Phyre^2

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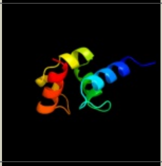
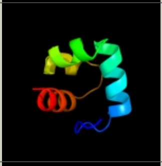
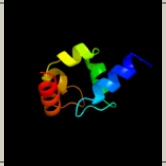
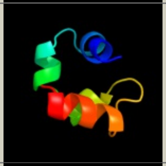
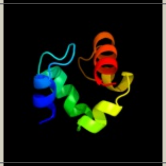
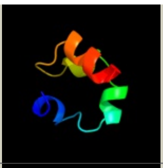
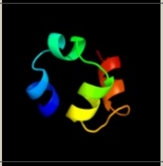
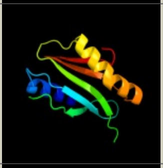
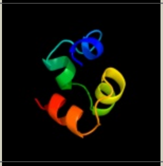
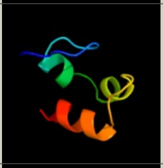
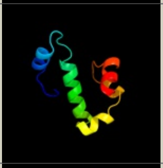
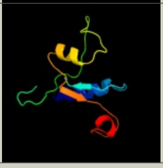
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qlcC_	Alignment		100.0	31	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein radc homolog; **PDBTitle:** the crystal structure of dna repair protein radc from chlorobium2 tepidum tls
2	d2bgwa1	Alignment		98.2	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
3	c3c1zA_	Alignment		98.0	14	**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
4	d1x2ia1	Alignment		98.0	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
5	d2a1jb1	Alignment		97.8	25	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
6	c2bhnD_	Alignment		97.7	32	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xpf endonuclease; **PDBTitle:** xpf from aeropyrum pernix
7	c1kftA_	Alignment		97.6	22	**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
8	d1kfta_	Alignment		97.6	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
9	d1dgsa1	Alignment		97.2	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
10	c2owoA_	Alignment		96.8	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
11	c1dgsB_	Alignment		96.8	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis

12	d2i1qa1	Alignment		96.7	15	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
13	c2nrzB_	Alignment		96.7	26	**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
14	d1oi0a_	Alignment		96.6	18	**Fold:**Cytidine deaminase-like **Superfamily:**JAB1/MPN domain **Family:**JAB1/MPN domain
15	c1v9pB_	Alignment		96.5	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
16	d1pzna1	Alignment		96.4	15	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
17	d1szpa1	Alignment		96.1	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
18	d2aq0a1	Alignment		96.1	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
19	d1pu6a_	Alignment		95.7	19	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
20	c2kcqA_	Alignment		95.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mov34/mpn/pad-1 family; **PDBTitle:** solution structure of protein sru_2040 from salinibacter2 ruber (strain dsm 13855) . northeast structural genomics3 consortium target srr106
21	d1szpb1	Alignment	not modelled	95.3	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
22	d1b22a_	Alignment	not modelled	95.1	15	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
23	c1b22A_	Alignment	not modelled	95.1	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
24	c1ixrA_	Alignment	not modelled	95.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
25	c1hjpA_	Alignment	not modelled	94.7	19	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
26	c1rrqA_	Alignment	not modelled	94.2	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
27	d1cuka2	Alignment	not modelled	93.7	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
28	c2kksA_	Alignment	not modelled	93.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein dsy2949 from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr27
						Fold:SAM domain-like

29	d1ixra1	Alignment	not modelled	92.0	18	**Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
30	c2h5xA_	Alignment	not modelled	91.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
31	c1yqmA_	Alignment	not modelled	91.5	27	**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
32	c3n5nX_	Alignment	not modelled	91.3	14	**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
33	d1ngna_	Alignment	not modelled	90.4	19	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
34	d2noha1	Alignment	not modelled	89.9	22	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
35	d2abka_	Alignment	not modelled	89.8	15	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
36	d1rrqa1	Alignment	not modelled	89.8	16	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
37	c1ko9A_	Alignment	not modelled	89.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**8-oxoguanine dna glycosylase; **PDBTitle:** native structure of the human 8-oxoguanine dna glycosylase2 hogg1
38	c3f10A_	Alignment	not modelled	89.7	13	**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
39	d1orna_	Alignment	not modelled	89.7	15	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
40	d1kg2a_	Alignment	not modelled	89.4	13	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
41	d1keaa_	Alignment	not modelled	89.1	17	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
42	c1d8lA_	Alignment	not modelled	88.7	21	**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
43	d1lb2b_	Alignment	not modelled	88.2	10	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
44	d1z3eb1	Alignment	not modelled	87.7	20	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
45	d1doqa_	Alignment	not modelled	86.6	24	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
46	d1cooa_	Alignment	not modelled	85.7	10	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
47	d1bvsa2	Alignment	not modelled	85.1	21	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
48	c2w6rA_	Alignment	not modelled	84.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit **PDBTitle:** crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
49	d1u9la_	Alignment	not modelled	81.6	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**NusA extra C-terminal domains
50	d1mpga1	Alignment	not modelled	78.9	13	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
51	d2axtu1	Alignment	not modelled	78.6	9	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
52	c1s5lu_	Alignment	not modelled	78.6	9	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
53	d3bzka1	Alignment		78.0	6	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
54	c3fhgA_	Alignment	not modelled	76.5	13	**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	d2duya1	Alignment	not modelled	75.5	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
56	d2csba4	Alignment	not modelled	74.3	21	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
57	c3s6iA_	Alignment	not modelled	73.0	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosylase 1; **PDBTitle:** schizosaccaromyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
58	c3tdmD_	Alignment	not modelled	72.9	13	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
59	d2a1ja1	Alignment	not modelled	71.5	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
60	d2edua1	Alignment	not modelled	70.9	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
61	c2yciX_	Alignment	not modelled	68.1	12	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
62	d1d8ba_	Alignment	not modelled	67.4	12	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
63	c3e49A_	Alignment	not modelled	66.0	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849 with a tim barrel fold; **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bxe_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
64	c2jhnB_	Alignment	not modelled	64.4	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase; **PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
65	d2e1fa1	Alignment	not modelled	63.4	16	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
66	c3n0uB_	Alignment	not modelled	62.9	21	**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
67	d2fmpa1	Alignment	not modelled	59.6	7	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
68	c3jrkG_	Alignment	not modelled	59.0	21	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
69	d2csua1	Alignment	not modelled	57.0	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
70	c2yg8B_	Alignment	not modelled	54.7	21	**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
71	d2bcqa1	Alignment	not modelled	54.6	22	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
72	d1f6ya_	Alignment	not modelled	52.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
73	d1jmsa1	Alignment	not modelled	51.0	19	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
74	d1wuda1	Alignment	not modelled	50.3	21	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
75	d1ka9f_	Alignment	not modelled	49.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
76	d2csba1	Alignment	not modelled	49.1	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
77	c3lotC_	Alignment	not modelled	47.3	25	**PDB header:**structure genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
78	c3c6cA_	Alignment	not modelled	44.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
79	d1nzpa_	Alignment	not modelled	44.2	21	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
80	c3q94B_	Alignment	not modelled	40.9	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate

						aldolase from2 bacillus anthracis str. 'ames ancestor'
81	c2bcuA_	Alignment	not modelled	39.5	21	**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
82	d1gvfa_	Alignment	not modelled	38.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
83	d1xo1a1	Alignment	not modelled	38.9	27	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
84	c3op1A_	Alignment	not modelled	38.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
85	c3e02A_	Alignment	not modelled	38.4	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849; **PDBTitle:** crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
86	d2odgc1	Alignment	not modelled	38.2	27	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
87	d1oxja2	Alignment	not modelled	37.9	12	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**PHAT domain
88	c1nomA_	Alignment	not modelled	37.8	28	**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)
89	c3kntC_	Alignment	not modelled	37.2	14	**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
90	c1wcnA_	Alignment	not modelled	36.5	17	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** nmr structure of the carboxyterminal domains of escherichia2 coli nusa
91	c2csdB_	Alignment	not modelled	36.4	50	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
92	c3c52B_	Alignment	not modelled	35.7	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
93	d1gjja2	Alignment	not modelled	35.2	19	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
94	c2iswB_	Alignment	not modelled	34.8	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
95	c3pm6B_	Alignment	not modelled	34.8	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
96	c1kdhA_	Alignment	not modelled	34.8	19	**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
97	c3k13A_	Alignment	not modelled	34.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
98	d1i94m_	Alignment	not modelled	34.0	20	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
99	c2rrdA_	Alignment	not modelled	33.9	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hrdc domain from bloom syndrome protein; **PDBTitle:** structure of hrdc domain from human bloom syndrome protein, blm
100	d2gy9m1	Alignment	not modelled	33.4	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
101	c3iz6M_	Alignment	not modelled	33.4	15	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s18 (s13p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
102	d1dk2a_	Alignment	not modelled	33.1	7	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
103	c3av0A_	Alignment	not modelled	32.7	24	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
104	c2xznM_	Alignment	not modelled	32.4	22	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**rps18e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
						PDB header:hydrolase

105	c1mpgB_	Alignment	not modelled	32.0	12	**Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
106	c2zkqm_	Alignment	not modelled	29.7	15	**PDB header:**ribosomal protein/rna **Chain:** M: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
107	d1rvga_	Alignment	not modelled	29.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
108	c2y7eA_	Alignment	not modelled	29.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
109	c8iczA_	Alignment	not modelled	28.8	7	**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)
110	d1jeia_	Alignment	not modelled	28.6	25	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
111	d1hl9a2	Alignment	not modelled	28.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
112	c3chvA_	Alignment	not modelled	27.8	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
113	d1h5ya_	Alignment	not modelled	27.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
114	d2uubm1	Alignment	not modelled	26.7	22	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
115	d1b43a1	Alignment	not modelled	26.7	26	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
116	c3majA_	Alignment	not modelled	26.6	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna processing chain a; **PDBTitle:** crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
117	c3t18D_	Alignment	not modelled	26.4	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
118	d1mc8a1	Alignment	not modelled	26.4	43	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
119	c1ut8B_	Alignment	not modelled	26.4	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** divalent metal ions (zinc) bound to t5 5'-exonuclease
120	d1ii7a_	Alignment	not modelled	26.3	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease