Phyre^2

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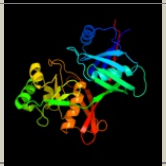
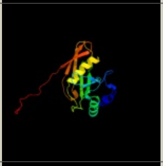
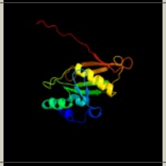
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qy9B_	Alignment		100.0	98	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ydde; **PDBTitle:** crystal structure of e. coli se-met protein ydde
2	c3ednB_	Alignment		100.0	32	**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
3	c1ym5A_	Alignment		100.0	23	**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.
4	c1u1wA_	Alignment		100.0	30	**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
5	c1u0kA_	Alignment		100.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gene product pa4716; **PDBTitle:** the structure of a predicted epimerase pa4716 from pseudomonas2 aeruginosa
6	d1s7ja_	Alignment		100.0	31	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
7	c3ekmE_	Alignment		100.0	16	**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
8	c2otnB_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of the catalytically active form of diaminopimelate2 epimerase from bacillus anthracis
9	c2gkjA_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of diaminopimelate epimerase in complex2 with an irreversible inhibitor dl-azidap
10	c2azpA_	Alignment		100.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa1268; **PDBTitle:** crystal structure of pa1268 solved by sulfur sad
11	c1w62B_	Alignment		100.0	13	**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)

12	d1qy9a1	Alignment		100.0	99	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
13	c3fveA_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of diaminopimelate epimerase mycobacterium2 tuberculosis dapf
14	d1u0ka1	Alignment		100.0	26	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
15	d1xuba1	Alignment		100.0	33	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
16	d1qy9a2	Alignment		100.0	98	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
17	d1tm0a_	Alignment		100.0	14	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Proline racemase
18	d1xuba2	Alignment		100.0	30	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
19	d1u0ka2	Alignment		99.9	30	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
20	d2gkea1	Alignment		99.9	20	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
21	d2gkea2	Alignment	not modelled	99.8	13	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
22	c3g7kD_	Alignment	not modelled	98.2	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**3-methylitaconate isomerase; **PDBTitle:** crystal structure of methylitaconate-delta-isomerase
23	c2pw0A_	Alignment	not modelled	98.1	18	**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	96.0	23	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
25	c3ldgA_	Alignment	not modelled	40.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.472; **PDBTitle:** crystal structure of smu.472, a putative methyltransferase complexed2 with sah
26	c3k0bA_	Alignment	not modelled	38.8	18	**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
27	d1g60a_	Alignment	not modelled	36.5	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Type II DNA methylase
28	d1booa_	Alignment	not modelled	33.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases

						Family: Type II DNA methylase
29	c2zifB_	Alignment	not modelled	32.7	23	**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
30	d1euza2	Alignment	not modelled	31.7	26	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
31	d1bgva2	Alignment	not modelled	31.5	19	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
32	d1v9la2	Alignment	not modelled	31.0	19	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
33	c1nw6A_	Alignment	not modelled	29.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**modification methylase rsri; **PDBTitle:** structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin
34	d1o9ga_	Alignment	not modelled	28.7	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase AviRa
35	d1gtma2	Alignment	not modelled	26.6	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
36	d1eg2a_	Alignment	not modelled	24.2	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Type II DNA methylase
37	c3lduA_	Alignment	not modelled	23.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methylase; **PDBTitle:** the crystal structure of a possible methylase from2 clostridium difficile 630.
38	d1bvua2	Alignment	not modelled	23.4	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
39	d2ar0a1	Alignment	not modelled	22.3	36	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
40	d2fug21	Alignment	not modelled	21.7	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
41	d1b26a2	Alignment	not modelled	21.7	26	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
42	c2waqG_	Alignment	not modelled	20.6	27	**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
43	c3khkA_	Alignment	not modelled	20.2	21	**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.
44	d1hwxa2	Alignment	not modelled	19.3	29	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
45	d2okca1	Alignment	not modelled	17.8	29	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
46	c2l3bA_	Alignment	not modelled	17.4	33	**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
47	d2f8la1	Alignment	not modelled	17.2	36	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
48	c2l7qA_	Alignment	not modelled	16.3	27	**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
49	c3p9nA_	Alignment	not modelled	16.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible methyltransferase (methylase); **PDBTitle:** rv2966c of m. tuberculosis is a rsmd-like methyltransferase
50	c1g38A_	Alignment	not modelled	15.4	7	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**modification methylase taqi; **PDBTitle:** adenine-specific methyltransferase m. taq i/dna complex
51	c3sb1B_	Alignment	not modelled	15.4	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hydrogenase expression protein; **PDBTitle:** hydrogenase expression protein huph from thiobacillus denitrificans2 atcc 25259
52	c1aqjB_	Alignment	not modelled	15.4	7	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**adenine-n6-dna-methyltransferase taqi; **PDBTitle:** structure of adenine-n6-dna-methyltransferase taqi
53	d1uhsa_	Alignment	not modelled	15.2	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Homeodomain
54	d2ih2a1	Alignment	not modelled	14.0	7	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**DNA methylase TaqI, N-terminal domain
55	d1l1fa2	Alignment	not modelled	14.0	29	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
56	c3lkdB_	Alignment	not modelled	13.5	21	**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
57	d1s7ea1	Alignment	not modelled	13.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
58	d1j6ua1	Alignment	not modelled	13.1	12	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
59	d1ko7a1	Alignment	not modelled	13.1	13	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
60	d2p81a1	Alignment	not modelled	12.2	41	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
61	c3itcA_	Alignment	not modelled	12.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
62	c3k8zD_	Alignment	not modelled	11.8	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
63	d1pjza_	Alignment	not modelled	11.7	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
64	c3c6vB_	Alignment	not modelled	11.2	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**probable tautomerase/dehalogenase au4130; **PDBTitle:** crystal structure of au4130/apc7354, a probable enzyme from the2 thermophilic fungus aspergillus fumigatus
65	c1v9lA_	Alignment	not modelled	11.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
66	d1e3oc1	Alignment	not modelled	11.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
67	d1knxa1	Alignment	not modelled	10.9	3	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
68	d1wy7a1	Alignment	not modelled	10.8	33	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
69	c2i5gB_	Alignment	not modelled	10.6	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
70	c1bvuF_	Alignment	not modelled	10.4	23	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** glutamate dehydrogenase from thermococcus litoralis
71	c2vi6F_	Alignment	not modelled	10.3	41	**PDB header:**transcription **Chain:** F: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** crystal structure of the nanog homeodomain
72	c2da4A_	Alignment	not modelled	10.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
73	c3lu2B_	Alignment	not modelled	10.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2462 protein; **PDBTitle:** structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
74	d1o4xa1	Alignment	not modelled	10.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
75	c3s1sA_	Alignment	not modelled	10.0	29	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**restriction endonuclease bpusi; **PDBTitle:** characterization and crystal structure of the type iig restriction2 endonuclease bpusi
76	d1p7ia_	Alignment	not modelled	9.8	41	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
77	c2da2A_	Alignment	not modelled	9.7	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
78	c2tmgD_	Alignment	not modelled	9.5	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
						Fold:S-adenosyl-L-methionine-dependent methyltransferases

79	d1ne2a_	Alignment	not modelled	9.4	36	**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ta1320-like
80	d2hi3a1	Alignment	not modelled	9.3	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
81	d1ws6a1	Alignment	not modelled	9.3	29	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
82	c2da1A_	Alignment	not modelled	9.2	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
83	d2ifta1	Alignment	not modelled	9.0	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
84	c2yfqA_	Alignment	not modelled	9.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
85	c2l9rA_	Alignment	not modelled	8.9	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein nkx-3.1; **PDBTitle:** solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
86	d2cqxa1	Alignment	not modelled	8.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
87	c2ragB_	Alignment	not modelled	8.8	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidase; **PDBTitle:** crystal structure of aminohydrolase from caulobacter crescentus
88	d2cuea1	Alignment	not modelled	8.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
89	c3aogA_	Alignment	not modelled	8.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
90	d1au7a1	Alignment	not modelled	8.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
91	c2dmuA_	Alignment	not modelled	8.5	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
92	d1jgga_	Alignment	not modelled	8.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
93	d2j85a1	Alignment	not modelled	8.5	20	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
94	c3fdgA_	Alignment	not modelled	8.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidase ac. metallo peptidase. merops family m19; **PDBTitle:** the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
95	d2hddb_	Alignment	not modelled	8.1	41	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
96	d1f43a_	Alignment	not modelled	8.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
97	d1le8a_	Alignment	not modelled	8.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
98	d1ztra1	Alignment	not modelled	7.9	41	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
99	c1ko7B_	Alignment	not modelled	7.9	13	**PDB header:**transferase,hydrolase **Chain:** B: **PDB Molecule:**hpr kinase/phosphatase; **PDBTitle:** x-ray structure of the hpr kinase/phosphatase from2 staphylococcus xylosus at 1.95 a resolution