



# Phyre2

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Description	RVBD3040c_(-)_3400203_3401069
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3qsjA_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
2	<a href="#">c5t3pB_</a>	 Alignment		99.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal coenzyme a diphosphatase nudt7; <b>PDBTitle:</b> crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
3	<a href="#">c4dywA_</a>	 Alignment		99.4	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt nudix hydrolase from burkholderia2 pseudomallei
4	<a href="#">d1sjya_</a>	 Alignment		99.4	28	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
5	<a href="#">d2b0va1</a>	 Alignment		99.4	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
6	<a href="#">c5gg7A_</a>	 Alignment		99.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family protein; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (I)
7	<a href="#">d1ktga_</a>	 Alignment		99.4	24	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
8	<a href="#">d1jkna_</a>	 Alignment		99.3	28	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
9	<a href="#">d2fkba1</a>	 Alignment		99.3	23	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
10	<a href="#">d1nqza_</a>	 Alignment		99.3	29	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
11	<a href="#">c2kdvA_</a>	 Alignment		99.3	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna pyrophosphohydrolase; <b>PDBTitle:</b> solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli

12	<a href="#">c5lf8A_</a>	Alignment		99.3	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 17; <b>PDBTitle:</b> human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
13	<a href="#">d1ppva_</a>	Alignment		99.3	18	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
14	<a href="#">c3sonB_</a>	Alignment		99.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical nudix hydrolase; <b>PDBTitle:</b> crystal structure of a putative nudix hydrolase (Imof2365_2679) from <i>Listeria monocytogenes</i> str. 4b f2365 at 1.70 Å resolution
15	<a href="#">d1xsba_</a>	Alignment		99.3	16	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
16	<a href="#">c5cfiC_</a>	Alignment		99.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> bis(5'-nucleosyl)-tetraphosphatase (diadenosine) <b>PDBTitle:</b> structural and functional attributes of malaria parasite ap4a2 hydrolase
17	<a href="#">c4kyxA_</a>	Alignment		99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribose pyrophosphatase mutt; <b>PDBTitle:</b> crystal structure of adp-ribose pyrophosphatase mutt from <i>Rickettsia felis</i>
18	<a href="#">c3grnB_</a>	Alignment		99.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt related protein; <b>PDBTitle:</b> crystal structure of mutt protein from <i>Methanosarcina mazei</i> go1
19	<a href="#">c3hhjA_</a>	Alignment		99.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> crystal structure of mutator mutt from <i>Bartonella henselae</i>
20	<a href="#">c3fjyB_</a>	Alignment		99.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable mutt1 protein; <b>PDBTitle:</b> crystal structure of a probable mutt1 protein from <i>Bifidobacterium adolescentis</i>
21	<a href="#">d1puna_</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
22	<a href="#">c2rrkA_</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp pyrophosphohydrolase; <b>PDBTitle:</b> solution structure of the <i>E. coli</i> orf135 protein
23	<a href="#">c5gp0F_</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nudix hydrolase 1; <b>PDBTitle:</b> crystal structure of geraniol-nudx1 complex
24	<a href="#">d1hzta_</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> IPP isomerase-like
25	<a href="#">d2fmla2</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
26	<a href="#">c5bonC_</a>	Alignment	not modelled	99.2	30	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable 8-oxo-dgtp diphosphatase nudt15; <b>PDBTitle:</b> crystal structure of human nudt15 (mth2)
27	<a href="#">c2yvoA_</a>	Alignment	not modelled	99.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of ndx2 in complex with mg2+ and amp from <i>Thermus2 thermophilus</i> hb8
28	<a href="#">c2pq1B_</a>	Alignment	not modelled	99.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ap4a hydrolase; <b>PDBTitle:</b> crystal structure of ap4a hydrolase complexed with amp and 2 ATP (aq_158) from <i>Aquifex aeolicus</i> vf5
29	<a href="#">d1x51a1</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like

30	<a href="#">c3gz8C_</a>	Alignment	not modelled	99.2	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> cocrystal structure of nudix domain of shewanella oneidensis nrtr2 complexed with adp ribose
31	<a href="#">c2o1cB_</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> datp pyrophosphohydrolase; <b>PDBTitle:</b> structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
32	<a href="#">d1u20a1</a>	Alignment	not modelled	99.1	28	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
33	<a href="#">c3n77B_</a>	Alignment	not modelled	99.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoside triphosphatase nudix; <b>PDBTitle:</b> crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
34	<a href="#">c3dkuB_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphohydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase orf153, ymfB, from escherichia2 coli k-1
35	<a href="#">c5c7tB_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nudf protein; <b>PDBTitle:</b> crystal structure of the bdellovibrio bacteriovorus nucleoside2 diphosphate sugar hydrolase in complex with adp-ribose
36	<a href="#">c2jvbA_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna-decapping enzyme subunit 2; <b>PDBTitle:</b> solution structure of catalytic domain of ydcp2
37	<a href="#">c5zrhA_</a>	Alignment	not modelled	99.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mutator protein mutt2/nudix hydrolase; <b>PDBTitle:</b> m. smegmatis antimutator protein mutt2 in complex with cmp
38	<a href="#">d2fb1a2</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
39	<a href="#">c3gwyA_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ctp pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
40	<a href="#">c3ef5A_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable pyrophosphohydrolase; <b>PDBTitle:</b> structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
41	<a href="#">c3r03B_</a>	Alignment	not modelled	99.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> the crystal structure of nudix hydrolase from rhodospirillum rubrum
42	<a href="#">c5x1xA_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> solution nmr structure of dna mismatch repair protein mutt (family2 nudix hydrolase) from methicillin resistant staphylococcus aureus 252
43	<a href="#">d2o5fa1</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> I PP isomerase-like
44	<a href="#">c3h95A_</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 6; <b>PDBTitle:</b> crystal structure of the nudix domain of nudt6
45	<a href="#">d2azwa1</a>	Alignment	not modelled	99.0	25	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
46	<a href="#">c5mp0D_</a>	Alignment	not modelled	99.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> m7gpppn-mrna hydrolase; <b>PDBTitle:</b> human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
47	<a href="#">c3i9xA_</a>	Alignment	not modelled	99.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mutt/nudix family protein from listeria innocua
48	<a href="#">c6o3pA_</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal nadh pyrophosphatase nudt12; <b>PDBTitle:</b> crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
49	<a href="#">d1k2ea_</a>	Alignment	not modelled	99.0	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
50	<a href="#">c4ilqA_</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ct771; <b>PDBTitle:</b> 2.60a resolution structure of ct771 from chlamydia trachomatis
51	<a href="#">c3cngC_</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from nitrosomonas europaea
52	<a href="#">c5lopA_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kla0f23980p; <b>PDBTitle:</b> structure of the active form of /k. lactis/ dcp1-dcp2-edc3 decapping2 complex bound to m7gdp
53	<a href="#">d1ryaa_</a>	Alignment	not modelled	99.0	22	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> GDP-mannose mannosyl hydrolase NudD
54	<a href="#">c2fvvA_</a>	Alignment	not modelled	99.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> diphosphoinositol polyphosphate phosphohydrolase 1; <b>PDBTitle:</b> human diphosphoinositol polyphosphate phosphohydrolase 1 <b>Fold:</b> Nudix

