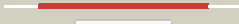



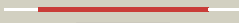




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3733c_(-)_4184190_4184690
Date	Fri Aug 9 18:20:43 BST 2019
Unique Job ID	a1c0bb1066fb7072

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fyjB_	 Alignment		99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
2	c5gg7A_	 Alignment		99.9	33	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family protein; PDBTitle: crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
3	d1ktga_	 Alignment		99.9	23	Fold: Nudix Superfamily: Nudix Family: MutT-like
4	d1xsba_	 Alignment		99.9	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
5	c4dywA_	 Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt nudix hydrolase from burkholderia2 pseudomallei
6	c3sonB_	 Alignment		99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical nudix hydrolase; PDBTitle: crystal structure of a putative nudix hydrolase (lmo2365_2679) from2 listeria monocytogenes str. 4b f2365 at 1.70 a resolution
7	d2b0va1	 Alignment		99.9	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
8	c3gz8C_	 Alignment		99.9	16	PDB header: dna binding protein Chain: C: PDB Molecule: mutt/nudix family protein; PDBTitle: cocrystal structure of nudix domain of shewanella oneidensis nrtr2 complexed with adp ribose
9	c2kdvA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: rna pyrophosphohydrolase; PDBTitle: solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
10	c3dkuB_	 Alignment		99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of nudix hydrolase orf153, ymfb, from escherichia2 coli k-1
11	c5cfiC_	 Alignment		99.8	18	PDB header: hydrolase Chain: C: PDB Molecule: bis(5'-nucleosyl)-tetrphosphatase (diadenosine PDBTitle: structural and functional attributes of malaria parasite ap4a2 hydrolase

12	d2fb1a2	Alignment		99.8	16	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
13	c2pq1B_	Alignment		99.8	28	PDB header: hydrolase Chain: B: PDB Molecule: ap4a hydrolase; PDBTitle: crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5
14	c5gp0F_	Alignment		99.8	16	PDB header: hydrolase Chain: F: PDB Molecule: nudix hydrolase 1; PDBTitle: crystal structure of geraniol-nudx1 complex
15	c5bonC_	Alignment		99.8	18	PDB header: hydrolase Chain: C: PDB Molecule: probable 8-oxo-dgtp diphosphatase nudt15; PDBTitle: crystal structure of human nudt15 (mth2)
16	c2o1cB_	Alignment		99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: datp pyrophosphohydrolase; PDBTitle: structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
17	c3fcmA_	Alignment		99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a nudix hydrolase from clostridium perfringens
18	d1jkna_	Alignment		99.8	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
19	c2fvvA_	Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: diphosphoinositol polyphosphate phosphohydrolase 1; PDBTitle: human diphosphoinositol polyphosphate phosphohydrolase 1
20	d2fvva1	Alignment		99.8	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
21	c4ilqA_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: ct771; PDBTitle: 2.60a resolution structure of ct771 from chlamydia trachomatis
22	d1vcda1	Alignment	not modelled	99.8	26	Fold: Nudix Superfamily: Nudix Family: MutT-like
23	c4kyxA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribose pyrophosphatase mutt; PDBTitle: crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
24	c3q4iA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase (mutt/nudix family protein); PDBTitle: crystal structure of cdp-chase in complex with gd3+
25	d1sjya_	Alignment	not modelled	99.8	27	Fold: Nudix Superfamily: Nudix Family: MutT-like
26	c2gb5B_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
27	c2yyhC_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: C: PDB Molecule: 8-oxo-dgtpase domain; PDBTitle: crystal structure of nudix family protein from aquifex aeolicus
28	c2fb1A_	Alignment	not modelled	99.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0354 from bacteroides thetaiotaomicron
						Fold: Nudix

