

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qxxA_	Alignment		100.0	99	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: bifunctional dctp deaminase: dutpase from mycobacterium tuberculosis2 in complex with dttp
2	d1xs1a_	Alignment		100.0	43	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
3	c4xjcD_	Alignment		100.0	37	PDB header: hydrolase Chain: D: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: dctp deaminase-dutpase from bacillus halodurans
4	c2qlpC_	Alignment		100.0	99	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: bifunctional dctp deaminase:dutpase from mycobacterium tuberculosis,2 apo form
5	c2r9qD_	Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
6	d1pkha_	Alignment		100.0	35	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
7	c2vzjB_	Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 167aa long hypothetical dutpase; PDBTitle: crystal structure of dctp deaminase from sulfolobus tokodaii
8	c3km3B_	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: crystal structure of eoexcytidine triphosphate deaminase from2 anaplasma phagocytophilum at 2.1a resolution
9	c4dhkB_	Alignment		100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: crystal structure of a deoxycytidine triphosphate deaminase (dctp2 deaminase) from burkholderia thailandensis
10	d1duna_	Alignment		99.9	28	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
11	c3mbqC_	Alignment		99.9	24	PDB header: hydrolase Chain: C: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5'-triphosphate nucleotidohydrolase2 from brucella melitensis, orthorhombic crystal form

12	d1f7ra_	Alignment		99.9	32	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
13	c3ehwA_	Alignment		99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: dutp pyrophosphatase; PDBTitle: human dutpase in complex with alpha,beta-imido-dutp and mg2+ :2 visualization of the full-length c-termini in all monomers and3 suggestion for an additional metal ion binding site
14	d1sixa_	Alignment		99.9	29	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
15	c6maiA_	Alignment		99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5'-triphosphate nucleotidohydrolase2 from legionella pneumophila philadelphia 1
16	c3tqzA_	Alignment		99.9	32	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii
17	c3so2A_	Alignment		99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: chlorella dutpase
18	c3ca9A_	Alignment		99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
19	d1euwa_	Alignment		99.9	24	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
20	d1rnja_	Alignment		99.9	26	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
21	c3c3iA_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
22	c3f4fB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of dut1p, a dutpase from saccharomyces cerevisiae
23	c2okdB_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: B: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: high resolution crystal structures of vaccinia virus dutpase
24	d3ehwa1	Alignment	not modelled	99.9	23	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
25	d1sjna_	Alignment	not modelled	99.9	31	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
26	d1f7da_	Alignment	not modelled	99.9	34	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
27	d1q5uz_	Alignment	not modelled	99.9	25	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
28	c3lqwA_	Alignment	not modelled	99.9	31	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5'-triphosphate2 nucleotidohydrolase from entamoeba histolytica

29	d1vyqa1	Alignment	not modelled	99.9	23	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
30	c3h6xA	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: dutpase; PDBTitle: crystal structure of dutpase from streptococcus mutans
31	c2p9oB	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: dutp pyrophosphatase-like protein; PDBTitle: structure of dutpase from arabidopsis thaliana
32	c2bazA	Alignment	not modelled	99.9	21	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein bsu20020; PDBTitle: structure of yoss, a putative dutpase from bacillus subtilis
33	c5vjyC	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: C: PDB Molecule: dutp pyrophosphatase; PDBTitle: crystal structure of dutp pyrophosphatase protein, from naegleria2 fowleri
34	c3zf6A	Alignment	not modelled	99.9	28	PDB header: hydrolase Chain: A: PDB Molecule: dutpase; PDBTitle: phage dutpases control transfer of virulence genes by a proto-2 oncogenic g protein-like mechanism. (staphylococcus bacteriophage3 80alpha dutpase d81a d110c s168c mutant with dupnhpp).
35	c2d4nA	Alignment	not modelled	99.9	30	PDB header: hydrolase Chain: A: PDB Molecule: du; PDBTitle: crystal structure of m-pmv dutpase complexed with dupnpp, substrate2 analogue
36	c5y5pB	Alignment	not modelled	99.9	26	PDB header: viral protein Chain: B: PDB Molecule: wsv112; PDBTitle: crystal structure of the dutpase of white spot syndrome virus in2 complex with du,ppi and mg2+
37	c3ecyA	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: cg4584-pa, isoform a (bcdna.Id08534); PDBTitle: crystal structural analysis of drosophila melanogaster dutpase
38	d2bsya2	Alignment	not modelled	99.8	24	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
39	d2bsya1	Alignment	not modelled	99.8	26	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
40	c2bt1A	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: epstein barr virus dutpase in complex with a,b-imino dutp
41	c3p43A	Alignment	not modelled	28.4	19	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and activities of archaeal members of the ligd 3'2 phosphoesterase dna repair enzyme superfamily
42	d1tula	Alignment	not modelled	25.6	15	Fold: beta-clip Superfamily: Tlp20, baculovirus telokin-like protein Family: Tlp20, baculovirus telokin-like protein
43	d1vioa2	Alignment	not modelled	25.2	14	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
44	c5dmpA	Alignment	not modelled	21.4	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the archaeal nhej phosphoesterase from methanocella2 paludicola.
45	c3n9dA	Alignment	not modelled	20.7	26	PDB header: ligase Chain: A: PDB Molecule: probable atp-dependent dna ligase; PDBTitle: monoclinic structure of p. aeruginosa ligd phosphoesterase domain
46	c1dm9A	Alignment	not modelled	20.1	13	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
47	d1dm9a	Alignment	not modelled	20.1	13	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kd
48	c4mqdB	Alignment	not modelled	17.0	13	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: dna-entry nuclease inhibitor; PDBTitle: crystal structure of comj, inhibitor of the dna degrading activity of2 nuca, from bacillus subtilis
49	d1vqop1	Alignment	not modelled	14.6	17	Fold: Ribosomal protein L19 (L19e) Superfamily: Ribosomal protein L19 (L19e) Family: Ribosomal protein L19 (L19e)
50	c1kskA	Alignment	not modelled	13.8	17	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
51	c3j21Q	Alignment	not modelled	13.7	21	PDB header: ribosome Chain: Q: PDB Molecule: 50s ribosomal protein l19e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
52	c2istA	Alignment	not modelled	13.4	10	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of rlud from e. coli
53	c4a17O	Alignment	not modelled	12.3	22	PDB header: ribosome Chain: O: PDB Molecule: rp119; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
54	d2visc	Alignment	not modelled	12.1	19	Fold: Viral protein domain Superfamily: Viral protein domain