55	<a href="#">d2fvva1</a>	Alignment	not modelled	99.0	27	<b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
56	<a href="#">c3f6aA_</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family; <b>PDBTitle:</b> crystal structure of a hydrolase, nudix family from2 clostridium perfringens
57	<a href="#">c4v14A_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> structure and function analysis of mutt from the2 psychrophile fish pathogen alivibrio salmonicida and the3 mesophile vibrio cholerae
58	<a href="#">c3o8sA_</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribose pyrophosphatase; <b>PDBTitle:</b> crystal structure of an adp-ribose pyrophosphatase (ssu98_1448) from2 streptococcus suis 89-1591 at 2.27 a resolution
59	<a href="#">d2a6ta2</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> mRNA decapping enzyme-like
60	<a href="#">c2qjoB_</a>	Alignment	not modelled	99.0	31	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional nmn adenylyltransferase/nudix hydrolase; <b>PDBTitle:</b> crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
61	<a href="#">d1vcda1</a>	Alignment	not modelled	98.9	30	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
62	<a href="#">c2w4eA_</a>	Alignment	not modelled	98.9	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
63	<a href="#">c2r5wA_</a>	Alignment	not modelled	98.9	21	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinamide-nucleotide adenylyltransferase; <b>PDBTitle:</b> crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
64	<a href="#">c3exqA_</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nudix family hydrolase; <b>PDBTitle:</b> crystal structure of a nudix family hydrolase from2 lactobacillus brevis
65	<a href="#">c3id9B_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
66	<a href="#">d1iryA_</a>	Alignment	not modelled	98.9	25	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
67	<a href="#">c4hfqB_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of udp-x diphosphatase
68	<a href="#">c3fk9B_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> crystal structure of mmutator mutt protein from bacillus halodurans
69	<a href="#">d1vk6a2</a>	Alignment	not modelled	98.9	26	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> NADH pyrophosphatase
70	<a href="#">d1v8ya_</a>	Alignment	not modelled	98.9	28	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
71	<a href="#">c2gb5B_</a>	Alignment	not modelled	98.9	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh pyrophosphatase; <b>PDBTitle:</b> crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
72	<a href="#">c2yyhC_</a>	Alignment	not modelled	98.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 8-oxo-dgtpase domain; <b>PDBTitle:</b> crystal structure of nudix family protein from aquifex aeolicus
73	<a href="#">d2b06a1</a>	Alignment	not modelled	98.9	28	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
74	<a href="#">d1vhza_</a>	Alignment	not modelled	98.8	18	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
75	<a href="#">c2fmlB_</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family protein from enterococcus2 faecalis
76	<a href="#">c2pqvA_</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family protein from streptococcus2 pneumoniae
77	<a href="#">c3q4iA_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphohydrolase (mutt/nudix family protein); <b>PDBTitle:</b> crystal structure of cdp-chase in complex with gd3+
78	<a href="#">d1g0sa_</a>	Alignment	not modelled	98.8	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
79	<a href="#">d1mqea_</a>	Alignment	not modelled	98.7	25	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
80	<a href="#">c3hm4B_</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adp-sugar pyrophosphatase;

80	<a href="#">c3b14B</a>	Alignment	not modelled	98.7	18	<b>PDBTitle:</b> crystal structure of human adp-ribose pyrophosphatase nudt5 in complex2 with magnesium and ampccpr <b>PDB header:</b> dna binding protein/dna
81	<a href="#">c3gz6A</a>	Alignment	not modelled	98.7	23	<b>Chain:</b> A; <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of shewanella oneidensis nrtr complexed with a 27mer2 dna
82	<a href="#">c3fcmA</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hydrolase, nudix family; <b>PDBTitle:</b> crystal structure of a nudix hydrolase from clostridium perfringens
83	<a href="#">c2qkmF</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> spac19a8.12 protein; <b>PDBTitle:</b> the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
84	<a href="#">c2i6kA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 1; <b>PDBTitle:</b> crystal structure of human type i ipp isomerase complexed with a2 substrate analog
85	<a href="#">c2fb1A</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of protein bt0354 from bacteroides thetaiotaomicron
86	<a href="#">c4zbpC</a>	Alignment	not modelled	98.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> nudix hydrolase 7; <b>PDBTitle:</b> crystal structure of the ampccpr-bound atnudt7
87	<a href="#">d1viva</a>	Alignment	not modelled	98.6	24	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
88	<a href="#">d1q33a</a>	Alignment	not modelled	98.6	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
89	<a href="#">c4jztA</a>	Alignment	not modelled	98.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dgtp pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
90	<a href="#">c5if9A</a>	Alignment	not modelled	98.6	24	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 22; <b>PDBTitle:</b> crystal structure of human nudt22
91	<a href="#">c3gg6A</a>	Alignment	not modelled	98.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 18; <b>PDBTitle:</b> crystal structure of the nudix domain of human nudt18
92	<a href="#">c1rrqA</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> muty; <b>PDBTitle:</b> muty adenine glycosylase in complex with dna containing an2 a:oxog pair
93	<a href="#">c3f13A</a>	Alignment	not modelled	98.5	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative nudix hydrolase family member; <b>PDBTitle:</b> crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
94	<a href="#">c3edsA</a>	Alignment	not modelled	98.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
95	<a href="#">c3dupB</a>	Alignment	not modelled	98.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
96	<a href="#">d1rrqa2</a>	Alignment	not modelled	98.3	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
97	<a href="#">c3e57A</a>	Alignment	not modelled	98.2	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein tm1382; <b>PDBTitle:</b> crystal structure of tm1382, a putative nudix hydrolase
98	<a href="#">c3rh7A</a>	Alignment	not modelled	98.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
99	<a href="#">c3q91D</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> uridine diphosphate glucose pyrophosphatase; <b>PDBTitle:</b> crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
100	<a href="#">c2pnyA</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 2; <b>PDBTitle:</b> structure of human isopentenyl-diphosphate delta-isomerase 2
101	<a href="#">c4v1aj</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
102	<a href="#">c2j8qB</a>	Alignment	not modelled	97.5	28	<b>PDB header:</b> nuclear protein <b>Chain:</b> B; <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor 5; <b>PDBTitle:</b> crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
103	<a href="#">c3couA</a>	Alignment	not modelled	97.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 16; <b>PDBTitle:</b> crystal structure of human nudix motif 16 (nudt16)
104	<a href="#">c3kvhA</a>	Alignment	not modelled	93.0	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein syndesmos; <b>PDBTitle:</b> crystal structure of human protein syndesmos (nudt16-like protein)
						<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> myo-inositol-1-phosphate synthase-related

105	<a href="#">c3cinA_</a>	Alignment	not modelled	74.6	21	protein; <b>PDBTitle:</b> crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
106	<a href="#">c1gr0A_</a>	Alignment	not modelled	70.2	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol-3-phosphate synthase; <b>PDBTitle:</b> myo-inositol 1-phosphate synthase from mycobacterium2 tuberculosis in complex with nad and zinc.
107	<a href="#">d1nvpb_</a>	Alignment	not modelled	63.6	36	<b>Fold:</b> Transcription factor IIA (TFIIA), alpha-helical domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), alpha-helical domain <b>Family:</b> Transcription factor IIA (TFIIA), alpha-helical domain
108	<a href="#">c1nvpB_</a>	Alignment	not modelled	63.6	36	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcription initiation factor iia alpha chain; <b>PDBTitle:</b> human tfiia/tbp/dna complex
109	<a href="#">d1vkya_</a>	Alignment	not modelled	63.2	24	<b>Fold:</b> QueA-like <b>Superfamily:</b> QueA-like <b>Family:</b> QueA-like
110	<a href="#">c1u1iC_</a>	Alignment	not modelled	62.7	21	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> myo-inositol-1-phosphate synthase; <b>PDBTitle:</b> myo-inositol phosphate synthase mips from a. fulgidus
111	<a href="#">d1vjpa1</a>	Alignment	not modelled	57.2	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
112	<a href="#">d1nh2b_</a>	Alignment	not modelled	52.3	43	<b>Fold:</b> Transcription factor IIA (TFIIA), alpha-helical domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), alpha-helical domain <b>Family:</b> Transcription factor IIA (TFIIA), alpha-helical domain
113	<a href="#">c2q0oC_</a>	Alignment	not modelled	51.2	19	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional repressor tram; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
114	<a href="#">c1vw46_</a>	Alignment	not modelled	26.8	28	<b>PDB header:</b> ribosome <b>Chain:</b> 6: <b>PDB Molecule:</b> 54s ribosomal protein l17, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
115	<a href="#">c1rm1C_</a>	Alignment	not modelled	25.8	43	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transcription initiation factor iia large chain; <b>PDBTitle:</b> structure of a yeast tfiia/tbp/tata-box dna complex
116	<a href="#">c4ewpD_</a>	Alignment	not modelled	24.5	30	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> crystal structure of fabh from micrococcus luteus
117	<a href="#">c1p1hD_</a>	Alignment	not modelled	23.4	26	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> inositol-3-phosphate synthase; <b>PDBTitle:</b> crystal structure of the 1l-myo-inositol/nad+ complex
118	<a href="#">d1u6ea1</a>	Alignment	not modelled	23.1	17	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
119	<a href="#">c1vkoA_</a>	Alignment	not modelled	23.1	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol-3-phosphate synthase; <b>PDBTitle:</b> crystal structure of inositol-3-phosphate synthase (ce21227) from2 caenorhabditis elegans at 2.30 a resolution
120	<a href="#">c3il3A_</a>	Alignment	not modelled	22.8	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> structure of haemophilus influenzae fabh