Phyre^2

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Description	Q93K97
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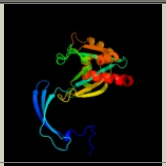
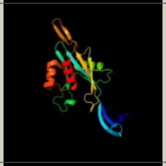
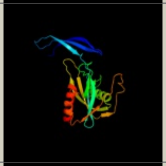
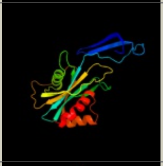
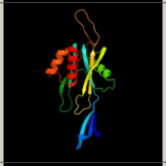
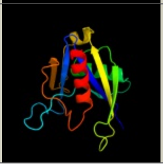
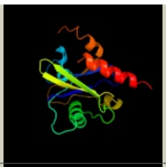
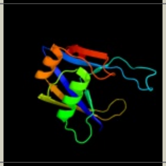
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g0sa_	Alignment		100.0	99	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
2	d1viua_	Alignment		100.0	30	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
3	d1vhza_	Alignment		100.0	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
4	c3bm4B_	Alignment		100.0	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
5	c2yvoA_	Alignment		100.0	26	**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
6	d1mqea_	Alignment		100.0	25	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
7	c3q91D_	Alignment		100.0	28	**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	31	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
9	c2w4eA_	Alignment		100.0	26	**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	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
11	d1vk6a2	Alignment		99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase

12	c2jvbA_	Alignment		99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
13	d2o5fa1	Alignment		99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
14	d2fkba1	Alignment		99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
15	d1nqza_	Alignment		99.8	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
16	c2gb5B_	Alignment		99.8	17	**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
17	d2b0va1	Alignment		99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
18	c3dkuB_	Alignment		99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1
19	c2o1cB_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase; **PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
20	c2kdvA_	Alignment		99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
21	d2a6ta2	Alignment	not modelled	99.7	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
22	c2r5wA_	Alignment	not modelled	99.7	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
23	c3h95A_	Alignment	not modelled	99.7	18	**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	c2fvvA_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
25	d2fvva1	Alignment	not modelled	99.7	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
26	d1ppva_	Alignment	not modelled	99.7	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
27	d1ktga_	Alignment	not modelled	99.7	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
28	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
29	c3sonB_	Alignment	not modelled	99.7	24	**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
30	d1ryaa_	Alignment	not modelled	99.7	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
31	c2pq1B_	Alignment	not modelled	99.7	20	**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
32	c3grnB_	Alignment	not modelled	99.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt related protein; **PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1
33	d1vcda1	Alignment	not modelled	99.7	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
34	d2azwa1	Alignment	not modelled	99.7	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
35	d1hzta_	Alignment	not modelled	99.7	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
36	c3hhjA_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
37	d1irya_	Alignment	not modelled	99.7	26	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
38	c3gg6A_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 18; **PDBTitle:** crystal structure of the nudix domain of human nudt18
39	c2qjoB_	Alignment	not modelled	99.7	14	**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.
40	c3fjyB_	Alignment	not modelled	99.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
41	c3o8sA_	Alignment	not modelled	99.7	15	**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
42	c3i9xA_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from listeria innocua
43	c3gz8C_	Alignment	not modelled	99.7	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
44	c3id9B_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
45	d1jkna_	Alignment	not modelled	99.7	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
46	c3gwyA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
47	d2fb1a2	Alignment	not modelled	99.7	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
48	c2qkmF_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
49	c3q4iA_	Alignment	not modelled	99.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
50	c3ef5A_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
51	c3fcmA_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens
52	c3fk9B_	Alignment	not modelled	99.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mmutator mutt protein from bacillus2 halodurans
53	d2b06a1	Alignment	not modelled	99.6	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like

54	c2yyhC_	Alignment	not modelled	99.6	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain; **PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus
55	c3exqA_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
56	d1xsba_	Alignment	not modelled	99.6	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
57	d1puna_	Alignment	not modelled	99.6	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
58	c3r03B_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
59	c3e57A_	Alignment	not modelled	99.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
60	c3n77B_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
61	c2pqvA_	Alignment	not modelled	99.6	11	**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
62	c3gz6A_	Alignment	not modelled	99.5	15	**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
63	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
64	c3f6aA_	Alignment	not modelled	99.5	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
65	d2fmla2	Alignment	not modelled	99.5	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
66	c2fb1A_	Alignment	not modelled	99.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
67	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
68	c3edsA_	Alignment	not modelled	99.5	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	d1k2ea_	Alignment	not modelled	99.5	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
70	c3f13A_	Alignment	not modelled	99.4	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
71	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
72	c2fmlB_	Alignment	not modelled	99.4	24	**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
73	c2pnyA_	Alignment	not modelled	99.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
74	d1q33a_	Alignment	not modelled	99.3	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
75	d1u20a1	Alignment	not modelled	99.3	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
76	d1x51a1	Alignment	not modelled	99.2	8	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
77	c3qsjA_	Alignment	not modelled	99.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
78	c1rrqA_	Alignment	not modelled	99.1	15	**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	99.0	9	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 5;

79	c2j8qB_	Alignment	not modelled	99.0	9	**PDBTitle:** crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
80	d1rrqa2	Alignment	not modelled	99.0	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
81	c3couA_	Alignment	not modelled	98.4	16	**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	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	83.2	14	**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	12.8	20	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Peptidylarginine deiminase Pad4, catalytic C-terminal domain
85	c1w63T_	Alignment	not modelled	12.7	14	**PDB header:**endocytosis **Chain:** T: **PDB Molecule:**adapter-related protein complex 1 sigma 1a **PDBTitle:** ap1 clathrin adaptor core
86	c2hf6A_	Alignment	not modelled	11.6	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit zeta-1; **PDBTitle:** solution structure of human zeta-cop
87	c3h76A_	Alignment	not modelled	11.5	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pqs biosynthetic enzyme; **PDBTitle:** crystal structure of pqsd, a key enzyme in pseudomonas2 aeruginosa quinolone signal biosynthesis pathway
88	d1gw5m2	Alignment	not modelled	10.6	19	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Clathrin coat assembly domain
89	d1gw5s_	Alignment	not modelled	10.3	11	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Clathrin coat assembly domain
90	c2jswA_	Alignment	not modelled	8.2	17	**PDB header:**actin-binding protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the talin c-terminal actin binding site
91	d1aopa2	Alignment	not modelled	7.9	13	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
92	d2fug21	Alignment	not modelled	7.4	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
93	c3s3lB_	Alignment	not modelled	7.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cerj; **PDBTitle:** crystal structure of cerj from streptomyces tendae
94	c3lx6B_	Alignment	not modelled	6.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cytosine-specific methyltransferase; **PDBTitle:** structure of probable cytosine-specific methyltransferase from2 shigella flexneri
95	d1ub7a1	Alignment	not modelled	6.4	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
96	d1bm8a_	Alignment	not modelled	6.1	20	**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	c3lmaC_	Alignment	not modelled	5.9	29	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**stage v sporulation protein ad (spovad); **PDBTitle:** crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
98	c1w63P_	Alignment	not modelled	5.7	17	**PDB header:**endocytosis **Chain:** P: **PDB Molecule:**adaptor-related protein complex 1, mu 1 subunit; **PDBTitle:** ap1 clathrin adaptor core
99	d1p9qc3	Alignment	not modelled	5.2	25	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**Hypothetical protein AF0491, C-terminal domain