Phyre²

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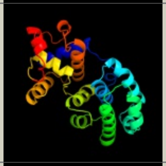
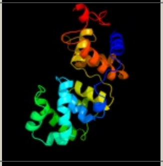
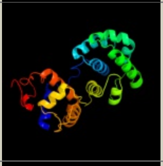
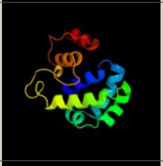
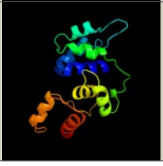
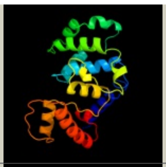
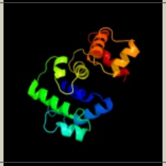
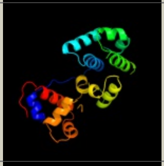
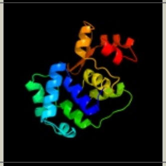
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rrqA_	Alignment		100.0	36	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
2	d1kg2a_	Alignment		100.0	100	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
3	c3n5nX_	Alignment		100.0	45	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase; **PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
4	d1rrqa1	Alignment		100.0	47	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
5	d1keaa_	Alignment		100.0	28	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
6	d1orna_	Alignment		100.0	23	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
7	d2abka_	Alignment		100.0	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
8	d1pu6a_	Alignment		100.0	15	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
9	d1ngna_	Alignment		100.0	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
10	c3kntC_	Alignment		100.0	16	**PDB header:**hydrolase, lyase/dna **Chain:** C: **PDB Molecule:**n-glycosylase/dna lyase; **PDBTitle:** crystal structure of methanocaldococcus jannaschii 8-2 oxoguanine glycosylase/lyase in complex with 15mer dna3 containing 8-oxoguanine
11	c3n0uB_	Alignment		100.0	16	**PDB header:**hydrolase, lyase **Chain:** B: **PDB Molecule:**probable n-glycosylase/dna lyase; **PDBTitle:** crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima

12	c3fhgA_	Alignment		99.9	14	**PDB header:**dna repair, hydrolase, lyase **Chain:** A: **PDB Molecule:**n-glycosylase/dna lyase; **PDBTitle:** crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
13	c3f10A_	Alignment		99.9	20	**PDB header:**hydrolase, lyase **Chain:** A: **PDB Molecule:**8-oxoguanine-dna-glycosylase; **PDBTitle:** crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine
14	c3s6iA_	Alignment		99.9	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosylase 1; **PDBTitle:** schizosaccaromyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
15	d2noha1	Alignment		99.9	26	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
16	c1yqmA_	Alignment		99.9	24	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**n-glycosylase/dna lyase; **PDBTitle:** catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna
17	c1ko9A_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**8-oxoguanine dna glycosylase; **PDBTitle:** native structure of the human 8-oxoguanine dna glycosylase2 hogg1
18	c2yg8B_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna-3-methyladenine glycosidase ii, putative; **PDBTitle:** structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans
19	d1mpga1	Alignment		99.9	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
20	d1x51a1	Alignment		99.9	27	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
21	d1rrqa2	Alignment	not modelled	99.9	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
22	c2jhnB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase; **PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
23	c2h56C_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of dna-3-methyladenine glycosidase (10174367) from2 bacillus halodurans at 2.55 a resolution
24	c1mpgB_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
25	d1puna_	Alignment	not modelled	99.8	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
26	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
27	c3gwyA_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
28	c3hhjA_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
						PDB header:hydrolase

29	c3grnB_	Alignment	not modelled	99.7	14	**Chain:** B: **PDB Molecule:**mutt related protein; **PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1
30	c3r03B_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
31	c3cngC_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
32	c3fk9B_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mmutator mutt protein from bacillus2 halodurans
33	c2pq1B_	Alignment	not modelled	99.6	11	**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
34	c2gb5B_	Alignment	not modelled	99.6	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
35	c3exqA_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
36	c3n77B_	Alignment	not modelled	99.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
37	d2b06a1	Alignment	not modelled	99.5	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
38	d1irya_	Alignment	not modelled	99.5	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
39	d1vcda1	Alignment	not modelled	99.5	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
40	c3q4iA_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
41	c2qjoB_	Alignment	not modelled	99.5	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.
42	c3dkuB_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1
43	c3rh7A_	Alignment	not modelled	99.5	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical oxidoreductase; **PDBTitle:** crystal structure of a hypothetical oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
44	d2b0va1	Alignment	not modelled	99.5	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
45	d1k2ea_	Alignment	not modelled	99.5	13	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
46	d1vk6a2	Alignment	not modelled	99.5	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
47	c2kdvA_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
48	c3o8sA_	Alignment	not modelled	99.5	14	**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
49	d2azwa1	Alignment	not modelled	99.4	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
50	c2pqvA_	Alignment	not modelled	99.4	10	**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
51	c3fcmA_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens
52	d1ryaa_	Alignment	not modelled	99.4	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
53	d2fkba1	Alignment	not modelled	99.4	13	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
54	c2o1cB_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase; **PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase

55	c3id9B_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
56	c3gz8C_	Alignment	not modelled	99.4	20	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** cocrystal structure of nudix domain of shewanella oneidensis2 nrtr complexed with adp ribose
57	c3h95A_	Alignment	not modelled	99.4	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 6; **PDBTitle:** crystal structure of the nudix domain of nudt6
58	c3sonB_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical nudix hydrolase; **PDBTitle:** crystal structure of a hypothetical nudix hydrolase (lmof2365_2679)2 from listeria monocytogenes (atcc 19115) at 1.70 a resolution
59	c3gg6A_	Alignment	not modelled	99.4	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
60	c3f6aA_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
61	d2fb1a2	Alignment	not modelled	99.4	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
62	c2jvbA_	Alignment	not modelled	99.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
63	c3fjyB_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
64	d1ktga_	Alignment	not modelled	99.3	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
65	c3f13A_	Alignment	not modelled	99.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nudix hydrolase family member; **PDBTitle:** crystal structure of putative nudix hydrolase family member2 from chromobacterium violaceum
66	d1sjya_	Alignment	not modelled	99.3	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
67	c2r5wA_	Alignment	not modelled	99.3	17	**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
68	c2yyhC_	Alignment	not modelled	99.3	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain; **PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus
69	c3i9xA_	Alignment	not modelled	99.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from listeria innocua
70	d1xsba_	Alignment	not modelled	99.3	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
71	c3gz6A_	Alignment	not modelled	99.3	21	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of shewanella oneidensis nrtr complexed2 with a 27mer dna
72	d2a6ta2	Alignment	not modelled	99.2	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
73	c2fb1A_	Alignment	not modelled	99.2	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
74	d1jkna_	Alignment	not modelled	99.2	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
75	d2fvva1	Alignment	not modelled	99.2	13	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
76	c2fvvA_	Alignment	not modelled	99.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
77	d2o5fa1	Alignment	not modelled	99.2	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
78	d1ppva_	Alignment	not modelled	99.2	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
79	c3edsA_	Alignment	not modelled	99.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
80	d1nqza_	Alignment	not modelled	99.2	18	**Fold:**Nudix **Superfamily:**Nudix

						Family: MutT-like
81	d1hzta_	Alignment	not modelled	99.2	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
82	c2qkmF_	Alignment	not modelled	99.1	12	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
83	d2fmla2	Alignment	not modelled	99.1	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
84	c2w4eA_	Alignment	not modelled	99.1	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
85	d1g0sa_	Alignment	not modelled	99.1	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
86	d1vhza_	Alignment	not modelled	99.0	16	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
87	c3e57A_	Alignment	not modelled	99.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
88	d1v8ya_	Alignment	not modelled	99.0	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
89	c2yvoA_	Alignment	not modelled	98.9	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
90	d1q33a_	Alignment	not modelled	98.9	11	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
91	c2i6kA_	Alignment	not modelled	98.9	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 1; **PDBTitle:** crystal structure of human type i ipp isomerase complexed2 with a substrate analog
92	c3bm4B_	Alignment	not modelled	98.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-sugar pyrophosphatase; **PDBTitle:** crystal structure of human adp-ribose pyrophosphatase nudt52 in complex with magnesium and ampcpr
93	c2fmlB_	Alignment	not modelled	98.9	18	**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
94	d1mqea_	Alignment	not modelled	98.8	9	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
95	c2pnyA_	Alignment	not modelled	98.7	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
96	c3q91D_	Alignment	not modelled	98.7	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
97	d1viua_	Alignment	not modelled	98.7	14	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
98	c2j8qB_	Alignment	not modelled	98.5	10	**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.
99	c3dupB_	Alignment	not modelled	98.4	8	**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	c3qsjA_	Alignment	not modelled	98.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
101	d1u20a1	Alignment	not modelled	98.1	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
102	c3couA_	Alignment	not modelled	97.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 16; **PDBTitle:** crystal structure of human nudix motif 16 (nudt16)
103	c3kvhA_	Alignment	not modelled	95.3	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
104	c2h5xA_	Alignment	not modelled	94.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
105	d1jmsa1	Alignment	not modelled	94.8	9	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like

106	d2bcqa1	Alignment	not modelled	94.6	20	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
107	d1dgsa1	Alignment	not modelled	94.5	31	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
108	d1ixra1	Alignment	not modelled	94.4	33	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
109	d1nzpa_	Alignment	not modelled	94.3	20	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
110	c1ixrA_	Alignment	not modelled	94.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
111	d1cuka2	Alignment	not modelled	94.2	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
112	d2bgwa1	Alignment	not modelled	93.5	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
113	d2fmpa1	Alignment	not modelled	93.5	25	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
114	d1szpa1	Alignment	not modelled	93.4	23	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
115	d1bvsa2	Alignment	not modelled	93.2	31	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
116	c1d8lA_	Alignment	not modelled	92.8	27	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva); **PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
117	d1x2ia1	Alignment	not modelled	92.6	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
118	d1dk2a_	Alignment	not modelled	91.9	26	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
119	c1kftA_	Alignment	not modelled	91.9	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
120	d1kfta_	Alignment	not modelled	91.9	28	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain