

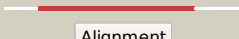

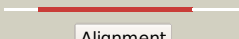








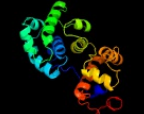










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3589_(mutY)_4030672_4031586
Date	Fri Aug 9 18:20:27 BST 2019
Unique Job ID	1d1773aeb77be8e4

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	c3n5nX_	 Alignment		100.0	36	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
3	d1kq2a_	 Alignment		100.0	33	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
4	d1rrqa1	 Alignment		100.0	36	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
5	d1keaa_	 Alignment		100.0	26	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
6	d2abka_	 Alignment		100.0	24	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
7	d1orna_	 Alignment		100.0	23	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
8	c4uobA_	 Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
9	c4unfA_	 Alignment		100.0	30	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
10	d1pu6a_	 Alignment		100.0	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
11	d1ngna_	 Alignment		100.0	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase

12	c3n0uB_	Alignment		100.0	14	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
13	c3kntC_	Alignment		100.0	13	PDB header: hydrolase, lyase/dna Chain: C: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of methanocaldococcus jannaschii 8-oxoguanine2 glycosylase/lyase in complex with 15mer dna containing 8-oxoguanine
14	c4b24A_	Alignment		100.0	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: probable dna-3-methyladenine glycosylase 2; PDBTitle: unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
15	c3fhgA_	Alignment		100.0	11	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)
16	c3f10A_	Alignment		100.0	17	PDB header: hydrolase, lyase Chain: A: PDB Molecule: 8-oxoguanine-dna-glycosylase; PDBTitle: crystal structure of clostridium acetobutylicum 8-oxoguanine dna2 glycosylase in complex with 8-oxoguanosine
17	c3s6iA_	Alignment		100.0	17	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.
18	d2noha1	Alignment		100.0	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
19	c4ejvA_	Alignment		100.0	18	PDB header: hydrolase/dna Chain: A: PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mbogg1 in complex with high affinity dna ligand
20	c2yg8B_	Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: dna-3-methyladenine glycosidase ii, putative; PDBTitle: structure of an unusual 3-methyladenine dna glycosylase ii (alka) from2 deinococcus radiodurans
21	c1yqmA_	Alignment	not modelled	99.9	20	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
22	c1ko9A_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
23	d1mpga1	Alignment	not modelled	99.9	20	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
24	c2jhnB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
25	c2h56C_	Alignment	not modelled	99.9	17	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
26	c1mpgB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
27	c2jg6A_	Alignment	not modelled	96.1	14	PDB header: hydrolase Chain: A: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus
28	d2bcqa1	Alignment	not modelled	96.0	16	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
						Fold: SAM domain-like

29	d1jmsa1	Alignment	not modelled	95.7	5	Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
30	d2fmpa1	Alignment	not modelled	95.6	18	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
31	d1nkua_	Alignment	not modelled	95.6	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)
32	d1dgsa1	Alignment	not modelled	95.5	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD ⁺ -dependent DNA ligase, domain 3
33	d1nzpa_	Alignment	not modelled	95.4	16	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
34	d1ixra1	Alignment	not modelled	95.2	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
35	c6h5hA_	Alignment	not modelled	95.1	18	PDB header: unknown function Chain: A: PDB Molecule: polb4; PDBTitle: a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
36	d2bgwa1	Alignment	not modelled	94.5	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
37	c8icza_	Alignment	not modelled	94.5	18	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), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
38	d1dk2a_	Alignment	not modelled	94.4	17	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
39	d1mkma1	Alignment	not modelled	94.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
40	c2h5xA_	Alignment	not modelled	94.1	20	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
41	c2mutA_	Alignment	not modelled	94.0	18	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
42	c1ixrA_	Alignment	not modelled	94.0	22	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
43	d1bvsa2	Alignment	not modelled	94.0	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
44	c1vddC_	Alignment	not modelled	93.7	35	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
45	d1vdda_	Alignment	not modelled	93.7	35	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
46	d1szpa1	Alignment	not modelled	93.6	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
47	d1cuka2	Alignment	not modelled	93.2	36	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
48	c1d8IA_	Alignment	not modelled	93.2	36	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
49	c1ixrB_	Alignment	not modelled	93.1	32	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
50	c2owoA_	Alignment	not modelled	93.1	33	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
51	c2bcuA_	Alignment	not modelled	93.0	16	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 t:t mismatch
52	c5zvqA_	Alignment	not modelled	92.8	38	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
53	d1x2ia1	Alignment	not modelled	92.8	15	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
54	d1kfta_	Alignment	not modelled	92.7	11	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
55	c1kftA_	Alignment	not modelled	92.7	11	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
56	c3c1zA_	Alignment	not modelled	92.7	22 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 damage sensor2 protein
57	c1mkmA_	Alignment	not modelled	92.5	17 PDB header: transcription Chain: A: PDB Molecule: iclr transcriptional regulator; PDBTitle: crystal structure of the thermotoga maritima iclr
58	c2ihmA_	Alignment	not modelled	92.4	19 PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
59	c5z2vB_	Alignment	not modelled	92.4	38 PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
60	d2a1jb1	Alignment	not modelled	92.4	18 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
61	c3auoB_	Alignment	not modelled	92.3	26 PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
62	d2i1qa1	Alignment	not modelled	92.0	13 Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
63	d2duya1	Alignment	not modelled	91.8	35 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
64	d2edua1	Alignment	not modelled	91.8	17 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
65	c1kdhA_	Alignment	not modelled	91.5	5 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
66	c4qlxA_	Alignment	not modelled	91.4	33 PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
67	d1pzna1	Alignment	not modelled	91.4	19 Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
68	d2hr3a1	Alignment	not modelled	90.3	24 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
69	c1b22A_	Alignment	not modelled	90.0	13 PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
70	d1b22a_	Alignment	not modelled	90.0	13 Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
71	c2bhnD_	Alignment	not modelled	90.0	19 PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
72	d1ku9a_	Alignment	not modelled	89.8	14 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding protein Mj223
73	c1hjpA_	Alignment	not modelled	89.5	30 PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
74	c5h1aC_	Alignment	not modelled	89.3	15 PDB header: transcription regulator Chain: C: PDB Molecule: iclr transcription factor homolog; PDBTitle: crystal structure of an iclr homolog from microbacterium sp. strain2 hm58-2
75	d2axtu1	Alignment	not modelled	89.3	14 Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
76	d3bzka1	Alignment	not modelled	89.2	16 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HHH-containing domain-like
77	c2h09A_	Alignment	not modelled	89.2	14 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
78	c1f5tA_	Alignment	not modelled	89.1	16 PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
79	c1s5lu_	Alignment	not modelled	88.9	14 PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
80	c2it0A_	Alignment	not modelled	88.9	16 PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
81	c1dgsB_	Alignment	not modelled	88.8	19 PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
					PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor,

82	c5o19A_	Alignment	not modelled	88.4	4	mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
83	c5jbrA_	Alignment	not modelled	88.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bcav_2135; PDBTitle: crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
84	c3mq0A_	Alignment	not modelled	87.4	24	PDB header: transcription repressor Chain: A: PDB Molecule: transcriptional repressor of the blcabc operon; PDBTitle: crystal structure of agobacterium tumefaciens repressor blcr
85	c4bxoA_	Alignment	not modelled	87.4	10	PDB header: hydrolase/dna Chain: A: PDB Molecule: fanconi anemia group m protein; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
86	c2kp7A_	Alignment	not modelled	86.7	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
87	c3psfA_	Alignment	not modelled	86.3	17	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)
88	c5y6iB_	Alignment	not modelled	86.0	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of pseudomonas aeruginosa hmgr
89	c2o0yB_	Alignment	not modelled	85.9	23	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
90	c2va8A_	Alignment	not modelled	85.9	18	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
91	c6gmhM_	Alignment	not modelled	85.8	23	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
92	c1v9pB_	Alignment	not modelled	85.4	19	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
93	c2xroE_	Alignment	not modelled	85.4	13	PDB header: dna-binding protein/dna Chain: E: PDB Molecule: hth-type transcriptional regulator ttgv; PDBTitle: crystal structure of ttgv in complex with its dna operator
94	c1fx7C_	Alignment	not modelled	85.2	16	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
95	d1z6ra1	Alignment	not modelled	85.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
96	c5w1eA_	Alignment	not modelled	84.8	21	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: pobr in complex with phb
97	c6cmvA_	Alignment	not modelled	84.8	18	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator lrs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from2 sulfolobus acidocaldarius
98	c5whmB_	Alignment	not modelled	84.7	12	PDB header: transcription Chain: B: PDB Molecule: iclr family transcriptional regulator; PDBTitle: crystal structure of iclr family transcriptional regulator from2 brucella abortus
99	c6iv7B_	Alignment	not modelled	84.6	20	PDB header: transferase Chain: B: PDB Molecule: methyltransferase lepi; PDBTitle: the crystal structure of a sam-dependent enzyme from aspergillus2 flavus
100	c5zb8B_	Alignment	not modelled	84.4	7	PDB header: dna binding protein Chain: B: PDB Molecule: pfuendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
101	d1tw3a1	Alignment	not modelled	84.3	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Plant O-methyltransferase, N-terminal domain
102	d1z05a1	Alignment	not modelled	84.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
103	c2lyhA_	Alignment	not modelled	83.9	19	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
104	c2oceA_	Alignment	not modelled	83.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
105	c2g7uB_	Alignment	not modelled	83.5	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
106	d2fbha1	Alignment	not modelled	83.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
107	c4bxoB_	Alignment	not modelled	83.2	19	PDB header: hydrolase/dna Chain: B: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex

108	c1nomA_	Alignment	not modelled	82.7	29	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)
109	c5cviB_	Alignment	not modelled	82.3	13	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
110	c3psiA_	Alignment	not modelled	82.3	17	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)
111	c2x4hA_	Alignment	not modelled	82.0	10	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus
112	d1szpb1	Alignment	not modelled	81.9	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
113	d1g3wa1	Alignment	not modelled	81.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
114	c2i5hA_	Alignment	not modelled	81.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
115	d2i5ha1	Alignment	not modelled	81.7	24	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like
116	c4nb5D_	Alignment	not modelled	81.5	20	PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator
117	c4o6jA_	Alignment	not modelled	81.5	13	PDB header: metal binding protein Chain: A: PDB Molecule: iron-dependent transcription repressor related protein; PDBTitle: crystal sturcture of t. acidophilum ider
118	c2csdB_	Alignment	not modelled	81.4	25	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
119	c5agaA_	Alignment	not modelled	81.2	12	PDB header: transferase Chain: A: PDB Molecule: dna polymerase theta; PDBTitle: crystal structure of the helicase domain of human dna2 polymerase theta in complex with ampnp
120	c3deuB_	Alignment	not modelled	80.8	19	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator slya; PDBTitle: crystal structure of transcription regulatory protein slya from2 salmonella typhimurium in complex with salicylate ligands