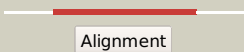

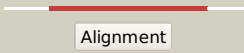



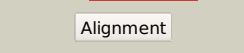



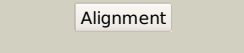

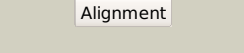
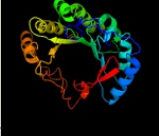


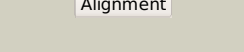

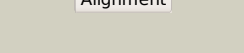

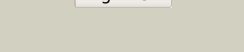
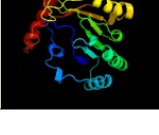








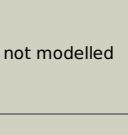


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3138_(pfIA)_3504192_3505280
Date	Thu Aug 8 16:20:32 BST 2019
Unique Job ID	661ac8c92fd5f8b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c8fA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate formate-lyase 1-activating enzyme; PDBTitle: 4fe-4s-pyruvate formate-lyase activating enzyme with partially2 disordered adomet
2	c6fz6B_	 Alignment		99.9	17	PDB header: transferase Chain: B; PDB Molecule: probable dual-specificity rna methyltransferase rlmn; PDBTitle: crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
3	c3rfaB_	 Alignment		99.9	13	PDB header: oxidoreductase Chain: B; PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
4	c3canA_	 Alignment		99.9	18	PDB header: lyase activator Chain: A; PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
5	c3rfaA_	 Alignment		99.9	13	PDB header: oxidoreductase Chain: A; PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
6	c2yx0A_	 Alignment		99.9	17	PDB header: metal binding protein Chain: A; PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
7	d1tv8a_	 Alignment		99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
8	c5v1tA_	 Alignment		99.9	17	PDB header: metal binding protein Chain: A; PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis sub bound to precursor2 peptide sua
9	c6efnA_	 Alignment		99.9	14	PDB header: oxidoreductase Chain: A; PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
10	c4njkA_	 Alignment		99.9	21	PDB header: lyase Chain: A; PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
11	c5th5C_	 Alignment		99.8	13	PDB header: lyase Chain: C; PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound

12	c6b4cH_	Alignment		99.8	13	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
13	c4u0pB_	Alignment		99.8	16	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
14	c6nhlB_	Alignment		99.8	15	PDB header: lyase Chain: B: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli
15	c4k39A_	Alignment		99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmecepe with bound adomet and cp18cys peptide
16	c5vslB_	Alignment		99.8	14	PDB header: antiviral protein Chain: B: PDB Molecule: radical s-adenosyl methionine domain-containing protein 2; PDBTitle: crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)
17	c5wggA_	Alignment		99.8	12	PDB header: peptide binding protein Chain: A: PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the biosynthesis2 of sactipeptides
18	c4wxcC_	Alignment		99.7	17	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydgc: a maturase of the [fefe]-hydrogenase
19	c5exkG_	Alignment		99.7	16	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
20	c2z2uA_	Alignment		99.7	21	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
21	c2a5hC_	Alignment	not modelled	99.6	13	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
22	d1r30a_	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
23	c1r30A_	Alignment	not modelled	99.6	17	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
24	c3t7vA_	Alignment	not modelled	99.6	13	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
25	c3cixA_	Alignment	not modelled	99.6	13	PDB header: adomet binding protein Chain: A: PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
26	c6c8vA_	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
27	c4jc0B_	Alignment	not modelled	99.5	13	PDB header: transferase Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77 PDB header: biosynthetic protein

28	c6fd2B_	Alignment	not modelled	99.4	18	Chain: B: PDB Molecule: putative apramycin biosynthetic oxidoreductase 4; PDBTitle: radical sam 1,2-diol dehydratase aprd4 in complex with its substrate2 paromamine
29	c4rtbA_	Alignment	not modelled	99.3	12	PDB header: lyase Chain: A: PDB Molecule: hydgd protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydgd from2 carboxydotherrmus hydrogenoformans
30	d1olta_	Alignment	not modelled	99.3	11	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
31	c4m7tA_	Alignment	not modelled	99.2	14	PDB header: metal binding protein Chain: A: PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
32	c5l7jA_	Alignment	not modelled	99.2	15	PDB header: translation Chain: A: PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
33	c5ul4A_	Alignment	not modelled	99.0	11	PDB header: metal binding protein Chain: A: PDB Molecule: oxsb protein; PDBTitle: structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
34	c4r33A_	Alignment	not modelled	98.8	15	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
35	c6qk7C_	Alignment	not modelled	98.8	15	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
36	c2qgqF_	Alignment	not modelled	98.7	14	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm_1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima. northeast2 structural genomics consortium target vr77
37	c4fheA_	Alignment	not modelled	98.7	11	PDB header: lyase Chain: A: PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
38	c6iazA_	Alignment	not modelled	98.1	12	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
39	c3e49A_	Alignment	not modelled	95.9	17	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
40	c3no5C_	Alignment	not modelled	95.6	14	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
41	c2y0fD_	Alignment	not modelled	95.1	27	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
42	c3c6cA_	Alignment	not modelled	94.9	14	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
43	c3noyA_	Alignment	not modelled	94.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
44	c2y7eA_	Alignment	not modelled	94.0	14	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
45	c3e02A_	Alignment	not modelled	94.0	15	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
46	c3chvA_	Alignment	not modelled	93.7	11	PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
47	c5zmyF_	Alignment	not modelled	92.9	15	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
48	d1x7fa2	Alignment	not modelled	92.8	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
49	c1x7fA_	Alignment	not modelled	92.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
50	c4u3eA_	Alignment	not modelled	88.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
51	c5fkvA_	Alignment	not modelled	87.7	18	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: cryo-em structure of the e. coli replicative dna

						polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
52	c2gb5B_	Alignment	not modelled	86.2	16	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
53	c6o3pA_	Alignment	not modelled	86.2	13	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
54	c6hmsB_	Alignment	not modelled	85.5	30	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
55	c5vrvA_	Alignment	not modelled	83.4	18	PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: protein regulated by acid ph; PDBTitle: 2.05 angstrom resolution crystal structure of c-terminal domain2 (duf2156) of putative lysylphosphatidylglycerol synthetase from3 agrobacterium fabrum.
56	c3qc3B_	Alignment	not modelled	82.6	14	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
57	c5flmI_	Alignment	not modelled	82.6	23	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
58	c1i3qI_	Alignment	not modelled	82.3	20	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
59	c3hgzP_	Alignment	not modelled	81.7	29	PDB header: transferase Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
60	c3cc4Z_	Alignment	not modelled	81.4	28	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
61	c3lotC_	Alignment	not modelled	80.2	16	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
62	c3zf7o_	Alignment	not modelled	80.2	24	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
63	c4a17Y_	Alignment	not modelled	79.9	24	PDB header: ribosome Chain: Y: PDB Molecule: rp137a; 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.
64	c2hnhA_	Alignment	not modelled	78.7	17	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
65	c2qa4Z_	Alignment	not modelled	78.0	28	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
66	c3floD_	Alignment	not modelled	77.5	23	PDB header: transferase Chain: D: PDB Molecule: dna polymerase alpha catalytic subunit a; PDBTitle: crystal structure of the carboxyl-terminal domain of yeast dna2 polymerase alpha in complex with its b subunit
67	c4gx9A_	Alignment	not modelled	77.4	17	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit epsilon,dna polymerase iii PDBTitle: crystal structure of a dna polymerase iii alpha-epsilon chimera
68	d1ffkw_	Alignment	not modelled	76.8	34	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
69	c4v36B_	Alignment	not modelled	76.6	19	PDB header: transferase Chain: B: PDB Molecule: lysyl-trna-dependent l-ysyl-phosphatidylglycerol synthase; PDBTitle: the structure of l-pgs from bacillus licheniformis
70	d1muwa_	Alignment	not modelled	76.5	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
71	c6k0aC_	Alignment	not modelled	76.3	15	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ribonuclease p protein component 3; PDBTitle: cryo-em structure of an archaeal ribonuclease p
72	c3ct7E_	Alignment	not modelled	76.3	14	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
73	c4b6ap_	Alignment	not modelled	75.8	21	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
74	c1yshD_	Alignment	not modelled	75.6	24	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
75	c3j39p_	Alignment	not modelled	75.4	21	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
						PDB header: ribosomal protein/rna

76	c2zkrz_	Alignment	not modelled	75.3	24	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
77	d1hjsa_	Alignment	not modelled	75.2	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
78	d1jj2y_	Alignment	not modelled	75.0	31	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
79	d1vqoz1	Alignment	not modelled	74.7	28	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
80	c3h0gl_	Alignment	not modelled	74.2	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
81	c3j2i_	Alignment	not modelled	73.9	34	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)
82	c2qkdA_	Alignment	not modelled	73.7	15	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
83	d7rega2	Alignment	not modelled	73.4	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
84	c3izrm_	Alignment	not modelled	72.9	24	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
85	c3jyw9_	Alignment	not modelled	72.6	21	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
86	c3dx5A_	Alignment	not modelled	72.3	10	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
87	c5zb8B_	Alignment	not modelled	71.5	14	PDB header: dna binding protein Chain: B: PDB Molecule: pfuendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
88	c5y06A_	Alignment	not modelled	71.3	25	PDB header: unknown function Chain: A: PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis
89	c3axtA_	Alignment	not modelled	70.5	17	PDB header: transferase Chain: A: PDB Molecule: probable n(2),n(2)-dimethylguanosine trna methyltransferase PDBTitle: complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
90	c6ncsB_	Alignment	not modelled	70.3	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-acetylneuraminic acid (sialic acid) synthetase; PDBTitle: crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
91	c4k3zA_	Alignment	not modelled	69.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-erythrose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
92	c2nb9A_	Alignment	not modelled	69.9	32	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
93	c5ijlA_	Alignment	not modelled	69.0	27	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
94	c4c2mX_	Alignment	not modelled	69.0	20	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
95	d1xima_	Alignment	not modelled	68.9	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
96	d1bxca_	Alignment	not modelled	68.6	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
97	c4l9mA_	Alignment	not modelled	68.3	22	PDB header: signaling protein Chain: A: PDB Molecule: ras guanyl-releasing protein 1; PDBTitle: autoinhibited state of the ras-specific exchange factor rasgrp1
98	c4yddF_	Alignment	not modelled	68.2	3	PDB header: oxidoreductase Chain: F: PDB Molecule: dms0 reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
99	c1s1i9_	Alignment	not modelled	67.8	21	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. PDB header: transferase

100	c3rmjB_	Alignment	not modelled	67.6	10	Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
101	d1qt1a_	Alignment	not modelled	67.3	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
102	c4ur7B_	Alignment	not modelled	67.2	6	PDB header: lyase Chain: B; PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
103	c3j21e_	Alignment	not modelled	67.0	35	PDB header: ribosome Chain: E; PDB Molecule: 50s ribosomal protein l5p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
104	d1yx1a1	Alignment	not modelled	66.6	11	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
105	c3ogrA_	Alignment	not modelled	66.4	14	PDB header: hydrolase Chain: A; PDB Molecule: beta-galactosidase; PDBTitle: complex structure of beta-galactosidase from trichoderma reesei with2 galactose
106	c3e35A_	Alignment	not modelled	66.4	12	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein sco1997; PDBTitle: actinobacteria-specific protein of unknown function, sco1997
107	c5zhzA_	Alignment	not modelled	66.2	15	PDB header: dna binding protein Chain: A; PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of the apurinic/aprimidinic endonuclease iv from2 mycobacterium tuberculosis
108	c3bicA_	Alignment	not modelled	65.2	12	PDB header: isomerase Chain: A; PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
109	d1bxbA_	Alignment	not modelled	64.1	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
110	c1dvbA_	Alignment	not modelled	63.8	35	PDB header: electron transport Chain: A; PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
111	c2lqA_	Alignment	not modelled	63.4	28	PDB header: metal binding protein Chain: A; PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
112	c1hk8A_	Alignment	not modelled	63.4	15	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 dgtp
113	d1hk8a_	Alignment	not modelled	63.4	15	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
114	c4ru1A_	Alignment	not modelled	63.3	29	PDB header: isomerase/dna Chain: A; PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
115	d1ujpa_	Alignment	not modelled	63.1	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
116	d2apob1	Alignment	not modelled	63.1	28	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
117	c2p0oA_	Alignment	not modelled	63.1	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
118	d2q02a1	Alignment	not modelled	63.0	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lol1-like
119	c1yuzB_	Alignment	not modelled	62.7	36	PDB header: oxidoreductase Chain: B; PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
120	c2zaeB_	Alignment	not modelled	61.8	21	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