





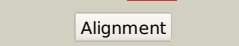



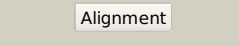
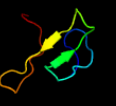
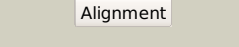

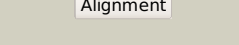
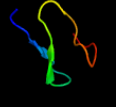
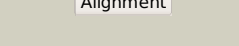

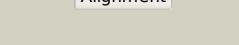

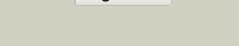

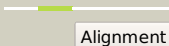
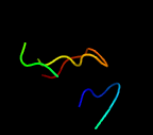
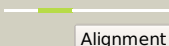


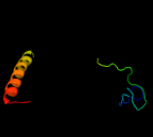



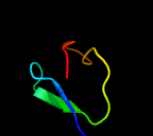







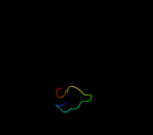
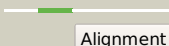


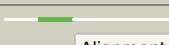



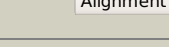


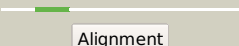
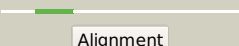

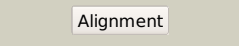
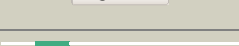
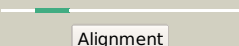

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2568c_(-)_2892456_2893481
Date	Wed Aug 7 12:50:20 BST 2019
Unique Job ID	1c99bafde09b759e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fpca_	 Alignment		96.7	23	PDB header: hydrolase Chain: A: PDB Molecule: pro-pro endopeptidase; PDBTitle: structure of the pro-pro endopeptidase (ppep-2) from paenibacillus2 alvei
2	c5a0sa_	 Alignment		96.1	26	PDB header: hydrolase Chain: A: PDB Molecule: zinc metalloprotease zmp1; PDBTitle: apo-structure of metalloprotease zmp1 variant e143a from clostridium2 difficile
3	c4l7aB_	 Alignment		95.2	50	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative zinc-binding metallo-peptidase2 (baccac_01431) from bacteroides caccae atcc 43185 at 2.10 a3 resolution
4	dlj7na2	 Alignment		94.1	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Anthrax toxin lethal factor, N- and C-terminal domains
5	c2l0ra_	 Alignment		87.1	28	PDB header: hydrolase,toxin Chain: A: PDB Molecule: lethal factor; PDBTitle: conformational dynamics of the anthrax lethal factor catalytic center
6	dlp91a_	 Alignment		71.9	26	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase RImA
7	c3hcb_	 Alignment		70.1	35	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: structure of msrb from xanthomonas campestris (oxidized2 form)
8	c2lk1A_	 Alignment		69.4	23	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 5; PDBTitle: solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
9	c2lk0A_	 Alignment		69.4	23	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 5; PDBTitle: solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
10	c1vzb_	 Alignment		68.9	22	PDB header: oxidoreductase Chain: B: PDB Molecule: desulfoferrodoxin; PDBTitle: structure of superoxide reductase bound to ferrocyanide and active2 site expansion upon x-ray induced photoreduction
11	c2l1uA_	 Alignment		67.8	30	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b2, mitochondrial; PDBTitle: structure-functional analysis of mammalian msrb2 protein

12	c3k7aM_	 Alignment		66.9	33	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
13	c3cezA_	 Alignment		61.7	34	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
14	c6f42V_	 Alignment		61.7	36	PDB header: transcription Chain: V: PDB Molecule: transcription factor iiib 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
15	c6ok1B_	 Alignment		61.3	29	PDB header: transport protein Chain: B: PDB Molecule: chsh2(duf35); PDBTitle: ltp2-chsh2(duf35) aldolase
16	c5iy9O_	 Alignment		61.0	27	PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)
17	c5mg5W_	 Alignment		59.6	23	PDB header: transferase Chain: W: PDB Molecule: 2,4-diacetylphloroglucinol biosynthesis protein; PDBTitle: a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (magg)
18	c5fa9B_	 Alignment		58.9	23	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
19	c2mxvA_	 Alignment		58.8	29	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 10; PDBTitle: nmr structure of the first zinc finger domain of rbm10
20	d2gnra1	 Alignment		58.7	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: SSO2064-like
21	c5fz5M_	 Alignment	not modelled	57.1	33	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
22	d2dsxa1	 Alignment	not modelled	56.8	36	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
23	c6et9H_	 Alignment	not modelled	56.3	16	PDB header: transferase Chain: H: PDB Molecule: pfam duf35; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
24	c4bpo9_	 Alignment	not modelled	55.5	28	PDB header: ribosome Chain: 9: PDB Molecule: 40s ribosomal protein rps31e; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 3
25	c4v1oM_	 Alignment	not modelled	54.9	33	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
26	c6cnbR_	 Alignment	not modelled	54.8	26	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iiib 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex
27	c3e0mB_	 Alignment	not modelled	54.6	30	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
28	c6o38A_	 Alignment	not modelled	51.4	71	PDB header: sugar binding protein Chain: A: PDB Molecule: acinetobacter secreted protease cpaa; PDBTitle: structure of a chaperone-substrate complex

29	c3g9yA_	 Alignment	not modelled	50.1	24	PDB header: transcription/rna Chain: A: PDB Molecule: zinc finger ran-binding domain-containing protein 2; PDBTitle: crystal structure of the second zinc finger from zranb2/znf265 bound2 to 6 nt nrna sequence agguaa
30	c2gb5B_	 Alignment	not modelled	50.1	15	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
31	c2pziA_	 Alignment	not modelled	49.8	38	PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
32	c3a44D_	 Alignment	not modelled	49.1	42	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
33	d2cu8a1	 Alignment	not modelled	49.0	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
34	c5oqjW_	 Alignment	not modelled	48.3	27	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
35	c5jy9M_	 Alignment	not modelled	48.2	29	PDB header: transcription, transferase/dna/rna Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: human holo-pic in the initial transcribing state (no iis)
36	d1bxa_	 Alignment	not modelled	48.1	22	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
37	c4ultN_	 Alignment	not modelled	47.8	21	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of verrucarin bound to the yeast 80s ribosome
38	c2f9iD_	 Alignment	not modelled	47.8	24	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
39	c5ijjA_	 Alignment	not modelled	47.8	38	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
40	c4uloO_	 Alignment	not modelled	47.6	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of phyllanthoside bound to the yeast 80s ribosome
41	c4ujjO_	 Alignment	not modelled	47.6	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of narciclasine bound to the yeast 80s ribosome
42	c4ul3O_	 Alignment	not modelled	47.6	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of geneticin bound to the yeast 80s ribosome
43	c4uldO_	 Alignment	not modelled	47.6	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of nagilactone c bound to the yeast 80s ribosome
44	c4ukoN_	 Alignment	not modelled	47.6	21	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of cryptopleurine bound to the yeast 80s ribosome
45	c4ul8O_	 Alignment	not modelled	47.6	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of homoharringtonine bound to the yeast 80s ribosome
46	c4uk3O_	 Alignment	not modelled	47.6	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of anisomycin bound to the yeast 80s ribosome
47	c4ujoO_	 Alignment	not modelled	47.6	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of lycorine bound to the yeast 80s ribosome
48	c4b6aW_	 Alignment	not modelled	47.4	21	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
49	c4ukjN_	 Alignment	not modelled	47.4	21	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of blasticidin s bound to the yeast 80s ribosome
50	c4byuW_	 Alignment	not modelled	47.4	21	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet2 eukaryotic translation initiation complex
51	c4ukeO_	 Alignment	not modelled	47.4	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of cycloheximide bound to the yeast 80s ribosome
52	c4ukyO_	 Alignment	not modelled	47.4	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of edeine bound to the yeast 80s ribosome
53	c3u5iW_	 Alignment	not modelled	47.4	21	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a

						resolution. this2 entry contains proteins of the 60s subunit, ribosome b
54	c4bynW_	Alignment	not modelled	47.4	21	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet eukaryotic2 translation initiation complex
55	c1vxvX_	Alignment	not modelled	47.4	21	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l24; PDBTitle: structures of yeast 80s ribosome-trna complexes in the rotated and2 non-rotated conformations (class ii - rotated ribosome with 1 trna,3 this entry contains the large ribosomal subunit proteins)
56	c4uk8O_	Alignment	not modelled	47.3	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of cca trinucleotide bound to the yeast 80s ribosome
57	c4ujtO_	Alignment	not modelled	47.3	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of lactimidomycin bound to the yeast 80s ribosome
58	c4uliO_	Alignment	not modelled	47.3	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of pactamycin bound to the yeast 80s ribosome
59	c4ujyN_	Alignment	not modelled	47.1	21	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of t-2 toxin bound to the yeast 80s ribosome
60	c3cngC_	Alignment	not modelled	46.7	25	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
61	c5flmI_	Alignment	not modelled	45.7	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
62	d1dl6a_	Alignment	not modelled	45.2	31	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
63	c3k1fM_	Alignment	not modelled	45.1	31	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
64	d1ltla_	Alignment	not modelled	45.1	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA replication initiator (cdc21/cdc54) N-terminal domain
65	c4uktO_	Alignment	not modelled	44.9	21	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of deoxynivalenol bound to the yeast 80s ribosome
66	c6g99B_	Alignment	not modelled	44.1	27	PDB header: rna binding protein Chain: B: PDB Molecule: rna-binding protein fus; PDBTitle: solution structure of fus-znf bound to uggug
67	d1ynjd1	Alignment	not modelled	43.8	43	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
68	c6gymW_	Alignment	not modelled	43.3	27	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccd1st)
69	c6o9lQ_	Alignment	not modelled	43.3	31	PDB header: transcription/dna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state
70	c5oqmW_	Alignment	not modelled	42.9	27	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
71	c3j39W_	Alignment	not modelled	42.8	18	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
72	c6fhjA_	Alignment	not modelled	42.0	28	PDB header: hydrolase Chain: A: PDB Molecule: protein,protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase, native.
73	d6rxna_	Alignment	not modelled	41.8	28	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
74	c5flmL_	Alignment	not modelled	41.3	18	PDB header: transcription Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc4; PDBTitle: structure of transcribing mammalian rna polymerase ii
75	c6k1hF_	Alignment	not modelled	41.3	21	PDB header: protein transport Chain: F: PDB Molecule: pts system mannose-specific eiid component; PDBTitle: structure of membrane protein
76	c1lttE_	Alignment	not modelled	41.3	39	PDB header: replication Chain: E: PDB Molecule: dna replication initiator (cdc21/cdc54); PDBTitle: the dodecamer structure of mcm from archaean m.2 thermoautotrophicum
77	d1imla1	Alignment	not modelled	40.9	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
78	c2xzn9_	Alignment	not modelled	40.8	31	PDB header: ribosome Chain: 9: PDB Molecule: rps31e; 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
79	c5x51X	Alignment	not modelled	40.7	14	PDB header: transferase Chain: X: PDB Molecule: rna polymerase subunit, found in rna polymerase complexes PDBTitle: rna polymerase ii from komagataella pastoris (type-3 crystal)
80	c2xzm9	Alignment	not modelled	40.6	31	PDB header: ribosome Chain: 9: PDB Molecule: rps31e; 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 1
81	c6j9eD	Alignment	not modelled	40.4	33	PDB header: transcription Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: cryo-em structure of xanthomonos oryzae transcription elongation2 complex with nusa and the bacteriophage protein p7
82	c2ja6L	Alignment	not modelled	40.3	18	PDB header: transferase Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii 7.7 kda PDBTitle: cpd lesion containing rna polymerase ii elongation complex b
83	c2owoA	Alignment	not modelled	38.9	36	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
84	d4rxna	Alignment	not modelled	38.6	28	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
85	c6fhnA	Alignment	not modelled	38.2	28	PDB header: hydrolase Chain: A: PDB Molecule: protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase (pt derivative)
86	c6hmsB	Alignment	not modelled	38.2	38	PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna polymerase ii large PDBTitle: cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
87	d1hfca	Alignment	not modelled	37.4	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
88	d1ctla1	Alignment	not modelled	37.1	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
89	c1n0zA	Alignment	not modelled	36.9	32	PDB header: transcription Chain: A: PDB Molecule: znf265; PDBTitle: solution structure of the first zinc-finger domain from2 znf265
90	d2k4xa1	Alignment	not modelled	36.3	29	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
91	c1s24A	Alignment	not modelled	35.8	28	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from pseudomonas oleovorans
92	d1s24a	Alignment	not modelled	35.8	28	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
93	d1m2ka	Alignment	not modelled	35.6	33	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
94	d1lroa	Alignment	not modelled	35.6	28	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
95	d1pfta	Alignment	not modelled	35.5	26	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
96	c3pkIF	Alignment	not modelled	35.5	22	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
97	c2v3bB	Alignment	not modelled	35.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex rubredoxin -2 rubredoxin reductase from pseudomonas aeruginosa.
98	d2apob1	Alignment	not modelled	35.0	37	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
99	d1smyd	Alignment	not modelled	34.1	36	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
100	d1vzia2	Alignment	not modelled	33.6	23	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulfiredoxin
101	d2rdva	Alignment	not modelled	33.4	28	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
102	d1iqca1	Alignment	not modelled	33.2	26	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
103	c4g7oN	Alignment	not modelled	33.1	43	PDB header: transcription, transferase/dna Chain: N: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure of thermus thermophilus transcription

						initiation2 complex containing 2 nt of rna
104	c2lo2A_	Alignment	not modelled	33.0	42	PDB header: transcription Chain: A: PDB Molecule: saga-associated factor 11; PDBTitle: solution structure of sgf11(63-99) zinc finger domain
105	c5x22D_	Alignment	not modelled	32.9	38	PDB header: transferase/dna Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: crystal structure of thermus thermophilus transcription initiation2 complex with gpa and cmppcp
106	c6em4u_	Alignment	not modelled	32.2	24	PDB header: ribosome Chain: U: PDB Molecule: PDBTitle: state b architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
107	c1i3qL_	Alignment	not modelled	32.0	25	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii 14.2kd PDBTitle: rna polymerase ii crystal form i at 3.1 a resolution
108	c3k35D_	Alignment	not modelled	31.3	22	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
109	d1dfxa2	Alignment	not modelled	31.0	23	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulfiredoxin
110	d1fbla2	Alignment	not modelled	30.8	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
111	c5zvqA_	Alignment	not modelled	30.3	30	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
112	c2kdxA_	Alignment	not modelled	30.2	25	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
113	c3izcZ_	Alignment	not modelled	29.8	21	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein rpl24 (l24e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
114	c3h0gL_	Alignment	not modelled	29.5	21	PDB header: transcription Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc4; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
115	c5an9G_	Alignment	not modelled	29.1	15	PDB header: translation Chain: G: PDB Molecule: 60s ribosomal protein l24; PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit
116	c4c2mX_	Alignment	not modelled	28.6	35	PDB header: transcription Chain: X: PDB Molecule: dna-directed rna polymerase i subunit rpa12; PDBTitle: structure of rna polymerase i at 2.8 a resolution
117	c4a1eT_	Alignment	not modelled	28.3	21	PDB header: ribosome Chain: T: PDB Molecule: rpl24; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
118	c3j65p_	Alignment	not modelled	27.8	24	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l5; PDBTitle: arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
119	c5o10B_	Alignment	not modelled	27.6	30	PDB header: hydrolase Chain: B: PDB Molecule: putative silent information regulator 2,putative silent PDBTitle: structure of leishmania infantum silent information regulator 22 related protein 1 (lisir2rp1) in complex with acetylated p53 peptide
120	d2fiya1	Alignment	not modelled	27.6	20	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like