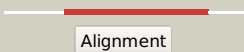

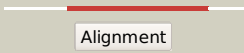



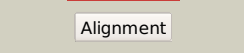



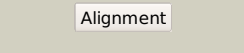
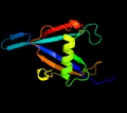
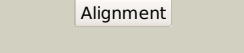



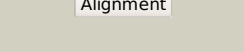

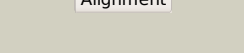

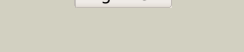



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3672c_(-)_4113699_4114520
Date	Fri Aug 9 18:20:36 BST 2019
Unique Job ID	c92f4785e232fb4c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5t3pB_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal coenzyme a diphosphatase nudt7; <b>PDBTitle:</b> crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
2	<a href="#">d1nqza_</a>	 Alignment		100.0	32	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
3	<a href="#">c5if8A_</a>	 Alignment		99.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 17; <b>PDBTitle:</b> human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
4	<a href="#">c3gz8C_</a>	 Alignment		99.7	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> cocrystal structure of nudix domain of shewanella oneidensis nrtr2 complexed with adp ribose
5	<a href="#">c3h95A_</a>	 Alignment		99.7	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 6; <b>PDBTitle:</b> crystal structure of the nudix domain of nudt6
6	<a href="#">c3qsjA_</a>	 Alignment		99.6	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
7	<a href="#">c5bonC_</a>	 Alignment		99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable 8-oxo-dgtp diphosphatase nudt15; <b>PDBTitle:</b> crystal structure of human nudt15 (mth2)
8	<a href="#">d2fb1a2</a>	 Alignment		99.6	16	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
9	<a href="#">d2fkba1</a>	 Alignment		99.6	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
10	<a href="#">d1sjya_</a>	 Alignment		99.6	25	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
11	<a href="#">c3gz6A_</a>	 Alignment		99.6	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of shewanella oneidensis nrtr complexed with a 27mer2 dna

12	<a href="#">c3i9xA_</a>	Alignment		99.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mutt/nudix family protein from listeria innocua
13	<a href="#">c4kyxA_</a>	Alignment		99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribose pyrophosphatase mutt; <b>PDBTitle:</b> crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
14	<a href="#">c2yvoA_</a>	Alignment		99.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of ndx2 in complex with mg2+ and amp from thermus2 thermophilus hb8
15	<a href="#">c3hhjA_</a>	Alignment		99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> crystal structure of mutator mutt from bartonella henselae
16	<a href="#">c4dywA_</a>	Alignment		99.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt nudix hydrolase from burkholderia2 pseudomallei
17	<a href="#">c2r5wA_</a>	Alignment		99.5	18	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinamide-nucleotide adenylyltransferase; <b>PDBTitle:</b> crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
18	<a href="#">c2rrkA_</a>	Alignment		99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp pyrophosphohydrolase; <b>PDBTitle:</b> solution structure of the e. coli orf135 protein
19	<a href="#">c5gg7A_</a>	Alignment		99.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family protein; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
20	<a href="#">d1ktga_</a>	Alignment		99.5	23	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
21	<a href="#">c3grnB_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt related protein; <b>PDBTitle:</b> crystal structure of mutt protein from methanosarcina mazei go1
22	<a href="#">d2b0va1</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
23	<a href="#">c3exqA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nudix family hydrolase; <b>PDBTitle:</b> crystal structure of a nudix family hydrolase from2 lactobacillus brevis
24	<a href="#">c2fb1A_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of protein bt0354 from bacteroides thetaiotaomicron
25	<a href="#">c2qjoB_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional nmn adenylyltransferase/nudix hydrolase; <b>PDBTitle:</b> crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
26	<a href="#">d1ppva_</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
27	<a href="#">c3dkuB_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphohydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase orf153, ymfb, from escherichia2 coli k-1
28	<a href="#">c3n77B_</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoside triphosphatase nudix; <b>PDBTitle:</b> crystal structure of idp01880, putative ntp

						pyrophosphohydrolase of 2 salmonella typhimurium lt2
29	<a href="#">d1hzta</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
30	<a href="#">d1puna</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
31	<a href="#">c2kdvA</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna pyrophosphohydrolase; <b>PDBTitle:</b> solution structure of rna pyrophosphohydrolase rpph from 2 escherichia coli
32	<a href="#">c3id9B</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mutt/nudix family protein from 2 bacillus thuringiensis
33	<a href="#">d1u20a1</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
34	<a href="#">d1vk6a2</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> NADH pyrophosphatase
35	<a href="#">d2fvva1</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
36	<a href="#">c2fvvA</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> diphosphoinositol polyphosphate phosphohydrolase 1; <b>PDBTitle:</b> human diphosphoinositol polyphosphate phosphohydrolase 1
37	<a href="#">c4zbpC</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase 7; <b>PDBTitle:</b> crystal structure of the ampcpr-bound atnud7
38	<a href="#">d1lrya</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
39	<a href="#">d1ryaa</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> GDP-mannose mannosyl hydrolase NudD
40	<a href="#">c5gp0F</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nudix hydrolase 1; <b>PDBTitle:</b> crystal structure of geraniol-nudx1 complex
41	<a href="#">c2gb5B</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh pyrophosphatase; <b>PDBTitle:</b> crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from 2 escherichia coli k12 at 2.30 a resolution
42	<a href="#">d2fmla2</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
43	<a href="#">c2yyhC</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 8-oxo-dgtpase domain; <b>PDBTitle:</b> crystal structure of nudix family protein from aquifex aeolicus
44	<a href="#">c5cfcC</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> bis(5'-nucleosyl)-tetraphosphatase (diadenosine <b>PDBTitle:</b> structural and functional attributes of malaria parasite ap4a2 hydrolase
45	<a href="#">c5zrhA</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mutator protein mutt2/nudix hydrolase; <b>PDBTitle:</b> m. smegmatis antimutator protein mutt2 in complex with cmp
46	<a href="#">d2azwa1</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
47	<a href="#">c3ef5A</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable pyrophosphohydrolase; <b>PDBTitle:</b> structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
48	<a href="#">c3fjyB</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable mutt1 protein; <b>PDBTitle:</b> crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
49	<a href="#">c5c7tB</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nudf protein; <b>PDBTitle:</b> crystal structure of the bdellovibrio bacteriovorus nucleoside2 diphosphate sugar hydrolase in complex with adp-ribose
50	<a href="#">d1xsba</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
51	<a href="#">c2jvbA</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna-decapping enzyme subunit 2; <b>PDBTitle:</b> solution structure of catalytic domain of ydcp2
52	<a href="#">c3r03B</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> the crystal structure of nudix hydrolase from rhodospirillum rubrum
53	<a href="#">c6o3pA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal nadh pyrophosphatase nudt12; <b>PDBTitle:</b> crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
54	<a href="#">c3cncC</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase;

54	<a href="#">c3hgc_</a>	Alignment	not modelled	99.4	10	<b>PDBTitle:</b> crystal structure of nudix hydrolase from nitrosomonas europaea
55	<a href="#">d1vhza_</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
56	<a href="#">c5x1xA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> solution nmr structure of dna mismatch repair protein mutt (family2 nudix hydrolase) from methicillin resistant staphylococcus aureus 252
57	<a href="#">c2w4eA</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
58	<a href="#">d1g0sa_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
59	<a href="#">c5mp0D_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> m7gpppn-mrna hydrolase; <b>PDBTitle:</b> human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
60	<a href="#">d1jkna_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
61	<a href="#">d1vcda1</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
62	<a href="#">c2pq1B_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ap4a hydrolase; <b>PDBTitle:</b> crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5
63	<a href="#">c3fk9B_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> crystal structure of mmutator mutt protein from bacillus halodurans
64	<a href="#">c3sonB_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical nudix hydrolase; <b>PDBTitle:</b> crystal structure of a putative nudix hydrolase (lmoF2365_2679) from2 listeria monocytogenes str. 4b f2365 at 1.70 a resolution
65	<a href="#">d2b06a1</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
66	<a href="#">c4hfbQ_</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of udp-x diphosphatase
67	<a href="#">c3gg6A_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 18; <b>PDBTitle:</b> crystal structure of the nudix domain of human nudt18
68	<a href="#">c3q4iA_</a>	Alignment	not modelled	99.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphohydrolase (mutt/nudix family protein); <b>PDBTitle:</b> crystal structure of cdp-chase in complex with gd3+
69	<a href="#">c3gwyA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ctp pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
70	<a href="#">c2o1cB_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> datp pyrophosphohydrolase; <b>PDBTitle:</b> structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
71	<a href="#">c2fmlB_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family protein from enterococcus2 faecalis
72	<a href="#">c4jztA_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dgtp pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
73	<a href="#">c2pqvA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family protein from streptococcus2 pneumoniae
74	<a href="#">c3bm4B_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adp-sugar pyrophosphatase; <b>PDBTitle:</b> crystal structure of human adp-ribose pyrophosphatase nudt5 in complex2 with magnesium and ampcpr
75	<a href="#">c3o8sA_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribose pyrophosphatase; <b>PDBTitle:</b> crystal structure of an adp-ribose pyrophosphatase (ssu98_1448) from2 streptococcus suis 89-1591 at 2.27 a resolution
76	<a href="#">d1k2ea_</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
77	<a href="#">d2o5fa1</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
78	<a href="#">c5lopA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> klla0f23980p; <b>PDBTitle:</b> structure of the active form of /k. lactis/ dcp1-dcp2-edc3 decapping2 complex bound to m7gdp
79	<a href="#">c4v14A_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> structure and function analysis of mutt from the2 psychrophile fish pathogen alivibrio salmonicida and the3 mesophile vibrio cholerae

80	<a href="#">c3edsA</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
81	<a href="#">c4ilqA</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ct771; <b>PDBTitle:</b> 2.60a resolution structure of ct771 from chlamydia trachomatis
82	<a href="#">c2qkmF</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> spac19a8.12 protein; <b>PDBTitle:</b> the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
83	<a href="#">c3f6aA</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family; <b>PDBTitle:</b> crystal structure of a hydrolase, nudix family from2 clostridium perfringens
84	<a href="#">c5if9A</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 22; <b>PDBTitle:</b> crystal structure of human nudt22
85	<a href="#">d1mqea</a>	Alignment	not modelled	99.2	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
86	<a href="#">d2a6ta2</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> mRNA decapping enzyme-like
87	<a href="#">c2i6kA</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 1; <b>PDBTitle:</b> crystal structure of human type i ipp isomerase complexed with a2 substrate analog
88	<a href="#">c3dupB</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
89	<a href="#">c3fcmA</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family; <b>PDBTitle:</b> crystal structure of a nudix hydrolase from clostridium perfringens
90	<a href="#">d1x51a1</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
91	<a href="#">d1q33a</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
92	<a href="#">d1v8ya</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
93	<a href="#">d1viua</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
94	<a href="#">c3q91D</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uridine diphosphate glucose pyrophosphatase; <b>PDBTitle:</b> crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
95	<a href="#">c3f13A</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nudix hydrolase family member; <b>PDBTitle:</b> crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
96	<a href="#">c1rrqA</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> muty; <b>PDBTitle:</b> muty adenine glycosylase in complex with dna containing an2 a:oxog pair
97	<a href="#">c3rh7A</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
98	<a href="#">c3e57A</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein tm1382; <b>PDBTitle:</b> crystal structure of tm1382, a putative nudix hydrolase
99	<a href="#">c2pnyA</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 2; <b>PDBTitle:</b> structure of human isopentenyl-diphosphate delta-isomerase 2
100	<a href="#">d1rrqa2</a>	Alignment	not modelled	98.8	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
101	<a href="#">c2j8qB</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor 5; <b>PDBTitle:</b> crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
102	<a href="#">c4v1aj</a>	Alignment	not modelled	98.3	11	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
103	<a href="#">c3couA</a>	Alignment	not modelled	98.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 16; <b>PDBTitle:</b> crystal structure of human nudix motif 16 (nudt16)
104	<a href="#">c3kvhA</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein syndesmos; <b>PDBTitle:</b> crystal structure of human protein syndesmos (nudt16-like protein)
						<b>PDB header:</b> rna binding protein

105	<a href="#">c3p5tE_</a>	Alignment	not modelled	90.6	19	<b>Chain:</b> E: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor subunit 5; <b>PDBTitle:</b> cfim25-cfim68 complex
106	<a href="#">c6drkD_</a>	Alignment	not modelled	86.6	16	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> transient receptor potential cation channel, subfamily m, <b>PDBTitle:</b> structure of trpm2 ion channel receptor by single particle electron2 cryo-microscopy, apo state
107	<a href="#">c6mizC_</a>	Alignment	not modelled	63.4	21	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> human trpm2 ion channel in an adpr-bound state
108	<a href="#">c1vw46_</a>	Alignment	not modelled	62.8	24	<b>PDB header:</b> ribosome <b>Chain:</b> 6: <b>PDB Molecule:</b> 54s ribosomal protein l17, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
109	<a href="#">c6d73B_</a>	Alignment	not modelled	57.6	29	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transient receptor potential cation channel, subfamily m; <b>PDBTitle:</b> cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+
110	<a href="#">c5ghaF_</a>	Alignment	not modelled	28.1	39	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> sulfur carrier ttub; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
111	<a href="#">d1aopa2</a>	Alignment	not modelled	21.8	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3