Phyre^2

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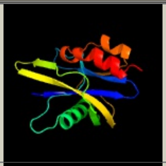
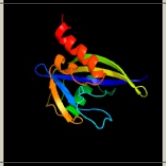
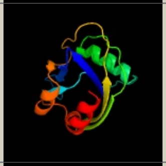
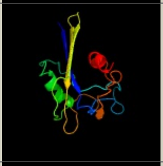
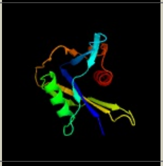
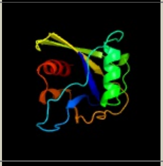
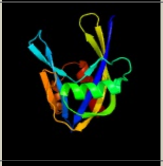
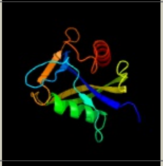
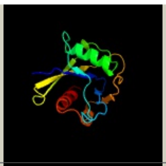
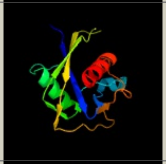
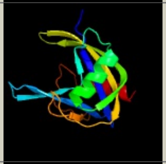
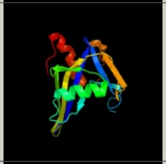
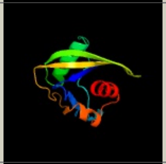
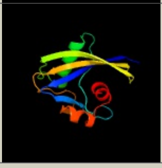
Description	RVBD1160_(mutT2)_1286600_1287025
Date	Wed Jul 31 22:05:24 BST 2019
Unique Job ID	157b1029c3337fec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zrhA_	Alignment		100.0	59	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mutator protein mutt2/nudix hydrolase; **PDBTitle:** m. smegmatis antimutator protein mutt2 in complex with cmp
2	c2rrkA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ctp pyrophosphohydrolase; **PDBTitle:** solution structure of the e. coli orf135 protein
3	c3ef5A_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
4	d1puna_	Alignment		100.0	27	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
5	c5x1xA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** solution nmr structure of dna mismatch repair protein mutt (family2 nudix hydrolase) from methicillin resistant staphylococcus aureus 252
6	c3gwyA_	Alignment		99.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
7	c3hhjA_	Alignment		99.9	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
8	c2pq1B_	Alignment		99.9	19	**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	d2b0va1	Alignment		99.9	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
10	c4hfqB_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of udp-x diphosphatase
11	c4dywA_	Alignment		99.9	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt nudix hydrolase from burkholderia2 pseudomallei

12	c3r03B_	Alignment		99.9	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
13	c3q4iA_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
14	c3dkuB_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from escherichia2 coli k-1
15	d1irya_	Alignment		99.9	27	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
16	c3exqA_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
17	c3o8sA_	Alignment		99.9	22	**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
18	c3cngC_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
19	c4v14A_	Alignment		99.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** structure and function analysis of mutt from the2 psychrofile fish pathogen aliivibrio salmonicida and the3 mesophile vibrio cholerae
20	c3n77B_	Alignment		99.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
21	c5gg7A_	Alignment	not modelled	99.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family protein; **PDBTitle:** crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
22	c3grnB_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt related protein; **PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1
23	c3gz8C_	Alignment	not modelled	99.9	19	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** cocrystal structure of nudix domain of shewanella oneidensis nrtr2 complexed with adp ribose
24	c5gp0F_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nudix hydrolase 1; **PDBTitle:** crystal structure of geraniol-nudx1 complex
25	d2b06a1	Alignment	not modelled	99.9	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
26	d1vcda1	Alignment	not modelled	99.9	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
27	c3fk9B_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mmutator mutt protein from bacillus halodurans
28	c2gb5B_	Alignment	not modelled	99.9	23	**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
						Fold: Nudix

29	d1vk6a2	Alignment	not modelled	99.9	22	**Superfamily:**Nudix **Family:**NADH pyrophosphatase
30	d1k2ea_	Alignment	not modelled	99.9	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
31	c5bonC_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable 8-oxo-dgtp diphosphatase nudt15; **PDBTitle:** crystal structure of human nudt15 (mth2)
32	c4kyxA_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribose pyrophosphatase mutt; **PDBTitle:** crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
33	c2qjoB_	Alignment	not modelled	99.9	28	**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.
34	c3h95A_	Alignment	not modelled	99.9	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
35	c2yyhC_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain; **PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus
36	d2fb1a2	Alignment	not modelled	99.9	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
37	c3fjyB_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
38	c3gg6A_	Alignment	not modelled	99.9	20	**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	c2pqvA_	Alignment	not modelled	99.9	22	**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
40	c2kdvA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
41	c1rrqA_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
42	d1ktga_	Alignment	not modelled	99.9	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
43	c3i9xA_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from listeria innocua
44	d1ryaa_	Alignment	not modelled	99.9	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
45	d2fkba1	Alignment	not modelled	99.9	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
46	c3rh7A_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
47	d1sjya_	Alignment	not modelled	99.9	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
48	c3gz6A_	Alignment	not modelled	99.9	18	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of shewanella oneidensis nrtr complexed with a 27mer2 dna
49	c3f6aA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
50	c3sonB_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical nudix hydrolase; **PDBTitle:** crystal structure of a putativel nudix hydrolase (lmof2365_2679) from2 listeria monocytogenes str. 4b f2365 at 1.70 a resolution
51	c2r5wA_	Alignment	not modelled	99.9	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
52	d1rrqa2	Alignment	not modelled	99.9	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
53	c2fb1A_	Alignment	not modelled	99.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
54	c2o1cB	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase;

