
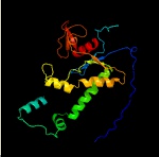
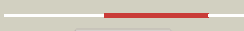
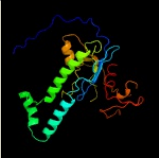

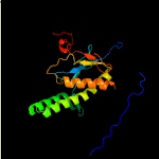





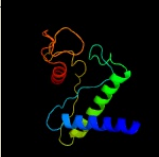

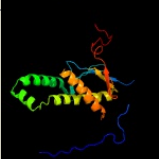







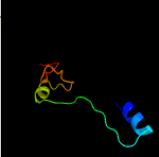


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2978c (-) _3333795_3335174
Date	Thu Aug 8 16:20:14 BST 2019
Unique Job ID	35b620ec8cf0f48c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wtiZ_	 Alignment		98.8	23	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
2	c6e7aY_	 Alignment		98.7	21	PDB header: dna binding protein/dna/rna Chain: Y: PDB Molecule: casx; PDBTitle: casx-grna-dna(30bp) state ii
3	c5id6A_	 Alignment		98.1	19	PDB header: hydrolase Chain: A: PDB Molecule: cpf1; PDBTitle: structure of cpf1/rna complex
4	c6iv6A_	 Alignment		97.9	17	PDB header: immune system/rna Chain: A: PDB Molecule: nuclease; PDBTitle: cryo-em structure of acrva5-acetylated mbcas12a in complex with crrna
5	c5mgaA_	 Alignment		97.6	18	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: structure of the cpf1 endonuclease r-loop complex after dna cleavage
6	c5wqeA_	 Alignment		97.5	17	PDB header: rna binding protein Chain: A: PDB Molecule: crispr-associated endonuclease c2c1; PDBTitle: crystal structure of alicyclobacillus acidoterrestis c2c1 in complex2 with single-guide rna at 3.1 angstrom resolution
7	c5nfvA_	 Alignment		97.4	18	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	c5b43A_	 Alignment		97.3	21	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
9	c5u31A_	 Alignment		97.0	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	c2gb5B_	 Alignment		95.0	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
11	d1hk8a_	 Alignment		93.9	13	Fold: PFL-like glycyI radical enzymes Superfamily: PFL-like glycyI radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit

12	c1hk8A_	Alignment		93.9	13	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	c4u3eA_	Alignment		93.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
14	c5fz5M_	Alignment		92.3	17	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
15	c3ky9B_	Alignment		91.5	19	PDB header: apoptosis Chain: B: PDB Molecule: proto-oncogene vav; PDBTitle: autoinhibited vav1
16	c4a17Y_	Alignment		91.4	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.
17	c1yuzB_	Alignment		91.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
18	d2akla2	Alignment		91.4	16	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
19	c2qa4Z_	Alignment		91.3	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
20	c2aklA_	Alignment		91.0	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
21	c2vrwB_	Alignment	not modelled	91.0	20	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
22	c4b6ap_	Alignment	not modelled	91.0	23	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
23	c5iy9M_	Alignment	not modelled	91.0	18	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)
24	d1pfta_	Alignment	not modelled	90.7	24	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
25	c3cc4Z_	Alignment	not modelled	90.6	27	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
26	d1vqoz1	Alignment	not modelled	90.6	27	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
27	d1ffkw_	Alignment	not modelled	90.6	19	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
28	c3izrm_	Alignment	not modelled	90.6	23	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 PDB header: ribosome

29	c3zf7o_	Alignment	not modelled	90.6	27	Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 Brucei ribosome
30	c6f42V_	Alignment	not modelled	90.6	23	PDB header: transcription Chain: V: PDB Molecule: transcription factor iib 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
31	c3j39p_	Alignment	not modelled	90.4	27	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
32	c3j21i_	Alignment	not modelled	90.4	27	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)
33	c2zkrz_	Alignment	not modelled	90.2	23	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
34	d1jj2y_	Alignment	not modelled	90.1	19	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
35	c3k1fM_	Alignment	not modelled	89.9	17	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
36	c1yshD_	Alignment	not modelled	89.9	23	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
37	c3bjia_	Alignment	not modelled	89.7	21	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
38	c4v1oM_	Alignment	not modelled	89.7	22	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
39	c3k7aM_	Alignment	not modelled	89.6	19	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
40	c2hr5B_	Alignment	not modelled	89.6	24	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
41	c3cngC_	Alignment	not modelled	89.5	21	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
42	c1s1i9_	Alignment	not modelled	89.0	23	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.
43	d1dl6a_	Alignment	not modelled	88.6	19	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
44	c6cnbR_	Alignment	not modelled	88.5	22	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
45	d1twfi2	Alignment	not modelled	88.5	27	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
46	c1dvbA_	Alignment	not modelled	87.7	33	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
47	c3jyw9_	Alignment	not modelled	87.7	23	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
48	c3wwnB_	Alignment	not modelled	87.3	23	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
49	c2qkdA_	Alignment	not modelled	86.9	19	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
50	d2fiya1	Alignment	not modelled	86.9	19	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
51	c1i3ql_	Alignment	not modelled	86.0	22	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
52	c2lcqA_	Alignment	not modelled	85.6	12	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
53	c5ijlA_	Alignment	not modelled	85.3	24	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
54	c1nnjA_	Alignment	not modelled	85.3	11	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 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
55	c6g5iy_	Alignment	not modelled	85.1	24	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
56	c4c2mX_	Alignment	not modelled	85.1	14	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
57	c5flmI_	Alignment	not modelled	84.7	17	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
58	c2opfA_	Alignment	not modelled	84.2	16	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
59	c2ba1B_	Alignment	not modelled	84.2	22	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
60	c3zyqA_	Alignment	not modelled	83.7	21	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)
61	c5iy9O_	Alignment	not modelled	83.3	22	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
62	c2f9iD_	Alignment	not modelled	83.0	16	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
63	c2kdxA_	Alignment	not modelled	82.2	26	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
64	c1ee8A_	Alignment	not modelled	82.1	26	PDB header: transferase/transcription Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis complex
65	c1pqvS_	Alignment	not modelled	82.0	20	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
66	d2k4xa1	Alignment	not modelled	82.0	22	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
67	c1dvpA_	Alignment	not modelled	81.8	21	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
68	c6hmsB_	Alignment	not modelled	81.8	22	PDB header: transferase/transcription/dna-rna hybrid Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis-dna/rna complex
69	c1y1yS_	Alignment	not modelled	81.8	20	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
70	c1k82D_	Alignment	not modelled	81.4	15	PDB header: hydrolase/rna Chain: I: PDB Molecule: exosome complex component csl4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
71	c4ifdl_	Alignment	not modelled	80.7	4	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
72	c2f9yB_	Alignment	not modelled	80.4	20	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
73	d2f9yb1	Alignment	not modelled	80.4	20	PDB header: transcription/rna Chain: U: PDB Molecule: general transcription elongation factor tfiis; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
74	c5xonU_	Alignment	not modelled	79.5	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
75	c2f5qA_	Alignment	not modelled	78.9	22	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
76	c2nn6I_	Alignment	not modelled	78.8	11	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
77	c5fywW_	Alignment	not modelled	78.7	13	Fold: RING/U-box

78	d2ct7a1	Alignment	not modelled	78.7	17	Superfamily: RING/U-box Family: lBR domain
79	c5x51X	Alignment	not modelled	78.6	24	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	c4bpo9	Alignment	not modelled	78.5	21	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
81	c1kcfB	Alignment	not modelled	78.4	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
82	c3h0gl	Alignment	not modelled	78.0	13	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
83	c4rvga	Alignment	not modelled	77.9	19	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
84	c3ndjA	Alignment	not modelled	77.8	31	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
85	c2xzn9	Alignment	not modelled	77.7	16	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
86	c2xzm9	Alignment	not modelled	77.5	16	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
87	c5iycU	Alignment	not modelled	77.0	20	PDB header: transcription, transferase/dna Chain: U: PDB Molecule: transcription elongation factor a protein 1; PDBTitle: human core-pic in the initial transcribing state
88	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 phorbo2 esters/diacylglycerol binding domain of human protein3 kinase c alpha type
89	c3pfqA	Alignment	not modelled	76.6	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
90	c2nb9A	Alignment	not modelled	76.6	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
91	d1kcfA2	Alignment	not modelled	76.1	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain
92	c3h0gL	Alignment	not modelled	75.9	24	PDB header: transcription Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc4; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
93	c3gn5B	Alignment	not modelled	75.8	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)
94	c5flmL	Alignment	not modelled	75.7	20	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
95	c2ja6L	Alignment	not modelled	75.6	16	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
96	d1yuza2	Alignment	not modelled	75.5	24	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
97	d1nnqa2	Alignment	not modelled	75.3	24	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
98	c1nuiA	Alignment	not modelled	75.1	18	PDB header: replication Chain: A: PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
99	c3w0fA	Alignment	not modelled	74.7	24	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mneil3)
100	c5fjal	Alignment	not modelled	74.1	14	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase iii subunit rpc10; PDBTitle: cryo-em structure of yeast rna polymerase iii at 4.7 a
101	d1lkoa2	Alignment	not modelled	73.9	22	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
102	c2enzA	Alignment	not modelled	73.3	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
						Fold: Rubredoxin-like

103	d1tfia_	Alignment	not modelled	72.9	21	Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
104	c2ennA_	Alignment	not modelled	72.8	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
105	d1tbna_	Alignment	not modelled	72.7	18	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
106	c1pd0A_	Alignment	not modelled	72.6	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)
107	d1x3za1	Alignment	not modelled	72.5	32	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
108	d1ptqa_	Alignment	not modelled	72.3	15	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
109	c6gymW_	Alignment	not modelled	72.2	23	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccd1st)
110	c5oqjW_	Alignment	not modelled	71.8	23	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
111	c6o3pA_	Alignment	not modelled	71.4	19	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
112	d1xa6a3	Alignment	not modelled	71.2	15	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
113	d2j0151	Alignment	not modelled	70.8	21	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
114	c3bvoA_	Alignment	not modelled	70.4	21	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb, mitochondrial precursor; PDBTitle: crystal structure of human co-chaperone protein hscb
115	c1y8fA_	Alignment	not modelled	70.1	15	PDB header: endocytosis/exocytosis,signaling protein Chain: A: PDB Molecule: unc-13 homolog a; PDBTitle: solution structure of the munc13-1 c1-domain
116	d1zbdb_	Alignment	not modelled	70.1	13	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: FYVE, a phosphatidylinositol-3-phosphate binding domain
117	c2pziA_	Alignment	not modelled	69.9	14	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
118	d1qypa_	Alignment	not modelled	69.9	27	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
119	c1m2vB_	Alignment	not modelled	69.2	26	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
120	d2nn6i1	Alignment	not modelled	69.1	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like