

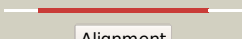

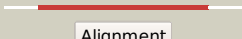
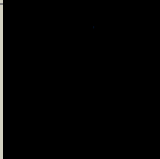
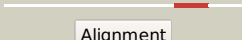

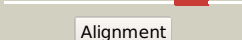


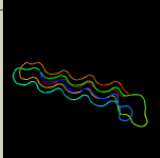
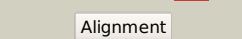
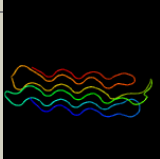
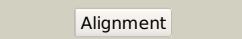
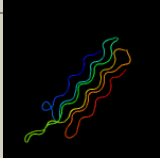
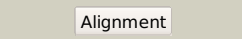
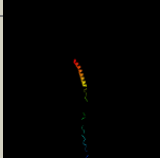
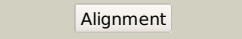
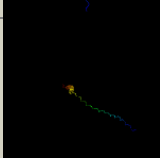
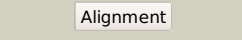
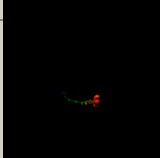
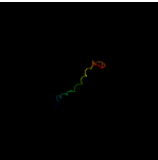
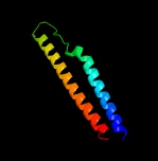

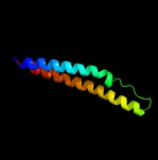
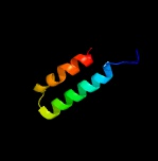
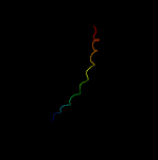

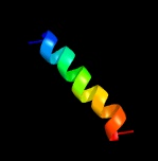
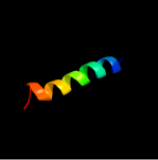


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0278c_(PE_PGRS3)_333437_336310
Date	Tue Jul 23 14:50:34 BST 2019
Unique Job ID	413aff65fb332cd4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	 Alignment		100.0	24	PDB header: structural protein/contractile protein Chain: A: PDB Molecule: collagen i alpha 1; PDBTitle: the structure of collagen type i. single type i collagen2 molecule: rigid refinement
2	c3hqvB_	 Alignment		100.0	28	PDB header: structural protein, contractile protein Chain: B: PDB Molecule: collagen alpha-2(i) chain; PDBTitle: low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
3	c1y0fB_	 Alignment		100.0	27	PDB header: structural protein/contractile protein Chain: B: PDB Molecule: collagen i alpha 2; PDBTitle: the structure of collagen type i. single type i collagen2 molecule
4	c3bogB_	 Alignment		97.3	33	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
5	c3bogA_	 Alignment		97.3	33	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
6	c2pneA_	 Alignment		97.0	39	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
7	c3boiB_	 Alignment		97.0	39	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
8	c3boiA_	 Alignment		97.0	39	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
9	c5ctdB_	 Alignment		96.7	15	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-2(i) chain, collagen alpha-2(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
10	c5ctiC_	 Alignment		96.7	18	PDB header: structural protein Chain: C: PDB Molecule: collagen alpha-1(i) chain, collagen alpha-3(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
11	c5ctdA_	 Alignment		95.9	21	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(i) chain, collagen alpha-1(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen

12	c1nayC_	Alignment		93.8	20	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
13	c2g38A_	Alignment		92.8	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
14	d2g38a1	Alignment		92.8	30	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
15	c5xfsA_	Alignment		92.4	51	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp5 from m.2 tuberculosis
16	d2ddha2	Alignment		82.9	15	Fold: Bromodomain-like Superfamily: Acyl-CoA dehydrogenase C-terminal domain-like Family: acyl-CoA oxidase C-terminal domains
17	c2klwA_	Alignment		81.9	28	PDB header: de novo protein Chain: A: PDB Molecule: (pkg)10; PDBTitle: solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
18	c1etgB_	Alignment		75.5	52	PDB header: viral protein/rna Chain: B: PDB Molecule: rev peptide; PDBTitle: rev response element (rre) rna complexed with rev peptide,2 nmr, 19 structures
19	c1etfB_	Alignment		75.5	52	PDB header: viral protein/rna Chain: B: PDB Molecule: rev peptide; PDBTitle: rev response element (rre) rna complexed with rev peptide,2 nmr, minimized average structure
20	c2m1aA_	Alignment		73.7	52	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 rev arginine-rich motif (arm); PDBTitle: hiv-1 rev arm peptide (residues t34-r50)
21	c4rv7C_	Alignment	not modelled	65.4	39	PDB header: transferase Chain: C: PDB Molecule: diadenylate cyclase; PDBTitle: characterization of an essential diadenylate cyclase
22	c6gyyB_	Alignment	not modelled	65.3	28	PDB header: transferase Chain: B: PDB Molecule: diadenylate cyclase; PDBTitle: crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant
23	c5ooll_	Alignment	not modelled	65.1	44	PDB header: ribosome Chain: L: PDB Molecule: 39s ribosomal protein l14, mitochondrial; PDBTitle: structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rna
24	c5ooml_	Alignment	not modelled	65.1	44	PDB header: ribosome Chain: L: PDB Molecule: 39s ribosomal protein l14, mitochondrial; PDBTitle: structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rna
25	c4ndkA_	Alignment	not modelled	61.4	67	PDB header: fluorescent protein, de novo protein Chain: A: PDB Molecule: e23p-yfp, gfp-like fluorescent chromoprotein fp506, PDBTitle: crystal structure of a computational designed engrailed homeodomain2 variant fused with yfp
26	c2x7IP_	Alignment	not modelled	61.1	56	PDB header: immune system Chain: P: PDB Molecule: protein rev; PDBTitle: implications of the hiv-1 rev dimer structure at 3.2a resolution for2 multimeric binding to the rev response element
27	d2fb5a1	Alignment	not modelled	59.3	33	Fold: Yojj-like Superfamily: Yojj-like Family: Yojj-like
28	c4zhjA_	Alignment	not modelled	58.3	12	PDB header: metal binding protein Chain: A: PDB Molecule: mg-chelatase subunit chlh; PDBTitle: crystal structure of the catalytic subunit of magnesium chelatase

29	c3lphD_	Alignment	not modelled	56.4	56	PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer
30	c3ob4A_	Alignment	not modelled	56.2	23	PDB header: allergen Chain: A: PDB Molecule: maltose abc transporter periplasmic protein, arah 2; PDBTitle: mbp-fusion protein of the major peanut allergen ara h 2
31	c2p7nA_	Alignment	not modelled	55.3	14	PDB header: cell invasion Chain: A: PDB Molecule: pathogenicity island 1 effector protein; PDBTitle: crystal structure of the pathogenicity island 1 effector protein from2 chromobacterium violaceum. northeast structural genomics consortium3 (nesgc) target cvr69.
32	c2zj6A_	Alignment	not modelled	52.7	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
33	c2cuoF_	Alignment	not modelled	51.4	31	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
34	c2cuoC_	Alignment	not modelled	51.4	31	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
35	c4witB_	Alignment	not modelled	51.3	13	PDB header: lipid transport Chain: B: PDB Molecule: predicted protein; PDBTitle: tmem16 lipid scramblase in crystal form 2
36	c5ys9A_	Alignment	not modelled	50.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coenzyme a oxidase 3; PDBTitle: crystal structure of acyl-coa oxidase3 from yarrowia lipolytica
37	c3ah9D_	Alignment	not modelled	49.2	29	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
38	c1e5wA_	Alignment	not modelled	48.9	19	PDB header: membrane protein Chain: A: PDB Molecule: moesin; PDBTitle: structure of isolated ferm domain and first long helix of moesin
39	d1o9ga_	Alignment	not modelled	48.5	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase AviRa
40	c4ndlC_	Alignment	not modelled	48.2	83	PDB header: de novo protein Chain: C: PDB Molecule: enh-c2b, computational designed homodimer; PDBTitle: computational design and experimental verification of a symmetric2 homodimer
41	c5ys2C_	Alignment	not modelled	47.0	18	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein b,envelope glycoprotein b; PDBTitle: structure of the domain iv(d_iv) of pseudorabies virus glycoprotein b(2 prv gb)
42	c3ah9A_	Alignment	not modelled	46.6	32	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
43	c3ah9F_	Alignment	not modelled	45.9	31	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
44	c3ah9E_	Alignment	not modelled	44.9	31	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
45	c3ah9C_	Alignment	not modelled	44.9	31	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
46	c3ah9B_	Alignment	not modelled	44.9	31	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
47	c3fvcA_	Alignment	not modelled	44.4	33	PDB header: viral protein Chain: A: PDB Molecule: glycoprotein gp110; PDBTitle: crystal structure of a trimeric variant of the epstein-barr virus2 glycoprotein b
48	c3c1zA_	Alignment	not modelled	42.1	33	PDB header: dna binding protein Chain: A: PDB Molecule: dna integrity scanning protein disa; PDBTitle: structure of the ligand-free form of a bacterial dna damage sensor2 protein
49	c5f0kE_	Alignment	not modelled	40.6	40	PDB header: protein transport Chain: E: PDB Molecule: vacuolar protein sorting-associated protein 35; PDBTitle: structure of vps35 n terminal region
50	c2ml3A_	Alignment	not modelled	39.3	18	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
51	c1k6fE_	Alignment	not modelled	38.5	30	PDB header: structural protein Chain: E: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
52	c1k6fC_	Alignment	not modelled	38.5	30	PDB header: structural protein Chain: C: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
53	c1k6fB_	Alignment	not modelled	38.5	30	PDB header: structural protein Chain: B: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
54	c1k6fF_	Alignment	not modelled	38.5	30	PDB header: structural protein Chain: F: PDB Molecule: collagen triple helix;

54	c1k6fI_	Alignment	not modelled	38.5	30	PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3 PDB header: structural protein
55	c1k6fA_	Alignment	not modelled	38.5	30	Chain: A: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3 PDB header: structural protein
56	c1k6fD_	Alignment	not modelled	38.5	30	Chain: D: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3 PDB header: structural protein
57	c2cuoE_	Alignment	not modelled	38.0	32	Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 PDB header: structural protein
58	c2cuoD_	Alignment	not modelled	38.0	32	Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 PDB header: structural protein
59	c2cuoA_	Alignment	not modelled	38.0	32	Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 PDB header: structural protein
60	c2cuoB_	Alignment	not modelled	38.0	32	Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 PDB header: structural protein
61	c3a0mF_	Alignment	not modelled	37.5	31	Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal PDB header: structural protein
62	c1k7qA_	Alignment	not modelled	37.4	21	Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtc from erwinia chrysanthemi: e189a mutant PDB header: hydrolase
63	c4jhdF_	Alignment	not modelled	36.6	25	Chain: F: PDB Molecule: protein cordon-bleu; PDBTitle: crystal structure of an actin dimer in complex with the actin2 nucleator cordon-bleu PDB header: structural protein/protein binding
64	c4tqvI_	Alignment	not modelled	36.5	20	Chain: I: PDB Molecule: algm1; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate PDB header: transport protein
65	d1ug7a_	Alignment	not modelled	36.4	15	Fold: Four-helical up-and-down bundle Superfamily: Domain from hypothetical 2610208m17rik protein Family: Domain from hypothetical 2610208m17rik protein
66	c4cw5B_	Alignment	not modelled	36.2	19	Chain: B: PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens PDB header: oxidoreductase
67	c1jiwP_	Alignment	not modelled	35.9	23	Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex PDB header: hydrolase/hyrolase inhibitor
68	d1isna2	Alignment	not modelled	35.4	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Third domain of FERM
69	c3sjdD_	Alignment	not modelled	34.8	39	Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: crystal structure of s. cerevisiae get3 with bound adp-mg2+ in complex2 with get2 cytosolic domain PDB header: hydrolase/transport protein
70	c3sjdE_	Alignment	not modelled	34.8	39	Chain: E: PDB Molecule: golgi to er traffic protein 2; PDBTitle: crystal structure of s. cerevisiae get3 with bound adp-mg2+ in complex2 with get2 cytosolic domain PDB header: hydrolase/transport protein
71	c5v2sA_	Alignment	not modelled	34.6	21	Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i PDB header: viral protein
72	c3zs9C_	Alignment	not modelled	34.5	39	Chain: C: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment PDB header: hydrolase/transport protein
73	c3j04A_	Alignment	not modelled	33.0	16	Chain: A: PDB Molecule: myosin-11; PDBTitle: em structure of the heavy meromyosin subfragment of chick smooth2 muscle myosin with regulatory light chain in phosphorylated state PDB header: structural protein
74	d1kapp1	Alignment	not modelled	32.5	23	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
75	c6ansD_	Alignment	not modelled	31.7	22	Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia cenocepacia PDB header: unknown function
76	c4a1eF_	Alignment	not modelled	31.6	17	Chain: F: PDB Molecule: rpl7a; 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 PDB header: ribosome
77	c4lb6B_	Alignment	not modelled	31.1	21	Chain: B: PDB Molecule: protein kinase containing z-dna binding domains; PDBTitle: crystal structure of pkz alpaha in complex with ds(cg)6 (tetragonal2 form) PDB header: transferase/dna
78	c5j9tG_	Alignment	not modelled	31.1	15	Chain: G: PDB Molecule: enhancer of polycomb-like protein 1; PDBTitle: crystal structure of the nua4 core complex PDB header: transferase
79	c4jx2B_	Alignment	not modelled	31.1	20	Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative secreted protein (lpg1979) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 2.653 a resolution PDB header: structural genomics, unknown function

80	d2dlqa1	Alignment	not modelled	30.7	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
81	c6em5b_	Alignment	not modelled	30.5	28	PDB header: ribosome Chain: B; PDB Molecule: 60s ribosomal protein l3; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
82	c5c6tA_	Alignment	not modelled	30.0	36	PDB header: viral protein/immue system Chain: A; PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of hcmv glycoprotein b in complex with 1g2 fab
83	d1e5wa2	Alignment	not modelled	29.7	22	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Third domain of FERM
84	d2guma1	Alignment	not modelled	29.6	18	Fold: Viral glycoprotein ectodomain-like Superfamily: Viral glycoprotein ectodomain-like Family: Glycoprotein B-like
85	c2ml2A_	Alignment	not modelled	29.5	17	PDB header: isomerase Chain: A; PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
86	c6bm8A_	Alignment	not modelled	29.5	21	PDB header: viral protein Chain: A; PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
87	c2agmA_	Alignment	not modelled	29.2	21	PDB header: isomerase Chain: A; PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
88	c3j66s_	Alignment	not modelled	28.1	17	PDB header: ribosome Chain: S; PDB Molecule: PDBTitle: arx1 pre-60s particle. this entry contains the alternative position2 for rlp7.
89	d3e9la1	Alignment	not modelled	27.9	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Prp8 beta-finger domain-like
90	c3nw8B_	Alignment	not modelled	27.4	18	PDB header: viral protein Chain: B; PDB Molecule: envelope glycoprotein b; PDBTitle: glycoprotein b from herpes simplex virus type 1, y179s mutant, high-ph
91	d1k7ia1	Alignment	not modelled	26.9	22	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
92	c6escA_	Alignment	not modelled	26.9	18	PDB header: viral protein Chain: A; PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of pseudorabies virus glycoprotein b
93	c1vw4a_	Alignment	not modelled	25.8	18	PDB header: ribosome Chain: A; PDB Molecule: PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
94	c4nqa1_	Alignment	not modelled	25.6	21	PDB header: transcription regulator/dna Chain: I; PDB Molecule: liver x nuclear receptor beta; PDBTitle: crystal structure of liganded hrxr-alpha/hlxr-beta heterodimer on dna
95	c5k3jA_	Alignment	not modelled	25.5	17	PDB header: oxidoreductase Chain: A; PDB Molecule: acyl-coenzyme a oxidase; PDBTitle: crystals structure of acyl-coa oxidase-2 in caenorhabditis elegans2 bound with fad, ascaroside-coa, and atp
96	c6ah3B_	Alignment	not modelled	24.9	23	PDB header: hydrolase/rna Chain: B; PDB Molecule: ribonucleases p/mrp protein subunit pop1; PDBTitle: cryo-em structure of yeast ribonuclease p with pre-trna substrate
97	d1yq2a4	Alignment	not modelled	24.6	18	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: beta-Galactosidase, domain 5
98	c4v1aq_	Alignment	not modelled	24.0	27	PDB header: ribosome Chain: Q; PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
99	c2ddhA_	Alignment	not modelled	23.7	15	PDB header: oxidoreductase Chain: A; PDB Molecule: acyl-coa oxidase; PDBTitle: crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
100	c2mk0A_	Alignment	not modelled	23.5	71	PDB header: structural protein Chain: A; PDB Molecule: hep200 protein; PDBTitle: structure of the pscd4-domain of the cell wall protein pleuralin-12 from the diatom cylindrotheca fusiformis
101	d1jz8a4	Alignment	not modelled	23.3	29	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: beta-Galactosidase, domain 5
102	c5b3hB_	Alignment	not modelled	23.3	14	PDB header: transcription Chain: B; PDB Molecule: protein short-root; PDBTitle: the crystal structure of the jackdaw/idd10 bound to the heterodimeric2 shr-scr complex
103	d1w07a2	Alignment	not modelled	23.2	8	Fold: Bromodomain-like Superfamily: Acyl-CoA dehydrogenase C-terminal domain-like Family: acyl-CoA oxidase C-terminal domains
104	c3a5tB_	Alignment	not modelled	23.1	13	PDB header: transcription regulator/dna Chain: B; PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
105	c6gcsG_	Alignment	not modelled	23.0	17	PDB header: oxidoreductase Chain: G; PDB Molecule: 30-kda protein (nugm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
						PDB header: hydrolase (serine protease)

106	c1satA_	Alignment	not modelled	22.9	23	Chain: A; PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
107	c1ydmC_	Alignment	not modelled	22.4	5	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: hypothetical protein yqgn; PDBTitle: x-ray structure of northeast structural genomics target sr44
108	c3zs9D_	Alignment	not modelled	22.4	39	PDB header: hydrolase/transport protein Chain: D; PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
109	c5zwo9_	Alignment	not modelled	22.0	42	PDB header: splicing Chain: 9; PDB Molecule: pre-mrna-splicing factor spp381; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
110	c5k3iH_	Alignment	not modelled	21.6	13	PDB header: oxidoreductase Chain: H; PDB Molecule: acyl-coenzyme a oxidase; PDBTitle: crystal structure of acyl-coa oxidase-1 in caenorhabditis elegans2 complexed with fad and atp
111	c2lo9A_	Alignment	not modelled	21.5	100	PDB header: toxin Chain: A; PDB Molecule: mu-conotoxin buiiiib; PDBTitle: nmr solution structure of mu-conotoxin buiiiib
112	c1yybA_	Alignment	not modelled	21.4	42	PDB header: apoptosis Chain: A; PDB Molecule: programmed cell death protein 5; PDBTitle: solution structure of 1-26 fragment of human programmed2 cell death 5 protein
113	c2locA_	Alignment	not modelled	21.3	100	PDB header: toxin Chain: A; PDB Molecule: mu-conotoxin buiiiib; PDBTitle: conotoxin analogue [d-ala2]buiiiiib