Phyre^2

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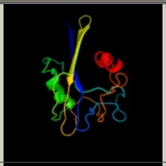
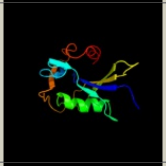
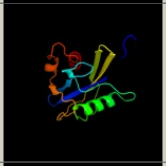
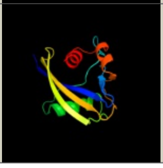
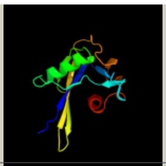
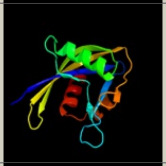
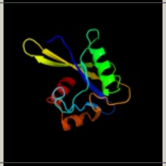
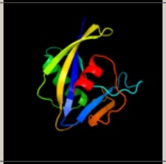
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1puna_	Alignment		100.0	100	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
2	c3gwyA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
3	c3ef5A_	Alignment		99.9	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
4	c3hhjA_	Alignment		99.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
5	c3r03B_	Alignment		99.9	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
6	d1irya_	Alignment		99.9	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
7	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
8	d1rrqa2	Alignment		99.9	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
9	c3exqA_	Alignment		99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
10	c1rrqA_	Alignment		99.9	21	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
11	c3n77B_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2

12	c3cngC_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
13	c2pq1B_	Alignment		99.9	26	**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
14	d2b06a1	Alignment		99.9	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
15	d1vk6a2	Alignment		99.9	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
16	c3o8sA_	Alignment		99.9	18	**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
17	c3fk9B_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mmutator mutt protein from bacillus2 halodurans
18	d2b0va1	Alignment		99.9	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
19	c2gb5B_	Alignment		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
20	d1vcda1	Alignment		99.9	25	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
21	c3dkuB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1
22	c3q4iA_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
23	c3gg6A_	Alignment	not modelled	99.9	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
24	c2qjoB_	Alignment	not modelled	99.9	22	**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.
25	c3h95A_	Alignment	not modelled	99.9	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 6; **PDBTitle:** crystal structure of the nudix domain of nudt6
26	d1x51a1	Alignment	not modelled	99.9	13	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
27	c3gz8C_	Alignment	not modelled	99.9	14	**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
28	d2fkba1	Alignment	not modelled	99.9	18	**Fold:**Nudix **Superfamily:**Nudix

						Family:IPP isomerase-like
29	d2fb1a2	Alignment	not modelled	99.9	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
30	d1k2ea_	Alignment	not modelled	99.9	25	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
31	c2kdvA_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
32	c2jvbA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
33	c2yyhC_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain; **PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus
34	c2o1cB_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase; **PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
35	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
36	d1sjya_	Alignment	not modelled	99.8	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
37	c3rh7A_	Alignment	not modelled	99.8	18	**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
38	c2r5wA_	Alignment	not modelled	99.8	23	**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
39	d2azwa1	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
40	c3gz6A_	Alignment	not modelled	99.8	14	**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
41	d1ryaa_	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
42	c2pqvA_	Alignment	not modelled	99.8	28	**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
43	c2fvvA_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
44	d2fvva1	Alignment	not modelled	99.8	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
45	c3fjyB_	Alignment	not modelled	99.8	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
46	d1ktga_	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
47	c2fb1A_	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
48	c3id9B_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
49	c2qkmF_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
50	d1xsba_	Alignment	not modelled	99.8	25	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
51	d2a6ta2	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
52	c3edsA_	Alignment	not modelled	99.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
53	c3f6aA_	Alignment	not modelled	99.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
						Fold: Nudix

54	d1vhza_	Alignment	not modelled	99.8	23	**Superfamily:**Nudix **Family:**MutT-like
55	c3fcmA_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens
56	c3sonB_	Alignment	not modelled	99.8	16	**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
57	d1nqza_	Alignment	not modelled	99.8	28	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
58	c2w4eA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
59	d2fmla2	Alignment	not modelled	99.8	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
60	d1ppva_	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
61	d1hzta_	Alignment	not modelled	99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
62	c2yvoA_	Alignment	not modelled	99.8	22	**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
63	d1jkna_	Alignment	not modelled	99.8	23	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
64	d1v8ya_	Alignment	not modelled	99.8	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
65	c3f13A_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nudix hydrolase family member; **PDBTitle:** crystal structure of putative nudix hydrolase family member2 from chromobacterium violaceum
66	c3e57A_	Alignment	not modelled	99.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
67	d1g0sa_	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
68	c3bm4B_	Alignment	not modelled	99.7	25	**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
69	c2fmlB_	Alignment	not modelled	99.7	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
70	d1mqea_	Alignment	not modelled	99.7	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
71	d2o5fa1	Alignment	not modelled	99.7	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
72	c2i6kA_	Alignment	not modelled	99.7	19	**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
73	d1viua_	Alignment	not modelled	99.6	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
74	c3q91D_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
75	c2pnyA_	Alignment	not modelled	99.6	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
76	d1q33a_	Alignment	not modelled	99.6	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
77	c3qsjA_	Alignment	not modelled	99.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
78	c3dupB_	Alignment	not modelled	99.4	15	**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	c2j8qB_	Alignment	not modelled	99.4	17	**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.
80	d1u20a1	Alignment	not modelled	99.4	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
81	c3couA_	Alignment	not modelled	98.8	22	**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	98.0	15	**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	96.7	17	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 5; **PDBTitle:** cfim25-cfim68 complex
84	d2dexx3	Alignment	not modelled	10.5	23	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Peptidylarginine deiminase Pad4, catalytic C-terminal domain
85	c2vldA_	Alignment	not modelled	9.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
86	d1tnsa_	Alignment	not modelled	8.1	28	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
87	d1nc7a_	Alignment	not modelled	6.9	33	**Fold:**Hypothetical protein TM1070 **Superfamily:**Hypothetical protein TM1070 **Family:**Hypothetical protein TM1070
88	c1zwvA_	Alignment	not modelled	6.8	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
89	d2nn6d2	Alignment	not modelled	6.8	15	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
90	c1kveB_	Alignment	not modelled	5.7	23	**PDB header:**toxin **Chain:** B: **PDB Molecule:**smk toxin; **PDBTitle:** killer toxin from halotolerant yeast
91	c2dexX_	Alignment	not modelled	5.5	23	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**protein-arginine deiminase type iv; **PDBTitle:** crystal structure of human peptidylarginine deiminase 4 in complex2 with histone h3 n-terminal peptide including arg17