

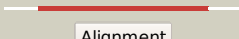

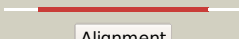














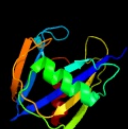




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1593c_(-)_1794004_1794714
Date	Fri Aug 2 13:30:18 BST 2019
Unique Job ID	914f727034ba4ced

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fb1A_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0354 from bacteroides thetaiotaomicron
2	c3gz6A_	 Alignment		100.0	29	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
3	c2fm1B_	 Alignment		100.0	28	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
4	d2fmla2	 Alignment		100.0	32	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
5	d2fb1a2	 Alignment		100.0	27	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
6	d1q33a_	 Alignment		100.0	13	Fold: Nudix Superfamily: Nudix Family: MutT-like
7	c3gz8C_	 Alignment		100.0	33	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
8	c3i9xA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from listeria innocua
9	c2qjoB_	 Alignment		100.0	27	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nmh adenylyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nmh adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
10	c2r5wA_	 Alignment		100.0	28	PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide adenylyltransferase; PDBTitle: crystal structure of a bifunctional nmh2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
11	c4zbpC_	 Alignment		100.0	19	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase 7; PDBTitle: crystal structure of the ampcpr-bound atnudt7

12	c2yyhC_	Alignment		99.9	20	PDB header: hydrolase Chain: C; PDB Molecule: 8-oxo-dgtpase domain; PDBTitle: crystal structure of nudix family protein from aquifex aeolicus
13	d2fb1a1	Alignment		99.9	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Nudix-associated domain
14	c3h95A_	Alignment		99.9	12	PDB header: gene regulation Chain: A; PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the nudix domain of nudt6
15	c5bonC_	Alignment		99.9	27	PDB header: hydrolase Chain: C; PDB Molecule: probable 8-oxo-dgtp diphosphatase nudt15; PDBTitle: crystal structure of human nudt15 (mth2)
16	c3cngC_	Alignment		99.9	22	PDB header: hydrolase Chain: C; PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
17	c2gb5B_	Alignment		99.9	14	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
18	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
19	c3fcmA_	Alignment		99.9	17	PDB header: hydrolase Chain: A; PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a nudix hydrolase from clostridium perfringens
20	d1iryA_	Alignment		99.9	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
21	d2b0va1	Alignment	not modelled	99.9	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
22	c3q4iA_	Alignment	not modelled	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+
23	c5gp0F_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: F; PDB Molecule: nudix hydrolase 1; PDBTitle: crystal structure of geraniol-nudx1 complex
24	c4kyxA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A; PDB Molecule: adp-ribose pyrophosphatase mutt; PDBTitle: crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
25	d1k2ea_	Alignment	not modelled	99.8	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
26	c4dywA_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A; PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt nudix hydrolase from burkholderia2 pseudomallei
27	d1vk6a2	Alignment	not modelled	99.8	13	Fold: Nudix Superfamily: Nudix Family: NADH pyrophosphatase
28	c4hfgB_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: B; PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of udp-x diphosphatase
						Fold: Nudix

29	d1ryaa_	Alignment	not modelled	99.8	18	Superfamily: Nudix Family: GDP-mannose mannosyl hydrolase NudD
30	c3o8sA_	Alignment	not modelled	99.8	18	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
31	d1ktga_	Alignment	not modelled	99.8	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
32	c2qkmF_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: F: PDB Molecule: spac19a8.12 protein; PDBTitle: the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
33	c5cfiC_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: C: PDB Molecule: bis(5'-nucleosyl)-tetrphosphatase (diadenosine) PDBTitle: structural and functional attributes of malaria parasite ap4a2 hydrolase
34	c2fvvA_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: diphosphoinositol polyphosphate phosphohydrolase 1; PDBTitle: human diphosphoinositol polyphosphate phosphohydrolase 1
35	d2fvva1	Alignment	not modelled	99.8	14	Fold: Nudix Superfamily: Nudix Family: MutT-like
36	c2jvbA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: mrna-decapping enzyme subunit 2; PDBTitle: solution structure of catalytic domain of ydcp2
37	d1vcda1	Alignment	not modelled	99.8	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
38	c5gg7A_	Alignment	not modelled	99.8	17	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)
39	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
40	c3gg6A_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 18; PDBTitle: crystal structure of the nudix domain of human nudt18
41	c3hhjA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mutator mutt from bartonella henselae
42	c3ef5A_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
43	c5zrhA_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: putative mutator protein mutt2/nudix hydrolase; PDBTitle: m. smegmatis antimutator protein mutt2 in complex with cmp
44	c3sonB_	Alignment	not modelled	99.8	16	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
45	d1xsba_	Alignment	not modelled	99.8	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
46	d1sjya_	Alignment	not modelled	99.8	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
47	c3f6aA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a hydrolase, nudix family from2 clostridium perfringens
48	c3fjyB_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
49	c2kdvA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: rna pyrophosphohydrolase; PDBTitle: solution structure of rna pyrophosphohydrolase rpqh from2 escherichia coli
50	c3dkuB_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of nudix hydrolase orf153, ymfb, from escherichia2 coli k-1
51	d2a6ta2	Alignment	not modelled	99.8	18	Fold: Nudix Superfamily: Nudix Family: mRNA decapping enzyme-like
52	c6o3pA_	Alignment	not modelled	99.8	17	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
53	c2rrkA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: ctp pyrophosphohydrolase; PDBTitle: solution structure of the e. coli orf135 protein
						PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein;

54	c4v14A_	Alignment	not modelled	99.7	14	PDBTitle: structure and function analysis of mutt from the2 psychrofile fish pathogen alivibrio salmonicida and the3 mesophile vibrio cholerae
55	c3fk9B_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mmutator mutt protein from bacillus halodurans
56	d2b06a1	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
57	c3r03B_	Alignment	not modelled	99.7	24	PDB header: hydrolase Chain: B: PDB Molecule: nudix hydrolase; PDBTitle: the crystal structure of nudix hydrolase from rhodospirillum rubrum
58	d2azwa1	Alignment	not modelled	99.7	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
59	c3edsA_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
60	c4ilqA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: ct771; PDBTitle: 2.60a resolution structure of ct771 from chlamydia trachomatis
61	c5mp0D_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: D: PDB Molecule: m7gpppn-mrna hydrolase; PDBTitle: human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
62	d1puna_	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
63	c3grnB_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: B: PDB Molecule: mutt related protein; PDBTitle: crystal structure of mutt protein from methanosarcina mazei go1
64	c4jztA_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: dgtp pyrophosphohydrolase; PDBTitle: crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
65	d1nqza_	Alignment	not modelled	99.7	21	Fold: Nudix Superfamily: Nudix Family: MutT-like
66	d1vhza_	Alignment	not modelled	99.7	12	Fold: Nudix Superfamily: Nudix Family: MutT-like
67	c3f13A_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: putative nudix hydrolase family member; PDBTitle: crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
68	c3gwyA_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: putative ctp pyrophosphohydrolase; PDBTitle: crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
69	c5lopA_	Alignment	not modelled	99.7	16	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
70	c2w4eA_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
71	d1u20a1	Alignment	not modelled	99.7	13	Fold: Nudix Superfamily: Nudix Family: MutT-like
72	c2yvoA_	Alignment	not modelled	99.7	15	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	c3n77B_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: B: PDB Molecule: nucleoside triphosphatase nudi; PDBTitle: crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
74	c2o1cB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: datp pyrophosphohydrolase; PDBTitle: structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
75	c5c7tB_	Alignment	not modelled	99.7	10	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
76	d1jkna_	Alignment	not modelled	99.7	12	Fold: Nudix Superfamily: Nudix Family: MutT-like
77	c5x1xA_	Alignment	not modelled	99.7	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 staphylococcus aureus 252
78	d2fkba1	Alignment	not modelled	99.7	14	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
79	c2ppqV_	Alignment	not modelled	99.7	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
						PDB header: hydrolase

80	c3id9B_	Alignment	not modelled	99.6	23	Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
81	d1g0sa_	Alignment	not modelled	99.6	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
82	c5lf8A_	Alignment	not modelled	99.6	22	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 17; PDBTitle: human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
83	d1hzta_	Alignment	not modelled	99.6	14	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
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	c5t3pB_	Alignment	not modelled	99.6	21	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal coenzyme a diphosphatase nudt7; PDBTitle: crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
86	c3bm4B_	Alignment	not modelled	99.6	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
87	d1v8ya_	Alignment	not modelled	99.6	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
88	d1ppva_	Alignment	not modelled	99.5	13	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
89	c3e57A_	Alignment	not modelled	99.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein tm1382; PDBTitle: crystal structure of tm1382, a putative nudix hydrolase
90	d2o5fa1	Alignment	not modelled	99.5	13	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
91	d1x51a1	Alignment	not modelled	99.5	15	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
92	d1mqea_	Alignment	not modelled	99.4	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
93	d1viua_	Alignment	not modelled	99.4	11	Fold: Nudix Superfamily: Nudix Family: MutT-like
94	c3q91D_	Alignment	not modelled	99.3	12	PDB header: hydrolase Chain: D: PDB Molecule: uridine diphosphate glucose pyrophosphatase; PDBTitle: crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
95	c2j8qB_	Alignment	not modelled	99.3	20	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.
96	d1rrqa2	Alignment	not modelled	99.3	16	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
97	c1rrqA_	Alignment	not modelled	99.3	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
98	c2i6kA_	Alignment	not modelled	99.0	15	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
99	c3dupB_	Alignment	not modelled	99.0	19	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	c4v1aj_	Alignment	not modelled	99.0	13	PDB header: ribosome Chain: J: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
101	c3qsjA_	Alignment	not modelled	98.9	32	PDB header: hydrolase Chain: A: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
102	c5lf9A_	Alignment	not modelled	98.8	14	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 22; PDBTitle: crystal structure of human nudt22
103	c2pnyA_	Alignment	not modelled	98.8	12	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 2; PDBTitle: structure of human isopentenyl-diphosphate delta-isomerase 2
104	c4ktbA_	Alignment	not modelled	98.7	16	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

105	d2fmla1	Alignment	not modelled	98.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Nudix-associated domain
106	c3couA	Alignment	not modelled	98.4	22	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudix motif 16 (nudt16)
107	c6drkD	Alignment	not modelled	98.1	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	97.8	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	c3kvhA	Alignment	not modelled	97.6	26	PDB header: rna binding protein Chain: A: PDB Molecule: protein syndesmos; PDBTitle: crystal structure of human protein syndesmos (nudt16-like protein)
110	c6d73B	Alignment	not modelled	96.9	17	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	c3p5tE	Alignment	not modelled	96.8	25	PDB header: rna binding protein Chain: E: PDB Molecule: cleavage and polyadenylation specificity factor subunit 5; PDBTitle: cfim25-cfim68 complex
112	c1vw46	Alignment	not modelled	93.8	18	PDB header: ribosome Chain: 6: PDB Molecule: 54s ribosomal protein l17, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
113	d1z05a1	Alignment	not modelled	84.7	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
114	c1z05A	Alignment	not modelled	68.7	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
115	c6d73C	Alignment	not modelled	61.9	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+
116	c4i98C	Alignment	not modelled	57.1	30	PDB header: cell cycle Chain: C: PDB Molecule: segregation and condensation protein b; PDBTitle: crystal structure of the complex between scpa(residues 1-160)-2 scpb(residues 1-183)
117	d1b79a	Alignment	not modelled	55.8	18	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
118	c3w6jC	Alignment	not modelled	55.2	28	PDB header: cell cycle Chain: C: PDB Molecule: scpb; PDBTitle: crystal structure of scpab core complex
119	c1t6sB	Alignment	not modelled	55.0	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
120	d2irfg	Alignment	not modelled	49.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Interferon regulatory factor