Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P28248
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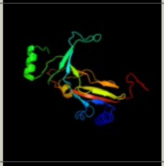
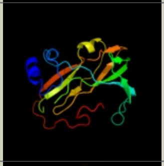
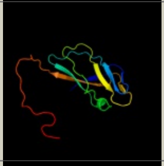
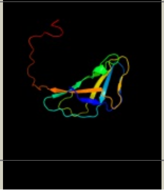
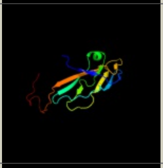
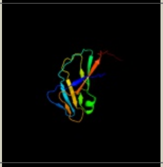
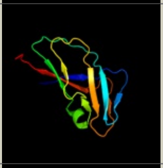
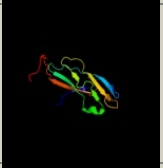
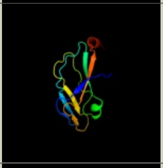
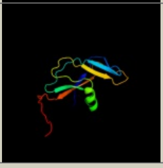
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xs1a_	Alignment		100.0	100	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
2	c2qxxA_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** bifunctional dctp deaminase: dutpase from mycobacterium tuberculosis2 in complex with dttp
3	c2qlpC_	Alignment		100.0	45	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** bifunctional dctp deaminase:dutpase from mycobacterium tuberculosis,2 apo form
4	d1pkha_	Alignment		100.0	29	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
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	c2yzjB_	Alignment		100.0	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**167aa long hypothetical dutpase; **PDBTitle:** crystal structure of dctp deaminase from sulfolobus tokodaii
7	c3km3B_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** crystal structure of eoxycytidine triphosphate deaminase from2 anaplasma phagocytophilum at 2.1a resolution
8	c3mbqC_	Alignment		99.9	26	**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
9	d1duna_	Alignment		99.9	23	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
10	d1f7ra_	Alignment		99.9	27	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
11	c3ehwA_	Alignment		99.9	27	**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

12	c3tqzA_	Alignment		99.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii
13	d1sixa_	Alignment		99.9	31	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
14	d1rnja_	Alignment		99.9	21	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
15	c2okdB_	Alignment		99.9	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** high resolution crystal structures of vaccinia virus dutpase
16	c3ca9A_	Alignment		99.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine triphosphatase; **PDBTitle:** evolution of chlorella virus dutpase
17	d1euwa_	Alignment		99.9	24	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
18	d1sjna_	Alignment		99.9	32	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
19	d1f7da_	Alignment		99.9	31	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
20	c3c3iA_	Alignment		99.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine triphosphatase; **PDBTitle:** evolution of chlorella virus dutpase
21	c3f4fB_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** crystal structure of dut1p, a dutpase from saccharomyces cerevisiae
22	d1q5uz_	Alignment	not modelled	99.9	30	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
23	d3ehwa1	Alignment	not modelled	99.9	29	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
24	d1vyqa1	Alignment	not modelled	99.9	19	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
25	c3lqwA_	Alignment	not modelled	99.9	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** crystal structure of deoxyuridine 5-triphosphate2 nucleotidohydrolase from entamoeba histolytica
26	c2p9oB_	Alignment	not modelled	99.9	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dutp pyrophosphatase-like protein; **PDBTitle:** structure of dutpase from arabidopsis thaliana
27	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
28	c3h6xA_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dutpase; **PDBTitle:** crystal structure of dutpase from streptococcus mutans
						PDB header:hydrolase

29	c2d4nA_	Alignment	not modelled	99.9	27	**Chain:** A: **PDB Molecule:**du; **PDBTitle:** crystal structure of m-pmv dutpase complexed with dupnpp, substrate2 analogue
30	c3ecyA_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg4584-pa, isoform a (bcdna.ld08534); **PDBTitle:** crystal structural analysis of drosophila melanogaster dutpase
31	d2bsya2	Alignment	not modelled	99.8	19	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
32	d2bsya1	Alignment	not modelled	99.8	24	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
33	c2bt1A_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** epstein barr virus dutpase in complex with a,b-imino dutp
34	d1tula_	Alignment	not modelled	25.3	10	**Fold:**beta-clip **Superfamily:**Tlp20, baculovirus telokin-like protein **Family:**Tlp20, baculovirus telokin-like protein
35	d1vioa2	Alignment	not modelled	13.7	14	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
36	d1dm9a_	Alignment	not modelled	12.4	11	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
37	c1dm9A_	Alignment	not modelled	12.4	11	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
38	d1vqop1	Alignment	not modelled	11.3	21	**Fold:**Ribosomal protein L19 (L19e) **Superfamily:**Ribosomal protein L19 (L19e) **Family:**Ribosomal protein L19 (L19e)
39	d1uwfa1	Alignment	not modelled	11.1	19	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
40	c4a1cO_	Alignment	not modelled	8.6	11	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rpl19; **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 4.
41	c3iz5T_	Alignment	not modelled	8.3	15	**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
42	d1v54b1	Alignment	not modelled	7.7	27	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
43	d2visc_	Alignment	not modelled	7.7	17	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
44	d2viua_	Alignment	not modelled	7.2	17	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
45	d1mqma_	Alignment	not modelled	7.1	18	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
46	c1ha0A_	Alignment	not modelled	6.2	17	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hemagglutinin precursor); **PDBTitle:** hemagglutinin precursor ha0
47	c2ebbA_	Alignment	not modelled	6.0	36	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
48	d2odgc1	Alignment	not modelled	5.5	25	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
49	d1zx5a1	Alignment	not modelled	5.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
50	d2phcb1	Alignment	not modelled	5.3	27	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like