human pus10, a novel pseudouridine2 synthase.
33	d1n0ua5	Alignment	not modelled	8.8	23	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
34	d2oara1	Alignment	not modelled	8.3	13	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
35	d1dwka1	Alignment	not modelled	8.0	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
36	d1g2ha_	Alignment	not modelled	7.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
37	c2b9sB_	Alignment	not modelled	6.7	38	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
38	c2oarA_	Alignment	not modelled	6.6	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
39	c1umqA_	Alignment	not modelled	6.4	19	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
40	d1umqa_	Alignment	not modelled	6.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
41	d1ddfa_	Alignment	not modelled	5.8	6	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
42	d2auwa1	Alignment	not modelled	5.7	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
43	d1gt1a_	Alignment	not modelled	5.5	18	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
44	c2knaA_	Alignment	not modelled	5.5	10	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** solution structure of uba domain of xiap