Phyre^2

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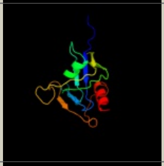
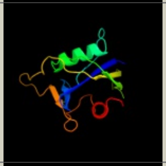
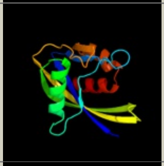
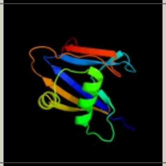
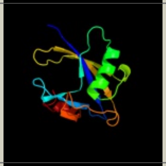
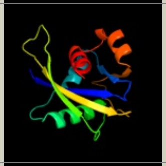
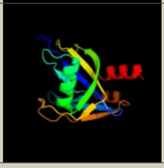
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dkuB_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1
2	d2b0va1	Alignment		100.0	36	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
3	c3cngC_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
4	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
5	c2qjoB_	Alignment		99.9	23	**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.
6	c3q4iA_	Alignment		99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
7	d1vk6a2	Alignment		99.9	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
8	c2pq1B_	Alignment		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
9	d2fb1a2	Alignment		99.9	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
10	c3gz8C_	Alignment		99.9	20	**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
11	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

12	c3h95A_	Alignment		99.9	22	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 6; **PDBTitle:** crystal structure of the nudix domain of nudt6
13	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
14	c2r5wA_	Alignment		99.9	29	**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
15	c2fb1A_	Alignment		99.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
16	d1ryaa_	Alignment		99.9	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
17	d1sjya_	Alignment		99.9	27	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
18	c3gg6A_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 18; **PDBTitle:** crystal structure of the nudix domain of human nudt18
19	d2fkba1	Alignment		99.8	23	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
20	d1vhza_	Alignment		99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
21	d1vcda1	Alignment	not modelled	99.8	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
22	d1irya_	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
23	c2pqvA_	Alignment	not modelled	99.8	18	**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
24	c3f6aA_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
25	c3grnB_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt related protein; **PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1
26	d2b06a1	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
27	c3rh7A_	Alignment	not modelled	99.8	16	**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
28	c3r03B_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
						PDB header:hydrolase

29	c2o1cB_	Alignment	not modelled	99.8	18	**Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase; **PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
30	d2azwa1	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
31	c3gwyA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
32	c3n77B_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
33	c3hhjA_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
34	c3ef5A_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
35	d1k2ea_	Alignment	not modelled	99.8	26	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
36	c2yyhC_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain; **PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus
37	d2fmla2	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
38	c3exqA_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
39	c3gz6A_	Alignment	not modelled	99.8	20	**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
40	d1puna_	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
41	c2kdvA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
42	c3fjyB_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
43	d2fvva1	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
44	c2fvvA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
45	c2qkmF_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
46	c2jvbA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
47	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
48	d1nqza_	Alignment	not modelled	99.8	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
49	d1ktga_	Alignment	not modelled	99.8	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
50	d1xsba_	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
51	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
52	c3fcmA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens
53	c2fmlB_	Alignment	not modelled	99.8	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
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
						PDB header:hydrolase

55	c2w4eA_	Alignment	not modelled	99.8	19	**Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
56	c3sonB_	Alignment	not modelled	99.8	23	**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	d1ppva_	Alignment	not modelled	99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
58	d1v8ya_	Alignment	not modelled	99.8	32	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
59	d2a6ta2	Alignment	not modelled	99.8	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
60	d1hzta_	Alignment	not modelled	99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
61	d1g0sa_	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
62	d1jkna_	Alignment	not modelled	99.7	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
63	c3e57A_	Alignment	not modelled	99.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
64	c3bm4B_	Alignment	not modelled	99.7	20	**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
65	d2o5fa1	Alignment	not modelled	99.7	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
66	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
67	d1mqea_	Alignment	not modelled	99.7	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
68	c3edsA_	Alignment	not modelled	99.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
69	c3q91D_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
70	d1viua_	Alignment	not modelled	99.7	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
71	d1q33a_	Alignment	not modelled	99.6	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
72	c1rrqA_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
73	d1x51a1	Alignment	not modelled	99.6	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
74	d1rrqa2	Alignment	not modelled	99.6	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
75	c2i6kA_	Alignment	not modelled	99.5	18	**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
76	c2pnyA_	Alignment	not modelled	99.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
77	d1u20a1	Alignment	not modelled	99.4	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
78	c3qsjA_	Alignment	not modelled	99.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
79	c3dupB_	Alignment	not modelled	99.3	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
80	c2j8qB_	Alignment	not modelled	99.3	18	**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	98.4	18	**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	16	**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	96.8	23	**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	9.7	6	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
85	c1wrjA_	Alignment	not modelled	9.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
86	d2hqya2	Alignment	not modelled	9.5	29	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
87	d2dexx3	Alignment	not modelled	9.4	19	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Peptidylarginine deiminase Pad4, catalytic C-terminal domain
88	c1kveB_	Alignment	not modelled	9.4	26	**PDB header:**toxin **Chain:** B: **PDB Molecule:**smk toxin; **PDBTitle:** killer toxin from halotolerant yeast
89	c2ii8F_	Alignment	not modelled	9.3	25	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**anabaena sensory rhodopsin transducer protein; **PDBTitle:** anabaena sensory rhodopsin transducer
90	c2hdnE_	Alignment	not modelled	8.9	27	**PDB header:**translation **Chain:** E: **PDB Molecule:**elongation factor ef-tu; **PDBTitle:** trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
91	d1nc7a_	Alignment	not modelled	8.7	28	**Fold:**Hypothetical protein TM1070 **Superfamily:**Hypothetical protein TM1070 **Family:**Hypothetical protein TM1070
92	c3enoB_	Alignment	not modelled	7.5	20	**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
93	c2hf6A_	Alignment	not modelled	6.6	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit zeta-1; **PDBTitle:** solution structure of human zeta-cop
94	d1ulqa2	Alignment	not modelled	6.4	24	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
95	d1zl8a1	Alignment	not modelled	6.4	50	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
96	c1zwvA_	Alignment	not modelled	6.4	31	**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
97	c2vldA_	Alignment	not modelled	6.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
98	d1jiha2	Alignment	not modelled	6.2	5	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
99	d1z3aa1	Alignment	not modelled	6.2	13	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like