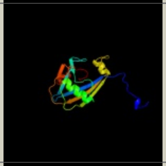
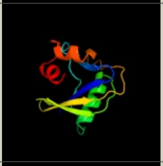
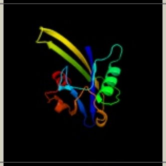
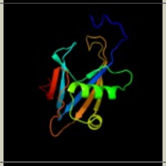
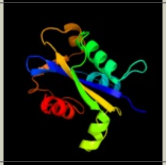
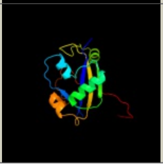
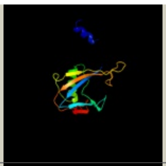
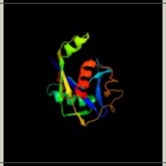
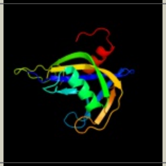
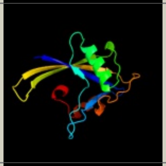
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P32056
Date	Thu Jan 5 11:49:03 GMT 2012
Unique Job ID	c161e7f841e0353e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ryaa_	Alignment		100.0	100	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
2	c3gz8C_	Alignment		99.9	19	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** cocrystal structure of nudix domain of shewanella oneidensis2 nrtr complexed with adp ribose
3	c2qjoB_	Alignment		99.9	20	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional nmn adenylyltransferase/nudix hydrolase; **PDBTitle:** crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
4	c3h95A_	Alignment		99.9	16	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 6; **PDBTitle:** crystal structure of the nudix domain of nudt6
5	c3cngC_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
6	c3grnB_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt related protein; **PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1
7	c2r5wA_	Alignment		99.9	20	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**nicotinamide-nucleotide adenylyltransferase; **PDBTitle:** crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
8	d2b0va1	Alignment		99.9	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
9	d2fb1a2	Alignment		99.9	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
10	d1sjya_	Alignment		99.9	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
11	c2fb1A_	Alignment		99.9	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron

12	d2fmla2	Alignment		99.9	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
13	c3q4iA_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
14	c3o8sA_	Alignment		99.9	16	**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
15	c3n77B_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
16	c3hhjA_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
17	c3gz6A_	Alignment		99.9	21	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of shewanella oneidensis nrtr complexed2 with a 27mer dna
18	c3dkuB_	Alignment		99.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1
19	c3exqA_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
20	c2fmlB_	Alignment		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
21	c3gg6A_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 18; **PDBTitle:** crystal structure of the nudix domain of human nudt18
22	c2kdvA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
23	c3f6aA_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
24	c3edsA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
25	c2pq1B_	Alignment	not modelled	99.9	17	**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
26	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
27	d1vcda1	Alignment	not modelled	99.9	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
28	d2b06a1	Alignment	not modelled	99.9	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
						PDB header:hydrolase

29	c3fk9B_	Alignment	not modelled	99.9	21	**Chain:** B: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mmutator mutt protein from bacillus2 halodurans
30	d1vk6a2	Alignment	not modelled	99.9	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
31	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
32	c2gb5B_	Alignment	not modelled	99.9	20	**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
33	d1irya_	Alignment	not modelled	99.9	23	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
34	d1ppva_	Alignment	not modelled	99.9	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
35	d2fvva1	Alignment	not modelled	99.9	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
36	c2fvvA_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
37	c2pqvA_	Alignment	not modelled	99.9	21	**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
38	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
39	d2fkba1	Alignment	not modelled	99.8	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
40	c3ef5A_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
41	d1jkna_	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
42	d1ktga_	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
43	c3gwyA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
44	c3sonB_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical nudix hydrolase; **PDBTitle:** crystal structure of a hypothetical nudix hydrolase (lmof2365_2679)2 from listeria monocytogenes (atcc 19115) at 1.70 a resolution
45	d2azwa1	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
46	d1hzta_	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
47	d1puna_	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
48	c3fcmA_	Alignment	not modelled	99.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens
49	d1xsba_	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
50	c2jvbA_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
51	d1nqza_	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
52	d1k2ea_	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
53	d2o5fa1	Alignment	not modelled	99.8	25	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
54	c3i9xA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from listeria innocua
55	c2qkmF_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping

						enzyme dcp1-dcp22 complex
56	d2a6ta2	Alignment	not modelled	99.8	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
57	c3rh7A_	Alignment	not modelled	99.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical oxidoreductase; **PDBTitle:** crystal structure of a hypothetical oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
58	c2yvoA_	Alignment	not modelled	99.8	20	**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
59	c3id9B_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
60	c2i6kA_	Alignment	not modelled	99.8	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 1; **PDBTitle:** crystal structure of human type i ipp isomerase complexed2 with a substrate analog
61	c2w4eA_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
62	c3fjyB_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
63	d1v8ya_	Alignment	not modelled	99.7	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
64	c2pnyA_	Alignment	not modelled	99.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
65	d1vhza_	Alignment	not modelled	99.7	10	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
66	d1q33a_	Alignment	not modelled	99.7	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
67	d1x51a1	Alignment	not modelled	99.7	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
68	d1g0sa_	Alignment	not modelled	99.7	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
69	d1mqea_	Alignment	not modelled	99.7	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
70	c3bm4B_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-sugar pyrophosphatase; **PDBTitle:** crystal structure of human adp-ribose pyrophosphatase nudt52 in complex with magnesium and ampcpr
71	c3f13A_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nudix hydrolase family member; **PDBTitle:** crystal structure of putative nudix hydrolase family member2 from chromobacterium violaceum
72	c1rrqA_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
73	c3e57A_	Alignment	not modelled	99.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
74	c3q91D_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
75	d1rrqa2	Alignment	not modelled	99.6	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
76	d1viua_	Alignment	not modelled	99.5	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
77	c2j8qB_	Alignment	not modelled	99.5	14	**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.
78	c3dupB_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
79	d1u20a1	Alignment	not modelled	99.4	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
80	c3qsjA_	Alignment	not modelled	99.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius

81	c3couA_	Alignment	not modelled	98.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 16; **PDBTitle:** crystal structure of human nudix motif 16 (nudt16)
82	c3kvhA_	Alignment	not modelled	97.7	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
83	c3p5tE_	Alignment	not modelled	97.3	17	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 5; **PDBTitle:** cfim25-cfim68 complex
84	c3brcA_	Alignment	not modelled	18.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein of unknown function; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
85	c3flcX_	Alignment	not modelled	13.0	18	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
86	c1glbG_	Alignment	not modelled	11.2	11	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
87	d1qpma_	Alignment	not modelled	10.6	13	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
88	c1lrzA_	Alignment	not modelled	10.3	14	**PDB header:**antibiotic inhibitor **Chain:** A: **PDB Molecule:**factor essential for expression of methicillin **PDBTitle:** x-ray crystal structure of staphylococcus aureus fema
89	d2dexx3	Alignment	not modelled	9.4	19	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Peptidylarginine deiminase Pad4, catalytic C-terminal domain
90	d1pn0a3	Alignment	not modelled	9.0	13	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**PHBH-like
91	c3c4nB_	Alignment	not modelled	8.2	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein dr_0571; **PDBTitle:** crystal structure of dr_0571 protein from deinococcus2 radiodurans in complex with adp. northeast structural3 genomics consortium target drr125
92	d1tnsa_	Alignment	not modelled	7.9	17	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
93	d1aopa2	Alignment	not modelled	7.9	10	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
94	c3ifrB_	Alignment	not modelled	7.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
95	d1nc7a_	Alignment	not modelled	7.6	22	**Fold:**Hypothetical protein TM1070 **Superfamily:**Hypothetical protein TM1070 **Family:**Hypothetical protein TM1070
96	c3enoB_	Alignment	not modelled	7.3	3	**PDB header:**hydrolase/unknown function **Chain:** B: **PDB Molecule:**putative o-sialoglycoprotein endopeptidase; **PDBTitle:** crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
97	c3g25B_	Alignment	not modelled	7.2	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
98	c3hz6A_	Alignment	not modelled	6.4	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
99	c2ii8F_	Alignment	not modelled	6.2	17	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**anabaena sensory rhodopsin transducer protein; **PDBTitle:** anabaena sensory rhodopsin transducer