Phyre^2

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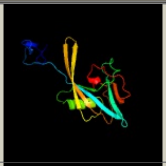
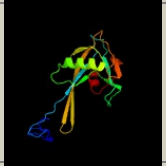
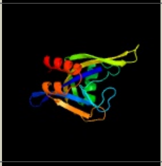
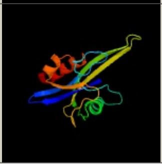
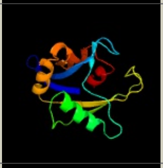
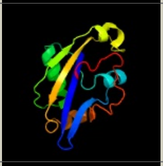
Description	RVBD0413_(mutT3)_499716_500369
Date	Tue Jul 23 14:50:48 BST 2019
Unique Job ID	ac2e8133bc5b61b2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gb5B_	Alignment		99.9	18	**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
2	c6o3pA_	Alignment		99.9	19	**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
3	c3cngC_	Alignment		99.9	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
4	c5gg7A_	Alignment		99.8	29	**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)
5	d1ktga_	Alignment		99.8	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
6	c3gz8C_	Alignment		99.8	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
7	c3hhjA_	Alignment		99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
8	c3fk9B_	Alignment		99.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mmutator mutt protein from bacillus halodurans
9	c2pq1B_	Alignment		99.8	26	**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
10	d1sjya_	Alignment		99.8	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
11	c2rrkA_	Alignment		99.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ctp pyrophosphohydrolase; **PDBTitle:** solution structure of the e. coli orf135 protein

12	c3exqA_	Alignment		99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
13	d2fb1a2	Alignment		99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
14	c3q4iA_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
15	c3i9xA_	Alignment		99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from listeria innocua
16	c2fb1A_	Alignment		99.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
17	d1nqza_	Alignment		99.8	30	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
18	c5cfiC_	Alignment		99.8	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**bis(5'-nucleosyl)-tetraphosphatase (diadenosine **PDBTitle:** structural and functional attributes of malaria parasite ap4a2 hydrolase
19	c3fjyB_	Alignment		99.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
20	c3ef5A_	Alignment		99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
21	c5bonC_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable 8-oxo-dgtp diphosphatase nudt15; **PDBTitle:** crystal structure of human nudt15 (mth2)
22	d1puna_	Alignment	not modelled	99.8	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
23	d1ryaa_	Alignment	not modelled	99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
24	c3gz6A_	Alignment	not modelled	99.8	19	**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
25	d2fmla2	Alignment	not modelled	99.8	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
26	c3n77B_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
27	c3sonB_	Alignment	not modelled	99.8	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
28	c2pqvA_	Alignment	not modelled	99.8	21	**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

29	c5zrhA_	Alignment	not modelled	99.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mutator protein mutt2/nudix hydrolase; **PDBTitle:** m. smegmatis antimutator protein mutt2 in complex with cmp
30	c2yyhC_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain; **PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus
31	c4kyxA_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribose pyrophosphatase mutt; **PDBTitle:** crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
32	c3r03B_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
33	c4hfqB_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of udp-x diphosphatase
34	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
35	c4v14A_	Alignment	not modelled	99.8	23	**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
36	c3grnB_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt related protein; **PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1
37	c3h95A_	Alignment	not modelled	99.8	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
38	c3gg6A_	Alignment	not modelled	99.8	19	**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	d2azwa1	Alignment	not modelled	99.8	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
40	d1vk6a2	Alignment	not modelled	99.7	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
41	d2fkba1	Alignment	not modelled	99.7	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
42	d2b06a1	Alignment	not modelled	99.7	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
43	c4dywA_	Alignment	not modelled	99.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt nudix hydrolase from burkholderia2 pseudomallei
44	c2qjoB_	Alignment	not modelled	99.7	17	**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.
45	c5gp0F_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nudix hydrolase 1; **PDBTitle:** crystal structure of geraniol-nudx1 complex
46	c5x1xA_	Alignment	not modelled	99.7	17	**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
47	d1vcda1	Alignment	not modelled	99.7	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
48	d2b0va1	Alignment	not modelled	99.7	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
49	d1xsba_	Alignment	not modelled	99.7	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
50	c5lf8A_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 17; **PDBTitle:** human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
51	c2fmlB_	Alignment	not modelled	99.7	20	**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
52	c4ilqA_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ct771; **PDBTitle:** 2.60a resolution structure of ct771 from chlamydia trachomatis
53	c3dkuB_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from escherichia2 coli k-1

