























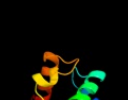







Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A809
Date	Thu Jan 5 11:06:34 GMT 2012
Unique Job ID	be9e6bd720e657ea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1hjpA_	 Alignment		100.0	99	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
2	c2h5xA_	 Alignment		100.0	38	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
3	c1d8lA_	 Alignment		100.0	100	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
4	c1ixrA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
5	d1cuka2	 Alignment		99.9	100	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
6	d1bvsa2	 Alignment		99.9	35	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
7	d1ixra1	 Alignment		99.9	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
8	d1cuka3	 Alignment		99.8	100	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
9	d1bvsa3	 Alignment		99.8	38	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
10	d1ixra2	 Alignment		99.8	37	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
11	d1cuka1	 Alignment		98.9	98	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain

12	dlx2ia1	Alignment		98.4	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
13	d1kfta_	Alignment		98.4	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
14	c1kfta_	Alignment		98.4	31	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
15	d2bgwa1	Alignment		98.3	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
16	d1dgsa1	Alignment		98.2	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
17	d2ilqa1	Alignment		98.1	30	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
18	d1pzna1	Alignment		98.1	25	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
19	d2a1jb1	Alignment		98.0	17	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
20	d1szpa1	Alignment		97.8	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
21	d1ixsa_	Alignment	not modelled	97.5	44	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
22	c2bhnD_	Alignment	not modelled	97.4	25	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
23	c1dgsB_	Alignment	not modelled	97.4	29	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
24	c2nrzB_	Alignment	not modelled	97.4	14	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
25	c1b22A_	Alignment	not modelled	97.4	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
26	d1b22a_	Alignment	not modelled	97.4	18	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
27	c2csdB_	Alignment	not modelled	97.3	25	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
28	c8icZA_	Alignment	not modelled	97.3	27	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase beta (e.c.2.7.7.7)); PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mnc12 (5 millimolar), and lithium sulfate4 (75

					millimolar)
29	c2w9mB_	Alignment	not modelled	97.3	25 PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
30	c2owoA_	Alignment	not modelled	97.2	19 PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
31	d1szpb1	Alignment	not modelled	97.1	23 Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
32	c1kdhA_	Alignment	not modelled	97.1	23 PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
33	c2ihmA_	Alignment	not modelled	97.1	21 PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
34	c2ziuA_	Alignment	not modelled	96.8	21 PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
35	c1vddC_	Alignment	not modelled	96.8	45 PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
36	d1vdda_	Alignment	not modelled	96.8	45 Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
37	c1v9pB_	Alignment	not modelled	96.7	19 PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
38	d2aq0a1	Alignment	not modelled	96.6	15 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
39	c3f10A_	Alignment	not modelled	96.4	24 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
40	c2bcuA_	Alignment	not modelled	96.3	22 PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a tt mismatch
41	d2axtu1	Alignment	not modelled	96.0	26 Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
42	c1s5lu_	Alignment	not modelled	95.8	26 PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
43	c1ko9A_	Alignment	not modelled	95.7	28 PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
44	d2duya1	Alignment	not modelled	95.7	43 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
45	d1rxwa1	Alignment	not modelled	95.7	17 Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
46	d1a77a1	Alignment	not modelled	95.6	19 Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
47	c2jhnB_	Alignment	not modelled	95.5	27 PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
48	c1yqmA_	Alignment	not modelled	95.5	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
49	d1b43a1	Alignment	not modelled	95.3	13 Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
50	d2edua1	Alignment	not modelled	95.2	25 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
51	d3bzka1	Alignment	not modelled	95.0	26 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
52	d1mc8a1	Alignment	not modelled	95.0	16 Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
53	c2vg8B_	Alignment	not modelled	94.7	26 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
54	c3fhgA_	Alignment	not modelled	94.6	25 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)

55	c2zixA	Alignment	not modelled	94.5	19	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: crystal structure of the mus81-eme1 complex
56	d1mpga1	Alignment	not modelled	94.3	28	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
57	d2noha1	Alignment	not modelled	93.9	27	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
58	clrxvA	Alignment	not modelled	93.8	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
59	d1xo1a1	Alignment	not modelled	93.6	15	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
60	c1nomA	Alignment	not modelled	93.5	22	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)
61	c3c1zA	Alignment	not modelled	93.5	16	PDB header: dna binding protein Chain: A: PDB Molecule: dna integrity scanning protein disa; PDBTitle: structure of the ligand-free form of a bacterial dna damage2 sensor protein
62	d1ngna	Alignment	not modelled	93.4	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
63	d2abka	Alignment	not modelled	93.2	31	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
64	d2p6ra2	Alignment	not modelled	93.2	17	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
65	dlorna	Alignment	not modelled	93.0	29	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
66	c1b43A	Alignment	not modelled	93.0	14	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
67	c3s6iA	Alignment	not modelled	92.8	37	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.
68	c2izoA	Alignment	not modelled	92.7	11	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
69	d1pu6a	Alignment	not modelled	92.6	28	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
70	d1rrqa1	Alignment	not modelled	92.4	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
71	d1keaa	Alignment	not modelled	92.3	25	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
72	d1ul1x1	Alignment	not modelled	92.2	28	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
73	d1bvsa1	Alignment	not modelled	91.9	24	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
74	d1kg2a	Alignment	not modelled	91.8	32	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
75	c1ut8B	Alignment	not modelled	91.7	11	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
76	c1mpgB	Alignment	not modelled	91.5	33	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
77	c2p6uA	Alignment	not modelled	91.2	28	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
78	c2oceA	Alignment	not modelled	91.0	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
79	d2csba3	Alignment	not modelled	90.9	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
80	c2va8A	Alignment	not modelled	90.9	24	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
81	c3oryA	Alignment	not modelled	90.5	18	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
82	c1rraA	Alignment	not modelled	90.2	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty;

82	c1nqa_	Alignment	not modelled	90.2	18	PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
83	d1veka_	Alignment	not modelled	90.1	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
84	c3n0uB_	Alignment	not modelled	89.5	25	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
85	d2bccqa1	Alignment	not modelled	89.0	35	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
86	c1ul1Y_	Alignment	not modelled	88.7	28	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
87	d2fmpa1	Alignment	not modelled	88.5	42	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
88	c3psiA_	Alignment	not modelled	88.4	19	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
89	d1cmwa1	Alignment	not modelled	88.3	28	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
90	c1a77A_	Alignment	not modelled	88.2	22	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
91	c3kntC_	Alignment	not modelled	87.6	21	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
92	d2i5ha1	Alignment	not modelled	87.6	39	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like
93	c2i5ha_	Alignment	not modelled	87.6	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
94	d1nzpa_	Alignment	not modelled	87.4	35	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
95	d1wiva_	Alignment	not modelled	87.2	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
96	c3q8lA_	Alignment	not modelled	87.2	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
97	c3n5nX_	Alignment	not modelled	87.0	32	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
98	c3psfA_	Alignment	not modelled	86.2	22	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
99	d1ifya_	Alignment	not modelled	85.4	9	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
100	c2zixB_	Alignment	not modelled	85.3	26	PDB header: hydrolase Chain: B: PDB Molecule: crossover junction endonuclease eme1; PDBTitle: crystal structure of the mus81-eme1 complex
101	c2dagA_	Alignment	not modelled	85.2	12	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 5; PDBTitle: solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
102	c3qeaZ_	Alignment	not modelled	85.0	18	PDB header: hydrolase/dna Chain: Z: PDB Molecule: exonuclease 1; PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii)
103	d1jmsa1	Alignment	not modelled	84.0	16	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
104	d1oqya1	Alignment	not modelled	83.6	7	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
105	d1cooa_	Alignment	not modelled	83.2	17	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
106	c2dakA_	Alignment	not modelled	82.9	15	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 5; PDBTitle: solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
107	d2crna1	Alignment	not modelled	82.8	13	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
108	d1whca_	Alignment	not modelled	82.6	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain

109	d2g3qa1	Alignment	not modelled	82.6	26	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
110	c2kp7A_	Alignment	not modelled	81.6	15	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
111	c2crnA_	Alignment	not modelled	81.5	12	PDB header: immune system Chain: A: PDB Molecule: ubash3a protein; PDBTitle: solution structure of the uba domain of human ubash3a2 protein
112	d1i94m_	Alignment	not modelled	81.2	35	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
113	d2fmpa2	Alignment	not modelled	81.2	26	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
114	c2cpwA_	Alignment	not modelled	80.8	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cbl-interacting protein sts-1 variant; PDBTitle: solution structure of rsgi ruh-031, a uba domain from human2 cdna
115	c2h56C_	Alignment	not modelled	80.2	29	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
116	d2vana1	Alignment	not modelled	80.1	20	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
117	d1dk2a_	Alignment	not modelled	80.1	42	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
118	d1lb2b_	Alignment	not modelled	79.7	24	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
119	d1vega_	Alignment	not modelled	79.2	12	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
120	d2bcqa2	Alignment	not modelled	79.1	16	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain