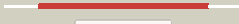



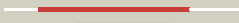




















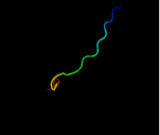
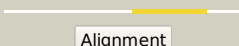

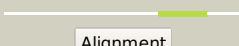
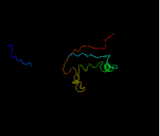
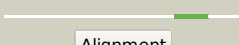

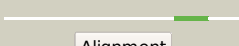

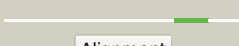


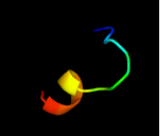




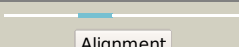
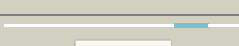

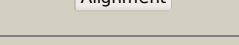





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2819c (-)_3126250_3127377
Date	Wed Aug 7 12:50:48 BST 2019
Unique Job ID	284802dcfae175cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ig0H_</a>	 Alignment		100.0	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> type iii-a crispr-associated ramp protein csm5; <b>PDBTitle:</b> type iii-a csm complex, cryo-em structure of csm-ctr1, atp bound
2	<a href="#">c6musF_</a>	 Alignment		100.0	22	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein csm5; <b>PDBTitle:</b> cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system
3	<a href="#">c6musK_</a>	 Alignment		99.6	21	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> K: <b>PDB Molecule:</b> uncharacterized protein csm3; <b>PDBTitle:</b> cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system
4	<a href="#">c4w8vA_</a>	 Alignment		99.6	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr6; <b>PDBTitle:</b> crystal structure of cmr6 from pyrococcus furiosus
5	<a href="#">c6ifnF_</a>	 Alignment		99.5	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> type iii-a crispr-associated ramp protein csm3; <b>PDBTitle:</b> crystal structure of type iii-a crispr csm complex
6	<a href="#">c4qtsC_</a>	 Alignment		99.4	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> crispr type iii-associated ramp protein csm3; <b>PDBTitle:</b> crystal structure of csm3-csm4 subcomplex in the type iii-a crispr-cas2 interference complex
7	<a href="#">c5yjdB_</a>	 Alignment		99.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> csm3; <b>PDBTitle:</b> structural insights into the crispr-cas-associated ribonuclease2 activity of staphylococcus epidermidis csm3
8	<a href="#">c6ae2B_</a>	 Alignment		99.3	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> csm3; <b>PDBTitle:</b> crystal structure of csm3 of the type iii-a crispr-cas effector2 complex
9	<a href="#">c3x1IE_</a>	 Alignment		99.3	27	<b>PDB header:</b> rna binding protein/rna/dna <b>Chain:</b> E: <b>PDB Molecule:</b> cmr4; <b>PDBTitle:</b> crystal structure of the crispr-cas rna silencing cmr complex bound to2 a target analog
10	<a href="#">c4n0IB_</a>	 Alignment		99.0	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> predicted component of a thermophile-specific dna repair <b>PDBTitle:</b> methanopyrus kandleri csm3 crystal structure
11	<a href="#">c4w8wB_</a>	 Alignment		99.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> crispr system cmr subunit cmr4; <b>PDBTitle:</b> crystal structure of oligomeric cmr4 from pyrococcus furiosus

12	<a href="#">c3x1H_</a>		Alignment		98.9	13	<b>PDB header:</b> rna binding protein/rna/dna <b>Chain:</b> H: <b>PDB Molecule:</b> cmr6; <b>PDBTitle:</b> crystal structure of the crispr-cas rna silencing cmr complex bound to2 a target analog
13	<a href="#">c4w8xA_</a>		Alignment		83.4	5	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr1-1; <b>PDBTitle:</b> crystal structure of cmr1 from pyrococcus furiosus bound to a2 nucleotide
14	<a href="#">c3ijeB_</a>		Alignment		77.3	15	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> crystal structure of the complete integrin alphavbeta3 ectodomain plus2 an alpha/beta transmembrane fragment
15	<a href="#">c3k6sB_</a>		Alignment		60.2	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-2; <b>PDBTitle:</b> structure of integrin alphaxbeta2 ectodomain
16	<a href="#">c1u3fA_</a>		Alignment		58.3	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 5,10-methenyltetrahydrofolate synthetase; <b>PDBTitle:</b> structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
17	<a href="#">d1sbqa_</a>		Alignment		58.3	38	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> Methenyltetrahydrofolate synthetase
18	<a href="#">c2jcbA_</a>		Alignment		52.2	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-formyltetrahydrofolate cyclo-ligase family protein; <b>PDBTitle:</b> the crystal structure of 5-formyl-tetrahydrofolate2 cycloligase from bacillus anthracis (ba4489)
19	<a href="#">c3hy4A_</a>		Alignment		50.1	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-formyltetrahydrofolate cyclo-ligase; <b>PDBTitle:</b> structure of human mthfs with n5-iminium phosphate
20	<a href="#">d1wkca_</a>		Alignment		48.7	31	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> Methenyltetrahydrofolate synthetase
21	<a href="#">c1ydmC_</a>		Alignment	not modelled	45.7	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein yqgn; <b>PDBTitle:</b> x-ray structure of northeast structural genomics target sr44
22	<a href="#">c1u8cB_</a>		Alignment	not modelled	40.9	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> a novel adaptation of the integrin psi domain revealed from its2 crystal structure
23	<a href="#">c2q6mA_</a>		Alignment	not modelled	39.8	30	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> cholix toxin; <b>PDBTitle:</b> catalytic fragment of cholix toxin from vibrio cholerae in complex2 with the pj34 inhibitor
24	<a href="#">d1soua_</a>		Alignment	not modelled	38.8	38	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> Methenyltetrahydrofolate synthetase
25	<a href="#">c4l6uB_</a>		Alignment	not modelled	36.9	33	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of af1868: cmr1 subunit of the cmr rna silencing2 complex
26	<a href="#">c4h4kA_</a>		Alignment	not modelled	33.5	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr3; <b>PDBTitle:</b> structure of the cmr2-cmr3 subcomplex of the cmr rna-silencing complex
27	<a href="#">d1qr0a1</a>		Alignment	not modelled	30.7	31	<b>Fold:</b> 4'-phosphopantetheinyl transferase <b>Superfamily:</b> 4'-phosphopantetheinyl transferase <b>Family:</b> 4'-Phosphopantetheinyl transferase SFP
28	<a href="#">c2q5tA_</a>		Alignment	not modelled	30.7	30	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> cholix toxin; <b>PDBTitle:</b> full-length cholix toxin from vibrio cholerae
							<b>PDB header:</b> protein binding

29	<a href="#">c2lycA</a>	Alignment	not modelled	28.6	67	<b>Chain:</b> A: <b>PDB Molecule:</b> spindle and kinetochore-associated protein 1 homolog; <b>PDBTitle:</b> structure of c-terminal domain of ska1
30	<a href="#">d1lkpa2</a>	Alignment	not modelled	25.3	41	<b>Fold:</b> ADP-ribosylation <b>Superfamily:</b> ADP-ribosylation <b>Family:</b> ADP-ribosylating toxins
31	<a href="#">d2ix0a3</a>	Alignment	not modelled	22.0	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
32	<a href="#">c4um9D</a>	Alignment	not modelled	20.7	22	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> integrin beta-6; <b>PDBTitle:</b> crystal structure of alpha v beta 6 with peptide
33	<a href="#">c6n1nA</a>	Alignment	not modelled	19.1	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of class d beta-lactamase from sebaldella termitidis2 atcc 33386
34	<a href="#">c2it0A</a>	Alignment	not modelled	18.7	42	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
35	<a href="#">c5bv3C</a>	Alignment	not modelled	18.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> m7gpppx diphosphatase; <b>PDBTitle:</b> yeast scavenger decapping enzyme in complex with m7gdp
36	<a href="#">c1ikqA</a>	Alignment	not modelled	16.9	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> exotoxin a; <b>PDBTitle:</b> pseudomonas aeruginosa exotoxin a, wild type
37	<a href="#">c1qr0A</a>	Alignment	not modelled	16.3	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4'-phosphopantetheinyl transferase sfp; <b>PDBTitle:</b> crystal structure of the 4'-phosphopantetheinyl transferase sfp-2 coenzyme a complex
38	<a href="#">c2ixsB</a>	Alignment	not modelled	15.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sdai restriction endonuclease; <b>PDBTitle:</b> structure of sdai restriction endonuclease
39	<a href="#">c1cjbB</a>	Alignment	not modelled	15.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (cytosolic phospholipase a2); <b>PDBTitle:</b> human cytosolic phospholipase a2
40	<a href="#">c4gn2A</a>	Alignment	not modelled	15.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxacillinase; <b>PDBTitle:</b> crystal structure of oxa-45, a class d beta-lactamase with extended2 spectrum activity
41	<a href="#">c4xpuA</a>	Alignment	not modelled	14.9	80	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> the crystal structure of endov from e.coli
42	<a href="#">c3ga2A</a>	Alignment	not modelled	14.6	80	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> crystal structure of the endonuclease_v (bsu36170) from bacillus2 subtilis, northeast structural genomics consortium target sr624
43	<a href="#">c2mmbA</a>	Alignment	not modelled	14.4	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein yp_001712342.1 from acinetobacter2 baumannii
44	<a href="#">c4xb6D</a>	Alignment	not modelled	14.3	36	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; <b>PDBTitle:</b> structure of the e. coli c-p lyase core complex
45	<a href="#">d1rutx3</a>	Alignment	not modelled	14.2	18	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
46	<a href="#">c3jszA</a>	Alignment	not modelled	14.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> legionella pneumophila glucosyltransferase lgt1 n293a with udp-glc
47	<a href="#">c4nspA</a>	Alignment	not modelled	14.1	80	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> crystal structure of human endov
48	<a href="#">c2moqA</a>	Alignment	not modelled	13.6	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> iron-regulated surface determinant protein b; <b>PDBTitle:</b> solution structure and molecular determinants of hemoglobin binding of2 the first neat domain of isdb in staphylococcus aureus
49	<a href="#">d1k38a</a>	Alignment	not modelled	13.5	40	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
50	<a href="#">d1isua</a>	Alignment	not modelled	13.4	50	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
51	<a href="#">c4kbfF</a>	Alignment	not modelled	13.3	63	<b>PDB header:</b> transcription/replication <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein pob3n; <b>PDBTitle:</b> structure of the spt16d pob3n heterodimer
52	<a href="#">c6bn3A</a>	Alignment	not modelled	13.2	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> ctx-m-151 class a extended-spectrum beta-lactamase apo crystal2 structure at 1.3 angstrom resolution.
53	<a href="#">c3gocB</a>	Alignment	not modelled	13.1	100	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
54	<a href="#">c2w36B</a>	Alignment	not modelled	13.0	80	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair

55	<a href="#">c5u1lA_</a>	Alignment	not modelled	12.8	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> p2x purinoceptor; <b>PDBTitle:</b> crystal structure of the atp-gated p2x7 ion channel in the closed, apo2 state
56	<a href="#">c4jbfB_</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidoglycan glycosyltransferase; <b>PDBTitle:</b> crystal structure of peptidoglycan glycosyltransferase from atopobium2 parvulum dsm 20469.
57	<a href="#">c1cm4B_</a>	Alignment	not modelled	12.6	30	<b>PDB header:</b> calcium-binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calmodulin-dependent protein kinase ii-alpha; <b>PDBTitle:</b> motions of calmodulin-four-conformer refinement
58	<a href="#">c1cm1B_</a>	Alignment	not modelled	12.6	30	<b>PDB header:</b> complex (calcium-binding/transferase) <b>Chain:</b> B: <b>PDB Molecule:</b> calmodulin-dependent protein kinase ii-alpha; <b>PDBTitle:</b> motions of calmodulin-single-conformer refinement
59	<a href="#">c1cdmB_</a>	Alignment	not modelled	12.6	30	<b>PDB header:</b> calcium-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> calmodulin; <b>PDBTitle:</b> modulation of calmodulin plasticity in molecular2 recognition on the basis of x-ray structures
60	<a href="#">c4k0xA_</a>	Alignment	not modelled	12.5	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> x-ray crystal structure of oxa-23 from acinetobacter baumannii
61	<a href="#">c3gp2B_</a>	Alignment	not modelled	12.5	30	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase type <b>PDBTitle:</b> calmodulin bound to peptide from calmodulin kinase ii2 (camkii)
62	<a href="#">c5xw6B_</a>	Alignment	not modelled	12.5	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> p2x purinoceptor; <b>PDBTitle:</b> crystal structure of the chicken atp-gated p2x7 receptor channel in2 the presence of competitive antagonist trp-atp at 3.1 angstroms
63	<a href="#">d1r5ba3</a>	Alignment	not modelled	12.3	40	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
64	<a href="#">c4hlxD_</a>	Alignment	not modelled	12.2	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> k9; <b>PDBTitle:</b> the crystal structure of the dna binding domain of virf-1 from the2 oncogenic kshv
65	<a href="#">d1xa1a_</a>	Alignment	not modelled	12.1	37	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
66	<a href="#">c3i5dC_</a>	Alignment	not modelled	11.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> p2x purinoceptor; <b>PDBTitle:</b> crystal structure of the atp-gated p2x4 ion channel in the closed, apo2 state at 3.5 angstroms (r3)
67	<a href="#">c6gnyD_</a>	Alignment	not modelled	11.6	33	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> telomere repeats-binding bouquet formation protein 2; <b>PDBTitle:</b> crystal structure of the majin-terb2 heterotetrameric complex
68	<a href="#">c2wd6B_</a>	Alignment	not modelled	11.6	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> agglutinin receptor; <b>PDBTitle:</b> crystal structure of the variable domain of the streptococcus gordonii2 surface protein sspb
69	<a href="#">c6gnxB_</a>	Alignment	not modelled	11.5	33	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> telomere repeats-binding bouquet formation protein 2; <b>PDBTitle:</b> crystal structure of the majin-terb2 heterotetrameric complex -2 selenomethionine derivative
70	<a href="#">c3fcuB_</a>	Alignment	not modelled	11.3	15	<b>PDB header:</b> cell adhesion/blood clotting <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> structure of headpiece of integrin aiibb3 in open conformation
71	<a href="#">c3vi3D_</a>	Alignment	not modelled	10.6	14	<b>PDB header:</b> cell adhesion/immune system <b>Chain:</b> D: <b>PDB Molecule:</b> integrin beta-1; <b>PDBTitle:</b> crystal structure of alpha5beta1 integrin headpiece (ligand-free form)
72	<a href="#">d2pifa1</a>	Alignment	not modelled	10.1	36	<b>Fold:</b> PSTPO5379-like <b>Superfamily:</b> PSTPO5379-like <b>Family:</b> PSTPO5379-like
73	<a href="#">c4kt3B_</a>	Alignment	not modelled	9.8	42	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> structure of a type vi secretion system effector-immunity complex from2 pseudomonas protegens
74	<a href="#">c3oqcB_</a>	Alignment	not modelled	9.6	63	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ufm1-specific protease 2; <b>PDBTitle:</b> ubiquitin-fold modifier 1 specific protease, ufsp2
75	<a href="#">c6nhsA_</a>	Alignment	not modelled	9.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the beta lactamase class d ybxi from nostoc
76	<a href="#">c4oh0A_</a>	Alignment	not modelled	9.6	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase oxa-58; <b>PDBTitle:</b> crystal structure of oxa-58 carbapenemase
77	<a href="#">c2jc7A_</a>	Alignment	not modelled	9.5	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase oxa-24; <b>PDBTitle:</b> the crystal structure of the carbapenemase oxa-24 reveals2 new insights into the mechanism of carbapenem-hydrolysis
78	<a href="#">c3j7yf_</a>	Alignment	not modelled	9.0	21	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> ul4; <b>PDBTitle:</b> structure of the large ribosomal subunit from human mitochondria
79	<a href="#">c4byrP_</a>	Alignment	not modelled	8.9	50	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b; <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnamet2 eukaryotic translation initiation complex

80	<a href="#">d1tza3</a>	Alignment	not modelled	8.8	30	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
81	<a href="#">c5ctmB</a>	Alignment	not modelled	8.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> structure of bpu1 beta-lactamase
82	<a href="#">d1irxa2</a>	Alignment	not modelled	8.6	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
83	<a href="#">c2hdnj</a>	Alignment	not modelled	8.6	50	<b>PDB header:</b> translation <b>Chain:</b> J: <b>PDB Molecule:</b> elongation factor ef-tu; <b>PDBTitle:</b> trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
84	<a href="#">c2z84A</a>	Alignment	not modelled	8.5	63	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ufm1-specific protease 1; <b>PDBTitle:</b> insights from crystal and solution structures of mouse ufsp1
85	<a href="#">d1rr7a</a>	Alignment	not modelled	8.3	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Middle operon regulator, Mor
86	<a href="#">c1rr7A</a>	Alignment	not modelled	8.3	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> middle operon regulator; <b>PDBTitle:</b> crystal structure of the middle operon regulator protein of2 bacteriophage mu
87	<a href="#">c2xi5D</a>	Alignment	not modelled	8.1	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> rna polymerase I; <b>PDBTitle:</b> n-terminal endonuclease domain of la crosse virus I-protein
88	<a href="#">c5cv1A</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> p granule abnormality protein 1; <b>PDBTitle:</b> c. elegans pgl-1 dimerization domain
89	<a href="#">d1tuba1</a>	Alignment	not modelled	8.0	29	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
90	<a href="#">c2xi7B</a>	Alignment	not modelled	8.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase I; <b>PDBTitle:</b> n-terminal endonuclease domain of la crosse virus I-protein
91	<a href="#">c3c26A</a>	Alignment	not modelled	8.0	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase ta0821; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase (np_394282.1) from2 thermoplasma acidophilum at 2.00 a resolution
92	<a href="#">c6k0bH</a>	Alignment	not modelled	8.0	22	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> H: <b>PDB Molecule:</b> ribonuclease p protein component 4; <b>PDBTitle:</b> cryo-em structure of archaeal ribonuclease p with mature trna
93	<a href="#">c5k0yS</a>	Alignment	not modelled	7.8	25	<b>PDB header:</b> translation <b>Chain:</b> S: <b>PDB Molecule:</b> eukaryotic initiation factor 2 gamma subunit (eif2-gamma); <b>PDBTitle:</b> m48s late-stage initiation complex, purified from rabbit reticulocytes2 lysates, displaying eif2 ternary complex and eif3 i and g subunits3 relocated to the intersubunit face
94	<a href="#">c6ei1A</a>	Alignment	not modelled	7.8	63	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger with ufm1-specific peptidase domain protein; <b>PDBTitle:</b> crystal structure of the covalent complex between deubiquitinase zufsp2 (zup1) and ubiquitin-pa
95	<a href="#">c3hbrD</a>	Alignment	not modelled	7.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> oxa-48; <b>PDBTitle:</b> crystal structure of oxa-48 beta-lactamase
96	<a href="#">c6gbsB</a>	Alignment	not modelled	7.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative mrna decapping protein; <b>PDBTitle:</b> crystal structure of the c. thermophilum scavenger decapping enzyme2 dcps apo form
97	<a href="#">c2cg5A</a>	Alignment	not modelled	7.6	14	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aminoadipate-semialdehyde dehydrogenase- <b>PDBTitle:</b> structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic acyl3 carrier protein and coenzyme a
98	<a href="#">d1tubb1</a>	Alignment	not modelled	7.5	18	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
99	<a href="#">c5e2fB</a>	Alignment	not modelled	7.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase ybxi; <b>PDBTitle:</b> crystal structure of beta-lactamase class d from bacillus subtilis