54	c5t3pB_	Alignment	not modelled	99.7	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal coenzyme a diphosphatase nudt7; **PDBTitle:** crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
55	c2o1cB_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase; **PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
56	d1ppva_	Alignment	not modelled	99.7	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
57	c3fcmA_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium perfringens
58	d1k2ea_	Alignment	not modelled	99.7	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
59	c5c7tB_	Alignment	not modelled	99.7	21	**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
60	c3o8sA_	Alignment	not modelled	99.7	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
61	c2r5wA_	Alignment	not modelled	99.7	16	**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
62	c2fvvA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase 1; **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
63	d2fvva1	Alignment	not modelled	99.7	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
64	d1irya_	Alignment	not modelled	99.7	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
65	d1hzta_	Alignment	not modelled	99.7	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
66	c2kdvA_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
67	c3f6aA_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
68	c3bm4B_	Alignment	not modelled	99.7	23	**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
69	c2jvbA_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
70	c5mp0D_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**m7gpppn-mrna hydrolase; **PDBTitle:** human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
71	d2o5fa1	Alignment	not modelled	99.7	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
72	c2yvoA_	Alignment	not modelled	99.7	23	**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
73	d1x51a1	Alignment	not modelled	99.7	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
74	d1vhza_	Alignment	not modelled	99.6	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
75	c3qsjA_	Alignment	not modelled	99.6	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
76	c2w4eA_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
77	c3id9B_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
78	c4zbpC_	Alignment	not modelled	99.6	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase 7; **PDBTitle:** crystal structure of the ampcpr-bound atnudt7
79	c3edsA	Alignment	not modelled	99.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein;

79	c3edsA_	Alignment	not modelled	99.6	23	**PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
80	d1g0sa_	Alignment	not modelled	99.6	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
81	c5lopA_	Alignment	not modelled	99.6	14	**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
82	d2a6ta2	Alignment	not modelled	99.6	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
83	c2qkmF_	Alignment	not modelled	99.6	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
84	c3rh7A_	Alignment	not modelled	99.6	17	**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
85	d1q33a_	Alignment	not modelled	99.6	25	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
86	d1v8ya_	Alignment	not modelled	99.6	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
87	d1jkna_	Alignment	not modelled	99.6	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
88	c4jztA_	Alignment	not modelled	99.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp pyrophosphohydrolase; **PDBTitle:** crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
89	d1mqea_	Alignment	not modelled	99.6	25	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
90	c1rrqA_	Alignment	not modelled	99.6	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
91	c3f13A_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nudix hydrolase family member; **PDBTitle:** crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
92	d1rrqa2	Alignment	not modelled	99.5	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
93	c2i6kA_	Alignment	not modelled	99.5	14	**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	c3q91D_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
95	d1u20a1	Alignment	not modelled	99.4	23	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
96	d1viua_	Alignment	not modelled	99.4	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
97	c3dupB_	Alignment	not modelled	99.4	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
98	c3e57A_	Alignment	not modelled	99.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
99	c2pnyA_	Alignment	not modelled	99.3	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
100	c2j8qB_	Alignment	not modelled	99.2	17	**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	c4v1aj_	Alignment	not modelled	99.2	21	**PDB header:**ribosome **Chain:** J: **PDB Molecule:** **PDBTitle:** structure of the large subunit of the mammalian mitoribosome, part 22 of 2
102	c5lf9A_	Alignment	not modelled	99.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 22; **PDBTitle:** crystal structure of human nudt22
103	c3couA_	Alignment	not modelled	98.2	30	**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	97.2	28	**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	96.2	18	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**54s ribosomal protein l17, mitochondrial; **PDBTitle:** structure of the yeast mitochondrial large ribosomal subunit
106	c3p5tE_	Alignment	not modelled	95.0	26	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 5; **PDBTitle:** cfim25-cfim68 complex
107	c6drkD_	Alignment	not modelled	94.2	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
108	c6mizC_	Alignment	not modelled	91.6	24	**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	c2aklA_	Alignment	not modelled	88.5	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
110	d2akla2	Alignment	not modelled	85.2	28	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
111	c6d73B_	Alignment	not modelled	84.8	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+m2
112	c4ktbA_	Alignment	not modelled	81.7	21	**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
113	c6d73C_	Alignment	not modelled	31.3	20	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transient receptor potential cation channel, subfamily m; **PDBTitle:** cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+m2
114	c4b6ap_	Alignment	not modelled	27.2	21	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l17-a; **PDBTitle:** cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
115	d1ffkw_	Alignment	not modelled	24.8	21	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
116	c3cc4Z_	Alignment	not modelled	24.4	29	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
117	c2qa4Z_	Alignment	not modelled	23.9	29	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
118	c3zf7o_	Alignment	not modelled	23.7	18	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l13a, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
119	c3izrm_	Alignment	not modelled	23.4	25	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l23 (l14p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
120	c3jyw9_	Alignment	not modelled	23.4	21	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution