







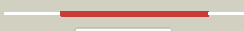















Phyre2

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Description	RVBD1259_(-)_1407345_1408244
Date	Wed Jul 31 22:05:35 BST 2019
Unique Job ID	00a12dd5dd262d6c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d3yA_	 Alignment		100.0	48	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8
2	c6ajrA_	 Alignment		100.0	26	PDB header: dna binding protein Chain: A: PDB Molecule: uracil dna glycosylase superfamily protein; PDBTitle: complex form of uracil dna glycosylase x and uracil
3	c4zbzA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: family 4 uracil-dna glycosylase from sulfolobus tokodaii (free form,2 x-ray wavelength=1.5418)
4	d1ui0a_	 Alignment		100.0	31	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
5	d1vk2a_	 Alignment		100.0	29	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
6	c3ikbB_	 Alignment		100.0	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a conserved protein from streptococcus2 mutans ua159.
7	c2rbaB_	 Alignment		100.0	16	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
8	c2c2pA_	 Alignment		100.0	17	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
9	d1muga_	 Alignment		100.0	16	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
10	c2d07A_	 Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: g/t mismatch-specific thymine dna glycosylase; PDBTitle: crystal structure of sumo-3-modified thymine-dna glycosylase
11	c5h93C_	 Alignment		99.6	24	PDB header: hydrolase Chain: C: PDB Molecule: geobacter metallireducens smug1; PDBTitle: crystal structure of geobacter metallireducens smug1

12	d1oe4a_	Alignment		99.4	21	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
13	c5h0jA_	Alignment		98.7	21	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of wt pedobacter heparinus smug2
14	c2l3fA_	Alignment		97.4	18	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
15	c5grkA_	Alignment		97.2	23	PDB header: hydrolase Chain: A: PDB Molecule: blr0248 protein; PDBTitle: crystal structure of uracil dna glycosylase -xanthine complex from2 bradyrhizobium diazoefficiens
16	d1laue_	Alignment		92.8	13	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
17	d3euqa_	Alignment		92.0	17	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
18	d2j8xa1	Alignment		91.3	19	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
19	c5nn7A_	Alignment		90.8	18	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: kshv uracil-dna glycosylase, apo form
20	c3cxmA_	Alignment		90.1	13	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil
21	d1okba_	Alignment	not modelled	89.9	14	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
22	c2booA_	Alignment	not modelled	88.5	17	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: the crystal structure of uracil-dna n-glycosylase (ung) from2 deinococcus radiodurans.
23	c3zogA_	Alignment	not modelled	85.8	13	PDB header: hydrolase/viral protein Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: structure of bsudg-p56 complex
24	d2hxma1	Alignment	not modelled	85.3	15	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
25	c3tr7A_	Alignment	not modelled	69.6	18	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: structure of a uracil-dna glycosylase (ung) from coxiella burnetii
26	c2owrD_	Alignment	not modelled	67.7	12	PDB header: hydrolase Chain: D: PDB Molecule: uracil-dna glycosylase; PDBTitle: crystal structure of vaccinia virus uracil-dna glycosylase
27	c5x3hA_	Alignment	not modelled	67.2	14	PDB header: dna binding protein Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: the y81g mutant of the ung crystal structure from nitratifactor2 salsuginis
28	c2zhxG_	Alignment	not modelled	54.5	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

29	d1t6ca2	Alignment	not modelled	50.0	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
30	c5x55A	Alignment	not modelled	44.9	16	PDB header: hydrolase Chain: A: PDB Molecule: probable uracil-dna glycosylase; PDBTitle: crystal structure of mimivirus uracil-dna glycosylase
31	c3anyB	Alignment	not modelled	24.6	14	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
32	c3absD	Alignment	not modelled	24.6	14	PDB header: lyase Chain: D: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adenylpentylcobalamin and ethanolamine
33	c5v2gB	Alignment	not modelled	12.5	27	PDB header: de novo protein Chain: B: PDB Molecule: 20-mer peptide; PDBTitle: de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
34	c5v2gA	Alignment	not modelled	12.5	27	PDB header: de novo protein Chain: A: PDB Molecule: 20-mer peptide; PDBTitle: de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
35	c5v2gC	Alignment	not modelled	12.5	27	PDB header: de novo protein Chain: C: PDB Molecule: 20-mer peptide; PDBTitle: de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
36	d1vjla	Alignment	not modelled	10.3	24	Fold: Hypothetical protein TM0160 Superfamily: Hypothetical protein TM0160 Family: Hypothetical protein TM0160
37	c5injA	Alignment	not modelled	10.2	35	PDB header: transferase Chain: A: PDB Molecule: prenyltransferase; PDBTitle: crystal structure of prenyltransferase prib ternary complex with l-2 tryptophan and dimethylallyl thiolodiphosphate (dmspp)
38	c4v1af	Alignment	not modelled	9.7	67	PDB header: ribosome Chain: F: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
39	d1nkua	Alignment	not modelled	8.6	38	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)
40	c1t6dB	Alignment	not modelled	8.3	28	PDB header: hydrolase Chain: B: PDB Molecule: exopolyphosphatase; PDBTitle: miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
41	c4ce5A	Alignment	not modelled	8.1	15	PDB header: transferase Chain: A: PDB Molecule: at-omegata; PDBTitle: first crystal structure of an (r)-selective omega-transaminase2 from aspergillus terreus
42	d1y5ea1	Alignment	not modelled	8.1	25	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
43	c5ooma	Alignment	not modelled	7.5	60	PDB header: ribosome Chain: A: PDB Molecule: 16s ribosomal rna; PDBTitle: structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rna
44	c6nstD	Alignment	not modelled	6.5	8	PDB header: transferase Chain: D: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of branched chain amino acid aminotransferase from2 pseudomonas aeruginosa
45	c3ty8A	Alignment	not modelled	6.2	29	PDB header: transferase Chain: A: PDB Molecule: polynucleotide 2',3'-cyclic phosphate phosphodiesterase / PDBTitle: crystal structure of c. thermocellum pnkp ligase domain apo form
46	c3nicA	Alignment	not modelled	6.2	31	PDB header: hydrolase/dna Chain: A: PDB Molecule: eco29kir; PDBTitle: dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
47	d2o3bb1	Alignment	not modelled	6.0	26	Fold: Nuclease A inhibitor (NuiA) Superfamily: Nuclease A inhibitor (NuiA) Family: Nuclease A inhibitor (NuiA)
48	c4e6nC	Alignment	not modelled	5.9	29	PDB header: protein binding Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of bacterial pnkp-c/hen1-n heterodimer
49	d1yc5a1	Alignment	not modelled	5.7	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
50	c5jqyA	Alignment	not modelled	5.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph)oxxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
51	c5ce8B	Alignment	not modelled	5.3	8	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: crystal structure of branched-chain aminotransferase from thermophilic2 archaea thermoproteus uzoniensis
52	c3hdCA	Alignment	not modelled	5.2	26	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin family protein; PDBTitle: the crystal structure of thioredoxin protein from geobacter2 metallireducens
53	c2ys2A	Alignment	not modelled	5.2	40	PDB header: transferase Chain: A: PDB Molecule: cytoplasmic tyrosine-protein kinase bmx; PDBTitle: solution structure of the btk motif of human cytoplasmic2 tyrosine-protein kinase bmx