

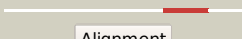

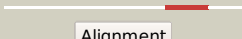

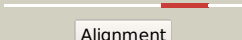

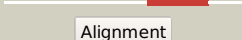
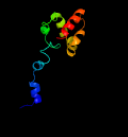


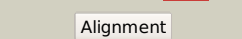

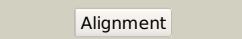

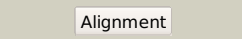

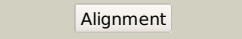

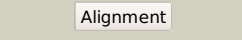



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2415c_(- )_2712901_2713794
Date	Wed Aug 7 12:50:03 BST 2019
Unique Job ID	cbb9130136e011da

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ol9A_</a>	 Alignment		99.8	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor, mitochondrial; <b>PDBTitle:</b> structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
2	<a href="#">d3bzka1</a>	 Alignment		99.8	32	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Tex HhH-containing domain-like
3	<a href="#">d2edua1</a>	 Alignment		99.7	32	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> ComEA-like
4	<a href="#">d2duya1</a>	 Alignment		99.7	47	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> ComEA-like
5	<a href="#">c1s5lu_</a>	 Alignment		99.7	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> U: <b>PDB Molecule:</b> photosystem ii 12 kda extrinsic protein; <b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center
6	<a href="#">d2axtu1</a>	 Alignment		99.7	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> PsbU/PolX domain-like <b>Family:</b> PsbU-like
7	<a href="#">c2oceA_</a>	 Alignment		99.6	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa5201; <b>PDBTitle:</b> crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
8	<a href="#">c6gmhM_</a>	 Alignment		99.4	24	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription elongation factor spt6,transcription <b>PDBTitle:</b> structure of activated transcription complex pol ii-dsif-paf-spt6
9	<a href="#">c3psiA_</a>	 Alignment		99.4	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt6; <b>PDBTitle:</b> crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
10	<a href="#">c3psfA_</a>	 Alignment		99.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt6; <b>PDBTitle:</b> crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
11	<a href="#">c2j58G_</a>	 Alignment		98.7	24	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> outer membrane lipoprotein wza; <b>PDBTitle:</b> the structure of wza

12	<a href="#">c2w8iG_</a>	Alignment		98.5	24	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> putative outer membrane lipoprotein wza; <b>PDBTitle:</b> crystal structure of wza24-345.
13	<a href="#">d2bgwa1</a>	Alignment		98.5	25	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
14	<a href="#">d1x2ia1</a>	Alignment		98.2	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
15	<a href="#">c1kfta_</a>	Alignment		98.1	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit c; <b>PDBTitle:</b> solution structure of the c-terminal domain of uvrc from e-2 coli
16	<a href="#">d1kfta_</a>	Alignment		98.1	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Excinuclease UvrC C-terminal domain
17	<a href="#">c5vtmX_</a>	Alignment		98.1	33	<b>PDB header:</b> transport protein <b>Chain:</b> X: <b>PDB Molecule:</b> type ii secretion system protein k; <b>PDBTitle:</b> the crystal structure of minor pseudopilin ternary complex of xcpvwx2 from the type 2 secretion system of pseudomonas aeruginosa
18	<a href="#">d2i1qa1</a>	Alignment		97.6	32	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
19	<a href="#">c3ci0K_</a>	Alignment		97.6	23	<b>PDB header:</b> protein transport <b>Chain:</b> K: <b>PDB Molecule:</b> pseudopilin gspk; <b>PDBTitle:</b> the crystal structure of the gspk-gspi-gspj complex from2 enterotoxigenic escherichia coli type 2 secretion system
20	<a href="#">c2hnhA_</a>	Alignment		97.6	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii alpha subunit; <b>PDBTitle:</b> crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
21	<a href="#">c2bcuA_</a>	Alignment	not modelled	97.6	23	<b>PDB header:</b> transferase, lyase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase lambda; <b>PDBTitle:</b> dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
22	<a href="#">d1pzna1</a>	Alignment	not modelled	97.5	28	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
23	<a href="#">c3p42D_</a>	Alignment	not modelled	97.5	28	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
24	<a href="#">d3ci0k2</a>	Alignment	not modelled	97.5	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> GspK insert domain-like <b>Family:</b> GspK insert domain-like
25	<a href="#">c3e0dA_</a>	Alignment	not modelled	97.4	27	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
26	<a href="#">c5lewA_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> dna polymerase
27	<a href="#">c3f2cA_</a>	Alignment	not modelled	97.4	31	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> geobacillus kaustophilus dna polc; <b>PDBTitle:</b> dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1531; <b>PDBTitle:</b> crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
28	<a href="#">c2i5hA_</a>	Alignment	not modelled	97.4	36	

29	<a href="#">d2i5ha1</a>	Alignment	not modelled	97.4	36	<b>Fold:</b> AF1531-like <b>Superfamily:</b> AF1531-like <b>Family:</b> AF1531-like
30	<a href="#">c3auoB_</a>	Alignment	not modelled	97.4	29	<b>PDB header:</b> transferase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase beta family (x family); <b>PDBTitle:</b> dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
31	<a href="#">d2a1jb1</a>	Alignment	not modelled	97.3	15	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
32	<a href="#">c1ixrA_</a>	Alignment	not modelled	97.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruva; <b>PDBTitle:</b> ruva-ruvb complex
33	<a href="#">c8iczA_</a>	Alignment	not modelled	97.3	33	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase beta (e.c.2.7.7.7)); <b>PDBTitle:</b> dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with 2 seven base pairs of dna; soaked in the presence of datp3 (1 millimolar), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
34	<a href="#">c5xf9E_</a>	Alignment	not modelled	97.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nad-reducing hydrogenase; <b>PDBTitle:</b> crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
35	<a href="#">d1cuka2</a>	Alignment	not modelled	97.3	26	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> DNA helicase RuvA subunit, middle domain
36	<a href="#">c5fkvA_</a>	Alignment	not modelled	97.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
37	<a href="#">c6q9gD_</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit f; <b>PDBTitle:</b> crystal structure of reduced aquifex aeolicus nadh-quinone2 oxidoreductase subunits nuo e g129d and nuof bound to nadh
38	<a href="#">d2fug13</a>	Alignment	not modelled	97.2	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Nqo1 middle domain-like <b>Family:</b> Nqo1 middle domain-like
39	<a href="#">d1ixra1</a>	Alignment	not modelled	97.2	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> DNA helicase RuvA subunit, middle domain
40	<a href="#">c2w9mB_</a>	Alignment	not modelled	97.1	25	<b>PDB header:</b> dna replication <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase x; <b>PDBTitle:</b> structure of family x dna polymerase from deinococcus2 radiodurans
41	<a href="#">c5lc5F_</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] flavoprotein 1, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
42	<a href="#">c1kdhA_</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> terminal deoxynucleotidyltransferase short <b>PDBTitle:</b> binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
43	<a href="#">c2zj8A_</a>	Alignment	not modelled	97.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ski2-type helicase; <b>PDBTitle:</b> archaeal dna helicase hjm apo state in form 2
44	<a href="#">c2ihmA_</a>	Alignment	not modelled	96.9	25	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase mu; <b>PDBTitle:</b> polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
45	<a href="#">c2mutA_</a>	Alignment	not modelled	96.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna excision repair protein ercc-1; <b>PDBTitle:</b> solution structure of the f231l mutant ercc1-xpf dimerization region
46	<a href="#">d1bvsa2</a>	Alignment	not modelled	96.9	33	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> DNA helicase RuvA subunit, middle domain
47	<a href="#">d1dgsa1</a>	Alignment	not modelled	96.8	16	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> NAD+-dependent DNA ligase, domain 3
48	<a href="#">c2fuga_</a>	Alignment	not modelled	96.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 1; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
49	<a href="#">d2aq0a1</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Hef domain-like
50	<a href="#">c4bxoA_</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> fanconi anemia group m protein; <b>PDBTitle:</b> architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
51	<a href="#">c1d8IA_</a>	Alignment	not modelled	96.6	26	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> protein (holliday junction dna helicase ruva); <b>PDBTitle:</b> e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
52	<a href="#">c2h5xA_</a>	Alignment	not modelled	96.4	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruva; <b>PDBTitle:</b> ruva from mycobacterium tuberculosis
53	<a href="#">c2nrzB_</a>	Alignment	not modelled	96.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uvrabc system protein c; <b>PDBTitle:</b> crystal structure of the c-terminal half of uvr c bound to its2 catalytic divalent cation

54	<a href="#">c1ixrB</a>	Alignment	not modelled	96.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction dna helicase ruva; <b>PDBTitle:</b> ruva-ruvb complex
55	<a href="#">c1hjpA</a>	Alignment	not modelled	96.1	26	<b>PDB header:</b> dna recombination <b>Chain:</b> A: <b>PDB Molecule:</b> ruva; <b>PDBTitle:</b> holliday junction binding protein ruva from e. coli
56	<a href="#">d1szpa1</a>	Alignment	not modelled	96.0	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
57	<a href="#">c2bhnD</a>	Alignment	not modelled	96.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> xpf endonuclease; <b>PDBTitle:</b> xpf from aeropyrum pernix
58	<a href="#">c4bxoB</a>	Alignment	not modelled	95.6	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fanconi anemia-associated protein of 24 kda; <b>PDBTitle:</b> architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
59	<a href="#">d2fmpa1</a>	Alignment	not modelled	95.6	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
60	<a href="#">d1jmsa1</a>	Alignment	not modelled	95.4	11	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
61	<a href="#">c4p4oA</a>	Alignment	not modelled	95.4	28	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase beta; <b>PDBTitle:</b> crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
62	<a href="#">c2lyhA</a>	Alignment	not modelled	95.3	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fanconi anemia-associated protein of 24 kda; <b>PDBTitle:</b> structure of faap24 residues 141-215
63	<a href="#">d1b22a</a>	Alignment	not modelled	95.1	17	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
64	<a href="#">c1b22A</a>	Alignment	not modelled	95.1	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> rad51 (n-terminal domain)
65	<a href="#">c2csdB</a>	Alignment	not modelled	94.5	29	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> topoisomerase v; <b>PDBTitle:</b> crystal structure of topoisomerase v (61 kda fragment)
66	<a href="#">c1dgsB</a>	Alignment	not modelled	94.4	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of nad+-dependent dna ligase from t.2 filiformis
67	<a href="#">c1v9pB</a>	Alignment	not modelled	94.3	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of nad+-dependent dna ligase
68	<a href="#">c2owoA</a>	Alignment	not modelled	94.2	21	<b>PDB header:</b> ligase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
69	<a href="#">c4glxA</a>	Alignment	not modelled	94.2	25	<b>PDB header:</b> ligase/ligase inhibitor/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> dna ligase a in complex with inhibitor
70	<a href="#">d3ci0k1</a>	Alignment	not modelled	94.2	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> GspK insert domain-like <b>Family:</b> GspK insert domain-like
71	<a href="#">d2p6ra2</a>	Alignment	not modelled	94.0	19	<b>Fold:</b> Sec63 N-terminal domain-like <b>Superfamily:</b> Sec63 N-terminal domain-like <b>Family:</b> Achaeal helicase C-terminal domain
72	<a href="#">c2p6uA</a>	Alignment	not modelled	93.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> afuhel308 helicase; <b>PDBTitle:</b> apo structure of the hel308 superfamily 2 helicase
73	<a href="#">c6flqF</a>	Alignment	not modelled	92.4	19	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> transcription termination/antitermination protein nusa; <b>PDBTitle:</b> cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
74	<a href="#">d1szpb1</a>	Alignment	not modelled	91.4	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
75	<a href="#">c6h5hA</a>	Alignment	not modelled	91.1	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> polb4; <b>PDBTitle:</b> a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
76	<a href="#">c1rrqA</a>	Alignment	not modelled	90.7	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> muty; <b>PDBTitle:</b> muty adenine glycosylase in complex with dna containing an2 a:oxog pair
77	<a href="#">c2kp7A</a>	Alignment	not modelled	90.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crossover junction endonuclease mus81; <b>PDBTitle:</b> solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
78	<a href="#">c1vddC</a>	Alignment	not modelled	90.2	38	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recombinational repair protein recr
79	<a href="#">d2bccq1</a>	Alignment	not modelled	90.0	24	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
80	<a href="#">c5zvqA</a>	Alignment	not modelled	89.9	43	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> recombination protein recr;

						<b>PDBTitle:</b> crystal structure of recombination mediator protein recr
81	<a href="#">d1vdda_</a>	Alignment	not modelled	89.9	38	<b>Fold:</b> Recombination protein RecR <b>Superfamily:</b> Recombination protein RecR <b>Family:</b> Recombination protein RecR
82	<a href="#">c5z2vB_</a>	Alignment	not modelled	89.9	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recr from pseudomonas aeruginosa pao1
83	<a href="#">d1mpga1</a>	Alignment	not modelled	89.6	24	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> DNA repair glycosylase, 2 C-terminal domains
84	<a href="#">d1pu6a_</a>	Alignment	not modelled	89.4	39	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> 3-Methyladenine DNA glycosylase III (MagIII)
85	<a href="#">d2fmpa2</a>	Alignment	not modelled	89.3	21	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> PsbU/PoIX domain-like <b>Family:</b> DNA polymerase beta-like, second domain
86	<a href="#">c4itqA_</a>	Alignment	not modelled	88.9	24	<b>PDB header:</b> gene regulation, structural protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sco1480; <b>PDBTitle:</b> crystal structure of hypothetical protein sco1480 bound to dna
87	<a href="#">d1dk2a_</a>	Alignment	not modelled	88.9	12	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
88	<a href="#">d1nzpa_</a>	Alignment	not modelled	88.7	24	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> DNA polymerase beta, N-terminal domain-like <b>Family:</b> DNA polymerase beta, N-terminal domain-like
89	<a href="#">c4unfA_</a>	Alignment	not modelled	88.6	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease iii-1; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans endonuclease iii-1
90	<a href="#">c3c1zA_</a>	Alignment	not modelled	88.6	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna integrity scanning protein disa; <b>PDBTitle:</b> structure of the ligand-free form of a bacterial dna damage sensor2 protein
91	<a href="#">d1kg2a_</a>	Alignment	not modelled	88.4	48	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
92	<a href="#">d2vana1</a>	Alignment	not modelled	88.3	22	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> PsbU/PoIX domain-like <b>Family:</b> DNA polymerase beta-like, second domain
93	<a href="#">c1mpgB_</a>	Alignment	not modelled	88.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyladenine dna glycosylase ii; <b>PDBTitle:</b> 3-methyladenine dna glycosylase ii from escherichia coli
94	<a href="#">d1keaa_</a>	Alignment	not modelled	88.0	32	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
95	<a href="#">d1rrqa1</a>	Alignment	not modelled	87.3	26	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Mismatch glycosylase
96	<a href="#">d1wg8a1</a>	Alignment	not modelled	87.2	37	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Putative methyltransferase TM0872, insert domain <b>Family:</b> Putative methyltransferase TM0872, insert domain
97	<a href="#">d1jmsa3</a>	Alignment	not modelled	86.8	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> PsbU/PoIX domain-like <b>Family:</b> DNA polymerase beta-like, second domain
98	<a href="#">c4p6vA_</a>	Alignment	not modelled	86.7	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit a; <b>PDBTitle:</b> crystal structure of the na <sup>+</sup> -translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
99	<a href="#">d2abka_</a>	Alignment	not modelled	86.7	36	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> Endonuclease III
100	<a href="#">c1wg8B_</a>	Alignment	not modelled	85.6	37	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted s-adenosylmethionine-dependent <b>PDBTitle:</b> crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
101	<a href="#">d1d8ba_</a>	Alignment	not modelled	85.6	4	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> HRDC domain from helicases
102	<a href="#">d2bcqa2</a>	Alignment	not modelled	85.0	25	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> PsbU/PoIX domain-like <b>Family:</b> DNA polymerase beta-like, second domain
103	<a href="#">c3tkaA_</a>	Alignment	not modelled	84.9	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase h; <b>PDBTitle:</b> crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
104	<a href="#">c3n5nX_</a>	Alignment	not modelled	84.5	50	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> a/g-specific adenine dna glycosylase; <b>PDBTitle:</b> crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
105	<a href="#">c4uobA_</a>	Alignment	not modelled	84.3	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease iii-3; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans endonuclease iii-3
106	<a href="#">d1orna_</a>	Alignment	not modelled	83.4	36	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase

					<b>Family:</b> Endonuclease III
107	<a href="#">d1a77a1</a>	Alignment	not modelled	82.8	38 <b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
108	<a href="#">c2va8A_</a>	Alignment	not modelled	82.1	23 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ski2-type helicase; <b>PDBTitle:</b> dna repair helicase hel308
109	<a href="#">c3zddA_</a>	Alignment	not modelled	81.6	23 <b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein xni; <b>PDBTitle:</b> structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
110	<a href="#">c5lm7A_</a>	Alignment	not modelled	81.5	21 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination/antitermination protein nusA; <b>PDBTitle:</b> crystal structure of the lambda n-nus factor complex
111	<a href="#">c4b24A_</a>	Alignment	not modelled	80.5	20 <b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> probable dna-3-methyladenine glycosylase 2; <b>PDBTitle:</b> unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
112	<a href="#">c1ut8B_</a>	Alignment	not modelled	80.4	24 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exodeoxyribonuclease; <b>PDBTitle:</b> divalent metal ions (zinc) bound to t5 5'-exonuclease
113	<a href="#">d1rxwa1</a>	Alignment	not modelled	80.3	13 <b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
114	<a href="#">c2jhnB_</a>	Alignment	not modelled	79.7	23 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyladenine dna-glycosylase; <b>PDBTitle:</b> 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
115	<a href="#">c2ziuA_</a>	Alignment	not modelled	78.2	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mus81 protein; <b>PDBTitle:</b> crystal structure of the mus81-eme1 complex
116	<a href="#">c3f10A_</a>	Alignment	not modelled	77.4	33 <b>PDB header:</b> hydrolase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-oxoguanine-dna-glycosylase; <b>PDBTitle:</b> crystal structure of clostridium acetobutylicum 8-oxoguanine dna2 glycosylase in complex with 8-oxoguanosine
117	<a href="#">c5e27B_</a>	Alignment	not modelled	76.6	30 <b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> resuscitation-promoting factor rpfb; <b>PDBTitle:</b> the structure of resuscitation promoting factor b from m. tuberculosis2 reveals unexpected ubiquitin-like domains
118	<a href="#">c1rxvA_</a>	Alignment	not modelled	76.5	13 <b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> flap structure-specific endonuclease; <b>PDBTitle:</b> crystal structure of a. fulgidus fen-1 bound to dna
119	<a href="#">c6c34A_</a>	Alignment	not modelled	75.8	33 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-3' exonuclease; <b>PDBTitle:</b> mycobacterium smegmatis dna flap endonuclease mutant d125n
120	<a href="#">d1ul1x1</a>	Alignment	not modelled	75.7	25 <b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain