Phyre2

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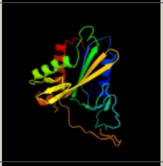
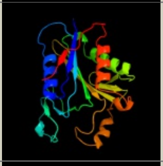
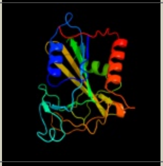
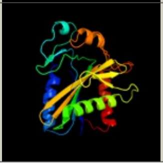
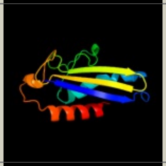
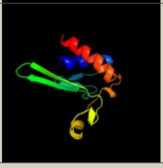
Description	P60720
Date	Thu Jan 5 12:07:03 GMT 2012
Unique Job ID	e76ed21bf11c66d4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w66a1	Alignment		100.0	31	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
2	c2qhvA_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoyltransferase; **PDBTitle:** structural basis of octanoic acid recognition by lipoate-protein2 ligase b
3	c2qhsA_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoyltransferase; **PDBTitle:** structural basis of octanoic acid recognition by lipoate-protein2 ligase b
4	c1x2gB_	Alignment		100.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lipoate-protein ligase a; **PDBTitle:** crystal structure of lipate-protein ligase a from2 escherichia coli
5	c1vqzA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
6	c2e5aA_	Alignment		100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoyltransferase 1; **PDBTitle:** crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
7	d1x2ga2	Alignment		100.0	17	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
8	d2c8ma1	Alignment		100.0	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
9	d1vqza2	Alignment		100.0	17	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
10	d2p5ia1	Alignment		100.0	13	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
11	d2p0la1	Alignment		100.0	11	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like

12	d2zgwa2	Alignment		99.2	20	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Biotin holoenzyme synthetase
13	c2ewnA_	Alignment		99.0	15	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
14	c2ej9A_	Alignment		99.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative biotin ligase; **PDBTitle:** crystal structure of biotin protein ligase from2 methanococcus jannaschii
15	c2eayB_	Alignment		98.9	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin [acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from aquifex2 aeolicus
16	c3bfmA_	Alignment		98.8	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**biotin protein ligase-like protein of unknown function; **PDBTitle:** crystal structure of a biotin protein ligase-like protein of unknown2 function (tm1040_0394) from silicibacter sp. tm1040 at 1.70 a3 resolution
17	c2dzcA_	Alignment		98.8	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin--[acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from pyrococcus2 horikoshii, mutation r48a
18	d1biaa3	Alignment		98.6	16	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Biotin holoenzyme synthetase
19	c2cghB_	Alignment		98.6	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin ligase; **PDBTitle:** crystal structure of biotin ligase from mycobacterium2 tuberculosis
20	d2ddza1	Alignment		97.5	20	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**PH0223-like
21	d2qfra2	Alignment	not modelled	22.8	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
22	c3lr4A_	Alignment	not modelled	19.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
23	d1knxa1	Alignment	not modelled	17.9	11	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
24	c1xzwB_	Alignment	not modelled	12.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** sweet potato purple acid phosphatase/phosphate complex
25	c1kbpB_	Alignment	not modelled	11.9	16	**PDB header:**hydrolase (phosphoric monoester) **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** kidney bean purple acid phosphatase
26	c3uotB_	Alignment	not modelled	10.1	11	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
27	d1ra0a1	Alignment	not modelled	9.8	17	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Cytosine deaminase
28	c1ponB_	Alignment	not modelled	8.2	15	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**troponin c; **PDBTitle:** site iii-site iv troponin c heterodimer, nmr

29	c2kd2A_	Alignment	not modelled	7.3	22	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** nmr structure of faim-ctd
30	d1m7ja1	Alignment	not modelled	7.2	31	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**D-aminoacylase
31	d1vsra_	Alignment	not modelled	7.2	23	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
32	c2j3tB_	Alignment	not modelled	6.9	9	**PDB header:**transport **Chain:** B: **PDB Molecule:**trafficking protein particle complex subunit 6a; **PDBTitle:** the crystal structure of the bet3-trs33-bet5-trs23 complex.
33	d1qbaa1	Alignment	not modelled	6.6	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
34	c2faoB_	Alignment	not modelled	6.5	20	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**probable atp-dependent dna ligase; **PDBTitle:** crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
35	c2iruA_	Alignment	not modelled	6.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative dna ligase-like protein rv0938/mt0965; **PDBTitle:** crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
36	d1xzwa2	Alignment	not modelled	5.6	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
37	d1kfia3	Alignment	not modelled	5.5	11	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
38	c2jpeA_	Alignment	not modelled	5.4	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear inhibitor of protein phosphatase 1; **PDBTitle:** fha domain of nipp1
39	d1k1da1	Alignment	not modelled	5.4	23	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)