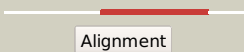

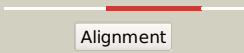



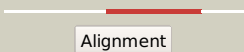

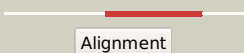
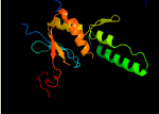
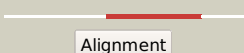







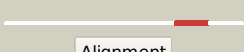

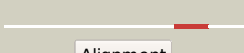



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2885c_(-)_3194176_3195558
Date	Thu Aug 8 16:20:03 BST 2019
Unique Job ID	d68b8b893d0ab2c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6e7aY_	 Alignment		98.9	20	PDB header: dna binding protein/dna/rna Chain: Y; PDB Molecule: casx; PDBTitle: casx-grna-dna(30bp) state ii
2	c5id6A_	 Alignment		98.5	17	PDB header: hydrolase Chain: A; PDB Molecule: cpf1; PDBTitle: structure of cpf1/rna complex
3	c5wtiZ_	 Alignment		98.4	18	PDB header: hydrolase/dna/rna Chain: Z; PDB Molecule: crispr-associated protein; PDBTitle: crystal structure of the crispr-associated protein in complex with2 crrna and dna
4	c6iv6A_	 Alignment		98.3	19	PDB header: immune system/rna Chain: A; PDB Molecule: nuclease; PDBTitle: cryo-em structure of acrva5-acetylated mbcas12a in complex with crrna
5	c5b43A_	 Alignment		98.2	22	PDB header: hydrolase/rna/dna Chain: A; PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: crystal structure of acidaminococcus sp. cpf1 in complex with crrna2 and target dna
6	c5mgaA_	 Alignment		98.1	19	PDB header: hydrolase Chain: A; PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: structure of the cpf1 endonuclease r-loop complex after dna cleavage
7	c5nfvA_	 Alignment		98.0	19	PDB header: hydrolase Chain: A; PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: crystal structure of catalytically inactive fncas12 mutant bound to an2 r-loop structure containing a pre-crrna mimic and full-length dna3 target
8	c5wqeA_	 Alignment		97.9	17	PDB header: rna binding protein Chain: A; PDB Molecule: crispr-associated endonuclease c2c1; PDBTitle: crystal structure of alicyclobacillus acidoterrestris c2c1 in complex2 with single-guide rna at 3.1 angstrom resolution
9	c5u31A_	 Alignment		97.4	21	PDB header: hydrolase/dna Chain: A; PDB Molecule: crispr-associated endonuclease c2c1; PDBTitle: crystal structure of aacc2c1-sgrna-8mer substrate dna ternary complex
10	c4u3eA_	 Alignment		95.1	16	PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
11	c2gb5B_	 Alignment		94.9	22	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

12	c1hk8A_	Alignment		94.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dntp
13	d1hk8a_	Alignment		94.9	12	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
14	c1yuzB_	Alignment		93.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
15	c3ky9B_	Alignment		92.8	16	PDB header: apoptosis Chain: B: PDB Molecule: proto-oncogene vav; PDBTitle: autoinhibited vav1
16	c2qa4Z_	Alignment		92.6	27	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
17	c2vrwB_	Alignment		92.5	18	PDB header: signaling protein Chain: B: PDB Molecule: proto-oncogene vav; PDBTitle: critical structural role for the ph and c1 domains of the2 vav1 exchange factor
18	c4a17Y_	Alignment		92.3	23	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
19	c4b6ap_	Alignment		92.2	27	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
20	d2akla2	Alignment		92.1	16	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
21	d1vqoz1	Alignment	not modelled	92.0	27	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
22	d1ffkw_	Alignment	not modelled	92.0	19	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
23	c3cc4Z_	Alignment	not modelled	91.9	27	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
24	c3izrm_	Alignment	not modelled	91.8	19	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l23 (l14p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
25	c5fz5M_	Alignment	not modelled	91.7	14	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
26	c3zf7o_	Alignment	not modelled	91.7	35	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
27	d1pfta_	Alignment	not modelled	91.7	21	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
28	c3j39p_	Alignment	not modelled	91.6	27	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
						PDB header: metal binding protein

29	c2lcqA_	Alignment	not modelled	91.6	12	Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
30	c5jy9M_	Alignment	not modelled	91.6	14	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)
31	c3j2i1_	Alignment	not modelled	91.6	31	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
32	c2zkrz_	Alignment	not modelled	91.5	27	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
33	c3bjia_	Alignment	not modelled	91.5	18	PDB header: signaling protein Chain: A: PDB Molecule: proto-oncogene vav; PDBTitle: structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
34	d1jj2y_	Alignment	not modelled	91.4	19	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
35	c6f42V_	Alignment	not modelled	91.4	15	PDB header: transcription Chain: V: PDB Molecule: transcription factor iib 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
36	c1yshD_	Alignment	not modelled	91.3	19	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
37	c2aklA_	Alignment	not modelled	91.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
38	c3k7aM_	Alignment	not modelled	91.2	18	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
39	c1s1i9_	Alignment	not modelled	90.6	27	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
40	c3k1fM_	Alignment	not modelled	89.7	15	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
41	c3jyw9_	Alignment	not modelled	89.7	27	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
42	c6cnbR_	Alignment	not modelled	89.6	15	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iib 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex
43	d1dl6a_	Alignment	not modelled	89.3	15	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
44	c4v1oM_	Alignment	not modelled	89.3	19	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
45	c5iy9Q_	Alignment	not modelled	89.1	22	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)
46	c2hr5B_	Alignment	not modelled	88.9	23	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
47	c4c2mX_	Alignment	not modelled	88.2	14	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
48	c2qkdA_	Alignment	not modelled	88.0	19	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
49	c3cngC_	Alignment	not modelled	87.5	22	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
50	c3zyqA_	Alignment	not modelled	87.5	21	PDB header: signaling Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
51	c5ijjA_	Alignment	not modelled	87.3	19	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
52	c3wwnB_	Alignment	not modelled	86.8	23	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
53	c1i3ql_	Alignment	not modelled	86.8	15	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

54	c1kcfB	Alignment	not modelled	86.8	14	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical 30.2 kd protein c25g10.02 in PDBTitle: crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
55	c1nnjA	Alignment	not modelled	86.6	15	PDB header: hydrolase Chain: A: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
56	c6g5iy	Alignment	not modelled	86.5	24	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
57	d1hjra	Alignment	not modelled	86.3	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
58	c1ee8A	Alignment	not modelled	86.3	26	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
59	d1twfi2	Alignment	not modelled	86.0	27	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
60	c1dvpA	Alignment	not modelled	85.8	20	PDB header: transferase Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine PDBTitle: crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
61	c2opfA	Alignment	not modelled	85.8	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
62	c5flml	Alignment	not modelled	85.7	17	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
63	c6hmsB	Alignment	not modelled	85.4	19	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
64	d1kcfA2	Alignment	not modelled	85.3	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain
65	c2f9iD	Alignment	not modelled	85.2	16	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
66	c3ndjA	Alignment	not modelled	84.9	29	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
67	c2f5qA	Alignment	not modelled	84.9	17	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
68	c5fywW	Alignment	not modelled	84.8	15	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
69	c2kdxA	Alignment	not modelled	84.1	26	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
70	d2k4xa1	Alignment	not modelled	84.0	22	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
71	c1dvaA	Alignment	not modelled	83.5	26	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
72	c2f9yB	Alignment	not modelled	82.9	20	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
73	d2f9yb1	Alignment	not modelled	82.9	20	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
74	d2fiya1	Alignment	not modelled	82.8	19	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
75	c1k82D	Alignment	not modelled	82.3	22	PDB header: hydrolase/dna Chain: D: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
76	c2ba1B	Alignment	not modelled	80.4	19	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
77	c3w0fA	Alignment	not modelled	80.4	24	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mnei)3
78	c4hnp9	Alignment	not modelled	80.2	23	PDB header: ribosome Chain: 9: PDB Molecule: 40s ribosomal protein rps31e;

78	c4upv9_	Alignment	not modelled	80.2	43	PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 3 PDB header: ribosome
79	c2xzn9_	Alignment	not modelled	80.1	18	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
80	c6gen5_	Alignment	not modelled	80.1	27	PDB header: nuclear protein Chain: 5: PDB Molecule: vacuolar protein sorting-associated protein 71; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
81	c2xzm9_	Alignment	not modelled	80.0	18	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
82	c3h0gl_	Alignment	not modelled	79.9	13	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
83	d2ct7a1	Alignment	not modelled	79.8	20	Fold: RING/U-box Superfamily: RING/U-box Family: !BR domain
84	d1pfva3	Alignment	not modelled	79.3	30	Fold: Rubredoxin-like Superfamily: Methionyl-tRNA synthetase (MetRS), Zn-domain Family: Methionyl-tRNA synthetase (MetRS), Zn-domain
85	c3j3v0_	Alignment	not modelled	79.1	19	PDB header: ribosome Chain: 0: PDB Molecule: 50s ribosomal protein l32; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
86	c3pfqA_	Alignment	not modelled	79.0	18	PDB header: transferase Chain: A: PDB Molecule: protein kinase c beta type; PDBTitle: crystal structure and allosteric activation of protein kinase c beta2 ii
87	c6gymW_	Alignment	not modelled	78.7	20	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccdist)
88	c5fmfR_	Alignment	not modelled	78.7	15	PDB header: transcription Chain: R: PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
89	c1pd0A_	Alignment	not modelled	78.6	26	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
90	d1qypa_	Alignment	not modelled	78.3	28	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
91	c5oqiW_	Alignment	not modelled	78.0	20	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
92	c5x51X_	Alignment	not modelled	77.7	29	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)
93	c5oqmW_	Alignment	not modelled	77.0	20	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
94	c2eliA_	Alignment	not modelled	76.8	18	PDB header: transferase Chain: A: PDB Molecule: protein kinase c alpha type; PDBTitle: solution structure of the second phorbol2 esters/diacylglycerol binding domain of human protein3 kinase c alpha type
95	c3gn5B_	Alignment	not modelled	76.7	14	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
96	c4qiwP_	Alignment	not modelled	76.5	23	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
97	c5y06A_	Alignment	not modelled	76.4	22	PDB header: unknown function Chain: A: PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis
98	c2enzA_	Alignment	not modelled	76.3	18	PDB header: transferase Chain: A: PDB Molecule: protein kinase c theta type; PDBTitle: solution structure of the second c1 domain from human2 protein kinase c theta
99	c4rvga_	Alignment	not modelled	76.2	19	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
100	c1m2vB_	Alignment	not modelled	76.0	26	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
101	d2j0151	Alignment	not modelled	75.8	20	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
102	c3h0gL_	Alignment	not modelled	75.6	25	PDB header: transcription Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc4;

						PDBTitle: rna polymerase ii from schizosaccharomyces pombe PDB header: replication Chain: A: PDB Molecule: dna primase/helicase;
103	c1nviA_	Alignment	not modelled	75.6	18	PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
104	c2zaeB_	Alignment	not modelled	75.5	24	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease p protein component 4; PDBTitle: crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
105	c2nn6I_	Alignment	not modelled	75.1	11	PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
106	c3eg9B_	Alignment	not modelled	74.6	22	PDB header: protein transport Chain: B: PDB Molecule: sec24 related gene family, member d; PDBTitle: crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
107	c3eh2B_	Alignment	not modelled	74.4	26	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24c; PDBTitle: crystal structure of the human copii-coat protein sec24c
108	c2nb9A_	Alignment	not modelled	74.3	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
109	d1ptqa_	Alignment	not modelled	74.3	15	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
110	c1y8fA_	Alignment	not modelled	74.2	12	PDB header: endocytosis/exocytosis, signaling protein Chain: A: PDB Molecule: unc-13 homolog a; PDBTitle: solution structure of the munc13-1 c1-domain
111	d1xa6a3	Alignment	not modelled	74.1	15	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
112	d2zjrz1	Alignment	not modelled	74.0	22	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
113	d1k3xa3	Alignment	not modelled	73.9	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
114	d1tbna_	Alignment	not modelled	73.8	18	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
115	c6o9lQ_	Alignment	not modelled	73.8	22	PDB header: transcription/dna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state
116	c2ennA_	Alignment	not modelled	73.7	21	PDB header: transferase Chain: A: PDB Molecule: protein kinase c theta type; PDBTitle: solution structure of the first c1 domain from human2 protein kinase c theta
117	c2ja6L_	Alignment	not modelled	73.3	17	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
118	c6qg3P_	Alignment	not modelled	73.3	24	PDB header: translation Chain: P: PDB Molecule: eukaryotic translation initiation factor 2 subunit beta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model b)
119	c3a44D_	Alignment	not modelled	73.3	19	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
120	c5flmL_	Alignment	not modelled	73.2	22	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