



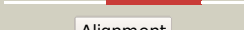

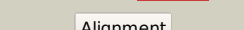
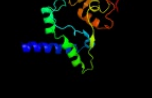

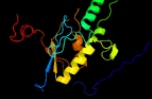

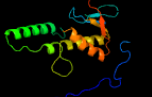


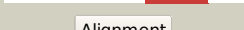

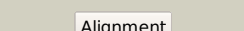




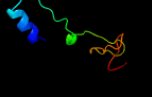


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2791c (-)_3100212_3101591
Date	Wed Aug 7 12:50:45 BST 2019
Unique Job ID	3c39e77cdbcb2b5

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6e7aY_	 Alignment		98.7	19	PDB header: dna binding protein/dna/rna Chain: Y: PDB Molecule: casx; PDBTitle: casx-grna-dna(30bp) state ii
2	c5id6A_	 Alignment		98.3	19	PDB header: hydrolase Chain: A: PDB Molecule: cpf1; PDBTitle: structure of cpf1/rna complex
3	c6iv6A_	 Alignment		98.2	20	PDB header: immune system/rna Chain: A: PDB Molecule: nuclease; PDBTitle: cryo-em structure of acrva5-acetylated mbcas12a in complex with crrna
4	c5wtiZ_	 Alignment		98.1	19	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
5	c5mgaA_	 Alignment		98.1	23	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: structure of the cpf1 endonuclease r-loop complex after dna cleavage
6	c5b43A_	 Alignment		98.0	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
7	c5nfvA_	 Alignment		97.8	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	c5wqeA_	 Alignment		97.5	19	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		96.7	19	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		95.3	28	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		94.0	18	Fold: PFL-like glycyI radical enzymes Superfamily: PFL-like glycyI radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit

12	c1hk8A_	Alignment		94.0	18	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		94.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
14	c3ky9B_	Alignment		93.4	20	PDB header: apoptosis Chain: B: PDB Molecule: proto-oncogene vav; PDBTitle: autoinhibited vav1
15	c2vrwB_	Alignment		93.2	17	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
16	c5fz5M_	Alignment		93.1	18	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
17	c1yu2B_	Alignment		92.5	29	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
18	c3bjia_	Alignment		92.4	20	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
19	c2qa4Z_	Alignment		91.9	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	c4b6ap_	Alignment		91.7	31	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
21	c4a17Y_	Alignment	not modelled	91.5	27	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.
22	c3k7aM_	Alignment	not modelled	91.3	21	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
23	d1ffkw_	Alignment	not modelled	91.3	27	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
24	c3cc4Z_	Alignment	not modelled	91.2	27	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
25	d2akla2	Alignment	not modelled	91.2	16	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
26	c6f42V_	Alignment	not modelled	91.1	15	PDB header: transcription Chain: V: PDB Molecule: transcription factor iib 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
27	c3cngC_	Alignment	not modelled	91.0	29	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
28	c3zf7o_	Alignment	not modelled	91.0	31	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

29	d1vqoz1	Alignment	not modelled	91.0	27	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
30	c3izrm	Alignment	not modelled	91.0	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
31	c3j39p	Alignment	not modelled	90.9	27	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
32	c2aklA	Alignment	not modelled	90.9	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
33	c2hr5B	Alignment	not modelled	90.7	33	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
34	c2lcqA	Alignment	not modelled	90.6	14	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
35	c3j21i	Alignment	not modelled	90.6	38	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)
36	c5iy9M	Alignment	not modelled	90.6	21	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)
37	c2zkrz	Alignment	not modelled	90.4	31	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
38	d1jj2y	Alignment	not modelled	90.3	27	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
39	d1pfta	Alignment	not modelled	90.3	17	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
40	c1yshD	Alignment	not modelled	90.2	23	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
41	c3k1fM	Alignment	not modelled	90.1	18	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
42	c1i3ql	Alignment	not modelled	89.8	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
43	c4v1oM	Alignment	not modelled	89.8	22	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
44	c5ijlA	Alignment	not modelled	89.5	32	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
45	c3zyqA	Alignment	not modelled	89.2	15	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
46	c1s1i9	Alignment	not modelled	89.2	31	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.
47	c1dvbA	Alignment	not modelled	89.1	43	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
48	c5flmI	Alignment	not modelled	88.9	17	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
49	c6cnbR	Alignment	not modelled	88.8	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
50	c6hmsB	Alignment	not modelled	88.7	32	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
51	c1ee8A	Alignment	not modelled	88.7	26	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
52	c1nnjA	Alignment	not modelled	88.5	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
53	c3jyw9	Alignment	not modelled	88.5	31	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
54	d2k4xa1	Alignment	not modelled	88.0	26	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
55	d1dl6a_	Alignment	not modelled	87.9	15	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
56	c6g5iy_	Alignment	not modelled	87.3	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	c2opfA_	Alignment	not modelled	87.1	26	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	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
59	c5iy9Q_	Alignment	not modelled	86.8	25	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)
60	c1dvpA_	Alignment	not modelled	86.5	15	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	c2kdxA_	Alignment	not modelled	86.2	26	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
62	c2f5qA_	Alignment	not modelled	86.2	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
63	c4bpo9_	Alignment	not modelled	86.1	24	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
64	c3wwnB_	Alignment	not modelled	85.7	31	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
65	c4c2mX_	Alignment	not modelled	85.4	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
66	c1k82D_	Alignment	not modelled	85.3	30	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
67	c2xzm9_	Alignment	not modelled	85.2	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
68	c2xzn9_	Alignment	not modelled	84.8	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 2
69	d2fiya1	Alignment	not modelled	84.6	19	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
70	d1twfi2	Alignment	not modelled	84.5	25	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
71	c3h0ql_	Alignment	not modelled	84.2	17	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
72	c2f9iD_	Alignment	not modelled	83.8	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
73	c2ba1B_	Alignment	not modelled	83.4	19	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
74	c1kcfB_	Alignment	not modelled	82.2	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
75	c5fywW_	Alignment	not modelled	82.1	15	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
76	d1kcfA2	Alignment	not modelled	82.0	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain
77	d2f9yb1	Alignment	not modelled	81.5	24	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain

78	c2f9yB	Alignment	not modelled	81.5	24	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from <i>Escherichia coli</i>
79	c4ifdl	Alignment	not modelled	81.4	11	PDB header: hydrolase/rna Chain: I: PDB Molecule: exosome complex component csl4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to 2 rna
80	d1qypa	Alignment	not modelled	80.7	28	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
81	d2j0151	Alignment	not modelled	80.7	23	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
82	c3j3v0	Alignment	not modelled	80.5	27	PDB header: ribosome Chain: 0: PDB Molecule: 50s ribosomal protein l32; PDBTitle: atomic model of the immature 50s subunit from <i>Bacillus subtilis</i> (state 2 i-a)
83	c5xonU	Alignment	not modelled	79.9	17	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
84	d2zjr1	Alignment	not modelled	79.6	25	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
85	c3w0fA	Alignment	not modelled	79.5	19	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mneil3)
86	c3pfqA	Alignment	not modelled	79.3	21	PDB header: transferase Chain: A: PDB Molecule: protein kinase c beta type; PDBTitle: crystal structure and allosteric activation of protein kinase c beta 2 ii
87	d1x3za1	Alignment	not modelled	79.3	32	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
88	d2ct7a1	Alignment	not modelled	79.0	17	Fold: RING/U-box Superfamily: RING/U-box Family: IBR domain
89	c2k5cA	Alignment	not modelled	78.9	50	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
90	c1nuiA	Alignment	not modelled	78.4	21	PDB header: replication Chain: A: PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
91	c5x51X	Alignment	not modelled	78.2	23	PDB header: transferase Chain: X: PDB Molecule: rna polymerase subunit, found in rna polymerase complexes PDBTitle: rna polymerase ii from <i>Komagataella pastoris</i> (type-3 crystal)
92	c2pziA	Alignment	not modelled	78.0	26	PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from <i>Mycobacterium tuberculosis</i> in complex with tetrahydrobenzothiophene ax20017
93	c2eliA	Alignment	not modelled	77.7	21	PDB header: transferase Chain: A: PDB Molecule: protein kinase c alpha type; PDBTitle: solution structure of the second phorbol 2 esters/diacylglycerol binding domain of human protein 3 kinase c alpha type
94	c3gn5B	Alignment	not modelled	77.3	19	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the <i>E. coli</i> protein mqsa (ygit/b3021)
95	c2nb9A	Alignment	not modelled	77.2	22	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
96	c3bvoA	Alignment	not modelled	77.0	29	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb, mitochondrial precursor; PDBTitle: crystal structure of human co-chaperone protein hscb
97	d1yuza2	Alignment	not modelled	77.0	29	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
98	d1nnqa2	Alignment	not modelled	76.9	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
99	c2nn6l	Alignment	not modelled	76.4	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
100	c3h0gL	Alignment	not modelled	76.4	28	PDB header: transcription Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc4; PDBTitle: rna polymerase ii from <i>Schizosaccharomyces pombe</i>
101	c1y1yS	Alignment	not modelled	76.1	21	PDB header: transferase/transcription/dna-rna hybrid Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis-dna/rna complex
102	c3eswA	Alignment	not modelled	76.0	32	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.

103	c1pqvS_	Alignment	not modelled	75.7	21	PDB header: transferase/transcription Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis complex
104	d1k3xa3	Alignment	not modelled	75.6	26	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
105	c3ndjA_	Alignment	not modelled	75.4	38	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
106	d1tdza3	Alignment	not modelled	75.2	20	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
107	c4rvqA_	Alignment	not modelled	75.2	26	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
108	c6gymW_	Alignment	not modelled	75.1	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)
109	d1ptqa_	Alignment	not modelled	74.8	18	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
110	d1tbna_	Alignment	not modelled	74.8	21	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
111	c2enzA_	Alignment	not modelled	74.7	21	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
112	c2ja6L_	Alignment	not modelled	74.7	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
113	c1y8fA_	Alignment	not modelled	74.6	12	PDB header: endocytosis/exocytosis,signaling protein Chain: A: PDB Molecule: unc-13 homolog a; PDBTitle: solution structure of the munc13-1 c1-domain
114	c5flmL_	Alignment	not modelled	74.2	24	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
115	c3a44D_	Alignment	not modelled	74.1	19	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
116	c5oqjW_	Alignment	not modelled	74.1	23	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
117	d1ee8a3	Alignment	not modelled	74.1	26	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
118	c4zlhB_	Alignment	not modelled	73.9	38	PDB header: metal binding protein Chain: B: PDB Molecule: lipopolysaccharide assembly protein b; PDBTitle: structure of the lapb cytoplasmic domain at 2 angstroms
119	c5iycU_	Alignment	not modelled	73.8	21	PDB header: transcription, transferase/dna Chain: U: PDB Molecule: transcription elongation factor a protein 1; PDBTitle: human core-pic in the initial transcribing state
120	d1zbdb_	Alignment	not modelled	73.7	16	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: FYVE, a phosphatidylinositol-3-phosphate binding domain