Phyre2

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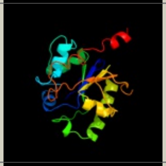
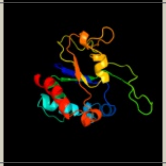
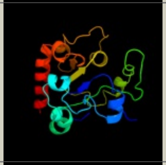
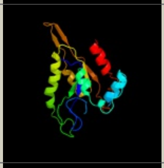
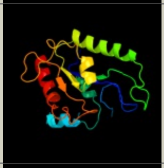
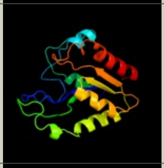
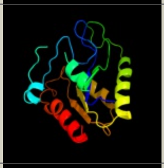
Description	P0A9H1
Date	Thu Jan 5 11:10:11 GMT 2012
Unique Job ID	0b654156fca3c0dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1muga_	Alignment		100.0	100	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
2	c2d07A_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g/t mismatch-specific thymine dna glycosylase; **PDBTitle:** crystal structure of sumo-3-modified thymine-dna glycosylase
3	c2rbaB_	Alignment		100.0	32	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**g/t mismatch-specific thymine dna glycosylase; **PDBTitle:** structure of human thymine dna glycosylase bound to abasic and2 undamaged dna
4	c2c2pA_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g/u mismatch-specific dna glycosylase; **PDBTitle:** the crystal structure of mismatch specific uracil-dna2 glycosylase (mug) from deinococcus radiodurans
5	c2l3fA_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a putative uracil dna glycosylase from2 methanosarcina acetivorans, northeast structural genomics consortium3 target mvr76
6	d1vk2a_	Alignment		100.0	23	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
7	c2d3yA_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8
8	d1ui0a_	Alignment		99.9	19	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
9	c3ikbB_	Alignment		99.9	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2 mutans ua159.
10	d1oe4a_	Alignment		99.5	21	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
11	c2owrD_	Alignment		96.5	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of vaccinia virus uracil-dna glycosylase

12	c3cxmA_	Alignment		95.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil
13	c3tr7A_	Alignment		95.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** structure of a uracil-dna glycosylase (ung) from coxiella burnetii
14	d3euga_	Alignment		95.3	13	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
15	d2hxma1	Alignment		94.6	11	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
16	c2zhxG_	Alignment		94.5	17	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** G: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from mycobacterium2 tuberculosis in complex with a proteinaceous inhibitor
17	d2j8xa1	Alignment		94.0	10	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
18	c2booA_	Alignment		93.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** the crystal structure of uracil-dna n-glycosylase (ung)2 from deinococcus radiodurans.
19	d1okba_	Alignment		93.1	14	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
20	d1laue_	Alignment		93.1	17	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
21	c3fpjA_	Alignment	not modelled	25.4	32	**PDB header:**biosynthetic protein, transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of e81q mutant of mtnas in complex with s-2 adenosylmethionine
22	c3absD_	Alignment	not modelled	18.2	24	**PDB header:**lyase **Chain:** D: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
23	c1v39A_	Alignment	not modelled	16.3	35	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**vp39; **PDBTitle:** dc26 mutant of vaccinia virus protein vp39 in complex with s-2 adenosylhomocysteine and m7g(5')pppg
24	c1vp3A_	Alignment	not modelled	16.3	35	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**vp39; **PDBTitle:** vaccinia virus protein vp39 in complex with s-adenosylhomocysteine
25	d1vpta_	Alignment	not modelled	16.2	32	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap methylase
26	c3anyB_	Alignment	not modelled	15.9	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
27	c2plwA_	Alignment	not modelled	10.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna methyltransferase, putative; **PDBTitle:** crystal structure of a ribosomal rna methyltransferase, putative, from2 plasmodium falciparum (pf13_0052).

28	c3jqoV_	Alignment	not modelled	8.8	15	**PDB header:**transport protein **Chain:** V: **PDB Molecule:**traf protein; **PDBTitle:** crystal structure of the outer membrane complex of a type iv2 secretion system
29	d2i7pa2	Alignment	not modelled	8.3	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
30	d1iv0a_	Alignment	not modelled	8.3	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
31	d2cyja1	Alignment	not modelled	7.6	25	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
32	c2h4bD_	Alignment	not modelled	6.7	38	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**pancreatic hormone; **PDBTitle:** cis-4-aminomethylphenylazobenzoic acid-avian pancreatic2 polypeptide
33	c2h4bC_	Alignment	not modelled	6.7	38	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**pancreatic hormone; **PDBTitle:** cis-4-aminomethylphenylazobenzoic acid-avian pancreatic2 polypeptide
34	c2h3sB_	Alignment	not modelled	6.7	38	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**pancreatic hormone; **PDBTitle:** cis-azobenzene-avian pancreatic polypeptide bound to dpc2 micelles
35	c2h3tB_	Alignment	not modelled	6.7	38	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**pancreatic hormone; **PDBTitle:** trans-(4-aminomethyl)phenylazobenzoic acid-app bound to dpc2 micelles
36	d1ihna_	Alignment	not modelled	6.5	14	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
37	d1jvaa2	Alignment	not modelled	5.5	25	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
38	d2q4qa1	Alignment	not modelled	5.3	15	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like