Phyre2

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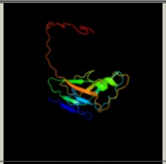
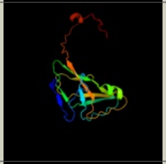
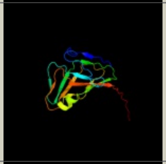
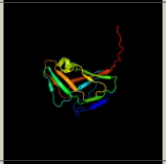
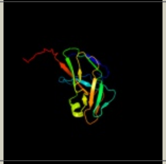
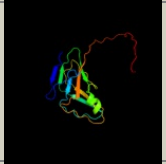
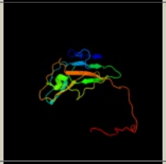
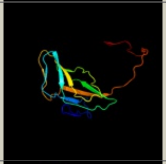
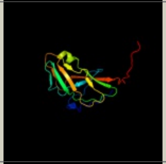
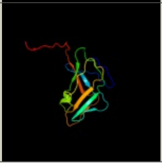
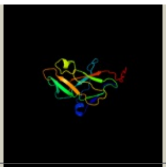
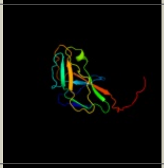
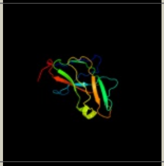
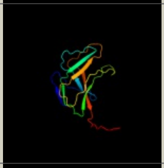
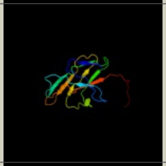
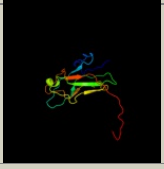
Description	P06968
Date	Thu Jan 5 10:59:35 GMT 2012
Unique Job ID	c4b402f3762d0bcc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ehwA_	Alignment		100.0	32	**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
2	d1sixa_	Alignment		100.0	32	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
3	d1rnja_	Alignment		100.0	99	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
4	d1euwa_	Alignment		100.0	100	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
5	c3tqzA_	Alignment		100.0	61	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii
6	d3ehwa1	Alignment		100.0	32	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
7	c3f4fB_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** crystal structure of dut1p, a dutpase from saccharomyces cerevisiae
8	d1f7ra_	Alignment		100.0	26	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
9	c3mbqC_	Alignment		100.0	44	**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
10	d1sjna_	Alignment		100.0	34	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
11	c3c3iA_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine triphosphatase; **PDBTitle:** evolution of chlorella virus dutpase

12	c3ca9A_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine triphosphatase; **PDBTitle:** evolution of chlorella virus dutpase
13	c3lqwA_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** crystal structure of deoxyuridine 5-triphosphate2 nucleotidohydrolase from entamoeba histolytica
14	d1vyqa1	Alignment		100.0	26	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
15	d1q5uz_	Alignment		100.0	29	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
16	c2p9oB_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dutp pyrophosphatase-like protein; **PDBTitle:** structure of dutpase from arabidopsis thaliana
17	c3h6xA_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dutpase; **PDBTitle:** crystal structure of dutpase from streptococcus mutans
18	c2okdB_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** high resolution crystal structures of vaccinia virus dutpase
19	c3ecyA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg4584-pa, isoform a (bcdna.ld08534); **PDBTitle:** crystal structural analysis of drosophila melanogaster dutpase
20	c2bazA_	Alignment		100.0	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu20020; **PDBTitle:** structure of yoss, a putative dutpase from bacillus subtilis
21	d1f7da_	Alignment	not modelled	100.0	26	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
22	d1duna_	Alignment	not modelled	100.0	21	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
23	c2d4nA_	Alignment	not modelled	100.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**du; **PDBTitle:** crystal structure of m-pmv dutpase complexed with dupnpp, substrate2 analogue
24	d2bsya2	Alignment	not modelled	100.0	20	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
25	c2bt1A_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** epstein barr virus dutpase in complex with a,b-imino dutp
26	c2qxxA_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** bifunctional dctp deaminase: dutpase from mycobacterium tuberculosis2 in complex with dttp
27	d2bsya1	Alignment	not modelled	99.9	21	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
28	d1xs1a_	Alignment	not modelled	99.9	22	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
						PDB header:hydrolase

29	c2qlpC_	Alignment	not modelled	99.9	26	**Chain:** C: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** bifunctional dctp deaminase:dutpase from mycobacterium tuberculosis,2 apo form
30	c3km3B_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** crystal structure of eoxycytidine triphosphate deaminase from2 anaplasma phagocytophilum at 2.1a resolution
31	d1pkha_	Alignment	not modelled	99.9	25	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
32	c2yzjB_	Alignment	not modelled	99.9	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**167aa long hypothetical dutpase; **PDBTitle:** crystal structure of dctp deaminase from sulfolobus tokodaii
33	c2r9qD_	Alignment	not modelled	99.8	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
34	d1tula_	Alignment	not modelled	44.2	18	**Fold:**beta-clip **Superfamily:**Tlp20, baculovirus telokin-like protein **Family:**Tlp20, baculovirus telokin-like protein
35	d1kwga1	Alignment	not modelled	17.6	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
36	c3kvpB_	Alignment	not modelled	13.8	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ymzc; **PDBTitle:** crystal structure of uncharacterized protein ymzc precursor2 from bacillus subtilis, northeast structural genomics3 consortium target sr378a
37	d1ng2a2	Alignment	not modelled	12.8	18	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
38	d1v7ra_	Alignment	not modelled	12.3	38	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
39	c3gzuB_	Alignment	not modelled	12.2	22	**PDB header:**virus **Chain:** B: **PDB Molecule:**inner capsid protein vp2; **PDBTitle:** vp7 recoated rotavirus dlp
40	c3h0dB_	Alignment	not modelled	12.1	44	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**ctsr; **PDBTitle:** crystal structure of ctsr in complex with a 26bp dna duplex
41	d1pmia_	Alignment	not modelled	12.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
42	c3kz4A_	Alignment	not modelled	11.5	20	**PDB header:**virus **Chain:** A: **PDB Molecule:**inner capsid protein vp2; **PDBTitle:** crystal structure of the rotavirus double layered particle
43	d1k7ka_	Alignment	not modelled	10.9	38	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
44	d1dj2a_	Alignment	not modelled	10.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
45	d1dj3a_	Alignment	not modelled	10.7	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
46	c3tquD_	Alignment	not modelled	10.7	38	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**non-canonical purine ntp pyrophosphatase; **PDBTitle:** structure of a ham1 protein from coxiella burnetii
47	d1qf5a_	Alignment	not modelled	10.3	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
48	d2cara1	Alignment	not modelled	9.7	44	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
49	c3ld1A_	Alignment	not modelled	8.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicase polyprotein 1a; **PDBTitle:** crystal structure of ibv nsp2a
50	d1o51a_	Alignment	not modelled	8.0	67	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
51	d1boba_	Alignment	not modelled	7.5	33	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
52	d3c0na1	Alignment	not modelled	7.2	18	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Aerolysin/Pertussis toxin (APT) domain
53	d1vp2a_	Alignment	not modelled	6.9	35	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
54	c1w1fA_	Alignment	not modelled	6.2	25	**PDB header:**sh3-domain **Chain:** A: **PDB Molecule:**tyrosine-protein kinase lyn; **PDBTitle:** sh3 domain of human lyn tyrosine kinase
55	d1uwfa1	Alignment	not modelled	6.1	17	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins

						Family: Pilus subunits
56	d1x7fa1	Alignment	not modelled	5.9	31	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Outer surface protein, C-terminal domain
57	c3nrfA_	Alignment	not modelled	5.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**apag protein; **PDBTitle:** crystal structure of an apag protein (pa1934) from pseudomonas2 aeruginosa pao1 at 1.50 a resolution
58	d1e5ba_	Alignment	not modelled	5.8	6	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family II
59	c3d82A_	Alignment	not modelled	5.6	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
60	d1qqfa_	Alignment	not modelled	5.3	21	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Complement components
61	c2oqbA_	Alignment	not modelled	5.3	26	**PDB header:**transferase,gene regulation **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** crystal structure of the n-terminal domain of coactivator-associated2 methyltransferase 1 (carm1)
62	d1cm0a_	Alignment	not modelled	5.2	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
63	c3h1yA_	Alignment	not modelled	5.2	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
64	c1xopA_	Alignment	not modelled	5.1	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** nmr structure of g1v mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
65	d2ot2a1	Alignment	not modelled	5.1	29	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
66	c3mwxA_	Alignment	not modelled	5.1	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**aldose 1-epimerase; **PDBTitle:** crystal structure of a putative galactose mutarotase (bsu18360) from2 bacillus subtilis at 1.45 a resolution