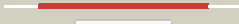























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2985_(mutT1)_3342175_3343128
Date	Thu Aug 8 16:20:15 BST 2019
Unique Job ID	21e527a3aa205e50

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5gg7A_	 Alignment		100.0	69	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)
2	c3fjyB_	 Alignment		100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
3	d1ktga_	 Alignment		100.0	28	Fold: Nudix Superfamily: Nudix Family: MuT-like
4	c3mxB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgam5, mitochondrial; PDBTitle: crystal structure of human phosphoglycerate mutase family member 52 (pgam5)
5	c2rfIB_	 Alignment		99.9	18	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
6	c4hbzA_	 Alignment		99.9	22	PDB header: hydrolase, isomerase Chain: A: PDB Molecule: putative phosphohistidine phosphatase, sixa; PDBTitle: the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartita.
7	d1e58a_	 Alignment		99.9	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
8	c1ujcA_	 Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
9	c2pq1B_	 Alignment		99.9	33	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
10	c3f2iD_	 Alignment		99.9	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr0221 protein; PDBTitle: crystal structure of the alr0221 protein from nostoc, northeast2 structural genomics consortium target nsr422.
11	c2yn0A_	 Alignment		99.9	27	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 55 kda subunit; PDBTitle: tau55 histidine phosphatase domain

12	d1xsba_	Alignment		99.9	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
13	c4embD_	Alignment		99.9	20	PDB header: isomerase Chain: D: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpma from borrelia2 burgdorferi b31
14	d1riia_	Alignment		99.9	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
15	c4pz9B_	Alignment		99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: glucosyl-3-phosphoglycerate phosphatase; PDBTitle: the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c
16	c4ilqA_	Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: ct771; PDBTitle: 2.60a resolution structure of ct771 from chlamydia trachomatis
17	c1vixD_	Alignment		99.9	17	PDB header: isomerase, hydrolase Chain: D: PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
18	d1xq9a_	Alignment		99.9	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
19	d1vcda1	Alignment		99.9	26	Fold: Nudix Superfamily: Nudix Family: MutT-like
20	c5um0A_	Alignment		99.9	18	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of 2,3-bisphosphoglycerate-dependent2 phosphoglycerate mutase from neisseria gonorrhoeae
21	d1qhfa_	Alignment	not modelled	99.9	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
22	c3sonB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical nudix hydrolase; PDBTitle: crystal structure of a putative nudix hydrolase (lmof2365_2679) from2 listeria monocytogenes str. 4b f2365 at 1.70 a resolution
23	c5vveA_	Alignment	not modelled	99.9	20	PDB header: isomerase Chain: A: PDB Molecule: phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from naegleria fowleri
24	c3dcyA_	Alignment	not modelled	99.9	21	PDB header: apoptosis regulator Chain: A: PDB Molecule: regulator protein; PDBTitle: crystal structure of a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.
25	c3ll4B_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
26	c3eznB_	Alignment	not modelled	99.9	20	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
27	c4hfqB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of udp-x diphosphatase
28	c5cfc_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: bis(5'-nucleosyl)-tetrakisphosphate (diadenosine)

