Phyre^2

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Description	P0A8G0
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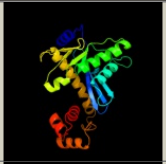
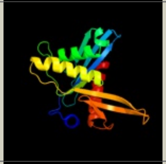
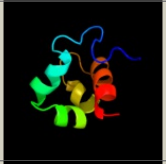
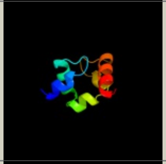
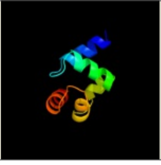
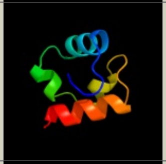
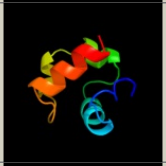
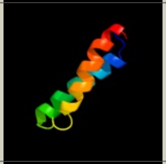
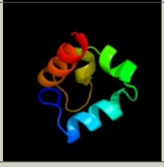
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nrzB_	Alignment		100.0	38	**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
2	c3c65A_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of bacillus stearothermophilus uvrc 5'2 endonuclease domain
3	c2nrrA_	Alignment		100.0	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal rnaseh endonuclase2 domain of uvrc
4	c1yd2A_	Alignment		99.9	34	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrc from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
5	c2wshC_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
6	c1yd6A_	Alignment		99.9	48	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrc; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
7	d1kfta_	Alignment		99.4	100	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
8	c1kftA_	Alignment		99.4	100	**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
9	d1x2ia1	Alignment		99.2	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
10	d2aq0a1	Alignment		99.2	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
11	d2bgwa1	Alignment		99.2	30	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like

12	d2a1jb1	Alignment		99.2	28	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
13	d2i1qa1	Alignment		98.9	27	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
14	d1pzna1	Alignment		98.8	35	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
15	d1mk0a_	Alignment		98.7	20	**Fold:**GIY-YIG endonuclease **Superfamily:**GIY-YIG endonuclease **Family:**GIY-YIG endonuclease
16	d1dgsa1	Alignment		98.7	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
17	c2bhnD_	Alignment		98.6	30	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xpf endonuclease; **PDBTitle:** xpf from aeropyrum pernix
18	d1szpa1	Alignment		98.5	15	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
19	d1e52a_	Alignment		98.5	37	**Fold:**Long alpha-hairpin **Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
20	c2owoA_	Alignment		98.4	31	**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
21	c1dgsB_	Alignment	not modelled	98.4	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
22	c1ixrA_	Alignment	not modelled	98.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
23	c1v9pB_	Alignment	not modelled	98.4	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
24	d1b22a_	Alignment	not modelled	98.3	21	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
25	c1b22A_	Alignment	not modelled	98.3	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
26	d1cuka2	Alignment	not modelled	98.2	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
27	d1ixra1	Alignment	not modelled	98.1	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
28	c3c1zA_	Alignment	not modelled	98.1	26	**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
29	d1szpb1	Alignment	not modelled	97.8	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like

						Family:DNA repair protein Rad51, N-terminal domain
30	c1hjpA_	Alignment	not modelled	97.8	31	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
31	c1d8lA_	Alignment	not modelled	97.8	31	**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
32	c2h5xA_	Alignment	not modelled	97.7	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
33	d1bvsa2	Alignment	not modelled	97.7	28	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
34	c2w36B_	Alignment	not modelled	97.5	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
35	c2va8A_	Alignment	not modelled	97.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
36	c2p6uA_	Alignment	not modelled	97.3	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
37	d2a1ja1	Alignment	not modelled	97.3	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
38	c3dlbA_	Alignment	not modelled	97.2	18	**PDB header:**nucleic acid binding protein/dna **Chain:** A: **PDB Molecule:**argonaute; **PDBTitle:** crystal structure of the guide-strand-containing argonaute2 protein silencing complex
39	d1qoja_	Alignment	not modelled	97.1	44	**Fold:**Long alpha-hairpin **Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
40	c1s5lu_	Alignment	not modelled	97.0	20	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
41	d2axtu1	Alignment	not modelled	96.9	20	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
42	c2d7dB_	Alignment	not modelled	96.9	32	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**40-mer from uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
43	d2p6ra2	Alignment	not modelled	96.8	16	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
44	c3ga2A_	Alignment	not modelled	96.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
45	c2csdB_	Alignment	not modelled	96.5	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
46	c3gocB_	Alignment	not modelled	96.5	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
47	c2izoA_	Alignment	not modelled	96.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** structure of an archaeal pcna1-pcna2-fen1 complex
48	c2ihmA_	Alignment	not modelled	96.4	10	**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
49	d1xo1a1	Alignment	not modelled	96.1	23	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
50	c2ziuA_	Alignment	not modelled	96.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mus81 protein; **PDBTitle:** crystal structure of the mus81-eme1 complex
51	c1ut8B_	Alignment	not modelled	95.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** divalent metal ions (zinc) bound to t5 5'-exonuclease
52	d2duya1	Alignment	not modelled	95.9	25	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
53	d1a77a1	Alignment	not modelled	95.8	23	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
54	c1kdhA_	Alignment	not modelled	95.8	18	**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
55	c2w9mB_	Alignment	not modelled	95.4	33	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x;

		Alignment	not modelled			**PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
56	d1ul1x1	Alignment	not modelled	95.4	27	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
57	d2edua1	Alignment	not modelled	95.3	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
58	c3mr2A_	Alignment	not modelled	95.3	10	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
59	d1rxwa1	Alignment	not modelled	95.2	26	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
60	c3nicA_	Alignment	not modelled	95.1	40	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**eco29kir; **PDBTitle:** dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
61	d3bzka1	Alignment	not modelled	95.1	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
62	c2zixA_	Alignment	not modelled	95.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81; **PDBTitle:** crystal structure of the mus81-eme1 complex
63	d1mc8a1	Alignment	not modelled	94.8	15	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
64	d1b43a1	Alignment	not modelled	94.8	15	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
65	c8iczA_	Alignment	not modelled	94.8	26	**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)
66	c1ywlA_	Alignment	not modelled	94.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0213 protein ef2693; **PDBTitle:** solution nmr structure of the protein ef2693 from e.2 faecalis: northeast structural genomics consortium target3 efr36
67	c2aq4A_	Alignment	not modelled	94.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
68	d2csba4	Alignment	not modelled	94.1	33	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
69	c3q8lA_	Alignment	not modelled	94.0	30	**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+
70	c1zg2A_	Alignment	not modelled	93.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0213 protein bh0048; **PDBTitle:** solution nmr structure of the upf0213 protein bh0048 from2 bacillus halodurans. northeast structural genomics target3 bhr2.
71	c1rxvA_	Alignment	not modelled	93.8	24	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** crystal structure of a. fulgidus fen-1 bound to dna
72	c2bcuA_	Alignment	not modelled	93.6	17	**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
73	c1a77A_	Alignment	not modelled	93.5	24	**PDB header:**5'-3' exo/endo nuclease **Chain:** A: **PDB Molecule:**flap endonuclease-1 protein; **PDBTitle:** flap endonuclease-1 from methanococcus jannaschii
74	c1b43A_	Alignment	not modelled	93.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (fen-1); **PDBTitle:** fen-1 from p. furiosus
75	c1nomA_	Alignment	not modelled	93.2	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)
76	d1cmwa1	Alignment	not modelled	92.9	31	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
77	d2csba3	Alignment	not modelled	92.8	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
78	c1ul1Y_	Alignment	not modelled	92.6	30	**PDB header:**hydrolase/dna binding protein **Chain:** Y: **PDB Molecule:**flap endonuclease-1; **PDBTitle:** crystal structure of the human fen1-pcna complex
79	d2q0zx1	Alignment	not modelled	92.4	7	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Sec63 N-terminal domain
80	d1t94a2	Alignment	not modelled	92.3	18	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
81			not modelled	92.0	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna processing chain a;

81	c3majA_	Alignment	not modelled	92.0	22	**PDBTitle:** crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
82	c1cmwA_	Alignment	not modelled	91.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
83	c2r8kB_	Alignment	not modelled	91.6	13	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
84	c3im2A_	Alignment	not modelled	91.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing helicase brr2; **PDBTitle:** structure of the c-terminal sec63 unit of yeast brr2, p41212 form
85	c2oceA_	Alignment	not modelled	91.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
86	c3oryA_	Alignment	not modelled	91.1	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
87	c1t3nB_	Alignment	not modelled	91.1	22	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**polymerase (dna directed) iota; **PDBTitle:** structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
88	c3gqcB_	Alignment	not modelled	90.4	12	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
89	d2bcqa1	Alignment	not modelled	90.4	23	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
90	c1jihA_	Alignment	not modelled	90.1	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
91	c2fllA_	Alignment	not modelled	89.3	24	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp
92	d1u04a2	Alignment	not modelled	88.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
93	c2d7dA_	Alignment	not modelled	88.5	37	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
94	c3psiA_	Alignment	not modelled	87.2	14	**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)
95	d1u9la_	Alignment	not modelled	86.9	16	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**NusA extra C-terminal domains
96	d1jmsa1	Alignment	not modelled	86.3	7	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
97	d1jx4a2	Alignment	not modelled	86.1	18	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
98	d2fmpa1	Alignment	not modelled	85.7	42	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
99	d1jiha2	Alignment	not modelled	85.2	17	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
100	d2uubb1	Alignment	not modelled	85.1	19	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
101	d1w9ha1	Alignment	not modelled	85.1	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
102	d2i5ha1	Alignment	not modelled	85.0	19	**Fold:**AF1531-like **Superfamily:**AF1531-like **Family:**AF1531-like
103	c2i5hA_	Alignment	not modelled	85.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1531; **PDBTitle:** crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
104	d1nzpa_	Alignment	not modelled	84.8	38	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
105	c3psfA_	Alignment	not modelled	84.8	15	**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)
106	d1kg2a_	Alignment	not modelled	84.7	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
107	d2csba1	Alignment	not modelled	83.2	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
						Fold:DNA-glycosylase

108	d1pu6a_	Alignment	not modelled	83.1	18	**Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
109	d1lb2b_	Alignment	not modelled	83.0	12	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
110	c2w42A_	Alignment	not modelled	82.8	12	**PDB header:**protein/dna complex **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the structure of a piwi protein from archaeoglobus fulgidus2 complexed with a 16nt dna duplex.
111	c2oh2B_	Alignment	not modelled	82.6	14	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
112	d1cooa_	Alignment	not modelled	82.2	12	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
113	d1k1sa2	Alignment	not modelled	80.7	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
114	d1dk2a_	Alignment	not modelled	79.6	38	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
115	c3qeaZ_	Alignment	not modelled	78.8	14	**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)
116	d2gy9b1	Alignment	not modelled	78.6	16	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
117	c2kp7A_	Alignment	not modelled	76.5	21	**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
118	d1keaa_	Alignment	not modelled	76.3	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
119	c3bbnB_	Alignment	not modelled	75.3	17	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
120	d1doqa_	Alignment	not modelled	75.2	21	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit