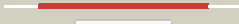



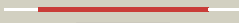


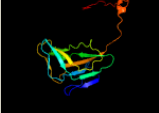



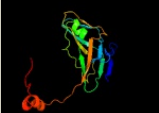



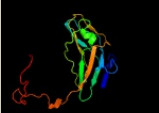








Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2697c_(dut)_3013693_3014157
 Date Wed Aug 7 12:50:35 BST 2019
 Unique Job ID 958f65ddcb86a8e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sixa_	 Alignment		100.0	92	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
2	c3zf6A_	 Alignment		100.0	38	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).
3	c3ehwA_	 Alignment		100.0	42	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
4	c3so2A_	 Alignment		100.0	45	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: chlorella dutpase
5	d1sjna_	 Alignment		100.0	100	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
6	d3ehwa1	 Alignment		100.0	42	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
7	c5y5pB_	 Alignment		100.0	35	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+
8	c3f4fB_	 Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of dut1p, a dutpase from saccharomyces cerevisiae
9	d1f7ra_	 Alignment		100.0	35	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
10	c5vjyC_	 Alignment		100.0	40	PDB header: hydrolase Chain: C: PDB Molecule: dutp pyrophosphatase; PDBTitle: crystal structure of dutp pyrophosphatase protein, from naegleria2 fowleri
11	d1euwa_	 Alignment		100.0	33	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like

12	c3ca9A_	Alignment		100.0	36	PDB header: hydrolase Chain: A; PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
13	d1rnja_	Alignment		100.0	32	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
14	c3c3iA_	Alignment		100.0	36	PDB header: hydrolase Chain: A; PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
15	c3tqzA_	Alignment		100.0	33	PDB header: hydrolase Chain: A; PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii
16	c3mbqC_	Alignment		100.0	47	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
17	c3lqwA_	Alignment		100.0	38	PDB header: hydrolase Chain: A; PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5-triphosphate2 nucleotidohydrolase from entamoeba histolytica
18	c6maiA_	Alignment		100.0	35	PDB header: hydrolase Chain: A; PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5'-triphosphate nucleotidohydrolase2 from legionella pneumophila philadelphia 1
19	d1q5uz_	Alignment		100.0	40	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
20	c2p9oB_	Alignment		100.0	37	PDB header: hydrolase Chain: B; PDB Molecule: dutp pyrophosphatase-like protein; PDBTitle: structure of dutpase from arabidopsis thaliana
21	c2okdB_	Alignment	not modelled	100.0	43	PDB header: hydrolase Chain: B; PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: high resolution crystal structures of vaccinia virus dutpase
22	d1vyqa1	Alignment	not modelled	100.0	31	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
23	c3h6xA_	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: A; PDB Molecule: dutpase; PDBTitle: crystal structure of dutpase from streptococcus mutans
24	c3ecyA_	Alignment	not modelled	100.0	36	PDB header: hydrolase Chain: A; PDB Molecule: cg4584-pa, isoform a (bcdna.ld08534); PDBTitle: crystal structural analysis of drosophila melanogaster dutpase
25	c2bazA_	Alignment	not modelled	100.0	29	PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein bsu20020; PDBTitle: structure of yoss, a putative dutpase from bacillus subtilis
26	d1f7da_	Alignment	not modelled	100.0	35	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
27	d1duna_	Alignment	not modelled	100.0	31	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
28	c2d4nA_	Alignment	not modelled	100.0	33	PDB header: hydrolase Chain: A; PDB Molecule: du; PDBTitle: crystal structure of m-pmv dutpase complexed with dupnpp, substrate2 analogue Fold: beta-clip

29	d2bsya2	Alignment	not modelled	100.0	24	Superfamily: dUTPase-like Family: dUTPase-like
30	c2bt1A	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: epstein barr virus dntpase in complex with a,b-imino dntp
31	c2qxxA	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: bifunctional dctp deaminase: dntpase from mycobacterium tuberculosis2 in complex with dntp
32	d2bsya1	Alignment	not modelled	100.0	19	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
33	d1xslA	Alignment	not modelled	100.0	32	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
34	c4xjcD	Alignment	not modelled	99.9	37	PDB header: hydrolase Chain: D: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: dctp deaminase-dntpase from bacillus halodurans
35	c2qjpC	Alignment	not modelled	99.9	28	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: bifunctional dctp deaminase:dntpase from mycobacterium tuberculosis,2 apo form
36	d1pkha	Alignment	not modelled	99.9	28	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
37	c4dhkB	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: B: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: crystal structure of a deoxycytidine triphosphate deaminase (dctp2 deaminase) from burkholderia thailandensis
38	c3km3B	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: crystal structure of eoxycytidine triphosphate deaminase from2 anaplasma phagocytophilum at 2.1a resolution
39	c2vziB	Alignment	not modelled	99.9	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 167aa long hypothetical dntpase; PDBTitle: crystal structure of dctp deaminase from sulfolobus tokodaii
40	c2r9qD	Alignment	not modelled	99.9	30	PDB header: hydrolase Chain: D: PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
41	d2viva	Alignment	not modelled	39.0	13	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
42	d1mqma	Alignment	not modelled	37.0	14	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
43	c5cl2A	Alignment	not modelled	33.7	17	PDB header: protein binding Chain: A: PDB Molecule: sporulation-control protein spo0m; PDBTitle: crystal structure of spo0m, sporulation control protein, from bacillus2 subtilis.
44	d1tula	Alignment	not modelled	31.4	24	Fold: beta-clip Superfamily: Tlp20, baculovirus telokin-like protein Family: Tlp20, baculovirus telokin-like protein
45	d1sdwa2	Alignment	not modelled	29.0	22	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: PHM/PNGase F Family: Peptidylglycine alpha-hydroxylating monooxygenase, PHM
46	d1vp2a	Alignment	not modelled	27.0	25	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
47	c4o4aD	Alignment	not modelled	26.3	16	PDB header: lipid binding protein Chain: D: PDB Molecule: lipoprotein, putative; PDBTitle: 2.75 angstrom crystal structure of putative lipoprotein from bacillus2 anthracis.
48	c1ha0A	Alignment	not modelled	25.8	13	PDB header: viral protein Chain: A: PDB Molecule: protein (hemagglutinin precursor); PDBTitle: hemagglutinin precursor ha0
49	d1uwfa1	Alignment	not modelled	24.7	20	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
50	d1k7ka	Alignment	not modelled	23.2	17	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
51	d2visc	Alignment	not modelled	22.6	13	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
52	c3ejhF	Alignment	not modelled	19.9	50	PDB header: cell adhesion Chain: F: PDB Molecule: collagen type-i a1 chain; PDBTitle: crystal structure of the fibronectin 8-9fni domain pair in complex2 with a type-i collagen peptide
53	c5sch1B	Alignment	not modelled	16.1	21	PDB header: transferase Chain: B: PDB Molecule: putative polycomb protein ezh2,putative polycomb protein PDBTitle: crystal structure of an active polycomb repressive complex 2 in the2 stimulated state
54	c4wsrA	Alignment	not modelled	14.8	22	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
55	c3ddvA	Alignment	not modelled	12.0	14	PDB header: luminescent protein Chain: A: PDB Molecule: lumazine protein;

55	c2uuuA	Alignment	not modelled	12.0	14	PDBTitle: structure of lumazine protein, an optical transponder of luminescent2 bacteria
56	c3a35B	Alignment	not modelled	11.9	14	PDB header: luminescent protein Chain: B: PDB Molecule: lumazine protein; PDBTitle: crystal structure of lump complexed with riboflavin
57	c4bngA	Alignment	not modelled	10.6	14	PDB header: hydrolase Chain: A: PDB Molecule: non-canonical purine ntp pyrophosphatase; PDBTitle: the structure of the staphylococcus aureus ham1 protein
58	c3kioC	Alignment	not modelled	9.1	42	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease h2 subunit c; PDBTitle: mouse rnase h2 complex
59	c2rfuA	Alignment	not modelled	8.8	13	PDB header: viral protein Chain: A: PDB Molecule: influenza b hemagglutinin (ha); PDBTitle: crystal structure of influenza b virus hemagglutinin in complex with2 lsc2 receptor analog
60	c2d7gD	Alignment	not modelled	8.4	27	PDB header: hydrolase Chain: D: PDB Molecule: primosomal protein n'; PDBTitle: crystal structure of the aa complex of the n-terminal domain of pria
61	c2oqbA	Alignment	not modelled	8.3	53	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	d1v7ra	Alignment	not modelled	8.1	15	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
63	c2wr2B	Alignment	not modelled	8.0	14	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: structure of influenza h2 avian hemagglutinin with avian2 receptor
64	c4n14H	Alignment	not modelled	7.9	26	PDB header: dna binding protein Chain: H: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to adp
65	c1yj5C	Alignment	not modelled	7.7	15	PDB header: transferase Chain: C: PDB Molecule: 5' polynucleotide kinase-3' phosphatase fha domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
66	c3gzub	Alignment	not modelled	7.7	24	PDB header: virus Chain: B: PDB Molecule: inner capsid protein vp2; PDBTitle: vp7 recoated rotavirus dlp
67	d1pmia	Alignment	not modelled	7.6	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Type I phosphomannose isomerase
68	d3c0na1	Alignment	not modelled	7.6	55	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Aerolysin/Pertussis toxin (APT) domain
69	d1boba	Alignment	not modelled	6.8	33	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
70	d1wb1a3	Alignment	not modelled	6.8	17	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
71	d1jsma	Alignment	not modelled	6.7	18	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
72	c3kz4A	Alignment	not modelled	6.5	22	PDB header: virus Chain: A: PDB Molecule: inner capsid protein vp2; PDBTitle: crystal structure of the rotavirus double layered particle
73	c3tquD	Alignment	not modelled	6.5	17	PDB header: hydrolase Chain: D: PDB Molecule: non-canonical purine ntp pyrophosphatase; PDBTitle: structure of a ham1 protein from coxiella burnetii
74	c4lhsA	Alignment	not modelled	6.3	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative gds1-like lipase (bacova_00914) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
75	c5d6aA	Alignment	not modelled	5.9	22	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase of the abc class; PDBTitle: 2.7 angstrom crystal structure of abc transporter atpase from vibrio2 vulnificus in complex with adenylyl-imidodiphosphate (amp-pnp)
76	d2ibxa1	Alignment	not modelled	5.7	13	Fold: Viral protein domain Superfamily: Viral protein domain Family: Influenza hemagglutinin headpiece
77	c3h0dB	Alignment	not modelled	5.3	44	PDB header: transcription/dna Chain: B: PDB Molecule: ctsr; PDBTitle: crystal structure of ctsr in complex with a 26bp dna duplex
78	c2vzyA	Alignment	not modelled	5.3	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1012; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
79	c4fqjA	Alignment	not modelled	5.1	13	PDB header: viral protein/immune system Chain: A: PDB Molecule: hemagglutinin; PDBTitle: influenza b/florida/4/2006 hemagglutinin fab cr8071 complex