					PDBTitle: structural and functional attributes of malaria parasite ap4a2 hydrolase
29	d1fzta_	Alignment	not modelled	99.9	19 Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
30	c2ikqA_	Alignment	not modelled	99.9	18 PDB header: signaling protein, immune system Chain: A: PDB Molecule: suppressor of t-cell receptor signaling 1; PDBTitle: crystal structure of mouse sts-1 pgm domain in complex with phosphate
31	c2qniA_	Alignment	not modelled	99.9	15 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu0299; PDBTitle: crystal structure of uncharacterized protein atu0299
32	c3d4iD_	Alignment	not modelled	99.9	21 PDB header: hydrolase Chain: D: PDB Molecule: sts-2 protein; PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2
33	c2fb1A_	Alignment	not modelled	99.9	18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0354 from bacteroides thetaiotaomicron
34	c3f3kA_	Alignment	not modelled	99.9	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
35	c2yn2A_	Alignment	not modelled	99.9	23 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ynl108c; PDBTitle: huf protein - paralogue of the tau55 histidine phosphatase domain
36	c4ij5B_	Alignment	not modelled	99.9	22 PDB header: hydrolase Chain: B: PDB Molecule: phosphoserine phosphatase 1; PDBTitle: crystal structure of a novel-type phosphoserine phosphatase from2 hydrogenobacter thermophilus tk-6
37	c3q4iA_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase (mutt/nudix family protein); PDBTitle: crystal structure of cdp-chase in complex with gd3+
38	c3gz8C_	Alignment	not modelled	99.9	19 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
39	d2fb1a2	Alignment	not modelled	99.9	17 Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
40	c1k6mA_	Alignment	not modelled	99.9	22 PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2- PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase
41	d2hhja1	Alignment	not modelled	99.9	26 Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
42	c3r7aA_	Alignment	not modelled	99.9	23 PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
43	c3hjbB_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-ribazole-5'-phosphate phosphatase cobc; PDBTitle: crystal structure of putative alpha-ribazole-5'-phosphate phosphatase2 cobc from vibrio parahaemolyticus
44	c2i1vB_	Alignment	not modelled	99.9	18 PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6- PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
45	c2a6pA_	Alignment	not modelled	99.9	21 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: possible phosphoglycerate mutase gpm2; PDBTitle: structure solution to 2.2 angstrom and functional characterisation of2 the open reading frame rv3214 from mycobacterium tuberculosis
46	d3pgma_	Alignment	not modelled	99.9	22 Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
47	c2o1cB_	Alignment	not modelled	99.9	21 PDB header: hydrolase Chain: B: PDB Molecule: datp pyrophosphohydrolase; PDBTitle: structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
48	c3fk9B_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: B: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mmulator mutt protein from bacillus halodurans
49	c3d8hB_	Alignment	not modelled	99.9	24 PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
50	c6e4bC_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: C: PDB Molecule: adenosylcobalamin/alpha-ribazole phosphatase; PDBTitle: the crystal structure of a putative alpha-ribazole-5'-p phosphatase2 from escherichia coli str. k-12 substr. mg1655
51	d2fvva1	Alignment	not modelled	99.9	21 Fold: Nudix Superfamily: Nudix Family: MuT-like
52	c2fvvA_	Alignment	not modelled	99.9	21 PDB header: hydrolase Chain: A: PDB Molecule: diphosphoinositol polyphosphate phosphohydrolase 1; PDBTitle: human diphosphoinositol polyphosphate phosphohydrolase 1
53	c3e9eB_	Alignment	not modelled	99.9	21 PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074;

53	c3e9eB	Alignment	not modelled	99.9	41	PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio PDB header: hydrolase
54	c3fcmA	Alignment	not modelled	99.9	14	Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a nudix hydrolase from clostridium perfringens
55	c5zkkA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphoglycerate mutase family protein, putative; PDBTitle: crystal structure of phosphoserine phosphatase from entamoeba2 histolytica
56	c4eo9A	Alignment	not modelled	99.9	22	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
57	d1k2ea	Alignment	not modelled	99.9	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
58	c3i9xA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from listeria innocua
59	c1bifA	Alignment	not modelled	99.9	19	PDB header: bifunctional enzyme Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; PDBTitle: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
60	d2azwa1	Alignment	not modelled	99.9	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
61	d1bifa2	Alignment	not modelled	99.9	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
62	c3gz6A	Alignment	not modelled	99.9	20	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
63	d1h2ea	Alignment	not modelled	99.9	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
64	c2kdvA	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: rna pyrophosphohydrolase; PDBTitle: solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
65	c3c7tB	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: B: PDB Molecule: ecdysteroid-phosphate phosphatase; PDBTitle: crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
66	c3o8sA	Alignment	not modelled	99.9	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
67	c3cngC	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
68	c3dkuB	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of nudix hydrolase orf153, ymf6, from escherichia2 coli k-1
69	c3gwyA	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: putative ctp pyrophosphohydrolase; PDBTitle: crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
70	d1k6ma2	Alignment	not modelled	99.9	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
71	c2yyhC	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: 8-oxo-dgtpase domain; PDBTitle: crystal structure of nudix family protein from aquifex aeolicus
72	c2rrkA	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: ctp pyrophosphohydrolase; PDBTitle: solution structure of the e. coli orf135 protein
73	d2b0va1	Alignment	not modelled	99.9	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
74	d2fmla2	Alignment	not modelled	99.9	18	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
75	c2jvbA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: mrna-decapping enzyme subunit 2; PDBTitle: solution structure of catalytic domain of ydcp2
76	c4dywA	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt nudix hydrolase from burkholderia2 pseudomallei
77	c3exqA	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: nudix family hydrolase; PDBTitle: crystal structure of a nudix family hydrolase from2 lactobacillus brevis
78	c3r03B	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: B: PDB Molecule: nudix hydrolase; PDBTitle: the crystal structure of nudix hydrolase from rhodospirillum rubrum

79	d1tipa_	Alignment	not modelled	99.9	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
80	d2b06a1	Alignment	not modelled	99.9	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
81	c5lopA_	Alignment	not modelled	99.9	16	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
82	c5x1xA_	Alignment	not modelled	99.9	20	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
83	c2fm1B_	Alignment	not modelled	99.9	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
84	c4v14A_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: structure and function analysis of mutt from the2 psychrophile fish pathogen alivibrio salmonicida and the3 mesophile vibrio cholerae
85	d1sjya_	Alignment	not modelled	99.9	23	Fold: Nudix Superfamily: Nudix Family: MutT-like
86	c5bonC_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: C: PDB Molecule: probable 8-oxo-dgtp diphosphatase nudt15; PDBTitle: crystal structure of human nudt15 (mth2)
87	c2gb5B_	Alignment	not modelled	99.9	21	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
88	c3hhjA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mutator mutt from bartonella henselae
89	c4zbpC_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase 7; PDBTitle: crystal structure of the ampccr-bound atnud7
90	c3f6aA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a hydrolase, nudix family from2 clostridium perfringens
91	d1nqza_	Alignment	not modelled	99.9	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
92	d1puna_	Alignment	not modelled	99.9	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
93	c3ef5A_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
94	d1vk6a2	Alignment	not modelled	99.9	21	Fold: Nudix Superfamily: Nudix Family: NADH pyrophosphatase
95	c4kyxA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribose pyrophosphatase mutt; PDBTitle: crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
96	d1jkna_	Alignment	not modelled	99.9	23	Fold: Nudix Superfamily: Nudix Family: MutT-like
97	c5zrhA_	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: A: PDB Molecule: putative mutator protein mutt2/nudix hydrolase; PDBTitle: m. smegmatis antimutator protein mutt2 in complex with cmp
98	c3grnB_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: B: PDB Molecule: mutt related protein; PDBTitle: crystal structure of mutt protein from methanosarcina mazei go1
99	c2r5wA_	Alignment	not modelled	99.8	18	PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide adenyllyltransferase; PDBTitle: crystal structure of a bifunctional nm2 adenyllyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
100	c5mp0D_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: D: PDB Molecule: m7gpppn-mrna hydrolase; PDBTitle: human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
101	c3eozB_	Alignment	not modelled	99.8	22	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
102	c2qjoB_	Alignment	not modelled	99.8	23	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nmn adenyllyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nmn adenyllyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
103	c3id9B_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein;

103	c3u2b_	Alignment	not modelled	99.8	43	PDBTitle: crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
104	c5gp0F_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: F: PDB Molecule: nudix hydrolase 1; PDBTitle: crystal structure of geraniol-nudx1 complex
105	c3h95A_	Alignment	not modelled	99.8	13	PDB header: gene regulation Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the nudix domain of nudt6
106	c2qkmF_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: F: PDB Molecule: spac19a8.12 protein; PDBTitle: the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
107	d1ryaa_	Alignment	not modelled	99.8	17	Fold: Nudix Superfamily: Nudix Family: GDP-mannose mannosyl hydrolase NudD
108	c2pqvA_	Alignment	not modelled	99.8	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
109	c3gg6A_	Alignment	not modelled	99.8	26	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 18; PDBTitle: crystal structure of the nudix domain of human nudt18
110	c6o3pA_	Alignment	not modelled	99.8	18	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
111	d1v37a_	Alignment	not modelled	99.8	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
112	d2fkba1	Alignment	not modelled	99.8	21	Fold: Nudix Superfamily: Nudix Family: IIPP isomerase-like
113	c3n77B_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: B: PDB Molecule: nucleoside triphosphatase nudt; PDBTitle: crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
114	c5c7tB_	Alignment	not modelled	99.8	23	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
115	c5lf8A_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 17; PDBTitle: human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
116	d1q33a_	Alignment	not modelled	99.8	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
117	c3f13A_	Alignment	not modelled	99.8	27	PDB header: hydrolase Chain: A: PDB Molecule: putative nudix hydrolase family member; PDBTitle: crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
118	d1irya_	Alignment	not modelled	99.8	20	Fold: Nudix Superfamily: Nudix Family: MutT-like
119	c3rh7A_	Alignment	not modelled	99.8	23	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
120	d2a6ta2	Alignment	not modelled	99.8	20	Fold: Nudix Superfamily: Nudix Family: mRNA decapping enzyme-like