
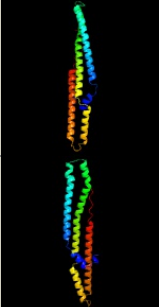

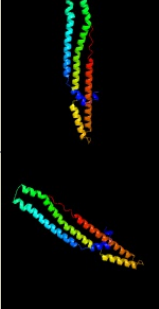

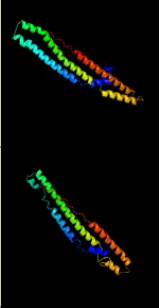

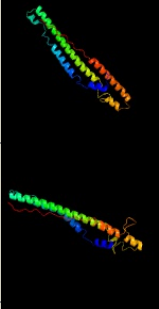

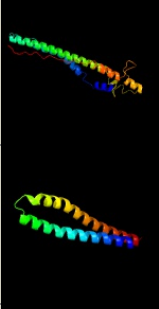

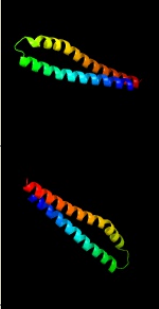

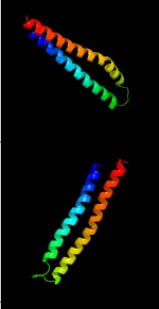

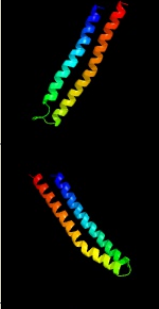

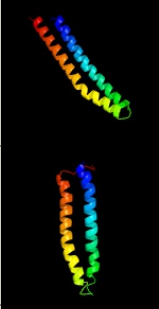

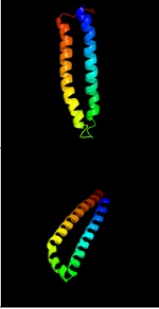




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1135c_(PPE16)_1262277_1264133
 Date Wed Jul 31 22:05:22 BST 2019
 Unique Job ID 8411f506d655b7d5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	51	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38B_	 Alignment		100.0	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	31	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	18	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		98.6	19	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		98.0	13	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.8	13	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c4iogD_	 Alignment		97.8	12	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
9	c3zbhC_	 Alignment		97.8	11	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.3	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		96.6	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	Alignment		96.4	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		96.2	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		95.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B_	Alignment		93.1	20	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ_	Alignment		77.5	20	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	d1ui5a2	Alignment		75.1	28	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	d1xkna_	Alignment		47.5	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
19	c5frgA_	Alignment		24.3	63	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
20	c2iu1A_	Alignment		24.2	33	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
21	c2kg7A_	Alignment	not modelled	23.0	25	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
22	c2ahmG_	Alignment	not modelled	21.1	18	PDB header: viral protein, replication Chain: G: PDB Molecule: replicase polyprotein 1ab, heavy chain; PDBTitle: crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
23	c2l5bA_	Alignment	not modelled	20.1	47	PDB header: apoptosis Chain: A: PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
24	c2fulE_	Alignment	not modelled	19.3	39	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
25	c2l5aA_	Alignment	not modelled	19.0	22	PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein cse4, protein scm3, PDBTitle: structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
26	c1bkvA_	Alignment	not modelled	18.4	44	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
27	c3zfsA_	Alignment	not modelled	18.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: f420-reducing hydrogenase, subunit alpha; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
28	c1bkvC_	Alianment	not modelled	17.2	44	PDB header: structural protein Chain: C: PDB Molecule: t3-785;

						PDBTitle: collagen
29	c1bkvB_	Alignment	not modelled	17.2	44	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
30	c2ke4A_	Alignment	not modelled	17.1	63	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cjp4
31	c3h6pB_	Alignment	not modelled	16.8	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
32	c3jywF_	Alignment	not modelled	16.7	52	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
33	c4n91A_	Alignment	not modelled	16.1	14	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate
34	c5lzkB_	Alignment	not modelled	16.0	9	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
35	c2hzbB_	Alignment	not modelled	15.0	17	PDB header: ligand binding, transport protein Chain: B: PDB Molecule: trap-t family sorbitol/mannitol transporter, periplasmic PDBTitle: crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
36	c3ub0D_	Alignment	not modelled	14.7	14	PDB header: replication Chain: D: PDB Molecule: non-structural protein 6, nsp6.; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of2 feline coronavirus
37	c3qthA_	Alignment	not modelled	14.5	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a dinb-like protein (cps_3021) from colwellia2 psychrerythraea 34h at 2.20 a resolution
38	c1paqA_	Alignment	not modelled	14.4	20	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
39	d1paqa_	Alignment	not modelled	14.4	20	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
40	c3trhl_	Alignment	not modelled	13.4	10	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
41	c3b50A_	Alignment	not modelled	13.2	15	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
42	c3r5zB_	Alignment	not modelled	12.9	12	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
43	c2kp7A_	Alignment	not modelled	12.6	20	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
44	c3juiA_	Alignment	not modelled	12.4	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
45	c4y9iA_	Alignment	not modelled	11.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
46	c5l4rA_	Alignment	not modelled	11.4	57	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
47	d2apla1	Alignment	not modelled	10.1	15	Fold: PG0816-like Superfamily: PG0816-like Family: PG0816-like
48	c3a9rA_	Alignment	not modelled	10.0	19	PDB header: isomerase Chain: A: PDB Molecule: d-arabinose isomerase; PDBTitle: x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
49	c3j3bF_	Alignment	not modelled	10.0	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
50	c4el8A_	Alignment	not modelled	9.8	31	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.bescii cela gh48 module
51	c3j21Y_	Alignment	not modelled	9.8	31	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l30p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em- implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
52	c5hl8B_	Alignment	not modelled	9.6	24	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein l; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic

						membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
53	c2kwuA	Alignment	not modelled	9.6	54	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
54	c6o9l6	Alignment	not modelled	9.6	40	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
55	d2ewoa1	Alignment	not modelled	9.3	24	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
56	d1luaa2	Alignment	not modelled	9.3	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
57	c4mnpA	Alignment	not modelled	9.2	15	PDB header: sugar binding protein Chain: A: PDB Molecule: n-acetylneuraminase-binding protein; PDBTitle: structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586
58	c3h96B	Alignment	not modelled	9.1	6	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
59	c3h8dC	Alignment	not modelled	9.0	13	PDB header: motor protein/signaling protein Chain: C: PDB Molecule: myosin-vi; PDBTitle: crystal structure of myosin vi in complex with dab2 peptide
60	c2np3A	Alignment	not modelled	8.9	14	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family regulator; PDBTitle: crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
61	c5vmoB	Alignment	not modelled	8.8	50	PDB header: viral protein/apoptosis Chain: B: PDB Molecule: bcl-2 interacting mediator of cell death; PDBTitle: crystal structure of grouper iridovirus giv66: bim complex
62	c2nviA	Alignment	not modelled	8.8	50	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
63	c2jerG	Alignment	not modelled	8.5	26	PDB header: hydrolase Chain: G: PDB Molecule: agmatine deiminase; PDBTitle: agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
64	c3j39F	Alignment	not modelled	8.5	38	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
65	c2lyyB	Alignment	not modelled	8.4	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
66	c4kkkA	Alignment	not modelled	8.4	19	PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
67	d1kx5a	Alignment	not modelled	8.3	20	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
68	c1bzgA	Alignment	not modelled	8.3	0	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone-related protein; PDBTitle: the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
69	c5ec0A	Alignment	not modelled	8.3	33	PDB header: structural protein Chain: A: PDB Molecule: alp7a; PDBTitle: crystal structure of actin-like protein alp7a
70	c3r5wO	Alignment	not modelled	8.3	21	PDB header: oxidoreductase Chain: O: PDB Molecule: deazaflavin-dependent nitroreductase; PDBTitle: structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
71	c4i6jB	Alignment	not modelled	8.1	11	PDB header: transcription Chain: B: PDB Molecule: cf-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
72	c3pe3D	Alignment	not modelled	8.1	16	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnae transferase and its complex with a peptide2 substrate
73	d1l1ya	Alignment	not modelled	8.0	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
74	c1l2aD	Alignment	not modelled	8.0	19	PDB header: hydrolase Chain: D: PDB Molecule: cellobiohydrolase; PDBTitle: the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
75	c4oanB	Alignment	not modelled	7.9	18	PDB header: membrane protein/protein transport Chain: B: PDB Molecule: trap dicarboxylate transporter dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodospseudomonas palustris haa2 (rpb_2686), target efi-510221, with3 density modeled as (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-4 acetolactate)
76	c2yfwC	Alignment	not modelled	7.8	20	PDB header: cell cycle Chain: C: PDB Molecule: histone h3-like centromeric protein cse4; PDBTitle: heterotetramer structure of kluyveromyces lactis cse4,h4
						PDB header: transferase

77	c5djsA_	Alignment	not modelled	7.8	22	Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnae transferase mutant - k341m
78	c3izce_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein rpl11 (I5p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
79	d1vkpa_	Alignment	not modelled	7.8	28	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
80	d2jera1	Alignment	not modelled	7.7	26	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
81	c4fusA_	Alignment	not modelled	7.7	31	PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related ca2+-binding protein; PDBTitle: the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
82	c6b2wB_	Alignment	not modelled	7.7	9	PDB header: hydrolase Chain: B: PDB Molecule: putative peptidyl-arginine deiminase family protein; PDBTitle: c. jejuni c315s agmatine deiminase with substrate bound
83	c2hueB_	Alignment	not modelled	7.6	20	PDB header: dna binding protein Chain: B: PDB Molecule: histone h3; PDBTitle: structure of the h3-h4 chaperone asf1 bound to histones h3 and h4
84	c3n6xA_	Alignment	not modelled	7.6	17	PDB header: ligase Chain: A: PDB Molecule: putative glutathionylspermidine synthase; PDBTitle: crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methylobacillus flagellatus kt at 2.35 a resolution
85	c2w82C_	Alignment	not modelled	7.6	2	PDB header: replication inhibitor Chain: C: PDB Molecule: orf18; PDBTitle: the structure of arda
86	c3r5yC_	Alignment	not modelled	7.5	12	PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
87	c4jijA_	Alignment	not modelled	7.4	19	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of t. fusca gh48 d224n mutant
88	c4u0zH_	Alignment	not modelled	7.4	17	PDB header: transferase Chain: H: PDB Molecule: adenosine monophosphate-protein transferase ficd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp
89	c4wpyA_	Alignment	not modelled	7.3	20	PDB header: de novo protein Chain: A: PDB Molecule: protein dl-rv1738; PDBTitle: racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
90	c6hu9u_	Alignment	not modelled	7.3	23	PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
91	c1d0rA_	Alignment	not modelled	7.3	40	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water
92	d1eqzg_	Alignment	not modelled	7.3	20	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
93	c4yicA_	Alignment	not modelled	7.2	15	PDB header: transport protein Chain: A: PDB Molecule: trap transporter solute binding protein; PDBTitle: crystal structure of a trap transporter solute binding protein2 (ipr025997) from bordetella bronchiseptica rb50 (bb0280, target efi-3 500035) with bound picolinic acid
94	c3zf7w_	Alignment	not modelled	7.1	25	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l23, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
95	c2vsnB_	Alignment	not modelled	7.1	16	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcnae2 transferase homolog: insight into molecular control of3 intracellular glycosylation
96	c4c5eG_	Alignment	not modelled	7.0	31	PDB header: transcription Chain: G: PDB Molecule: polycomb protein pho; PDBTitle: crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
97	c4c5eH_	Alignment	not modelled	7.0	31	PDB header: transcription Chain: H: PDB Molecule: polycomb protein pho; PDBTitle: crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
98	c3bb9D_	Alignment	not modelled	7.0	13	PDB header: unknown function Chain: D: PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
99	d1vqow1	Alignment	not modelled	7.0	19	Fold: Ribosomal protein L30p/L7e Superfamily: Ribosomal protein L30p/L7e Family: Ribosomal protein L30p/L7e