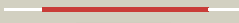
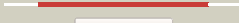
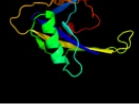
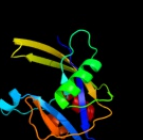
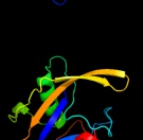
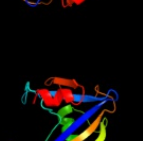


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ppva_	 Alignment		100.0	100	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
2	c2pnyA_	 Alignment		100.0	24	PDB header: isomerase Chain: A; PDB Molecule: isopentenyl-diphosphate delta-isomerase 2; PDBTitle: structure of human isopentenyl-diphosphate delta-isomerase 2
3	c2i6kA_	 Alignment		100.0	25	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
4	d1hzta_	 Alignment		100.0	100	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
5	d2fkba1	 Alignment		100.0	19	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
6	d2o5fa1	 Alignment		100.0	24	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
7	c3dupB_	 Alignment		99.9	18	PDB header: hydrolase Chain: B; PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
8	c3n77B_	 Alignment		99.9	22	PDB header: hydrolase Chain: B; PDB Molecule: nucleoside triphosphatase nudi; PDBTitle: crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
9	c3grnB_	 Alignment		99.8	20	PDB header: hydrolase Chain: B; PDB Molecule: mutt related protein; PDBTitle: crystal structure of mutt protein from methanosarcina mazei go1
10	d1ryaa_	 Alignment		99.8	20	Fold: Nudix Superfamily: Nudix Family: GDP-mannose mannosyl hydrolase NudD
11	d1sjya_	 Alignment		99.8	17	Fold: Nudix Superfamily: Nudix Family: MutT-like

12	d2b0va1	Alignment		99.8	11	Fold: Nudix Superfamily: Nudix Family: MutT-like
13	c3hhjA_	Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mutator mutt from bartonella henselae
14	d2azwa1	Alignment		99.8	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
15	c3dkuB_	Alignment		99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of nudix hydrolase orf153, ymf6, from2 escherichia coli k-1
16	c2pq1B_	Alignment		99.8	18	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
17	c2o1cB_	Alignment		99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: datp pyrophosphohydrolase; PDBTitle: structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
18	c2kdvA_	Alignment		99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: rna pyrophosphohydrolase; PDBTitle: solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
19	c3h95A_	Alignment		99.8	12	PDB header: gene regulation Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the nudix domain of nudt6
20	c3fk9B_	Alignment		99.8	23	PDB header: hydrolase Chain: B: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mmutator mutt protein from bacillus2 halodurans
21	c3f6aA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a hydrolase, nudix family from2 clostridium perfringens
22	d1jkna_	Alignment	not modelled	99.8	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
23	c2yv0A_	Alignment	not modelled	99.8	17	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
24	c3r03B_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: nudix hydrolase; PDBTitle: the crystal structure of nudix hydrolase from rhodospirillum rubrum
25	d1ktga_	Alignment	not modelled	99.7	20	Fold: Nudix Superfamily: Nudix Family: MutT-like
26	d1lrya_	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
27	c3gz8C_	Alignment	not modelled	99.7	24	PDB header: dna binding protein Chain: C: PDB Molecule: mutt/nudix family protein; PDBTitle: cocrystal structure of nudix domain of shewanella oneidensis2 ntrr complexed with adp ribose
28	d1xsba_	Alignment	not modelled	99.7	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
						PDB header: hydrolase

29	c3exqA	Alignment	not modelled	99.7	13	Chain: A: PDB Molecule: nudix family hydrolase; PDBTitle: crystal structure of a nudix family hydrolase from2 lactobacillus brevis
30	d1vcda1	Alignment	not modelled	99.7	24	Fold: Nudix Superfamily: Nudix Family: MutT-like
31	c2jvbA	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: mrna-decapping enzyme subunit 2; PDBTitle: solution structure of catalytic domain of ydcp2
32	d1nqza	Alignment	not modelled	99.7	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
33	d1puna	Alignment	not modelled	99.7	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
34	c3ef5A	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
35	d1vk6a2	Alignment	not modelled	99.7	15	Fold: Nudix Superfamily: Nudix Family: NADH pyrophosphatase
36	c2fvvA	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A: PDB Molecule: diphosphoinositol polyphosphate phosphohydrolase PDBTitle: human diphosphoinositol polyphosphate phosphohydrolase 1
37	d2fvva1	Alignment	not modelled	99.7	12	Fold: Nudix Superfamily: Nudix Family: MutT-like
38	c3fcmA	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a nudix hydrolase from clostridium2 perfringens
39	d2fb1a2	Alignment	not modelled	99.7	19	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
40	c3gg6A	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 18; PDBTitle: crystal structure of the nudix domain of human nudt18
41	c2qb5B	Alignment	not modelled	99.7	16	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
42	c3edsA	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
43	c3sonB	Alignment	not modelled	99.7	18	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
44	c2r5wA	Alignment	not modelled	99.7	14	PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide adenyltransferase; PDBTitle: crystal structure of a bifunctional nm2 adenyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
45	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
46	c3cngC	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
47	c2qjoB	Alignment	not modelled	99.7	20	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nm2 adenyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nm2 adenyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
48	c3o8sA	Alignment	not modelled	99.7	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
49	d2b06a1	Alignment	not modelled	99.7	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
50	d1g0sa	Alignment	not modelled	99.7	13	Fold: Nudix Superfamily: Nudix Family: MutT-like
51	c3q4iA	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase (mutt/nudix family protein); PDBTitle: crystal structure of cdp-chase in complex with gd3+
52	c3i9xA	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from listeria innocua
53	c3gz6A	Alignment	not modelled	99.7	22	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

54	c3id9B_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
55	c2vyhC_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: C: PDB Molecule: 8-oxo-dgtpase domain; PDBTitle: crystal structure of nudix family protein from aquifex aeolicus
56	c3e57A_	Alignment	not modelled	99.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein tm1382; PDBTitle: crystal structure of tm1382, a putative nudix hydrolase
57	c2fb1A_	Alignment	not modelled	99.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0354 from bacteroides thetaiotaomicron
58	c2pqvA_	Alignment	not modelled	99.6	25	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
59	d1k2ea_	Alignment	not modelled	99.6	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
60	d2fmla2	Alignment	not modelled	99.6	20	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
61	c3gwyA_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: putative ctp pyrophosphohydrolase; PDBTitle: crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
62	c2qkmF_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: F: PDB Molecule: spac19a8.12 protein; PDBTitle: the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
63	d2a6ta2	Alignment	not modelled	99.6	12	Fold: Nudix Superfamily: Nudix Family: mRNA decapping enzyme-like
64	d1v8ya_	Alignment	not modelled	99.6	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
65	d1vhza_	Alignment	not modelled	99.6	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
66	c3q91D_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: D: PDB Molecule: uridine diphosphate glucose pyrophosphatase; PDBTitle: crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudd14)
67	c3fjyB_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
68	d1x51a1	Alignment	not modelled	99.5	7	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
69	d1mqea_	Alignment	not modelled	99.5	14	Fold: Nudix Superfamily: Nudix Family: MutT-like
70	c3bm4B_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: B: PDB Molecule: adp-sugar pyrophosphatase; PDBTitle: crystal structure of human adp-ribose pyrophosphatase nudd52 in complex with magnesium and ampcpr
71	c2fmlB_	Alignment	not modelled	99.5	19	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
72	c3f13A_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: putative nudix hydrolase family member; PDBTitle: crystal structure of putative nudix hydrolase family member2 from chromobacterium violaceum
73	d1u20a1	Alignment	not modelled	99.5	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
74	d1viua_	Alignment	not modelled	99.4	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
75	c1rrqA_	Alignment	not modelled	99.4	12	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
76	c3rh7A_	Alignment	not modelled	99.4	9	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
77	d1rrqa2	Alignment	not modelled	99.3	15	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
78	d1q33a_	Alignment	not modelled	99.3	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
79	c3qsjA_	Alignment	not modelled	99.3	16	PDB header: hydrolase Chain: A: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
						PDB header: nuclear protein Chain: B: PDB Molecule: cleavage and polyadenylation specificity

80	c2j8qB_	Alignment	not modelled	99.2	9	factor 5; PDBTitle: crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
81	c3couA_	Alignment	not modelled	98.5	24	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	97.6	20	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	93.8	13	PDB header: rna binding protein Chain: E: PDB Molecule: cleavage and polyadenylation specificity factor subunit 5; PDBTitle: cfim25-cfim68 complex
84	d2yvxa2	Alignment	not modelled	52.2	10	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
85	c3brcA_	Alignment	not modelled	50.6	21	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
86	d2yzqa2	Alignment	not modelled	42.7	24	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
87	d1jr1a4	Alignment	not modelled	38.6	8	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
88	c2qh1B_	Alignment	not modelled	37.6	10	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ta0289; PDBTitle: structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
89	c1zfjA_	Alignment	not modelled	29.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
90	d2b78a1	Alignment	not modelled	27.5	21	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)
91	c1zxuA_	Alignment	not modelled	25.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: at5g01750 protein; PDBTitle: x-ray structure of protein from arabidopsis thaliana2 at5g01750
92	d1tifa_	Alignment	not modelled	24.0	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
93	d2q4ma1	Alignment	not modelled	23.1	17	Fold: Tubby C-terminal domain-like Superfamily: Tubby C-terminal domain-like Family: At5g01750-like
94	c2yvxD_	Alignment	not modelled	22.1	10	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
95	c3gf8A_	Alignment	not modelled	19.7	18	PDB header: carbohydrate binding protein Chain: A: PDB Molecule: putative polysaccharide binding proteins (duf1812); PDBTitle: crystal structure of putative polysaccharide binding proteins2 (duf1812) (np_809975.1) from bacteroides thetaiotaomicron vpi-5482 at3 2.20 a resolution
96	c3payB_	Alignment	not modelled	19.4	24	PDB header: cell adhesion Chain: B: PDB Molecule: putative adhesin; PDBTitle: crystal structure of a putative adhesin (bacova_04077) from2 bacteroides ovatus at 2.50 a resolution
97	c2hf6A_	Alignment	not modelled	16.6	13	PDB header: protein transport Chain: A: PDB Molecule: coatomer subunit zeta-1; PDBTitle: solution structure of human zeta-cop
98	c3flcX_	Alignment	not modelled	16.1	14	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
99	c2eq8C_	Alignment	not modelled	16.1	47	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp