



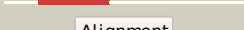











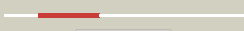












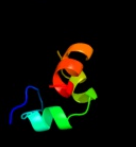
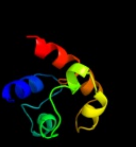


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P31337
Date	Tue Jul 17 17:05:10 BST 2012
Unique Job ID	8de979157a004c5f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qlcC_	 Alignment		100.0	44	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 t1s
2	d2bgwa1	 Alignment		98.2	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
3	c3c1zA_	 Alignment		98.0	19	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	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
5	d2a1jb1	 Alignment		97.7	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
6	c2bhnD_	 Alignment		97.6	21	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
7	c1kftA_	 Alignment		97.6	27	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	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
9	d1dgsa1	 Alignment		97.1	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
10	d2i1qa1	 Alignment		96.7	14	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
11	c2nrzB_	 Alignment		96.7	15	PDB header: hydrolase Chain: B: PDB Molecule: uvrc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation

12	c2owoA	Alignment		96.6	18	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
13	c1dgsB	Alignment		96.6	21	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
14	d1pzna1	Alignment		96.5	23	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
15	d2aq0a1	Alignment		96.5	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
16	d1oi0a	Alignment		96.4	28	Fold: Cytidine deaminase-like Superfamily: JAB1/MPN domain Family: JAB1/MPN domain
17	c1v9pB	Alignment		96.3	19	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
18	c1ixrA	Alignment		96.1	19	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
19	d1szpa1	Alignment		96.0	26	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
20	d1cuka2	Alignment		95.6	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
21	c1hjpA	Alignment	not modelled	95.5	21	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
22	c1b22A	Alignment	not modelled	95.2	20	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
23	d1b22a	Alignment	not modelled	95.2	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
24	d1szpb1	Alignment	not modelled	95.0	25	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
25	c2kcgA	Alignment	not modelled	95.0	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
26	c2kksA	Alignment	not modelled	94.8	17	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
27	c1d81A	Alignment	not modelled	94.6	25	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
28	c2h5xA	Alignment	not modelled	94.6	17	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva;

						PDBTitle: ruva from mycobacterium tuberculosis
29	dlixra1	Alignment	not modelled	94.5	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
30	d1pu6a	Alignment	not modelled	94.5	23	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
31	d1ngna	Alignment	not modelled	93.0	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
32	d1rrqa1	Alignment	not modelled	92.1	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
33	c1rrqA	Alignment	not modelled	91.9	11	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
34	d1kg2a	Alignment	not modelled	91.7	11	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
35	d1keaa	Alignment	not modelled	91.6	14	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
36	c3n5nX	Alignment	not modelled	91.6	13	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
37	d1bvsa2	Alignment	not modelled	91.5	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
38	d2abka	Alignment	not modelled	90.9	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
39	d1orna	Alignment	not modelled	90.6	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
40	c1yqmA	Alignment	not modelled	89.1	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
41	d1lb2b	Alignment	not modelled	88.7	20	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
42	d1z3eb1	Alignment	not modelled	87.8	32	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
43	c1ko9A	Alignment	not modelled	86.6	20	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
44	d1doqa	Alignment	not modelled	86.3	27	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
45	d1cooa	Alignment	not modelled	85.7	20	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
46	c3f10A	Alignment	not modelled	85.1	18	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
47	c2w6rA	Alignment	not modelled	82.1	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
48	d1u9la	Alignment	not modelled	78.1	23	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: NusA extra C-terminal domains
49	d1mpga1	Alignment	not modelled	75.2	7	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
50	c1s5lu	Alignment	not modelled	75.1	18	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
51	c3s6iA	Alignment	not modelled	74.8	15	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.
52	d2axtu1	Alignment	not modelled	74.2	18	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
53	d3bzka1	Alignment	not modelled	73.8	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
54	d2duya1	Alignment	not modelled	72.4	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
55	d2a1ja1	Alianment	not modelled	72.2	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like

						Family: Hef domain-like
56	c3tdmD	Alignment	not modelled	71.4	11	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
57	c3fhgA	Alignment	not modelled	70.4	19	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)
58	d2csba4	Alignment	not modelled	69.6	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
59	d1f6ya	Alignment	not modelled	69.4	23	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
60	c2jhnB	Alignment	not modelled	66.3	10	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
61	d2csba1	Alignment	not modelled	62.3	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
62	c3gzaB	Alignment	not modelled	62.3	10	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
63	c2yciX	Alignment	not modelled	61.3	22	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
64	c3n0uB	Alignment	not modelled	61.2	25	PDB header: hydrolase, lyase Chain: B: PDB Molecule: probable n-glycosylase/dna lyase; PDBTitle: crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima
65	c3auoB	Alignment	not modelled	60.8	15	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
66	c3q94B	Alignment	not modelled	60.1	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'
67	c2yg8B	Alignment	not modelled	59.8	23	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
68	d2edua1	Alignment	not modelled	59.8	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
69	d2noha1	Alignment	not modelled	58.7	12	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
70	d2e1fa1	Alignment	not modelled	58.2	12	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
71	d1d8ba	Alignment	not modelled	57.9	3	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
72	d1gvfa	Alignment	not modelled	57.4	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
73	c3eypB	Alignment	not modelled	57.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
74	c3c52B	Alignment	not modelled	55.1	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
75	d2fmpa1	Alignment	not modelled	54.5	21	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
76	c2iswB	Alignment	not modelled	54.4	11	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-bi-phosphate aldolase in2 complex with phosphoglycolohydroxamate
77	c2wvsD	Alignment	not modelled	54.3	18	PDB header: hydrolase Chain: D: PDB Molecule: alpha-l-fucosidase; PDBTitle: crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
78	d2csua1	Alignment	not modelled	53.1	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
79	c3pm6B	Alignment	not modelled	51.9	25	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-bi-phosphate aldolase from2 coccidioides immitis solved by combined sad mr
80	c3mo4B	Alignment	not modelled	50.6	19	PDB header: hydrolase Chain: B: PDB Molecule: alpha-1,3/4-fucosidase; PDBTitle: the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697

81	c1wcnA	Alignment	not modelled	50.3	29	PDB header: rna-binding protein Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: nmr structure of the carboxyterminal domains of escherichia2 coli nusa
82	c3jrkG	Alignment	not modelled	49.6	13	PDB header: lyase Chain: G: PDB Molecule: tagatose 1,6-diphosphate aldolase 2; PDBTitle: a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
83	d2bcqa1	Alignment	not modelled	49.6	26	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
84	d1rvga	Alignment	not modelled	49.3	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
85	c1mpgB	Alignment	not modelled	47.3	10	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
86	d1hl9a2	Alignment	not modelled	46.7	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Putative alpha-L-fucosidase, catalytic domain
87	d1wuda1	Alignment	not modelled	41.9	18	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
88	d1ka9f	Alignment	not modelled	41.6	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
89	d1nzpa	Alignment	not modelled	39.7	26	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
90	d1jmsa1	Alignment	not modelled	39.6	22	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
91	c3e49A	Alignment	not modelled	37.9	22	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 (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
92	c3elfA	Alignment	not modelled	37.5	16	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
93	c1nomA	Alignment	not modelled	37.1	53	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)
94	c3k13A	Alignment	not modelled	37.0	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
95	c3majA	Alignment	not modelled	36.2	6	PDB header: dna binding protein Chain: A: PDB Molecule: dna processing chain a; PDBTitle: crystal structure of putative dna processing protein dpra from2 rhodospseudomonas palustris cga009
96	c2csdB	Alignment	not modelled	34.9	22	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
97	c3qm3C	Alignment	not modelled	33.9	11	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
98	c2bcuA	Alignment	not modelled	33.9	25	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a tt mismatch
99	c2rrdA	Alignment	not modelled	33.4	14	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	c3op1A	Alignment	not modelled	33.3	15	PDB header: transferase Chain: A: PDB Molecule: macrolide-efflux protein; PDBTitle: crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
101	d1dosa	Alignment	not modelled	32.9	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
102	d1gjja2	Alignment	not modelled	32.2	22	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
103	d2p6ra2	Alignment	not modelled	31.5	20	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
104	c3stgA	Alignment	not modelled	30.9	9	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-oculonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
105	d1h5ya	Alignment	not modelled	29.4	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel

				Family:Histidine biosynthesis enzymes		
106	c3kntC_	Alignment	not modelled	29.0	18	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
107	c2ziuA_	Alignment	not modelled	28.9	18	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
108	d1jeia_	Alignment	not modelled	28.5	22	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
109	d1dk2a_	Alignment	not modelled	28.3	21	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
110	d1i94m_	Alignment	not modelled	27.2	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
111	d2odqc1	Alignment	not modelled	27.0	22	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
112	c3lotC_	Alignment	not modelled	25.6	21	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
113	c1kdhA_	Alignment	not modelled	25.4	22	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
114	d2gy9m1	Alignment	not modelled	25.0	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
115	d1b43a1	Alignment	not modelled	24.6	54	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
116	d1xo1a1	Alignment	not modelled	24.6	15	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
117	c3iz6M_	Alignment	not modelled	24.3	20	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
118	d1mc8a1	Alignment	not modelled	24.2	54	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
119	d1a77a1	Alignment	not modelled	24.1	54	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
120	c2xznM_	Alignment	not modelled	23.7	28	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