
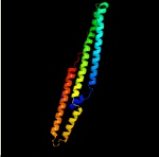
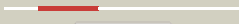
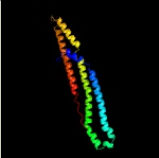

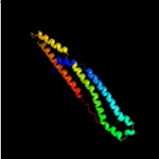

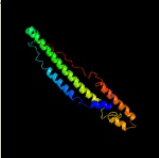

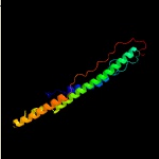

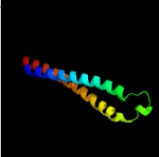



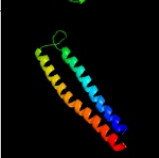

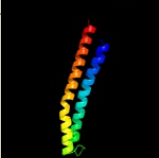



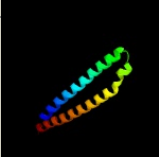


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2356c_(PPE40)_2637698_2639545
 Date Mon Aug 5 13:25:51 BST 2019
 Unique Job ID 43f6aab8cb29e0c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	53	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	d2g38b1	 Alignment		100.0	31	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	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
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		99.3	17	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		98.2	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		98.0	10	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		98.0	19	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		98.0	16	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.6	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		96.7	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	Alignment		96.6	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		96.5	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		95.8	23	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		94.3	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		91.9	28	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		75.3	30	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c2ahmG_	Alignment		38.9	22	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
19	c2iu1A_	Alignment		37.4	39	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
20	d1xkna_	Alignment		36.5	14	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
21	c3ub0D_	Alignment	not modelled	31.0	12	PDB header: replication Chain: D: PDB Molecule: non-structural protein 6, nsp6,; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of 2 feline coronavirus
22	c2fulE_	Alignment	not modelled	28.8	33	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
23	c2I5bA_	Alignment	not modelled	26.4	53	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	c5frgA_	Alignment	not modelled	24.5	75	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
25	c4wgiA_	Alignment	not modelled	22.8	16	PDB header: apoptosis/inhibitor Chain: A: PDB Molecule: maltose-binding periplasmic protein,induced myeloid protein,induced myeloid PDBTitle: a single diastereomer of a macrolactam core binds specifically to 2 myeloid cell leukemia 1 (mcl1)
26	c3fnbB_	Alignment	not modelled	22.6	12	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from 2 streptococcus mutans ua159
27	c1paqA_	Alignment	not modelled	22.4	15	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
28	d1paqa_	Alignment	not modelled	22.4	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like

29	c3h6pB	Alignment	not modelled	21.8	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein exxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
30	c2kg7A	Alignment	not modelled	21.1	37	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
31	c1bkvA	Alignment	not modelled	19.9	44	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
32	c1bkvC	Alignment	not modelled	18.6	44	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
33	c1bkvB	Alignment	not modelled	18.6	44	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
34	c3luiA	Alignment	not modelled	17.5	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
35	c2ke4A	Alignment	not modelled	16.8	75	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
36	c4n91A	Alignment	not modelled	16.1	15	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
37	c3jywF	Alignment	not modelled	15.9	54	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
38	c3r5zB	Alignment	not modelled	15.6	9	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
39	c3zfsA	Alignment	not modelled	13.9	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
40	c4y9iA	Alignment	not modelled	13.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
41	c2l5aA	Alignment	not modelled	12.6	19	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
42	c2kp7A	Alignment	not modelled	12.6	17	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
43	c5yysC	Alignment	not modelled	12.5	17	PDB header: transferase Chain: C: PDB Molecule: l-fucokinase, l-fucose-1-p guanylyltransferase; PDBTitle: cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis
44	c4oo3A	Alignment	not modelled	12.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative oxidoreductase (parmer_00841) from2 parabacteroides merdae atcc 43184 at 2.23 a resolution
45	c6epiC	Alignment	not modelled	12.4	13	PDB header: toxin Chain: C: PDB Molecule: epsilon_1 antitoxin; PDBTitle: structure of the epsilon_1 / zeta_1 antitoxin / toxin system from2 neisseria gonorrhoeae in complex with unam-4p.
46	c4devB	Alignment	not modelled	12.2	18	PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker.
47	c3mveB	Alignment	not modelled	11.4	17	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
48	c3j3bF	Alignment	not modelled	10.7	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
49	c3trhl	Alignment	not modelled	10.7	10	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
50	c5djsA	Alignment	not modelled	10.6	20	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnac transferase mutant - k341m
51	c3j2lY	Alignment	not modelled	10.6	25	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)
						PDB header: flavoprotein

52	c3h96B_	Alignment	not modelled	10.3	6	Chain: B; PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
53	c3r5wO_	Alignment	not modelled	10.1	15	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
54	c2lvyB_	Alignment	not modelled	9.8	13	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
55	c6hu9u_	Alignment	not modelled	9.7	18	PDB header: oxidoreductase/electron transport Chain: U; PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
56	c2kwuA_	Alignment	not modelled	9.7	38	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
57	c3j39F_	Alignment	not modelled	9.6	38	PDB header: ribosome Chain: F; PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
58	c4grdA_	Alignment	not modelled	9.6	19	PDB header: lyase, isomerase Chain: A; PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
59	c5hl8B_	Alignment	not modelled	9.5	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 gspl3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
60	c5lzkB_	Alignment	not modelled	9.2	9	PDB header: structural genomics Chain: B; PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
61	c3pe3D_	Alignment	not modelled	9.2	18	PDB header: transferase Chain: D; PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnac transferase and its complex with a peptide2 substrate
62	c3r5yC_	Alignment	not modelled	9.1	15	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
63	c4i6jB_	Alignment	not modelled	8.9	22	PDB header: transcription Chain: B; PDB Molecule: tf-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
64	c4oanB_	Alignment	not modelled	8.9	14	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)
65	c2zxxD_	Alignment	not modelled	8.7	14	PDB header: transport protein Chain: D; PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in2 complex with lactate
66	c5vmoB_	Alignment	not modelled	8.6	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
67	d1vqow1	Alignment	not modelled	8.5	19	Fold: Ribosomal protein L30p/L7e Superfamily: Ribosomal protein L30p/L7e Family: Ribosomal protein L30p/L7e
68	c2xqvA_	Alignment	not modelled	8.5	14	PDB header: viral protein Chain: A; PDB Molecule: psiv capsid n-terminal domain; PDBTitle: structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
69	c3qthA_	Alignment	not modelled	8.5	9	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
70	c2vsnB_	Alignment	not modelled	8.4	14	PDB header: transferase Chain: B; PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of f3 intracellular glycosylation
71	c3n6xA_	Alignment	not modelled	8.4	13	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
72	d2fgga1	Alignment	not modelled	8.4	40	Fold: dsRBD-like Superfamily: Rv2632c-like Family: Rv2632c-like
73	c6ghrF_	Alignment	not modelled	8.3	53	PDB header: photosynthesis Chain: F; PDB Molecule: cp12 polypeptide; PDBTitle: cyanobacterial gapdh with full-length cp12
74	c5i4rA_	Alignment	not modelled	8.3	43	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)
75	c3zf7w_	Alignment	not modelled	8.2	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
						PDB header: ribosome Chain: E; PDB Molecule: 60s ribosomal protein rpl11 (l5p);

76	c3izce_	Alignment	not modelled	8.2	19	PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
77	c2i3fA_	Alignment	not modelled	8.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glycolipid transfer-like protein; PDBTitle: crystal structure of a glycolipid transfer-like protein from galdieria2 sulphuraria
78	c5ec0A_	Alignment	not modelled	7.9	33	PDB header: structural protein Chain: A: PDB Molecule: alp7a; PDBTitle: crystal structure of actin-like protein alp7a
79	c2wybA_	Alignment	not modelled	7.8	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-homoserine lactone acylase pvdq subunit PDBTitle: the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
80	d1luaa2	Alignment	not modelled	7.7	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
81	c5kdiA_	Alignment	not modelled	7.6	15	PDB header: lipid transport Chain: A: PDB Molecule: pleckstrin homology domain-containing family a member 8; PDBTitle: how fapp2 selects simple glycosphingolipids using the gltp-fold
82	c4mnpA_	Alignment	not modelled	7.6	14	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
83	c4wpyA_	Alignment	not modelled	7.6	20	PDB header: de novo protein Chain: A: PDB Molecule: protein dl-rv1738; PDBTitle: racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
84	c6ansD_	Alignment	not modelled	7.5	16	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia cenocepacia
85	c1gk9A_	Alignment	not modelled	7.4	16	PDB header: antibiotic resistance Chain: A: PDB Molecule: penicillin g acylase alpha subunit; PDBTitle: crystal structures of penicillin acylase enzyme-substrate2 complexes: structural insights into the catalytic mechanism
86	c1d0rA_	Alignment	not modelled	7.1	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
87	d2apla1	Alignment	not modelled	7.1	10	Fold: PG0816-like Superfamily: PG0816-like Family: PG0816-like
88	c2hueB_	Alignment	not modelled	7.0	23	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
89	d1kx5a_	Alignment	not modelled	6.9	23	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
90	c2vh3B_	Alignment	not modelled	6.9	44	PDB header: unknown function Chain: B: PDB Molecule: ranasmurfin; PDBTitle: ranasmurfin
91	c6e0cA_	Alignment	not modelled	6.8	29	PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: cryo-em structure of the cenp-a nucleosome (w601) in complex with a2 single chain antibody fragment
92	c1jrjA_	Alignment	not modelled	6.7	27	PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
93	c6bc8B_	Alignment	not modelled	6.7	22	PDB header: replication Chain: B: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of rev7-r124a/rev3-rbm2 (residues 1988-2014) complex
94	c6bcdB_	Alignment	not modelled	6.7	22	PDB header: replication Chain: B: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of rev7-k44a/r124a/a135d in complex with rev3-rbm22 (residues 1988-2014)
95	c6ekmB_	Alignment	not modelled	6.7	22	PDB header: replication Chain: B: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of mammalian rev7 in complex with human rev3 second2 binding site
96	c6bi7D_	Alignment	not modelled	6.7	22	PDB header: replication Chain: D: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of rev7-wt/rev3 as a monomer under high-salt2 conditions
97	c3a9rA_	Alignment	not modelled	6.7	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
98	c6o9l6_	Alignment	not modelled	6.7	40	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
99	c4gyxC_	Alignment	not modelled	6.5	54	PDB header: structural protein, blood clotting Chain: C: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot