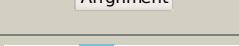
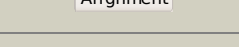
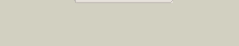
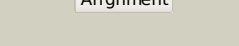
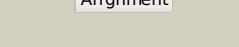
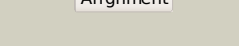


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlnqza_	 Alignment		100.0	36	Fold: Nudix Superfamily: Nudix Family: MutT-like
2	d2fkba1	 Alignment		99.8	20	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
3	c3gz8C_	 Alignment		99.8	27	PDB header: dna binding protein Chain: C: PDB Molecule: mutt/nudix family protein; PDBTitle: cocrystal structure of nudix domain of shewanella oneidensis2 nrtr complexed with adp ribose
4	d1hzta_	 Alignment		99.8	18	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
5	d2fb1a2	 Alignment		99.8	16	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
6	d1ppva_	 Alignment		99.8	18	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
7	d2b0va1	 Alignment		99.8	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
8	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
9	c3n77B_	 Alignment		99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: nucleoside triphosphatase nudi; PDBTitle: crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
10	c3gz6A_	 Alignment		99.8	28	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
11	c2gb5B_	 Alignment		99.8	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

12	c3dkuB_	Alignment		99.8	13	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of nudix hydrolase orf153, ymfB, from2 escherichia coli k-1
13	d1vk6a2	Alignment		99.8	18	Fold: Nudix Superfamily: Nudix Family: NADH pyrophosphatase
14	c3h95A_	Alignment		99.8	19	PDB header: gene regulation Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the nudix domain of nudt6
15	c3exqA_	Alignment		99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: nudix family hydrolase; PDBTitle: crystal structure of a nudix family hydrolase from2 lactobacillus brevis
16	d1sjya_	Alignment		99.8	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
17	d1lrya_	Alignment		99.8	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
18	d1vhza_	Alignment		99.8	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
19	c3hhjA_	Alignment		99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mutator mutt from bartonella henselae
20	c3ef5A_	Alignment		99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
21	d1ktga_	Alignment	not modelled	99.7	21	Fold: Nudix Superfamily: Nudix Family: MutT-like
22	c2yv0A_	Alignment	not modelled	99.7	23	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
23	d1g0sa_	Alignment	not modelled	99.7	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
24	c3qsjA_	Alignment	not modelled	99.7	35	PDB header: hydrolase Chain: A: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
25	d1puna_	Alignment	not modelled	99.7	20	Fold: Nudix Superfamily: Nudix Family: MutT-like
26	c2fb1A_	Alignment	not modelled	99.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0354 from bacteroides thetaiotaomicron
27	d2o5fa1	Alignment	not modelled	99.7	20	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
28	c2fvvA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: diphosphoinositol polyphosphate phosphohydrolase PDBTitle: human diphosphoinositol polyphosphate phosphohydrolase 1

29	d2fvva1	Alignment	not modelled	99.7	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
30	c2yyhC	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: C: PDB Molecule: 8-oxo-dgtpase domain; PDBTitle: crystal structure of nudix family protein from aquifex aeolicus
31	c2w4eA	Alignment	not modelled	99.7	24	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
32	d1ryaa	Alignment	not modelled	99.7	19	Fold: Nudix Superfamily: Nudix Family: GDP-mannose mannosyl hydrolase NudD
33	c2kdvA	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: rna pyrophosphohydrolase; PDBTitle: solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
34	c3bm4B	Alignment	not modelled	99.7	23	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
35	c2i6kA	Alignment	not modelled	99.7	15	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
36	c3i9xA	Alignment	not modelled	99.7	29	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from listeria innocua
37	c3gg6A	Alignment	not modelled	99.7	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
38	d2fmla2	Alignment	not modelled	99.7	21	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
39	c2o1cB	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: B: PDB Molecule: datp pyrophosphohydrolase; PDBTitle: structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
40	c2r5wA	Alignment	not modelled	99.7	21	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
41	c2jvbA	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A: PDB Molecule: mrna-decapping enzyme subunit 2; PDBTitle: solution structure of catalytic domain of ydcp2
42	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
43	d1xsba	Alignment	not modelled	99.7	23	Fold: Nudix Superfamily: Nudix Family: MutT-like
44	c3r03B	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: B: PDB Molecule: nudix hydrolase; PDBTitle: the crystal structure of nudix hydrolase from rhodospirillum rubrum
45	d2b06a1	Alignment	not modelled	99.7	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
46	c3fjyB	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
47	c3sonB	Alignment	not modelled	99.7	15	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
48	c3o8sA	Alignment	not modelled	99.7	19	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	c2qkmF	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: F: PDB Molecule: spac19a8.12 protein; PDBTitle: the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
50	c2qjoB	Alignment	not modelled	99.7	18	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.
51	d2azwa1	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
52	c3q4iA	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase (mutt/nudix family protein); PDBTitle: crystal structure of cdp-chase in complex with gd3+
53	c3i40B	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein;

53	c3ru2B_	Alignment	not modelled	99.7	14	PDBTitle: crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis PDB header: hydrolase
54	c3gwyA_	Alignment	not modelled	99.7	20	Chain: A: PDB Molecule: putative ctp pyrophosphohydrolase; PDBTitle: crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
55	c2pnyA_	Alignment	not modelled	99.7	13	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 2; PDBTitle: structure of human isopentenyl-diphosphate delta-isomerase 2
56	c3fk9B_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mmutator mutt protein from bacillus2 halodurans
57	c2pq1B_	Alignment	not modelled	99.6	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
58	d1mqea_	Alignment	not modelled	99.6	20	Fold: Nudix Superfamily: Nudix Family: MutT-like
59	d1vcda1	Alignment	not modelled	99.6	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
60	c3edsA_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from bacillus2 thuringiensis
61	d1jkna_	Alignment	not modelled	99.6	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
62	c3f6aA_	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a hydrolase, nudix family from2 clostridium perfringens
63	c2fmlB_	Alignment	not modelled	99.6	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
64	d1viua_	Alignment	not modelled	99.6	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
65	d1v8ya_	Alignment	not modelled	99.6	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
66	c2pqvA_	Alignment	not modelled	99.6	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
67	d2a6ta2	Alignment	not modelled	99.6	17	Fold: Nudix Superfamily: Nudix Family: mRNA decapping enzyme-like
68	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)
69	d1u20a1	Alignment	not modelled	99.6	27	Fold: Nudix Superfamily: Nudix Family: MutT-like
70	d1x51a1	Alignment	not modelled	99.5	14	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
71	c3fcmA_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a nudix hydrolase from clostridium2 perfringens
72	d1k2ea_	Alignment	not modelled	99.5	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
73	c3dupB_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
74	c3e57A_	Alignment	not modelled	99.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein tm1382; PDBTitle: crystal structure of tm1382, a putative nudix hydrolase
75	c3f13A_	Alignment	not modelled	99.5	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
76	c1rrqA_	Alignment	not modelled	99.5	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
77	d1q33a_	Alignment	not modelled	99.4	24	Fold: Nudix Superfamily: Nudix Family: MutT-like
78	c3rh7A_	Alignment	not modelled	99.4	12	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
79	d1rrqa2	Alignment	not modelled	99.4	16	Fold: Nudix Superfamily: Nudix

						Family: MutY C-terminal domain-like
80	c2j8qB_	 Alignment	not modelled	99.2	20	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.
81	c3couA_	 Alignment	not modelled	98.7	27	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	98.2	23	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	94.8	20	PDB header: rna binding protein Chain: E: PDB Molecule: cleavage and polyadenylation specificity factor subunit 5; PDBTitle: cfim25-cfim68 complex
84	d1aopa2	 Alignment	not modelled	33.2	19	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
85	d1zl8a1	 Alignment	not modelled	11.6	50	Fold: L27 domain Superfamily: L27 domain Family: L27 domain
86	d1cmca_	 Alignment	not modelled	10.7	31	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Met repressor, MetJ (MetR)
87	d2w6ka1	 Alignment	not modelled	10.4	11	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
88	c2eq8C_	 Alignment	not modelled	10.1	13	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
89	d1y74a1	 Alignment	not modelled	10.0	50	Fold: L27 domain Superfamily: L27 domain Family: L27 domain
90	c3enoB_	 Alignment	not modelled	8.9	21	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
91	c2eq7C_	 Alignment	not modelled	8.5	25	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
92	d1w4ha1	 Alignment	not modelled	7.4	31	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
93	c2cb4D_	 Alignment	not modelled	7.2	45	PDB header: toxin Chain: D: PDB Molecule: mosquitocidal toxin; PDBTitle: crystal structure of the catalytic domain of the2 mosquitocidal toxin from bacillus sphaericus, mutant e197q
94	c1w4kA_	 Alignment	not modelled	7.1	38	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase e2; PDBTitle: peripheral-subunit binding domains from mesophilic, 2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
95	d2cyua1	 Alignment	not modelled	7.1	31	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
96	d1w85i_	 Alignment	not modelled	7.1	19	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
97	c3dv0I_	 Alignment	not modelled	7.1	19	PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
98	c2eq9C_	 Alignment	not modelled	6.6	38	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
99	c2coaA_	 Alignment	not modelled	6.6	38	PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase component of branched- PDBTitle: solution structure of the e3 binding domain of2 dihydrolipoamide branched chaintransacylase