Phyre2

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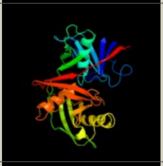
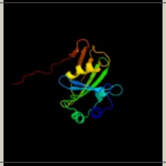
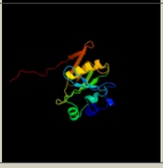
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gkjA_	Alignment		100.0	77	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of diaminopimelate epimerase in complex2 with an irreversible inhibitor dl-azidap
2	c3ekmE_	Alignment		100.0	41	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**diaminopimelate epimerase, chloroplastic; **PDBTitle:** crystal structure of diaminopimelate epimerase form2 arabidopsis thaliana in complex with irreversible inhibitor3 dl-azidap
3	c3fveA_	Alignment		100.0	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of diaminopimelate epimerase mycobacterium2 tuberculosis dapf
4	c2otnB_	Alignment		100.0	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of the catalytically active form of diaminopimelate2 epimerase from bacillus anthracis
5	c3ednB_	Alignment		100.0	20	**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
6	c1qy9B_	Alignment		100.0	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ydde; **PDBTitle:** crystal structure of e. coli se-met protein ydde
7	c1ym5A_	Alignment		100.0	17	**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.
8	d1s7ja_	Alignment		100.0	14	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
9	c1u1wA_	Alignment		100.0	20	**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
10	c1u0kA_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gene product pa4716; **PDBTitle:** the structure of a predicted epimerase pa4716 from pseudomonas2 aeruginosa
11	c2azpA_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa1268; **PDBTitle:** crystal structure of pa1268 solved by sulfur sad

12	d2gkea1	Alignment		100.0	81	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
13	c1w62B_	Alignment		100.0	15	**PDB header:**racemase **Chain:** B: **PDB Molecule:**b-cell mitogen; **PDBTitle:** proline racemase in complex with one molecule of pyrrole-2-2 carboxylic acid (hemi form)
14	d1tm0a_	Alignment		100.0	17	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Proline racemase
15	d2gkea2	Alignment		100.0	75	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
16	d1qy9a1	Alignment		99.9	21	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
17	d1xuba1	Alignment		99.9	17	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
18	d1xuba2	Alignment		99.9	20	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
19	d1u0ka1	Alignment		99.9	18	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
20	d1qy9a2	Alignment		99.8	15	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
21	d1u0ka2	Alignment	not modelled	99.7	20	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
22	c3g7kD_	Alignment	not modelled	98.6	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**3-methylitaconate isomerase; **PDBTitle:** crystal structure of methylitaconate-delta-isomerase
23	c2pw0A_	Alignment	not modelled	98.4	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prpf methylaconitate isomerase; **PDBTitle:** crystal structure of trans-aconitate bound to methylaconitate2 isomerase prpf from shewanella oneidensis
24	d2h9fa2	Alignment	not modelled	96.6	21	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
25	d2h9fa1	Alignment	not modelled	61.8	15	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
26	c3g12A_	Alignment	not modelled	39.2	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
27	c3ldgA_	Alignment	not modelled	36.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.472; **PDBTitle:** crystal structure of smu.472, a putative methyltransferase complexed2 with sah
28	c3sk1C_	Alignment	not modelled	31.5	24	**PDB header:**griseoluteate-binding protein **Chain:** C: **PDB Molecule:**ehpr; **PDBTitle:** crystal structure of phenazine resistance protein ehpr from2 enterobacter agglomerans (erwinia herbicola, pantoea agglomerans)3 eh1087, apo form

29	c2l3bA_	Alignment	not modelled	30.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
30	d1o9ga_	Alignment	not modelled	29.6	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase AviRa
31	c2l7qA_	Alignment	not modelled	27.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of conjugate transposon protein bvu_1572(27-2 141) from bacteroides vulgatus, northeast structural genomics3 consortium target bvr155
32	c3k0bA_	Alignment	not modelled	26.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted n6-adenine-specific dna methylase; **PDBTitle:** crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365
33	c1g38A_	Alignment	not modelled	22.2	38	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**modification methylase taqi; **PDBTitle:** adenine-specific methyltransferase m. taq i/dna complex
34	d2f8la1	Alignment	not modelled	21.0	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
35	d2ar0a1	Alignment	not modelled	19.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
36	d1c4qa_	Alignment	not modelled	19.6	15	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
37	c3lkdB_	Alignment	not modelled	19.0	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type i restriction-modification system **PDBTitle:** crystal structure of the type i restriction-modification2 system methyltransferase subunit from streptococcus3 thermophilus, northeast structural genomics consortium4 target sur80
38	c3lduA_	Alignment	not modelled	17.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methylase; **PDBTitle:** the crystal structure of a possible methylase from2 clostridium difficile 630.
39	d2ih2a1	Alignment	not modelled	17.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**DNA methylase TaqI, N-terminal domain
40	c2kjzA_	Alignment	not modelled	17.0	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**atc0852; **PDBTitle:** solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2.
41	d1sr8a_	Alignment	not modelled	16.4	19	**Fold:**CbiD-like **Superfamily:**CbiD-like **Family:**CbiD-like
42	c1aqjB_	Alignment	not modelled	15.6	21	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**adenine-n6-dna-methyltransferase taqi; **PDBTitle:** structure of adenine-n6-dna-methyltransferase taqi
43	d1r4pb_	Alignment	not modelled	15.4	17	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
44	c3owvA_	Alignment	not modelled	14.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-entry nuclease; **PDBTitle:** structural insights into catalytic and substrate binding mechanisms of2 the strategic enda nuclease from streptococcus pneumoniae
45	c2waqG_	Alignment	not modelled	14.6	25	**PDB header:**transcription **Chain:** G: **PDB Molecule:**dna-directed rna polymerase rpo8 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
46	d2okca1	Alignment	not modelled	13.9	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
47	c3fd5B_	Alignment	not modelled	13.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase 1; **PDBTitle:** crystal structure of human selenophosphate synthetase 12 complex with ampcp
48	c3khkA_	Alignment	not modelled	13.6	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**type i restriction-modification system **PDBTitle:** crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazei.
49	d1h6za2	Alignment	not modelled	13.1	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
50	c3hvzB_	Alignment	not modelled	12.9	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
51	c2xh3B_	Alignment	not modelled	12.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**spd1 nuclease; **PDBTitle:** extracellular nuclease
						PDB header:hydrolase

52	c2kmmA_	Alignment	not modelled	11.9	13	**Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
53	d1n2aa2	Alignment	not modelled	11.3	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
54	c2xznC_	Alignment	not modelled	10.7	12	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**kh domain containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
55	c3p9nA_	Alignment	not modelled	9.7	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible methyltransferase (methylase); **PDBTitle:** rv2966c of m. tuberculosis is a rsmd-like methyltransferase
56	c1wqaB_	Alignment	not modelled	9.5	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phospho-sugar mutase; **PDBTitle:** crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
57	d1twua_	Alignment	not modelled	9.1	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein YycE
58	c3ghjA_	Alignment	not modelled	9.0	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative integron gene cassette protein; **PDBTitle:** crystal structure from the mobile metagenome of halifax2 harbour sewage outfall: integron cassette protein hfx_cass4
59	c2ph0A_	Alignment	not modelled	9.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q6d2t7_erwct protein from erwinia2 carotovora. nesg target ewr41.
60	d2hqva1	Alignment	not modelled	8.9	13	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**ChuX-like
61	c3r6aB_	Alignment	not modelled	8.8	12	**PDB header:**isomerase, lyase **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein (hypothetical protein2 mm_3218) from methanosarcina mazei.
62	c2zifB_	Alignment	not modelled	8.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative modification methylase; **PDBTitle:** crystal structure of ttha0409, putative dna modification2 methylase from thermus thermophilus hb8- complexed with s-3 adenosyl-l-methionine
63	d1g60a_	Alignment	not modelled	8.5	46	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Type II DNA methylase
64	c2oviA_	Alignment	not modelled	7.9	17	**PDB header:**ligand binding protein, metal transport **Chain:** A: **PDB Molecule:**hypothetical protein chux; **PDBTitle:** structure of the heme binding protein chux
65	d1p3da1	Alignment	not modelled	7.8	18	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
66	d2bosa_	Alignment	not modelled	7.7	17	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
67	d1booa_	Alignment	not modelled	7.5	31	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Type II DNA methylase
68	c2f7lA_	Alignment	not modelled	7.5	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**455aa long hypothetical phospho-sugar mutase; **PDBTitle:** crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
69	c3m05A_	Alignment	not modelled	7.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480; **PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
70	c3s1sA_	Alignment	not modelled	7.3	20	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**restriction endonuclease bpusi; **PDBTitle:** characterization and crystal structure of the type iig restriction2 endonuclease bpusi
71	d1wy7a1	Alignment	not modelled	6.4	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
72	d1m7va_	Alignment	not modelled	6.3	18	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
73	d1ne2a_	Alignment	not modelled	6.3	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
74	c2fkdK_	Alignment	not modelled	6.2	30	**PDB header:**transcription regulator **Chain:** K: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of the c-terminal domain of bacteriophage2 186 repressor
75	d2hiya1	Alignment	not modelled	6.2	18	**Fold:**SP0830-like **Superfamily:**SP0830-like **Family:**SP0830-like
76	c3gm5A_	Alignment	not modelled	6.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**lactoylglutathione lyase and related lyases; **PDBTitle:** crystal structure of a putative methylmalonyl-coenzyme

						a2 epimerase from thermoanaerobacter tengcongensis at 2.0 a3 resolution
77	c2h8bB_	Alignment	not modelled	6.1	18	**PDB header:**hormone/growth factor **Chain:** B: **PDB Molecule:**insulin-like 3; **PDBTitle:** solution structure of insl3
78	d1j3aa_	Alignment	not modelled	6.1	10	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
79	d1nhya2	Alignment	not modelled	6.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
80	c1okgA_	Alignment	not modelled	6.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
81	c1nw6A_	Alignment	not modelled	6.0	43	**PDB header:**transferase **Chain:** A: **PDB Molecule:**modification methylase rsri; **PDBTitle:** structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin
82	d2esra1	Alignment	not modelled	5.9	40	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
83	c1c4gB_	Alignment	not modelled	5.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate **PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex
84	d1hksa_	Alignment	not modelled	5.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-shock transcription factor
85	d1xrka_	Alignment	not modelled	5.5	7	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
86	d1autl1	Alignment	not modelled	5.4	43	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
87	d1go4a_	Alignment	not modelled	5.4	18	**Fold:**The spindle assembly checkpoint protein mad2 **Superfamily:**The spindle assembly checkpoint protein mad2 **Family:**The spindle assembly checkpoint protein mad2
88	c2f40A_	Alignment	not modelled	5.3	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf1455; **PDBTitle:** structure of a novel protein from backbone-centered nmr data and nmr-2 assisted structure prediction
89	d1xo8a_	Alignment	not modelled	5.2	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like