						Family: Influenza hemagglutinin headpiece
55	c3iz5T_	Alignment	not modelled	11.3	22	PDB header: ribosome Chain: T; PDB Molecule: 60s ribosomal protein l19 (l19e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
56	c4a1eO_	Alignment	not modelled	11.0	22	PDB header: ribosome Chain: O; PDB Molecule: rpl19; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna, 5.8s rna3 and proteins of molecule 1
57	c4b6aR_	Alignment	not modelled	10.9	17	PDB header: ribosome Chain: R; PDB Molecule: 60s ribosomal protein l19-b; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
58	d2viva_	Alignment	not modelled	10.7	19	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
59	c4a1cO_	Alignment	not modelled	10.3	21	PDB header: ribosome Chain: O; PDB Molecule: rpl19; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 4.
60	c3p4hA_	Alignment	not modelled	10.2	14	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent dna ligase, n-terminal domain protein; PDBTitle: structures of archaeal members of the ligd 3'-phosphoesterase dna2 repair enzyme superfamily
61	c3j39R_	Alignment	not modelled	10.1	26	PDB header: ribosome Chain: R; PDB Molecule: 60s ribosomal protein l19; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
62	d1mqma_	Alignment	not modelled	9.9	19	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
63	c5hmqE_	Alignment	not modelled	9.8	31	PDB header: lyase Chain: E; PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
64	c3zf7T_	Alignment	not modelled	9.7	28	PDB header: ribosome Chain: T; PDB Molecule: 60s ribosomal protein l19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
65	c1ha0A_	Alignment	not modelled	9.0	19	PDB header: viral protein Chain: A; PDB Molecule: protein (hemagglutinin precursor); PDBTitle: hemagglutinin precursor ha0
66	c5z81A_	Alignment	not modelled	8.9	11	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 15; PDBTitle: trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
67	c2ahqA_	Alignment	not modelled	8.6	12	PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
68	c4uj3B_	Alignment	not modelled	8.6	12	PDB header: transport protein Chain: B; PDB Molecule: rab-3a-interacting protein; PDBTitle: crystal structure of human rab11-rabin8-fip3
69	c3mpbA_	Alignment	not modelled	8.3	17	PDB header: isomerase Chain: A; PDB Molecule: sugar isomerase; PDBTitle: z5688 from e. coli o157:h7 bound to fructose
70	c5oy0m_	Alignment	not modelled	7.0	33	PDB header: photosynthesis Chain: M; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
71	c5oy09_	Alignment	not modelled	7.0	33	PDB header: photosynthesis Chain: 9; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
72	c6hqbm_	Alignment	not modelled	7.0	33	PDB header: photosynthesis Chain: M; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: monomeric cyanobacterial photosystem i
73	c5oy0M_	Alignment	not modelled	7.0	33	PDB header: photosynthesis Chain: M; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
74	c4l6vM_	Alignment	not modelled	7.0	33	PDB header: electron transport Chain: M; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
75	c4l6v7_	Alignment	not modelled	7.0	33	PDB header: electron transport Chain: 7; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
76	d1v54b1	Alignment	not modelled	6.9	27	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
77	c2zkrp_	Alignment	not modelled	6.7	28	PDB header: ribosomal protein/rna Chain: P; PDB Molecule: rna expansion segment es31 part i; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
78	c2wwaj_	Alignment	not modelled	6.6	20	PDB header: ribosome Chain: J; PDB Molecule: 60s ribosomal protein l19; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the yeast 80s2 ribosome
79	c5dudB_	Alignment	not modelled	6.5	36	PDB header: unknown function Chain: B; PDB Molecule: ybgj; PDBTitle: crystal structure of e. coli ybgjk

80	c5olpB_	Alignment	not modelled	6.4	20	PDB header: hydrolase Chain: B: PDB Molecule: pectate lyase; PDBTitle: galacturonidase
81	c2psbA_	Alignment	not modelled	6.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yerb protein; PDBTitle: crystal structure of yerb protein from bacillus subtilis. northeast2 structural genomics target sr586
82	d2psba1	Alignment	not modelled	6.4	18	Fold: YerB-like Superfamily: YerB-like Family: YerB-like
83	d2q02a1	Alignment	not modelled	5.8	21	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
84	d1g6ea_	Alignment	not modelled	5.5	28	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Antifungal protein AFP1
85	d1uwfa1	Alignment	not modelled	5.5	19	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
86	d1zx5a1	Alignment	not modelled	5.3	17	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Type I phosphomannose isomerase