54	c2o1cB_	Alignment	not modelled	99.9	22	**PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
55	c5cfiC_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bis(5'-nucleosyl)-tetraphosphatase (diadenosine **PDBTitle:** structural and functional attributes of malaria parasite ap4a2 hydrolase
56	d2azwa1	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
57	d1x51a1	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
58	c4zbpC_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase 7; **PDBTitle:** crystal structure of the ampcpr-bound atnudt7
59	d1vhza_	Alignment	not modelled	99.8	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
60	c2fvvA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase 1; **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
61	d2fvva1	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
62	c5lf8A_	Alignment	not modelled	99.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 17; **PDBTitle:** human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
63	c3id9B_	Alignment	not modelled	99.8	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
64	c6o3pA_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peroxisomal nadh pyrophosphatase nudt12; **PDBTitle:** crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
65	d1xsba_	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
66	d2fmla2	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
67	d1jkna_	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
68	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 clostridium perfringens
69	c2jvbA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
70	c5c7tB_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudf protein; **PDBTitle:** crystal structure of the bdellovibrio bacteriovorus nucleoside2 diphosphate sugar hydrolase in complex with adp-ribose
71	c2qkmF_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
72	c5mp0D_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**m7gpppn-mrna hydrolase; **PDBTitle:** human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
73	d2a6ta2	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
74	c4jztA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp pyrophosphohydrolase; **PDBTitle:** crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
75	c2w4eA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
76	d1ppva_	Alignment	not modelled	99.8	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
77	c5lopA_	Alignment	not modelled	99.8	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**klla0f23980p; **PDBTitle:** structure of the active form of /k. lactis/ dcp1-dcp2-edc3 decapping2 complex bound to m7gdp
78	c4ilqA_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ct771; **PDBTitle:** 2.60a resolution structure of ct771 from chlamydia trachomatis
79	d1v8ya_	Alignment	not modelled	99.8	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
						PDB header:hydrolase

80	c3edsA_	Alignment	not modelled	99.8	24	**Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
81	d1nqza_	Alignment	not modelled	99.8	25	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
82	c3f13A_	Alignment	not modelled	99.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nudix hydrolase family member; **PDBTitle:** crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
83	d1hzta_	Alignment	not modelled	99.8	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
84	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
85	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
86	c3e57A_	Alignment	not modelled	99.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
87	d1g0sa_	Alignment	not modelled	99.7	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
88	c3bm4B_	Alignment	not modelled	99.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-sugar pyrophosphatase; **PDBTitle:** crystal structure of human adp-ribose pyrophosphatase nudt5 in complex2 with magnesium and ampcpr
89	d2o5fa1	Alignment	not modelled	99.7	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
90	d1mqea_	Alignment	not modelled	99.7	28	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
91	c5t3pB_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal coenzyme a diphosphatase nudt7; **PDBTitle:** crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
92	d1q33a_	Alignment	not modelled	99.7	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
93	c2i6kA_	Alignment	not modelled	99.6	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 1; **PDBTitle:** crystal structure of human type i ipp isomerase complexed with a2 substrate analog
94	d1viua_	Alignment	not modelled	99.6	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
95	c3q91D_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
96	c2pnyA_	Alignment	not modelled	99.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
97	c3qsjA_	Alignment	not modelled	99.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
98	c4v1aj_	Alignment	not modelled	99.5	19	**PDB header:**ribosome **Chain:** J: **PDB Molecule:** **PDBTitle:** structure of the large subunit of the mammalian mitoribosome, part 22 of 2
99	c3dupB_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
100	c2j8qB_	Alignment	not modelled	99.4	23	**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.
101	c5lf9A_	Alignment	not modelled	99.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 22; **PDBTitle:** crystal structure of human nudt22
102	d1u20a1	Alignment	not modelled	99.4	27	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
103	c3couA_	Alignment	not modelled	98.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 16; **PDBTitle:** crystal structure of human nudix motif 16 (nudt16)
104	c3kvhA_	Alignment	not modelled	98.0	30	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
105	c1vw46	Alignment	not modelled	97.9	20	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**54s ribosomal protein l17, mitochondrial;

105	c1vw46_	Alignment	not modelled	97.9	20	**PDBTitle:** structure of the yeast mitochondrial large ribosomal subunit
106	c6drkD_	Alignment	not modelled	97.4	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transient receptor potential cation channel, subfamily m, **PDBTitle:** structure of trpm2 ion channel receptor by single particle electron2 cryo-microscopy, apo state
107	c3p5tE_	Alignment	not modelled	97.0	27	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 5; **PDBTitle:** cfim25-cfim68 complex
108	c6mizC_	Alignment	not modelled	96.1	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**transient receptor potential cation channel subfamily m **PDBTitle:** human trpm2 ion channel in an adpr-bound state
109	c4ktbA_	Alignment	not modelled	88.6	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of posible asymmetric diadenosine tetraphosphate2 (ap(4)a) hydrolases from jonesia denitrificans dsm 20603
110	c6d73B_	Alignment	not modelled	76.5	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transient receptor potential cation channel, subfamily m; **PDBTitle:** cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+
111	c6gwjK_	Alignment	not modelled	36.7	23	**PDB header:**rna binding protein **Chain:** K: **PDB Molecule:**probable trna n6-adenosine threonylcarbamoyltransferase; **PDBTitle:** protein complex
112	c2bs5A_	Alignment	not modelled	22.7	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**fucose-binding lectin protein; **PDBTitle:** lectin from ralstonia solanacearum complexed with 2-fucosyllactose