29	d2azwa1	Alignment	not modelled	99.8	18	Superfamily: Nudix Family: MutT-like
30	d1ryaa_	Alignment	not modelled	99.8	17	Fold: Nudix Superfamily: Nudix Family: GDP-mannose mannosyl hydrolase NudD
31	c3i9xA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from listeria innocua
32	c3gwyA_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: putative ctp pyrophosphohydrolase; PDBTitle: crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
33	c3gz6A_	Alignment	not modelled	99.8	16	PDB header: dna binding protein/dna Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of shewanella oneidensis nrtr complexed with a 27mer2 dna
34	c6o3pA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
35	c4hfgB_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of udp-x diphosphatase
36	c3n77B_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: B: PDB Molecule: nucleoside triphosphatase nudix; PDBTitle: crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
37	c5mp0D_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: D: PDB Molecule: m7gpppn-mrna hydrolase; PDBTitle: human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
38	c2rrkA_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: ctp pyrophosphohydrolase; PDBTitle: solution structure of the e. coli orf135 protein
39	c3cngC_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
40	c5zrhA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: putative mutator protein mutt2/nudix hydrolase; PDBTitle: m. smegmatis antimutator protein mutt2 in complex with cmp
41	c5lopA_	Alignment	not modelled	99.8	20	PDB header: rna binding protein Chain: A: PDB Molecule: klla0f23980p; PDBTitle: structure of the active form of /k. lactis/ dcp1-dcp2-edc3 decapping2 complex bound to m7gdp
42	d2fmla2	Alignment	not modelled	99.8	21	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
43	d1vk6a2	Alignment	not modelled	99.8	18	Fold: Nudix Superfamily: Nudix Family: NADH pyrophosphatase
44	c3o8sA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribose pyrophosphatase; PDBTitle: crystal structure of an adp-ribose pyrophosphatase (ssu98_1448) from2 streptococcus suis 89-1591 at 2.27 a resolution
45	c2qjoB_	Alignment	not modelled	99.8	16	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nmh adenylyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nmh adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
46	c3grnB_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: mutt related protein; PDBTitle: crystal structure of mutt protein from methanosarcina mazei go1
47	d2b06a1	Alignment	not modelled	99.8	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
48	c2jvbA_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: mrna-decapping enzyme subunit 2; PDBTitle: solution structure of catalytic domain of ydcp2
49	c2r5wA_	Alignment	not modelled	99.8	15	PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide adenylyltransferase; PDBTitle: crystal structure of a bifunctional nmh2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
50	d1k2ea_	Alignment	not modelled	99.8	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
51	c3r03B_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: B: PDB Molecule: nudix hydrolase; PDBTitle: the crystal structure of nudix hydrolase from rhodospirillum rubrum
52	c3f6aA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a hydrolase, nudix family from2 clostridium perfringens
53	d2fkba1	Alignment	not modelled	99.8	15	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
						PDB header: hydrolase

54	c4v14A_	Alignment	not modelled	99.7	18	Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: structure and function analysis of mutt from the2 psychrofile fish pathogen alivibrio salmonicida and the3 mesophile vibrio cholerae
55	c3fk9B_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: B: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mmutator mutt protein from bacillus halodurans
56	c3hhjA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mutator mutt from bartonella henselae
57	d1puna_	Alignment	not modelled	99.7	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
58	c2qkmF_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: F: PDB Molecule: spac19a8.12 protein; PDBTitle: the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
59	c2fm1B_	Alignment	not modelled	99.7	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family protein from enterococcus2 faecalis
60	d1iryA_	Alignment	not modelled	99.7	24	Fold: Nudix Superfamily: Nudix Family: MutT-like
61	c3h95A_	Alignment	not modelled	99.7	17	PDB header: gene regulation Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the nudix domain of nudt6
62	d1nqza_	Alignment	not modelled	99.7	25	Fold: Nudix Superfamily: Nudix Family: MutT-like
63	c5lf8A_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 17; PDBTitle: human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
64	c3ef5A_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
65	d2a6ta2	Alignment	not modelled	99.7	21	Fold: Nudix Superfamily: Nudix Family: mRNA decapping enzyme-like
66	c3id9B_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
67	c4zbpC_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase 7; PDBTitle: crystal structure of the ampccr-bound atnudt7
68	c3gg6A_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 18; PDBTitle: crystal structure of the nudix domain of human nudt18
69	c3qsjA_	Alignment	not modelled	99.7	25	PDB header: hydrolase Chain: A: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
70	c3exqA_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: nudix family hydrolase; PDBTitle: crystal structure of a nudix family hydrolase from2 lactobacillus brevis
71	d1q33a_	Alignment	not modelled	99.7	21	Fold: Nudix Superfamily: Nudix Family: MutT-like
72	c5x1xA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: solution nmr structure of dna mismatch repair protein mutt (family2 nudix hydrolase) from methicillin resistant staphylococcus aureus 252
73	c3f13A_	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: putative nudix hydrolase family member; PDBTitle: crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
74	c2pqvA_	Alignment	not modelled	99.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family protein from streptococcus2 pneumoniae
75	c5c7tB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: nudf protein; PDBTitle: crystal structure of the bdellovibrio bacteriovorus nucleoside2 diphosphate sugar hydrolase in complex with adp-ribose
76	d2o5fa1	Alignment	not modelled	99.7	15	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
77	d1ppva_	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
78	d1hzta_	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
79	c3rh7A_	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution

80	c3edsA	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
81	c2yvoA	Alignment	not modelled	99.6	23	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of ndx2 in complex with mg2+ and amp from thermus2 thermophilus hb8
82	c2w4eA	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
83	d1vhza	Alignment	not modelled	99.6	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
84	d1v8ya	Alignment	not modelled	99.6	26	Fold: Nudix Superfamily: Nudix Family: MutT-like
85	d1g0sa	Alignment	not modelled	99.6	24	Fold: Nudix Superfamily: Nudix Family: MutT-like
86	c3bm4B	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: adp-sugar pyrophosphatase; PDBTitle: crystal structure of human adp-ribose pyrophosphatase nudt5 in complex2 with magnesium and ampcpr
87	c4jztA	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: dgtp pyrophosphohydrolase; PDBTitle: crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
88	c5t3pB	Alignment	not modelled	99.6	22	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal coenzyme a diphosphatase nudt7; PDBTitle: crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
89	d1x51a1	Alignment	not modelled	99.5	13	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
90	c3q91D	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: D: PDB Molecule: uridine diphosphate glucose pyrophosphatase; PDBTitle: crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
91	d1mqea	Alignment	not modelled	99.5	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
92	d1u20a1	Alignment	not modelled	99.4	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
93	d1viua	Alignment	not modelled	99.4	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
94	c3e57A	Alignment	not modelled	99.4	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein tm1382; PDBTitle: crystal structure of tm1382, a putative nudix hydrolase
95	c1rrqA	Alignment	not modelled	99.4	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
96	d1rrqa2	Alignment	not modelled	99.3	14	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
97	c2j8qB	Alignment	not modelled	99.3	18	PDB header: nuclear protein Chain: B: PDB Molecule: cleavage and polyadenylation specificity factor 5; PDBTitle: crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
98	c4v1aj	Alignment	not modelled	99.3	15	PDB header: ribosome Chain: J: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
99	c3dupB	Alignment	not modelled	99.3	10	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
100	c2i6kA	Alignment	not modelled	99.2	12	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 1; PDBTitle: crystal structure of human type i ipp isomerase complexed with a2 substrate analog
101	c2pnyA	Alignment	not modelled	99.0	13	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 2; PDBTitle: structure of human isopentenyl-diphosphate delta-isomerase 2
102	c5if9A	Alignment	not modelled	99.0	17	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 22; PDBTitle: crystal structure of human nudt22
103	c3couA	Alignment	not modelled	98.4	24	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudix motif 16 (nudt16)
104	c3kvhA	Alignment	not modelled	97.6	21	PDB header: rna binding protein Chain: A: PDB Molecule: protein syndesmos; PDBTitle: crystal structure of human protein syndesmos (nudt16-like protein) PDB header: ribosome

105	c1vw46_	Alignment	not modelled	97.4	20	Chain: 6: PDB Molecule: 54s ribosomal protein l17, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
106	c6drkD_	Alignment	not modelled	97.3	19	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel, subfamily m, PDBTitle: structure of trpm2 ion channel receptor by single particle electron2 cryo-microscopy, apo state
107	c3p5tE_	Alignment	not modelled	97.0	23	PDB header: rna binding protein Chain: E: PDB Molecule: cleavage and polyadenylation specificity factor subunit 5; PDBTitle: cfim25-cfim68 complex
108	c6mizC_	Alignment	not modelled	96.4	16	PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: human trpm2 ion channel in an adpr-bound state
109	c6d73B_	Alignment	not modelled	94.1	23	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+
110	c4ktbA_	Alignment	not modelled	88.1	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of posible asymmetric diadenosine tetraphosphate2 (ap(4)a) hydrolases from jonesia denitrificans dsm 20603
111	c6d73C_	Alignment	not modelled	81.7	12	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+