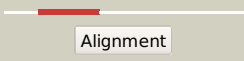
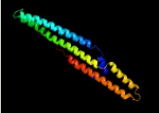
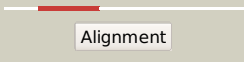
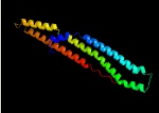
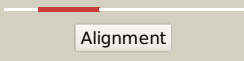
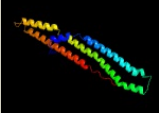
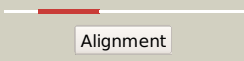
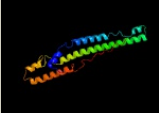
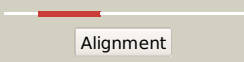
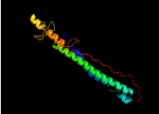
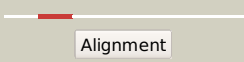
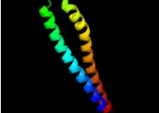
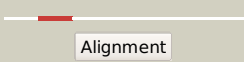

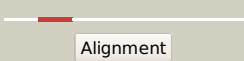

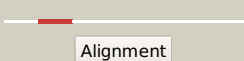

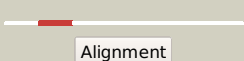
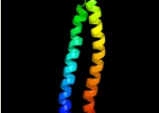
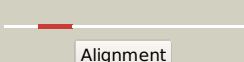
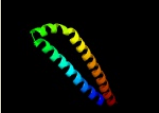


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3533c_(PPE62)_3970884_3972632
 Date Fri Aug 9 18:20:21 BST 2019
 Unique Job ID 96570b9c6b55bf40

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	52	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	29	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	29	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	20	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		98.8	21	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		98.1	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		97.9	11	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		97.9	17	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		97.4	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		96.8	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	Alignment		96.6	10	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		96.4	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		95.9	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		93.9	23	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		81.7	25	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		78.4	28	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c2ahmG_	Alignment		50.1	17	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	d1xkna_	Alignment		41.4	17	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
20	c3ub0D_	Alignment		38.8	17	PDB header: replication Chain: D: PDB Molecule: non-structural protein 6, nsp6,; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of f2 feline coronavirus
21	c3h6pB_	Alignment	not modelled	30.5	34	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
22	c2iu1A_	Alignment	not modelled	25.8	33	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
23	c5frgA_	Alignment	not modelled	25.7	50	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
24	c2lyyB_	Alignment	not modelled	24.1	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
25	c3zfsA_	Alignment	not modelled	23.1	14	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
26	c2kg7A_	Alignment	not modelled	22.3	22	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
27	c2fulE_	Alignment	not modelled	19.9	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
28	c4n91A_	Alignment	not modelled	19.0	16	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
29	c1bkvA_	Alignment	not modelled	18.7	31	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
30	c2l5bA_	Alignment	not modelled	18.4	59	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
31	c2ke4A_	Alignment	not modelled	18.0	50	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
32	c3jywF_	Alignment	not modelled	17.9	59	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	c1bkvC_	Alignment	not modelled	17.5	31	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
34	c1bkvB_	Alignment	not modelled	17.5	31	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
35	c2l5aA_	Alignment	not modelled	16.7	24	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
36	c2hzkB_	Alignment	not modelled	15.9	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
37	c4mnpA_	Alignment	not modelled	15.8	17	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
38	c3h8dC_	Alignment	not modelled	15.7	15	PDB header: motor protein/signaling protein Chain: C: PDB Molecule: myosin-vi; PDBTitle: crystal structure of myosin vi in complex with dab2 peptide
39	c2kp7A_	Alignment	not modelled	15.6	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
40	c3trhl_	Alignment	not modelled	14.3	14	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
41	c1paqA_	Alignment	not modelled	13.9	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
42	d1paqa_	Alignment	not modelled	13.9	20	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
43	c5lzkB_	Alignment	not modelled	13.5	9	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
44	c3juia_	Alignment	not modelled	13.0	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	c5im2A_	Alignment	not modelled	11.9	18	PDB header: transport protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of a trap solute binding protein from rhodospirillum rubrum ferredoxin-like protein 118 (rfer_2570, target efi-510210) in complex with3 copurified benzoate
46	c3b50A_	Alignment	not modelled	11.5	16	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.
47	c4p56C_	Alignment	not modelled	11.1	20	PDB header: solute-binding protein Chain: C: PDB Molecule: putative extracellular solute-binding protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 bordetella bronchiseptica, target efi-510038 (bb2442), with bound3 (r)-mandelate and (s)-mandelate
48	c5hl8B_	Alignment	not modelled	10.0	29	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein i; 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
49	c5i4rA_	Alignment	not modelled	9.9	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/cdi/ef-tu complex (trypsin-modified)
50	c3j3bF_	Alignment	not modelled	9.7	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
51	c2np3A_	Alignment	not modelled	9.6	11	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family regulator; PDBTitle: crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
						PDB header: ribosome

52	c3j21Y_	Alignment	not modelled	9.5	31	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)
53	d2fgga1	Alignment	not modelled	9.3	45	Fold: dsRBD-like Superfamily: Rv2632c-like Family: Rv2632c-like
54	c5ec0A_	Alignment	not modelled	9.1	33	PDB header: structural protein Chain: A; PDB Molecule: alp7a; PDBTitle: crystal structure of actin-like protein alp7a
55	c2kwuA_	Alignment	not modelled	8.9	31	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
56	c5vmoB_	Alignment	not modelled	8.9	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
57	c4el8A_	Alignment	not modelled	8.8	31	PDB header: hydrolase Chain: A; PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.bescii cela gh48 module
58	d2apla1	Alignment	not modelled	8.7	12	Fold: PG0816-like Superfamily: PG0816-like Family: PG0816-like
59	c5i7iB_	Alignment	not modelled	8.6	24	PDB header: transport protein Chain: B; PDB Molecule: trap solute binding protein; PDBTitle: crystal structure of a marine metagenome trap solute binding protein2 specific for aromatic acid ligands (sorcerer ii global ocean sampling3 expedition, unidentified microbe, locus tag gos_1523157) in complex4 with co-crystallized 3-hydroxybenzoate
60	c6o9l6_	Alignment	not modelled	8.5	50	PDB header: transcription/dna Chain: 6; PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
61	c4wpyA_	Alignment	not modelled	8.4	20	PDB header: de novo protein Chain: A; PDB Molecule: protein dl-rv1738; PDBTitle: racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
62	c4i6jB_	Alignment	not modelled	8.3	11	PDB header: transcription Chain: B; PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
63	c2nviA_	Alignment	not modelled	8.3	38	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
64	c5djsA_	Alignment	not modelled	8.3	20	PDB header: transferase Chain: A; PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnae transferase mutant -k341m
65	c3j39F_	Alignment	not modelled	8.3	38	PDB header: ribosome Chain: F; PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
66	c3a9rA_	Alignment	not modelled	8.1	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
67	c6hu9u_	Alignment	not modelled	7.9	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
68	c3pe3D_	Alignment	not modelled	7.9	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
69	c3qthA_	Alignment	not modelled	7.9	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	c4y9iA_	Alignment	not modelled	7.9	22	PDB header: oxidoreductase Chain: A; PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
71	c1bzgA_	Alignment	not modelled	7.7	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
72	c3izce_	Alignment	not modelled	7.6	19	PDB header: ribosome Chain: E; PDB Molecule: 60s ribosomal protein rpl11 (l5p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
73	c4u0zH_	Alignment	not modelled	7.6	12	PDB header: transferase Chain: H; PDB Molecule: adenosine monophosphate-protein transferase ficcd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp
74	c3n6xA_	Alignment	not modelled	7.5	16	PDB header: ligase Chain: A; PDB Molecule: putative glutathionylspermidine synthase; PDBTitle: crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methyllobacillus flagellatus kt at 2.35 a resolution
75	d1kx5a_	Alignment	not modelled	7.4	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
76	c4kka_	Alignment	not modelled	7.4	10	PDB header: hydrolase Chain: A; PDB Molecule: exoglucanase s;

76	c4kkaA	Alignment	not modelled	7.4	19	PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
77	d1l1ya	Alignment	not modelled	7.4	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
78	c1l2aD	Alignment	not modelled	7.4	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
79	c1gk9A	Alignment	not modelled	7.3	14	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
80	c6epiC	Alignment	not modelled	7.3	22	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.
81	c2jerG	Alignment	not modelled	7.2	22	PDB header: hydrolase Chain: G: PDB Molecule: agmatine deiminase; PDBTitle: agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
82	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
83	c4fusA	Alignment	not modelled	7.1	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
84	c2vsnB	Alignment	not modelled	7.1	10	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
85	d1rp3a1	Alignment	not modelled	7.0	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain PDB header: isomerase
86	c6o55B	Alignment	not modelled	7.0	14	Chain: B: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila
87	c3zf7w	Alignment	not modelled	6.9	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
88	c3u65B	Alignment	not modelled	6.9	6	PDB header: transport protein Chain: B: PDB Molecule: tp33 protein; PDBTitle: the crystal structure of tat-p(t) (tp0957)
89	c4jijA	Alignment	not modelled	6.9	19	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of t. fusca gh48 d224n mutant
90	c3r5zB	Alignment	not modelled	6.8	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
91	c1e3aA	Alignment	not modelled	6.8	18	PDB header: antibiotic resistance Chain: A: PDB Molecule: penicillin amidase alpha subunit; PDBTitle: a slow processing precursor penicillin acylase from escherichia coli
92	c3bb9D	Alignment	not modelled	6.7	9	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
93	c4yicA	Alignment	not modelled	6.7	14	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	c2lkqA	Alignment	not modelled	6.7	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
95	d1vqow1	Alignment	not modelled	6.7	19	Fold: Ribosomal protein L30p/L7e Superfamily: Ribosomal protein L30p/L7e Family: Ribosomal protein L30p/L7e
96	c2jwbB	Alignment	not modelled	6.7	17	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
97	c3fnbB	Alignment	not modelled	6.5	10	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
98	c4deyB	Alignment	not modelled	6.5	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.
99	d1eqzg	Alignment	not modelled	6.5	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones