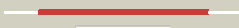






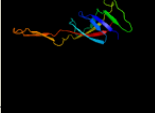


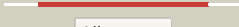



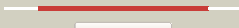
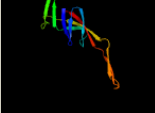

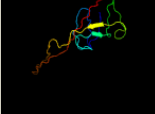
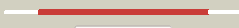
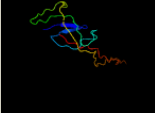

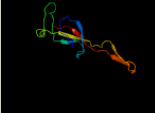
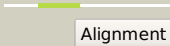
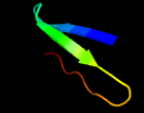
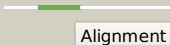
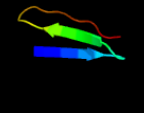
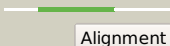


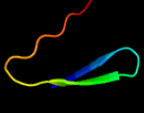

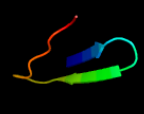
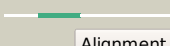
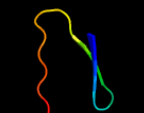
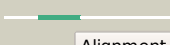
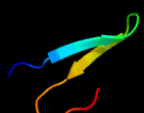

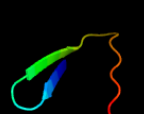


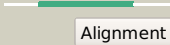



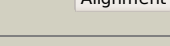
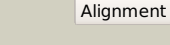
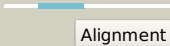



Phyre2

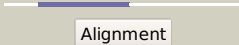
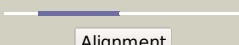
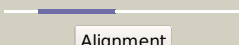
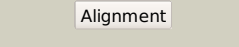
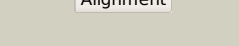
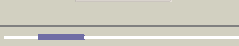

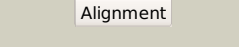
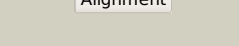
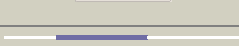

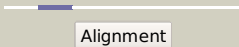
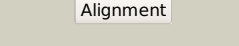



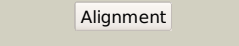
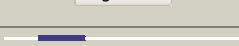



Email	mdejesus@rockefeller.edu
Description	RVBD2442c_(rplU)_2740057_2740371
Date	Wed Aug 7 12:50:06 BST 2019
Unique Job ID	4b36e290b38ec75f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60S_	 Alignment		100.0	88	PDB header: ribosome Chain: S; PDB Molecule: 50s ribosomal protein l21; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	c5mmiS_	 Alignment		100.0	29	PDB header: ribosome Chain: S; PDB Molecule: 50s ribosomal protein l21, chloroplastic; PDBTitle: structure of the large subunit of the chloroplast ribosome
3	c3j3vR_	 Alignment		100.0	40	PDB header: ribosome Chain: R; PDB Molecule: 50s ribosomal protein l21; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
4	c5mlcT_	 Alignment		100.0	29	PDB header: ribosome Chain: T; PDB Molecule: 50s ribosomal protein l21, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
5	d2qamr1	 Alignment		100.0	36	Fold: L21p-like Superfamily: L21p-like Family: Ribosomal protein L21p
6	c4v19V_	 Alignment		100.0	27	PDB header: ribosome Chain: V; PDB Molecule: mitoribosomal protein bl21m, mrpl21; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
7	c1vw4N_	 Alignment		100.0	20	PDB header: ribosome Chain: N; PDB Molecule: 54s ribosomal protein l49, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
8	c4ce4V_	 Alignment		100.0	27	PDB header: ribosome Chain: V; PDB Molecule: mrpl21; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
9	c3bboT_	 Alignment		100.0	30	PDB header: ribosome Chain: T; PDB Molecule: ribosomal protein l21; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
10	d2j01v1	 Alignment		100.0	46	Fold: L21p-like Superfamily: L21p-like Family: Ribosomal protein L21p
11	d2zjro1	 Alignment		100.0	46	Fold: L21p-like Superfamily: L21p-like Family: Ribosomal protein L21p

12	c5oo9A_	 Alignment		64.7	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative cupin_2 domain-containing isomerase; PDBTitle: streptomyces pac13 (y55f) with uridine
13	c2gu9B_	 Alignment		54.1	14	PDB header: immune system Chain: B: PDB Molecule: tetracenomycin polyketide synthesis protein; PDBTitle: crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
14	c3ossC_	 Alignment		50.0	24	PDB header: protein transport Chain: C: PDB Molecule: type 2 secretion system, gspc; PDBTitle: the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
15	c6nwoD_	 Alignment		48.2	29	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator bgar; PDBTitle: structures of the transcriptional regulator bgar, a lactose sensor.
16	c3ibmB_	 Alignment		46.9	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
17	c5j4fB_	 Alignment		46.8	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminally his6-tagged hp0902, an2 uncharacterized protein from helicobacter pylori 26695
18	c2ivwA_	 Alignment		46.7	24	PDB header: lipoprotein Chain: A: PDB Molecule: pilp pilot protein; PDBTitle: the solution structure of a domain from the neisseria meningitidis2 pilp pilot protein.
19	d2arca_	 Alignment		45.8	24	Fold: Double-stranded beta-helix Superfamily: Regulatory protein AraC Family: Regulatory protein AraC
20	c4h7lB_	 Alignment		44.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of plim_4148 protein from planctomyces limnophilus
21	c2lc4A_	 Alignment	not modelled	43.4	23	PDB header: structural protein Chain: A: PDB Molecule: pilp protein; PDBTitle: solution structure of pilp from pseudomonas aeruginosa
22	d1jala2	 Alignment	not modelled	40.9	39	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
23	c5tg0A_	 Alignment	not modelled	40.9	33	PDB header: lyase Chain: A: PDB Molecule: dimethylsulfoniopropionate lyase dddk; PDBTitle: crystal structure of the dimethylsulfoniopropionate (dmSP) lyase dddk2 complexed with iron and zinc
24	c3kgzA_	 Alignment	not modelled	40.2	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of a cupin 2 conserved barrel domain protein from2 rhodospseudomonas palustris
25	c4av2P_	 Alignment	not modelled	39.2	24	PDB header: protein transport Chain: P: PDB Molecule: pilp protein; PDBTitle: single particle electron microscopy of pilq dodecameric complexes from2 neisseria meningitidis.
26	c3d82A_	 Alignment	not modelled	38.7	9	PDB header: metal binding protein Chain: A: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
27	d1sq4a_	 Alignment	not modelled	37.5	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
28	d1sfna_	 Alignment	not modelled	36.2	24	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like

29	c2vpvA_	Alignment	not modelled	35.7	10	PDB header: cell cycle Chain: A: PDB Molecule: protein mif2; PDBTitle: dimerization domain of mif2p
30	c1sefA_	Alignment	not modelled	35.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
31	d1sefa_	Alignment	not modelled	35.6	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbaA-like
32	d1y9qa2	Alignment	not modelled	34.3	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Probable transcriptional regulator VC1968, C-terminal domain
33	d1vj2a_	Alignment	not modelled	34.2	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1459-like
34	c5u9eB_	Alignment	not modelled	33.5	14	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional activator rhar; PDBTitle: structure of the regulatory domain of the arac family transcriptional2 activator rhar
35	d1rc6a_	Alignment	not modelled	32.9	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbaA-like
36	c5uqpA_	Alignment	not modelled	32.6	29	PDB header: unknown function Chain: A: PDB Molecule: cupin; PDBTitle: the crystal structure of cupin protein from rhodococcus jostii rha1
37	c3cewA_	Alignment	not modelled	32.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized cupin protein; PDBTitle: crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
38	c4e2gE_	Alignment	not modelled	32.5	10	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of cupin fold protein sthe2323 from sphaerobacter2 thermophilus
39	c2lnvA_	Alignment	not modelled	30.4	25	PDB header: transport protein Chain: A: PDB Molecule: general secretion pathway protein c; PDBTitle: solution structure of gspc-hr of typeii secretion system
40	c3lwcA_	Alignment	not modelled	28.8	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
41	c3l2hD_	Alignment	not modelled	28.6	29	PDB header: isomerase Chain: D: PDB Molecule: putative sugar phosphate isomerase; PDBTitle: crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
42	c2ozjB_	Alignment	not modelled	27.2	19	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel; PDBTitle: crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
43	c3h7yA_	Alignment	not modelled	27.1	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: bacilysin biosynthesis protein bacb; PDBTitle: crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
44	c3fjsC_	Alignment	not modelled	26.0	19	PDB header: biosynthetic protein Chain: C: PDB Molecule: uncharacterized protein with rmlc-like cupin fold; PDBTitle: crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
45	d1yhfa1	Alignment	not modelled	25.2	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
46	c5fq0A_	Alignment	not modelled	25.2	19	PDB header: lyase Chain: A: PDB Molecule: kdgf; PDBTitle: the structure of kdgf from halomonas sp.
47	c3jzvA_	Alignment	not modelled	24.1	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rru_a2000; PDBTitle: crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
48	c4rd7A_	Alignment	not modelled	24.0	29	PDB header: unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: the crystal structure of a cupin 2 conserved barrel domain protein2 from salinispora arenicola cns-205
49	c4axoA_	Alignment	not modelled	23.1	14	PDB header: structural protein Chain: A: PDB Molecule: ethanolamine utilization protein; PDBTitle: structure of the clostridium difficile eutq protein
50	c4e2sE_	Alignment	not modelled	21.3	33	PDB header: hydrolase Chain: E: PDB Molecule: ureidoglycine aminohydrolase; PDBTitle: crystal structure of (s)-ureidoglycine aminohydrolase from arabidopsis2 thaliana in complex with its substrate, (s)-ureidoglycine
51	c2pfbB_	Alignment	not modelled	21.2	24	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
52	c5j7mB_	Alignment	not modelled	21.0	24	PDB header: unknown function Chain: B: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 conserved barrel domain protein from2 kribbella flavida dsm 17836
53	d1o4ta_	Alignment	not modelled	19.6	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like

54	c5ccbB_	 Alignment	not modelled	18.6	21	PDB header: transferase/rna non-catalytic Chain: B: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase PDBTitle: crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
55	c2ejgD_	 Alignment	not modelled	18.3	12	PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
56	c5zbfA_	 Alignment	not modelled	18.3	11	PDB header: isomerase Chain: A: PDB Molecule: cupin domain protein; PDBTitle: crystal structure of 4-hydroxyphenylpyruvic acid bound aere from2 microcystis aeruginosa
57	d1v70a_	 Alignment	not modelled	18.0	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
58	c3i7dB_	 Alignment	not modelled	17.7	10	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase; PDBTitle: crystal structure of sugar phosphate isomerase from a cupin2 superfamily spo2919 from silicibacter pomeroyi (yp_168127.1) from3 silicibacter pomeroyi dss-3 at 2.30 a resolution
59	c4i4aA_	 Alignment	not modelled	16.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: similar to unknown protein; PDBTitle: crystal structure of plu4264 protein from photorhabdus luminescens
60	d2pyta1	 Alignment	not modelled	15.9	27	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: EutQ-like
61	d2f4pa1	 Alignment	not modelled	15.8	24	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: TM1287-like
62	c5k2IA_	 Alignment	not modelled	15.6	33	PDB header: hydrolase Chain: A: PDB Molecule: chitinase, lysozyme; PDBTitle: crystal structure of lysm domain from volvox carteri chitinase
63	c6b8wB_	 Alignment	not modelled	15.4	11	PDB header: transcription Chain: B: PDB Molecule: xre family transcriptional regulator; PDBTitle: 1.9 angstrom resolution crystal structure of cupin_2 domain (pfam2 07883) of xre family transcriptional regulator from enterobacter3 cloacae.
64	c4npgA_	 Alignment	not modelled	14.4	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a hypothetical protein (bt1938) from bacteroides2 thetaiotaomicron vpi-5482 at 2.50 a resolution
65	d1uwwa_	 Alignment	not modelled	14.2	13	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 28 carbohydrate binding module, CBM28
66	c2go51_	 Alignment	not modelled	13.2	33	PDB header: translation/rna Chain: 1: PDB Molecule: signal recognition particle receptor alpha PDBTitle: structure of signal recognition particle receptor (sr) in2 complex with signal recognition particle (srp) and3 ribosome nascent chain complex
67	d2fh5a1	 Alignment	not modelled	13.0	33	Fold: Profilin-like Superfamily: SNARE-like Family: SRP alpha N-terminal domain-like
68	c2q30C_	 Alignment	not modelled	12.4	20	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a rmic-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
69	d1o5ua_	 Alignment	not modelled	12.0	41	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Hypothetical protein TM1112
70	c5nlaA_	 Alignment	not modelled	11.2	5	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator PDBTitle: crystal structure of the arac-like transcriptional activator cuxr
71	c3rnsA_	 Alignment	not modelled	10.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: cupin 2 conserved barrel domain protein from leptotrichia buccalis
72	c2i45C_	 Alignment	not modelled	10.4	23	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
73	c5bxxA_	 Alignment	not modelled	10.3	8	PDB header: lyase Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of the ectoine synthase from the cold-adapted marine2 bacterium sphingopyxis alaskensis
74	d1u0la1	 Alignment	not modelled	9.4	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
75	c5onoA_	Alignment	not modelled	9.2	22	PDB header: metal binding protein Chain: A: PDB Molecule: l-ectoine synthase; PDBTitle: crystal structure of ectoine synthase from p. lautus
76	c4la3B_	Alignment	not modelled	9.1	19	PDB header: lyase Chain: B: PDB Molecule: dimethylsulphoniopropionate (dmisp) lyase dddq; PDBTitle: crystal structure of dimethylsulphoniopropionate (dmisp) lyase dddq2 y131a in complex with dmisp
77	c3i0mA_	Alignment	not modelled	8.2	17	PDB header: cell cycle Chain: A: PDB Molecule: dna repair and telomere maintenance protein nbs1; PDBTitle: structure of the s. pombe nbs1 fha/brct-repeat domain PDB header: dna binding protein

78	c2wkdA	Alignment	not modelled	7.9	19	Chain: A: PDB Molecule: orf34p2; PDBTitle: crystal structure of a double ile-to-met mutant of protein orf34 from2 lactococcus phage p2
79	c3m9bk	Alignment	not modelled	7.7	14	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
80	d2b8ma1	Alignment	not modelled	7.7	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: MJ0764-like
81	c1d8lA	Alignment	not modelled	7.6	20	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
82	c2o8qA	Alignment	not modelled	7.4	5	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a protein with a cupin-like fold and unknown2 function (bx_e_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
83	d1tifa	Alignment	not modelled	7.3	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
84	d2fug33	Alignment	not modelled	7.0	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
85	c6ckaB	Alignment	not modelled	7.0	50	PDB header: viral protein Chain: B: PDB Molecule: paratox; PDBTitle: crystal structure of paratox
86	c3myxA	Alignment	not modelled	7.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pspto_0244; PDBTitle: crystal structure of the sixth cohesin from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
87	c5nrkA	Alignment	not modelled	6.8	27	PDB header: protein binding Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of the sixth cohesin from acetivibrio2 cellulolyticus' scaffoldin b in complex with cel5 dockerin s15i, i16n3 mutant
88	c3j8l1	Alignment	not modelled	6.8	19	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
89	d1dgwa	Alignment	not modelled	6.8	38	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
90	c2mkxA	Alignment	not modelled	6.8	31	PDB header: hydrolase Chain: A: PDB Molecule: autolysin; PDBTitle: solution structure of lysm the peptidoglycan binding domain of2 autolysin atla from enterococcus faecalis
91	c5fpzA	Alignment	not modelled	6.7	19	PDB header: hydrolase Chain: A: PDB Molecule: pectin degradation protein; PDBTitle: the structure of kdgf from yersinia enterocolitica with2 malonate bound in the active site.
92	d1a7ha	Alignment	not modelled	6.7	16	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Crystallins/Ca-binding development proteins
93	d1cuka3	Alignment	not modelled	6.7	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
94	c3accgA	Alignment	not modelled	6.6	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,4-endoglucanase; PDBTitle: crystal structure of carbohydrate-binding module family 28 from2 clostridium josui cel5a in complex with cellobiose
95	c1hjpA	Alignment	not modelled	6.4	20	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
96	d1hr0w	Alignment	not modelled	6.4	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
97	c2oqkA	Alignment	not modelled	6.2	31	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
98	d1jt8a	Alignment	not modelled	6.2	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
99	d2cqaa1	Alignment	not modelled	6.2	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain