



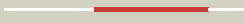






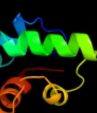












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2edua1	 Alignment		99.7	33	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
2	d3bzka1	 Alignment		99.7	34	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
3	d2duya1	 Alignment		99.7	42	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
4	c1s5lu_	 Alignment		99.7	20	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
5	d2axtu1	 Alignment		99.7	22	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
6	c2oceA_	 Alignment		99.4	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from pseudomonas aeruginosa
7	c3psiA_	 Alignment		99.1	20	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)
8	c3psfA_	 Alignment		99.0	21	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)
9	d2bgwa1	 Alignment		98.2	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
10	d1x2ia1	 Alignment		97.9	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
11	c1kftA_	 Alignment		97.8	29	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

12	d1kfta_	Alignment		97.8	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
13	d3ci0k2	Alignment		97.7	24	Fold: SAM domain-like Superfamily: GspK insert domain-like Family: GspK insert domain-like
14	c3ci0K_	Alignment		97.5	20	PDB header: protein transport Chain: K: PDB Molecule: pseudopilin gspk; PDBTitle: the crystal structure of the gspk-gspi-gspj complex from2 enterotoxigenic escherichia coli type 2 secretion system
15	d2i5ha1	Alignment		97.5	30	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like
16	c2i5hA_	Alignment		97.5	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
17	c2hnhA_	Alignment		97.4	27	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
18	c3f2cA_	Alignment		97.3	45	PDB header: transferase/dna Chain: A: PDB Molecule: geobacillus kaustophilus dna polc; PDBTitle: dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
19	c2bcuA_	Alignment		97.2	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
20	c3e0dA_	Alignment		97.2	33	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
21	d2i1qa1	Alignment	not modelled	97.2	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
22	d1pzna1	Alignment	not modelled	97.1	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
23	d1dgsa1	Alignment	not modelled	97.0	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
24	c8icza_	Alignment	not modelled	96.9	29	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)
25	d2a1jb1	Alignment	not modelled	96.9	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
26	clixrA_	Alignment	not modelled	96.8	30	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
27	c2w9mB_	Alignment	not modelled	96.7	27	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
28	d1cuka2	Alignment	not modelled	96.7	38	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain

29	dlixra1	Alignment	not modelled	96.5	37	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
30	dlszpa1	Alignment	not modelled	96.5	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
31	c1kdhA	Alignment	not modelled	96.4	17	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
32	d1bvsa2	Alignment	not modelled	96.3	32	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
33	c2ihmA	Alignment	not modelled	96.3	27	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
34	d2aq0a1	Alignment	not modelled	96.1	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
35	c1hjpA	Alignment	not modelled	96.1	40	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
36	c1d8lA	Alignment	not modelled	95.6	41	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
37	c2bhnD	Alignment	not modelled	95.6	26	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
38	c2h5xA	Alignment	not modelled	95.6	33	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
39	c1nomA	Alignment	not modelled	95.4	35	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)
40	c2nrzB	Alignment	not modelled	95.4	18	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
41	c1b22A	Alignment	not modelled	95.2	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
42	d1b22a	Alignment	not modelled	95.2	18	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
43	c1rrqA	Alignment	not modelled	94.7	17	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
44	d2p6ra2	Alignment	not modelled	94.1	23	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
45	d1kg2a	Alignment	not modelled	94.1	26	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
46	d1szpb1	Alignment	not modelled	94.1	26	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
47	d1jmsa1	Alignment	not modelled	94.0	16	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
48	c1wg8B	Alignment	not modelled	93.9	36	PDB header: transferase Chain: B: PDB Molecule: predicted s-adenosylmethionine-dependent PDBTitle: crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
49	c2p6uA	Alignment	not modelled	93.9	23	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
50	d1wg8a1	Alignment	not modelled	93.5	36	Fold: SAM domain-like Superfamily: Putative methyltransferase TM0872, insert domain Family: Putative methyltransferase TM0872, insert domain
51	d3ci0k1	Alignment	not modelled	93.1	17	Fold: SAM domain-like Superfamily: GspK insert domain-like Family: GspK insert domain-like
52	d2fmpa1	Alignment	not modelled	92.9	20	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
53	c2owoA	Alignment	not modelled	92.8	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
54	d1pu6a	Alignment	not modelled	92.8	24	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)

55	c1dgsB	Alignment	not modelled	92.7	22	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
56	c3n5nX	Alignment	not modelled	92.5	28	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
57	c1v9pB	Alignment	not modelled	92.5	21	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
58	d1rrqa1	Alignment	not modelled	92.0	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
59	d2bcqa1	Alignment	not modelled	91.6	22	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
60	c2csdB	Alignment	not modelled	91.5	27	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
61	c2kp7A	Alignment	not modelled	91.0	18	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
62	d1mpga1	Alignment	not modelled	90.7	26	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
63	d2abka	Alignment	not modelled	90.2	21	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
64	d1nzpa	Alignment	not modelled	90.2	22	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
65	d1orna	Alignment	not modelled	89.7	25	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
66	c1vddC	Alignment	not modelled	89.2	33	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
67	d2fmpa2	Alignment	not modelled	89.0	35	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
68	d1dk2a	Alignment	not modelled	89.0	20	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
69	d1vdda	Alignment	not modelled	88.9	33	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
70	d1keaa	Alignment	not modelled	88.2	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
71	c1ut8B	Alignment	not modelled	88.0	31	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
72	d1a77a1	Alignment	not modelled	87.5	33	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
73	d2vana1	Alignment	not modelled	87.4	38	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
74	d1rxwa1	Alignment	not modelled	87.0	25	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
75	c1mpgB	Alignment	not modelled	86.8	26	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
76	c1rxvA	Alignment	not modelled	86.2	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
77	c3n0uB	Alignment	not modelled	86.1	35	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
78	d2bcqa2	Alignment	not modelled	85.9	29	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
79	c3c1zA	Alignment	not modelled	85.2	23	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
80	d1m6ya1	Alignment	not modelled	85.1	35	Fold: SAM domain-like Superfamily: Putative methyltransferase TM0872, insert domain Family: Putative methyltransferase TM0872, insert domain
81	d1jmsa3	Alignment	not modelled	84.8	23	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
						Fold: SAM domain-like

82	dlul1x1	Alignment	not modelled	84.5	25	Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
83	dlcoa	Alignment	not modelled	83.9	26	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
84	dlxola1	Alignment	not modelled	83.8	33	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
85	c3s61a	Alignment	not modelled	82.5	30	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
86	d1lb2b	Alignment	not modelled	82.4	26	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
87	d2a1ja1	Alignment	not modelled	81.2	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
88	dlz3eb1	Alignment	not modelled	80.3	38	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
89	d1doqa	Alignment	not modelled	79.6	33	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
90	c2jhnB	Alignment	not modelled	79.6	33	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
91	c2ziuA	Alignment	not modelled	79.3	35	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
92	dlngna	Alignment	not modelled	79.2	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
93	d1d8ba	Alignment	not modelled	76.9	4	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
94	d1mc8a1	Alignment	not modelled	76.5	35	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
95	c3f10A	Alignment	not modelled	76.0	38	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
96	d1b43a1	Alignment	not modelled	75.0	42	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
97	c1a77A	Alignment	not modelled	74.8	33	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
98	d2noha1	Alignment	not modelled	74.4	29	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
99	c3kntC	Alignment	not modelled	74.2	27	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
100	d1u9la	Alignment	not modelled	73.6	25	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: NusA extra C-terminal domains
101	c2va8A	Alignment	not modelled	73.4	33	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
102	c3fhgA	Alignment	not modelled	73.1	25	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)
103	c1yqmA	Alignment	not modelled	72.8	30	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
104	c3q8lA	Alignment	not modelled	72.5	25	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+
105	c1ko9A	Alignment	not modelled	72.2	33	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
106	c2yg8B	Alignment	not modelled	72.1	24	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
107	c1ul1Y	Alignment	not modelled	71.1	25	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
108	c2h56C	Alignment	not modelled	69.8	21	PDB header: hydrolase Chain: C: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of dna-3-methyladenine glycosidase

					(10174367) from2 bacillus halodurans at 2.55 a resolution
109	d2ve8a1	Alignment	not modelled	69.7	23 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
110	c2izoA_	Alignment	not modelled	65.1	21 PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
111	d2uubm1	Alignment	not modelled	60.1	19 Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
112	d1cmwa1	Alignment	not modelled	60.0	30 Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
113	d2j5pa1	Alignment	not modelled	57.9	27 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
114	c1b43A_	Alignment	not modelled	54.0	41 PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
115	d2gy9m1	Alignment	not modelled	53.6	12 Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
116	c3f52A_	Alignment	not modelled	52.4	15 PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
117	d2e1fa1	Alignment	not modelled	51.0	26 Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
118	d1wuda1	Alignment	not modelled	50.8	25 Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
119	c2xznM_	Alignment	not modelled	50.5	11 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
120	c3rfaA_	Alignment	not modelled	50.1	8 PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine