

Phyre²

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pnyA_	Alignment		100.0	28	PDB header: isomerase Chain: A; PDB Molecule: isopentenyl-diphosphate delta-isomerase 2; PDBTitle: structure of human isopentenyl-diphosphate delta-isomerase 2
2	c2i6kA_	Alignment		100.0	28	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
3	d1ppva_	Alignment		100.0	45	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
4	d2fkba1	Alignment		100.0	20	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
5	d1hzta_	Alignment		100.0	45	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
6	d2o5fa1	Alignment		100.0	25	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
7	c3dupB_	Alignment		100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
8	c5lf8A_	Alignment		99.9	28	PDB header: hydrolase Chain: A; PDB Molecule: nucleoside diphosphate-linked moiety x motif 17; PDBTitle: human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
9	c3grnB_	Alignment		99.9	21	PDB header: hydrolase Chain: B; PDB Molecule: mutt related protein; PDBTitle: crystal structure of mutt protein from methanoscincus mazei go1
10	c3n77B_	Alignment		99.9	18	PDB header: hydrolase Chain: B; PDB Molecule: nucleoside triphosphatase nudi; PDBTitle: crystal structure of idp01880, putative ntp pyrophosphohydrolase of salmonella typhimurium lt2
11	d1ryaa_	Alignment		99.9	20	Fold: Nudix Superfamily: Nudix Family: GDP-mannose mannosyl hydrolase NudD

12	d1sjya	Alignment		99.9	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
13	c2rrkA	Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: ctp pyrophosphohydrolase; PDBTitle: solution structure of the e. coli orf135 protein
14	c3hhjA	Alignment		99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mutator mutt from bartonella henselae
15	c6o3pA	Alignment		99.8	22	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
16	d2b0va1	Alignment		99.8	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
17	c3f6aA	Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a hydrolase, nudix family from2 clostridium perfringens
18	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
19	c3r03B	Alignment		99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: nudix hydrolase; PDBTitle: the crystal structure of nudix hydrolase from rhodospirillum rubrum
20	c2o1cB	Alignment		99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: datp pyrophosphohydrolase; PDBTitle: structure of the e. coli dihydronoepterin triphosphate2 pyrophosphohydrolase
21	c4kyxA	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribose pyrophosphatase mutt; PDBTitle: crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
22	c3exqA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: nudix family hydrolase; PDBTitle: crystal structure of a nudix family hydrolase from2 lactobacillus brevis
23	c3dkuB	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of nudix hydrolase orf153, ymfb, from escherichia2 coli k-1
24	c3h95A	Alignment	not modelled	99.8	13	PDB header: gene regulation Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the nudix domain of nudt6
25	d1jkna	Alignment	not modelled	99.8	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
26	c2pq1B	Alignment	not modelled	99.8	15	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
27	d1puna	Alignment	not modelled	99.8	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
28	d2azwa1	Alignment	not modelled	99.8	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
						PDB header: hydrolase

29	c2kdvA_	Alignment	not modelled	99.8	25	Chain: A: PDB Molecule: rna pyrophosphohydrolase; PDBTitle: solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli PDB header: hydrolase
30	c5zrhA_	Alignment	not modelled	99.8	19	Chain: A: PDB Molecule: putative mutator protein mutt2/nudix hydrolase; PDBTitle: m. smegmatis antimutator protein mutt2 in complex with cmp
31	c5bonC_	Alignment	not modelled	99.8	15	Chain: C: PDB Molecule: probable 8-oxo-dgtp diphosphatase nudt15; PDBTitle: crystal structure of human nudt15 (mth2)
32	d1vcda1	Alignment	not modelled	99.8	21	Fold: Nudix Superfamily: Nudix Family: MutT-like
33	c4v14A_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: structure and function analysis of mutt from the2 psychrophile fish pathogen <i>alivibrio salmonicida</i> and the3 mesophile <i>vibrio cholerae</i>
34	d1iryA_	Alignment	not modelled	99.8	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
35	c3gz8C_	Alignment	not modelled	99.8	16	PDB header: dna binding protein Chain: C: PDB Molecule: mutt/nudix family protein; PDBTitle: cocrystal structure of nudix domain of shewanella oneidensis ntr2 complexed with adp ribose PDB header: hydrolase
36	c3ef5A_	Alignment	not modelled	99.8	16	Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
37	c5x1xA_	Alignment	not modelled	99.8	15	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 <i>staphylococcus aureus</i> 252
38	c4dywA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt nudix hydrolase from <i>burkholderia2 pseudomallei</i>
39	d1nqza_	Alignment	not modelled	99.8	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
40	c3fcmA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a nudix hydrolase from <i>clostridium perfringens</i>
41	d1xsba_	Alignment	not modelled	99.8	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
42	c5c7tB_	Alignment	not modelled	99.8	10	Chain: B: PDB Molecule: nudf protein; PDBTitle: crystal structure of the <i>bdellovibrio bacteriovorus</i> nucleoside 2 diphosphate sugar hydrolase in complex with adp-ribose PDB header: hydrolase
43	c5gg7A_	Alignment	not modelled	99.8	20	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)
44	c4ilqA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: ct771; PDBTitle: 2.60a resolution structure of ct771 from <i>chlamydia trachomatis</i>
45	c5gp0F_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: F: PDB Molecule: nudix hydrolase 1; PDBTitle: crystal structure of geraniol-nudx1 complex
46	d2b06a1	Alignment	not modelled	99.8	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
47	d1vk6a2	Alignment	not modelled	99.7	14	Fold: Nudix Superfamily: Nudix Family: NADH pyrophosphatase
48	d2fb1a2	Alignment	not modelled	99.7	19	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
49	c3edsA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mut/nudix family protein from <i>bacillus2 thuringiensis</i>
50	c2yvoA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of ndx2 in complex with mg2+ and amp from <i>thermus2 thermophilus hb8</i>
51	c2gb5B_	Alignment	not modelled	99.7	16	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
52	d1ktga_	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
53	d1g0sa_	Alignment	not modelled	99.7	25	Fold: Nudix Superfamily: Nudix Family: MutT-like
54	d2fvva1	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: MutT-like

55	c2fvvA	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: diphosphoinositol polyphosphate phosphohydrolase 1; PDBTitle: human diphosphoinositol polyphosphate phosphohydrolase 1
56	c3gg6A	Alignment	not modelled	99.7	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
57	c3o8sA	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribose pyrophosphatase; PDBTitle: crystal structure of an adp-ribose pyrophosphatase (ssu98_1448) from2 streptococcus suis 89-1591 at 2.27 a resolution
58	c2w4eA	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
59	c4hfqB	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of udp-x diphosphatase
60	c3q4iA	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase (mutt/nudix family protein); PDBTitle: crystal structure of cdp-chase in complex with gd3+
61	c3cngC	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
62	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
63	c2jvbA	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: mRNA-decapping enzyme subunit 2; PDBTitle: solution structure of catalytic domain of ydcp2
64	c3sonB	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical nudix hydrolase; PDBTitle: crystal structure of a putative nudix hydrolase (lmof2365_2679) from2 listeria monocytogenes str. 4b f2365 at 1.70 a resolution
65	c2qjoB	Alignment	not modelled	99.7	18	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nmn adenyllyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nmn adenyllyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
66	d2a6ta2	Alignment	not modelled	99.7	14	Fold: Nudix Superfamily: Nudix Family: mRNA decapping enzyme-like
67	c3gwyA	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: putative ctp pyrophosphohydrolase; PDBTitle: crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
68	c2r5wA	Alignment	not modelled	99.7	20	PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide adenyllyltransferase; PDBTitle: crystal structure of a bifunctional nmn2 adenyllyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
69	c3gz6A	Alignment	not modelled	99.7	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
70	c4zbpC	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase 7; PDBTitle: crystal structure of the ampcpr-bound atnudt7
71	d1mqa	Alignment	not modelled	99.7	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
72	c3i9xA	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from listeria innocua
73	c3id9B	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
74	c2yyhC	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: C: PDB Molecule: 8-oxo-dgtpase domain; PDBTitle: crystal structure of nudix family protein from aquifex aeolicus
75	c2pqvA	Alignment	not modelled	99.7	20	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
76	c5mp0D	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: D: PDB Molecule: m7gpppN-mRNA hydrolase; PDBTitle: human m7gpppN-mRNA hydrolase (dcp2, nudt20) catalytic domain
77	c2fb1A	Alignment	not modelled	99.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0354 from bacteroides thetaiotaomicron
78	c5cfiC	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: C: PDB Molecule: bis(5'-nucleosyl)-tetraphosphatase (diadenosine PDBTitle: structural and functional attributes of malaria parasite ap4a2 hydrolase

79	c3e57A	Alignment	not modelled	99.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein tm1382; PDBTitle: crystal structure of tm1382, a putative nudix hydrolase
80	c5lopA	Alignment	not modelled	99.6	18	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
81	d2fmla2	Alignment	not modelled	99.6	13	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
82	d1k2ea	Alignment	not modelled	99.6	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
83	d1u20a1	Alignment	not modelled	99.6	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
84	d1v8ya	Alignment	not modelled	99.6	20	Fold: Nudix Superfamily: Nudix Family: MutT-like
85	d1x51a1	Alignment	not modelled	99.6	17	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
86	c3fjyB	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
87	c3q91D	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: D: PDB Molecule: uridine diphosphate glucose pyrophosphatase; PDBTitle: crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
88	d1vhza	Alignment	not modelled	99.6	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
89	c4jztA	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: dgtp pyrophosphohydrolase; PDBTitle: crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
90	c3bm4B	Alignment	not modelled	99.5	14	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
91	c1rrqA	Alignment	not modelled	99.5	11	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
92	c2fmlB	Alignment	not modelled	99.5	14	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
93	c2gkmF	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: F: PDB Molecule: spac19a8.12 protein; PDBTitle: the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
94	c3f13A	Alignment	not modelled	99.5	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
95	c5lf9A	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 22; PDBTitle: crystal structure of human nudt22
96	c3rh7A	Alignment	not modelled	99.4	11	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
97	d1viau	Alignment	not modelled	99.4	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
98	d1rrqa2	Alignment	not modelled	99.4	11	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
99	c3qsjA	Alignment	not modelled	99.3	23	PDB header: hydrolase Chain: A: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
100	d1q33a	Alignment	not modelled	99.2	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
101	c2j8qB	Alignment	not modelled	99.1	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.
102	c4v1aj	Alignment	not modelled	99.1	16	PDB header: ribosome Chain: J: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
103	c3couA	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudt16 (nudt16)
104	c3kvhA	Alignment	not modelled	97.9	20	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	96.1	18	PDB header: ribosome Chain: 6; PDB Molecule: 54s ribosomal protein l17, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
106	c4ktbA		Alignment	not modelled	95.5	19	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of possible asymmetric diadenosine tetraphosphate2 (ap(4)a) hydrolases from jonesia denitrificans dsm 20603
107	c3p5tE		Alignment	not modelled	86.6	17	PDB header: rna binding protein Chain: E; PDB Molecule: cleavage and polyadenylation specificity factor subunit 5; PDBTitle: cfim25-cfim68 complex
108	c3brcA		Alignment	not modelled	62.8	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
109	c5d5pC		Alignment	not modelled	50.4	13	PDB header: transferase Chain: C; PDB Molecule: hcgb; PDBTitle: hcgb from methanococcus maripaludis
110	c6drkD		Alignment	not modelled	46.9	22	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
111	c3ivrA		Alignment	not modelled	38.8	19	PDB header: ligase Chain: A; PDB Molecule: putative long-chain-fatty-acid coa ligase; PDBTitle: crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
112	d1tifA		Alignment	not modelled	38.5	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
113	c6o6dA		Alignment	not modelled	38.3	21	PDB header: ligase Chain: A; PDB Molecule: translation initiation factor if-3; PDBTitle: n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori
114	c5nfIB		Alignment	not modelled	37.6	19	PDB header: cell adhesion Chain: B; PDB Molecule: minor fimbrium anchoring subunit mfa2; PDBTitle: the fimbrial anchor protein mfa2 from porphyromonas gingivalis
115	d2riha1		Alignment	not modelled	36.7	30	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
116	c4qdgB		Alignment	not modelled	36.0	15	PDB header: cell adhesion Chain: B; PDB Molecule: putative adhesin; PDBTitle: crystal structure of a putative adhesin (bt2657) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution (psi community target,3 nakayama)
117	d2b78a1		Alignment	not modelled	35.6	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)
118	d1zfja4		Alignment	not modelled	34.4	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
119	c3pkwA		Alignment	not modelled	33.5	23	PDB header: lyase Chain: A; PDB Molecule: toxoflavin lyase (tfla); PDBTitle: crystal structure of toxoflavin lyase (tfla) bound to mn(ii)
120	c2d3aj		Alignment	not modelled	30.8	5	PDB header: ligase Chain: J; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoxime phosphate