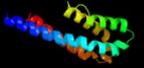
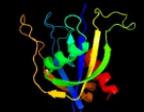
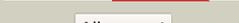
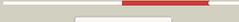


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2609c (-) _2936820_2937875
Date	Wed Aug 7 12:50:25 BST 2019
Unique Job ID	28f3cd6d098eb453

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2etda1</a>	 Alignment		99.9	32	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> LemA-like <b>Family:</b> LemA-like
2	<a href="#">c2kdvA</a>	 Alignment		99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna pyrophosphohydrolase; <b>PDBTitle:</b> solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
3	<a href="#">d1sjya</a>	 Alignment		99.8	29	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
4	<a href="#">d2o5fa1</a>	 Alignment		99.8	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> !PP isomerase-like
5	<a href="#">d1jkna</a>	 Alignment		99.8	18	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
6	<a href="#">c4hfgB</a>	 Alignment		99.8	17	<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
7	<a href="#">d1ryaa</a>	 Alignment		99.8	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> GDP-mannose mannosyl hydrolase NudD
8	<a href="#">c5c7tB</a>	 Alignment		99.8	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
9	<a href="#">c2pq1B</a>	 Alignment		99.8	26	<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
10	<a href="#">c5lf8A</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)
11	<a href="#">c5gg7A</a>	 Alignment		99.7	20	<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)

12	<a href="#">d1ppv_a</a>	Alignment		99.7	18	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> !PP isomerase-like
13	<a href="#">c2w4eA</a>	Alignment		99.7	22	<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
14	<a href="#">c3q4iA</a>	Alignment		99.7	20	<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+
15	<a href="#">c3grnB</a>	Alignment		99.7	21	<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
16	<a href="#">d2fkba1</a>	Alignment		99.7	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> !PP isomerase-like
17	<a href="#">c2yvoA</a>	Alignment		99.7	22	<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
18	<a href="#">d2azwa1</a>	Alignment		99.7	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
19	<a href="#">c3dkuB</a>	Alignment		99.7	22	<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
20	<a href="#">d2b0va1</a>	Alignment		99.7	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
21	<a href="#">c4kyxA</a>	Alignment	not modelled	99.7	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
22	<a href="#">c2rrkA</a>	Alignment	not modelled	99.7	20	<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
23	<a href="#">c2o1cB</a>	Alignment	not modelled	99.7	28	<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
24	<a href="#">d1mqea</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
25	<a href="#">c6o3pA</a>	Alignment	not modelled	99.7	19	<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
26	<a href="#">c3fjyB</a>	Alignment	not modelled	99.7	18	<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
27	<a href="#">c2pqvA</a>	Alignment	not modelled	99.7	21	<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
28	<a href="#">c3cngC</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from nitrosomonas europaea

29	<a href="#">c3h95A</a>	Alignment	not modelled	99.7	22	<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
30	<a href="#">c5bonC</a>	Alignment	not modelled	99.7	16	<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)
31	<a href="#">c2fvvA</a>	Alignment	not modelled	99.7	23	<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
32	<a href="#">d2fvva1</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
33	<a href="#">c2qjoB</a>	Alignment	not modelled	99.7	20	<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.
34	<a href="#">d1ktga</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
35	<a href="#">d1g0sa</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
36	<a href="#">c3exqA</a>	Alignment	not modelled	99.7	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
37	<a href="#">c2gb5B</a>	Alignment	not modelled	99.7	21	<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) from2 escherichia coli k12 at 2.30 a resolution
38	<a href="#">d1vcda1</a>	Alignment	not modelled	99.7	31	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
39	<a href="#">d1vk6a2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> NADH pyrophosphatase
40	<a href="#">d1xsba</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
41	<a href="#">c4zbpC</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase 7; <b>PDBTitle:</b> crystal structure of the ampccr-bound atnudt7
42	<a href="#">c3f6aA</a>	Alignment	not modelled	99.7	23	<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
43	<a href="#">c2r5wA</a>	Alignment	not modelled	99.7	19	<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
44	<a href="#">d1hztA</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> !PP isomerase-like
45	<a href="#">c5lopA</a>	Alignment	not modelled	99.7	17	<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
46	<a href="#">c3n77B</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoside triphosphatase nudt; <b>PDBTitle:</b> crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
47	<a href="#">c3sonB</a>	Alignment	not modelled	99.7	18	<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 (lmo2365_2679) from2 listeria monocytogenes str. 4b f2365 at 1.70 a resolution
48	<a href="#">c4dywA</a>	Alignment	not modelled	99.7	23	<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
49	<a href="#">c3edsA</a>	Alignment	not modelled	99.7	22	<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
50	<a href="#">c5gp0F</a>	Alignment	not modelled	99.7	19	<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
51	<a href="#">c3hhjA</a>	Alignment	not modelled	99.7	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
52	<a href="#">c3gg6A</a>	Alignment	not modelled	99.7	21	<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
53	<a href="#">d2fb1a2</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like

54	<a href="#">d1vhza_</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
55	<a href="#">c3gz8C_</a>	Alignment	not modelled	99.6	20	<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
56	<a href="#">c5mp0D_</a>	Alignment	not modelled	99.6	25	<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
57	<a href="#">c3fcmA_</a>	Alignment	not modelled	99.6	14	<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
58	<a href="#">c2qkmF_</a>	Alignment	not modelled	99.6	18	<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
59	<a href="#">c4v14A_</a>	Alignment	not modelled	99.6	22	<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 aliivibrio salmonicida and the3 mesophile vibrio cholerae
60	<a href="#">c3r03B_</a>	Alignment	not modelled	99.6	25	<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
61	<a href="#">c3o8sA_</a>	Alignment	not modelled	99.6	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
62	<a href="#">d2b06a1</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
63	<a href="#">c2jvbA_</a>	Alignment	not modelled	99.6	17	<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
64	<a href="#">d1v8ya_</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
65	<a href="#">d1puna_</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
66	<a href="#">c5x1xA_</a>	Alignment	not modelled	99.6	16	<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
67	<a href="#">d1lrya_</a>	Alignment	not modelled	99.6	31	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
68	<a href="#">c5zrhA_</a>	Alignment	not modelled	99.6	27	<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
69	<a href="#">c3bm4B_</a>	Alignment	not modelled	99.6	19	<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
70	<a href="#">c3gwyA_</a>	Alignment	not modelled	99.6	16	<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
71	<a href="#">c5cfiC_</a>	Alignment	not modelled	99.6	22	<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
72	<a href="#">c3ef5A_</a>	Alignment	not modelled	99.6	19	<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
73	<a href="#">d1k2ea_</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
74	<a href="#">c3fk9B_</a>	Alignment	not modelled	99.6	23	<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
75	<a href="#">c4ilqA_</a>	Alignment	not modelled	99.6	20	<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
76	<a href="#">c2fb1A_</a>	Alignment	not modelled	99.6	21	<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
77	<a href="#">c3id9B_</a>	Alignment	not modelled	99.6	22	<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 from2 bacillus thuringiensis
78	<a href="#">d1nqza_</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
						<b>Fold:</b> Nudix

79	<a href="#">d2a6ta2</a>	Alignment	not modelled	99.6	24	<b>Superfamily:</b> Nudix <b>Family:</b> mRNA decapping enzyme-like
80	<a href="#">c3gz6A</a>	Alignment	not modelled	99.5	22	<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
81	<a href="#">c2yyhC</a>	Alignment	not modelled	99.5	23	<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
82	<a href="#">c3rh7A</a>	Alignment	not modelled	99.5	22	<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
83	<a href="#">d2fmla2</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
84	<a href="#">d1viua</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
85	<a href="#">c4jztA</a>	Alignment	not modelled	99.5	21	<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
86	<a href="#">c3i9xA</a>	Alignment	not modelled	99.5	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
87	<a href="#">c3q91D</a>	Alignment	not modelled	99.5	21	<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)
88	<a href="#">c3f13A</a>	Alignment	not modelled	99.5	26	<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
89	<a href="#">c2fmlB</a>	Alignment	not modelled	99.4	18	<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
90	<a href="#">c3e57A</a>	Alignment	not modelled	99.4	14	<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
91	<a href="#">d1x51a1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
92	<a href="#">d1q33a</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
93	<a href="#">c2i6kA</a>	Alignment	not modelled	99.4	16	<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
94	<a href="#">c2j8qB</a>	Alignment	not modelled	99.3	20	<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.
95	<a href="#">c1rrqA</a>	Alignment	not modelled	99.3	17	<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
96	<a href="#">c2pnyA</a>	Alignment	not modelled	99.3	16	<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
97	<a href="#">c3qsjA</a>	Alignment	not modelled	99.3	24	<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
98	<a href="#">d1u20a1</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
99	<a href="#">c5t3pB</a>	Alignment	not modelled	99.1	20	<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
100	<a href="#">d1rrqa2</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
101	<a href="#">c4v1aj</a>	Alignment	not modelled	99.1	16	<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
102	<a href="#">c3dupB</a>	Alignment	not modelled	99.1	20	<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
103	<a href="#">c5lf9A</a>	Alignment	not modelled	98.8	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
104	<a href="#">c3ouA</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x

104	<a href="#">c3c0uA</a>	Alignment	not modelled	98.3	19	motif 16; <b>PDB header:</b> crystal structure of human nudix motif 16 (nudt16)
105	<a href="#">c3kvhA</a>	Alignment	not modelled	97.4	16	<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)
106	<a href="#">c1vw46</a>	Alignment	not modelled	97.3	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
107	<a href="#">c3p5tE</a>	Alignment	not modelled	96.7	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> E; <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor subunit 5; <b>PDBTitle:</b> cfim25-cfim68 complex
108	<a href="#">c4ktbA</a>	Alignment	not modelled	93.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of possible asymmetric diadenosine tetraphosphate2 (ap(4)a) hydrolases from jonesia denitrificans dsm 20603
109	<a href="#">c6drkD</a>	Alignment	not modelled	90.3	32	<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
110	<a href="#">c6mizC</a>	Alignment	not modelled	86.8	25	<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
111	<a href="#">c3brcA</a>	Alignment	not modelled	70.9	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved protein of unknown function; <b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
112	<a href="#">c3jcuJ</a>	Alignment	not modelled	66.4	15	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
113	<a href="#">d2axtj1</a>	Alignment	not modelled	65.9	23	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, PsbJ <b>Family:</b> PsbJ-like
114	<a href="#">c3a0hJ</a>	Alignment	not modelled	60.6	23	<b>PDB header:</b> electron transport <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
115	<a href="#">c5xnmj</a>	Alignment	not modelled	60.3	19	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from pismus2 sativum
116	<a href="#">c5d5pC</a>	Alignment	not modelled	54.3	17	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> hcgb; <b>PDBTitle:</b> hcgb from methanococcus maripaludis
117	<a href="#">c6d73B</a>	Alignment	not modelled	45.4	23	<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+
118	<a href="#">d1m56d</a>	Alignment	not modelled	42.7	24	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Bacterial aa3 type cytochrome c oxidase subunit IV <b>Family:</b> Bacterial aa3 type cytochrome c oxidase subunit IV
119	<a href="#">c5gkeB</a>	Alignment	not modelled	40.3	23	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> endonuclease endoms; <b>PDBTitle:</b> structure of endoms-dsdna1 complex
120	<a href="#">c2vldA</a>	Alignment	not modelled	39.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endonuclease nucs; <b>PDBTitle:</b> crystal structure of a repair endonuclease from pyrococcus abyssi