Phyre^2

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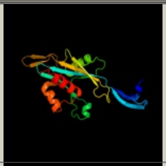
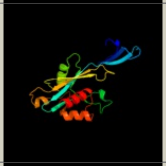
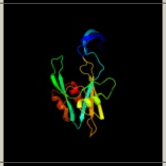
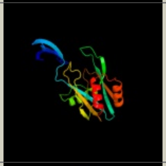
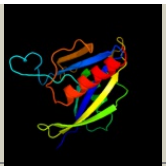
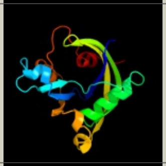
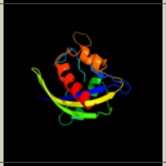
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1viua_	Alignment		100.0	97	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
2	d1g0sa_	Alignment		100.0	29	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
3	d1vhza_	Alignment		100.0	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
4	c3bm4B_	Alignment		100.0	26	**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
5	d1mqea_	Alignment		100.0	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
6	c2yvoA_	Alignment		100.0	27	**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
7	c3q91D_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
8	d1v8ya_	Alignment		100.0	29	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
9	c2w4eA_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
10	d1sjya_	Alignment		99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
11	d2o5fa1	Alignment		99.7	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like

12	d1vk6a2	Alignment		99.7	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
13	c2jvbA_	Alignment		99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
14	c2gb5B_	Alignment		99.7	19	**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
15	d1nqza_	Alignment		99.7	23	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
16	c3dkuB_	Alignment		99.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1
17	d2b0va1	Alignment		99.7	13	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
18	d2fkba1	Alignment		99.7	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
19	c2o1cB_	Alignment		99.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase; **PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
20	d2a6ta2	Alignment		99.7	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
21	c2fvvA_	Alignment	not modelled	99.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
22	d2fvva1	Alignment	not modelled	99.7	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
23	c3h95A_	Alignment	not modelled	99.7	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 6; **PDBTitle:** crystal structure of the nudix domain of nudt6
24	c2kdvA_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
25	c3gg6A_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 18; **PDBTitle:** crystal structure of the nudix domain of human nudt18
26	d2azwa1	Alignment	not modelled	99.6	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
27	c3cngC_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
28	d1ktga_	Alignment	not modelled	99.6	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like

29	c3fjyB_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
30	c2r5wA_	Alignment	not modelled	99.6	13	**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
31	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
32	d1irya_	Alignment	not modelled	99.6	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
33	d1jkna_	Alignment	not modelled	99.6	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
34	c3i9xA_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from listeria innocua
35	d1vcda1	Alignment	not modelled	99.6	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
36	c3hhjA_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
37	c2pq1B_	Alignment	not modelled	99.6	23	**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
38	c3grnB_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt related protein; **PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1
39	c3o8sA_	Alignment	not modelled	99.6	13	**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
40	d1ryaa_	Alignment	not modelled	99.6	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
41	c3gz8C_	Alignment	not modelled	99.6	16	**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
42	c3gwyA_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
43	c3sonB_	Alignment	not modelled	99.6	11	**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	c2qkmF_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
45	c3exqA_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
46	c2qjoB_	Alignment	not modelled	99.6	11	**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.
47	d2b06a1	Alignment	not modelled	99.6	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
48	c3e57A_	Alignment	not modelled	99.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
49	d2fb1a2	Alignment	not modelled	99.5	9	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
50	c3fcmA_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens
51	d1xsba_	Alignment	not modelled	99.5	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
52	d1ppva_	Alignment	not modelled	99.5	13	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
53	d1puna_	Alignment	not modelled	99.5	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like

54	c2yyhC_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain; **PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus
55	c3q4iA_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
56	c3ef5A_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
57	c3r03B_	Alignment	not modelled	99.5	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
58	d1hzta_	Alignment	not modelled	99.5	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
59	c3fk9B_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mmutator mutt protein from bacillus2 halodurans
60	c3n77B_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
61	c3dupB_	Alignment	not modelled	99.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
62	c2pqvA_	Alignment	not modelled	99.4	14	**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
63	c3f6aA_	Alignment	not modelled	99.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
64	c3gz6A_	Alignment	not modelled	99.4	16	**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
65	d1k2ea_	Alignment	not modelled	99.4	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
66	c2fb1A_	Alignment	not modelled	99.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
67	d2fmla2	Alignment	not modelled	99.3	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
68	c3edsA_	Alignment	not modelled	99.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
69	c3f13A_	Alignment	not modelled	99.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nudix hydrolase family member; **PDBTitle:** crystal structure of putative nudix hydrolase family member2 from chromobacterium violaceum
70	c2i6kA_	Alignment	not modelled	99.2	14	**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
71	c3rh7A_	Alignment	not modelled	99.2	11	**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
72	c3qsjA_	Alignment	not modelled	99.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
73	c2fmlB_	Alignment	not modelled	99.1	17	**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
74	c2pnyA_	Alignment	not modelled	99.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
75	d1x51a1	Alignment	not modelled	99.1	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
76	d1u20a1	Alignment	not modelled	99.1	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
77	d1q33a_	Alignment	not modelled	99.0	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
78	c1rrqA_	Alignment	not modelled	98.8	10	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
79	c2i8gB	Alignment	not modelled	98.8	13	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 5;

79	[illegible]	Alignment	not modelled	98.8	15	**PDBTitle:** crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
80	d1rrqa2	Alignment	not modelled	98.7	10	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
81	c3couA_	Alignment	not modelled	98.1	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	97.5	19	**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	78.0	12	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 5; **PDBTitle:** cfim25-cfim68 complex
84	c3pjyB_	Alignment	not modelled	22.0	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hypothetical signal peptide protein; **PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
85	c3m7aA_	Alignment	not modelled	18.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of saro_0823 (yp_496102.1) a protein of2 unknown function from novosphingobium aromaticivorans dsm3 12444 at 1.22 a resolution
86	c3pppA_	Alignment	not modelled	9.2	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline-binding protein; **PDBTitle:** structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
87	d2dw4a1	Alignment	not modelled	8.2	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
88	d2p12a1	Alignment	not modelled	7.9	17	**Fold:**FomD barrel-like **Superfamily:**FomD-like **Family:**FomD-like
89	c2hkoA_	Alignment	not modelled	7.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1
90	d2fug21	Alignment	not modelled	7.1	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
91	c2xagA_	Alignment	not modelled	7.1	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
92	c2v1dA_	Alignment	not modelled	7.1	22	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
93	c2hf6A_	Alignment	not modelled	6.8	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit zeta-1; **PDBTitle:** solution structure of human zeta-cop
94	c3d0wD_	Alignment	not modelled	6.6	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yflh protein; **PDBTitle:** crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326
95	d1gw5s_	Alignment	not modelled	6.0	21	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Clathrin coat assembly domain
96	d1bm8a_	Alignment	not modelled	5.8	14	**Fold:**DNA-binding domain of Mlu1-box binding protein MBP1 **Superfamily:**DNA-binding domain of Mlu1-box binding protein MBP1 **Family:**DNA-binding domain of Mlu1-box binding protein MBP1
97	d1wgga_	Alignment	not modelled	5.6	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
98	d1l3ga_	Alignment	not modelled	5.5	16	**Fold:**DNA-binding domain of Mlu1-box binding protein MBP1 **Superfamily:**DNA-binding domain of Mlu1-box binding protein MBP1 **Family:**DNA-binding domain of Mlu1-box binding protein MBP1
99	d1v86a_	Alignment	not modelled	5.4	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related