




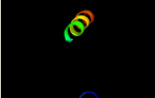

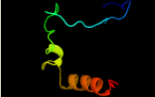

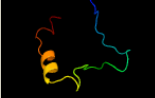









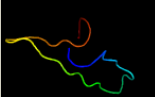



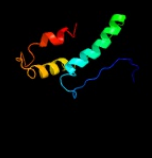
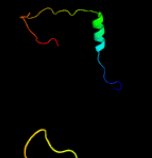
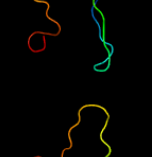
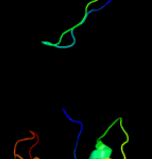
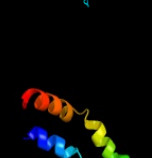
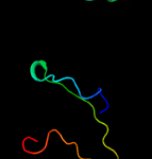
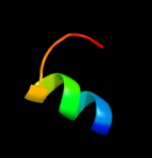
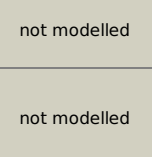


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3785 (-) _4231498_4232571
Date	Fri Aug 9 18:20:49 BST 2019
Unique Job ID	dc478003190e5dd5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rkhA_</a>	 Alignment		51.2	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative apha-like transcription factor; <b>PDBTitle:</b> crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution
2	<a href="#">c4dt1B_</a>	 Alignment		30.3	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> platinum sensitivity protein 3; <b>PDBTitle:</b> crystal structure of the psy3-csm2 complex
3	<a href="#">c2v6xB_</a>	 Alignment		28.5	50	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> doa4-independent degradation protein 4; <b>PDBTitle:</b> structural insight into the interaction between escrt-iii and vps4
4	<a href="#">d2pbka1</a>	 Alignment		22.2	35	<b>Fold:</b> Herpes virus serine proteinase, assemblin <b>Superfamily:</b> Herpes virus serine proteinase, assemblin <b>Family:</b> Herpes virus serine proteinase, assemblin
5	<a href="#">c3njqB_</a>	 Alignment		21.7	29	<b>PDB header:</b> viral protein/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> orf 17; <b>PDBTitle:</b> crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
6	<a href="#">d1at3a_</a>	 Alignment		21.3	46	<b>Fold:</b> Herpes virus serine proteinase, assemblin <b>Superfamily:</b> Herpes virus serine proteinase, assemblin <b>Family:</b> Herpes virus serine proteinase, assemblin
7	<a href="#">d2cyja1</a>	 Alignment		19.8	22	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
8	<a href="#">c2jqmA_</a>	 Alignment		19.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> envelope protein e; <b>PDBTitle:</b> yellow fever envelope protein domain iii nmr structure2 (s288-k398)
9	<a href="#">c3hjeA_</a>	 Alignment		18.3	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 704aa long hypothetical glycosyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus tokodaii hypothetical maltooligosyl2 trehalose synthase
10	<a href="#">c3egpA_</a>	 Alignment		17.7	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> crystal structure analysis of dengue-1 envelope protein2 domain iii
11	<a href="#">d2al3a1</a>	 Alignment		17.6	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain

12	<a href="#">d1iega_</a>	Alignment		16.3	22	<b>Fold:</b> Herpes virus serine proteinase, assemblin <b>Superfamily:</b> Herpes virus serine proteinase, assemblin <b>Family:</b> Herpes virus serine proteinase, assemblin
13	<a href="#">c1fx0B_</a>	Alignment		15.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase beta chain; <b>PDBTitle:</b> crystal structure of the chloroplast f1-atpase from spinach
14	<a href="#">c2vdcl_</a>	Alignment		15.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
15	<a href="#">c2h0pA_</a>	Alignment		15.5	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> nmr structure of the dengue-4 virus envelope protein domain2 iii
16	<a href="#">d1ok8a1</a>	Alignment		14.4	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Class II viral fusion proteins C-terminal domain
17	<a href="#">d2fmla2</a>	Alignment		12.4	20	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
18	<a href="#">c3nrhA_</a>	Alignment		12.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bf1032; <b>PDBTitle:</b> crystal structure of protein bf1032 from bacteroides fragilis,2 northeast structural genomics consortium target bfr309
19	<a href="#">d1s6na_</a>	Alignment		11.3	42	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Class II viral fusion proteins C-terminal domain
20	<a href="#">d2o3aa1</a>	Alignment		11.1	29	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> AF0751-like
21	<a href="#">d2fyta1</a>	Alignment	not modelled	11.0	18	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
22	<a href="#">c3uajA_</a>	Alignment	not modelled	10.9	22	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
23	<a href="#">d2fi9a1</a>	Alignment	not modelled	10.8	33	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
24	<a href="#">c2yrcA_</a>	Alignment	not modelled	10.7	71	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein sec23a; <b>PDBTitle:</b> solution structure of the zf-sec23_sec24 from human sec23a
25	<a href="#">c6epkA_</a>	Alignment	not modelled	10.7	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope protein e; <b>PDBTitle:</b> crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the yellow fever virus
26	<a href="#">c3fz5C_</a>	Alignment	not modelled	10.3	24	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> possible 2-hydroxychromene-2-carboxylate isomerase; <b>PDBTitle:</b> crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
27	<a href="#">c4ip8B_</a>	Alignment	not modelled	10.3	30	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> serum amyloid a-1 protein; <b>PDBTitle:</b> structure of human serum amyloid a1
28	<a href="#">d1fx0a3</a>	Alignment	not modelled	10.0	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)

29	<a href="#">d1o6ea</a>	Alignment	not modelled	9.9	25	<b>Fold:</b> Herpes virus serine proteinase, assemblin <b>Superfamily:</b> Herpes virus serine proteinase, assemblin <b>Family:</b> Herpes virus serine proteinase, assemblin
30	<a href="#">c2k2eA</a>	Alignment	not modelled	9.8	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bp2786; <b>PDBTitle:</b> solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
31	<a href="#">c5x51X</a>	Alignment	not modelled	9.7	38	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> rna polymerase subunit, found in rna polymerase complexes <b>PDBTitle:</b> rna polymerase ii from komagataella pastoris (type-3 crystal)
32	<a href="#">c2h6oA</a>	Alignment	not modelled	9.6	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> major outer envelope glycoprotein gp350; <b>PDBTitle:</b> epstein barr virus major envelope glycoprotein
33	<a href="#">c1uzgA</a>	Alignment	not modelled	9.5	25	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> major envelope protein e; <b>PDBTitle:</b> crystal structure of the dengue type 3 virus envelope2 protein
34	<a href="#">c2yxyA</a>	Alignment	not modelled	9.3	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein, gk0453; <b>PDBTitle:</b> crystal structure of hypothetical conserved protein, gk0453
35	<a href="#">c5zcrB</a>	Alignment	not modelled	9.3	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> maltoooligosyl trehalose synthase; <b>PDBTitle:</b> dsm5389 glycosyltrehalose synthase
36	<a href="#">d1dqna</a>	Alignment	not modelled	9.3	50	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
37	<a href="#">c2yy8B</a>	Alignment	not modelled	9.1	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0106 protein ph0461; <b>PDBTitle:</b> crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
38	<a href="#">d1ztxe1</a>	Alignment	not modelled	9.0	42	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Class II viral fusion proteins C-terminal domain
39	<a href="#">c6rdtY</a>	Alignment	not modelled	9.0	23	<b>PDB header:</b> proton transport <b>Chain:</b> Y: <b>PDB Molecule:</b> atp synthase subunit beta; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 composite map
40	<a href="#">c4xvwK</a>	Alignment	not modelled	8.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> K: <b>PDB Molecule:</b> dsba-like protein; <b>PDBTitle:</b> crystal structure of proteus mirabilis scsc in a compact conformation
41	<a href="#">d2iida1</a>	Alignment	not modelled	8.5	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
42	<a href="#">c3c6dB</a>	Alignment	not modelled	8.4	22	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> polyprotein; <b>PDBTitle:</b> the pseudo-atomic structure of dengue immature virus
43	<a href="#">d1pjwa</a>	Alignment	not modelled	8.2	39	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Class II viral fusion proteins C-terminal domain
44	<a href="#">d1z6ma1</a>	Alignment	not modelled	8.2	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
45	<a href="#">d2q4qa1</a>	Alignment	not modelled	7.9	22	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
46	<a href="#">c5whaF</a>	Alignment	not modelled	7.6	68	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> miniprotein 225-11; <b>PDBTitle:</b> kras g12v, bound to gdp and miniprotein 225-11
47	<a href="#">c1hznA</a>	Alignment	not modelled	7.6	45	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> cholecystokinin type a receptor; <b>PDBTitle:</b> nmr solution structure of the third extracellular loop of2 the cholecystokinin a receptor
48	<a href="#">d1na6a2</a>	Alignment	not modelled	7.6	19	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Type II restriction endonuclease catalytic domain
49	<a href="#">d2ifxa1</a>	Alignment	not modelled	7.5	39	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> MmlI-like
50	<a href="#">c6eh1D</a>	Alignment	not modelled	7.5	70	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> minor capsid protein micp; <b>PDBTitle:</b> sacbrood virus of honeybee - expansion state ii
51	<a href="#">c6egvD</a>	Alignment	not modelled	7.5	70	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> minor capsid protein micp; <b>PDBTitle:</b> sacbrood virus of honeybee
52	<a href="#">c6egxD</a>	Alignment	not modelled	7.5	70	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> minor capsid protein micp; <b>PDBTitle:</b> sacbrood virus of honeybee - expansion state i
53	<a href="#">c5oypD</a>	Alignment	not modelled	7.5	70	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> minor capsid protein micp; <b>PDBTitle:</b> sacbrood virus of honeybee
54	<a href="#">c5lsfD</a>	Alignment	not modelled	7.5	70	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> vp4; <b>PDBTitle:</b> sacbrood honeybee virus
						<b>PDB header:</b> transferase

55	<a href="#">c2ja6L</a>	Alignment	not modelled	7.1	38	<b>Chain:</b> L: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii 7.7 kda <b>PDBTitle:</b> cpd lesion containing rna polymerase ii elongation complex b
56	<a href="#">c6f5dE</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> atp synthase subunit beta, mitochondrial; <b>PDBTitle:</b> trypanosoma brucei f1-atpase
57	<a href="#">c4gxzB</a>	Alignment	not modelled	7.1	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> suppression of copper sensitivity protein; <b>PDBTitle:</b> crystal structure of a periplasmic thioredoxin-like protein from 2 salmonella enterica serovar typhimurium
58	<a href="#">c2gm2A</a>	Alignment	not modelled	7.1	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
59	<a href="#">c5flmL</a>	Alignment	not modelled	6.9	31	<b>PDB header:</b> transcription <b>Chain:</b> L: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc4; <b>PDBTitle:</b> structure of transcribing mammalian rna polymerase ii
60	<a href="#">c5j8tA</a>	Alignment	not modelled	6.9	0	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> choline binding protein; <b>PDBTitle:</b> nmr structure of excalibur domain of cbpl
61	<a href="#">c2yewB</a>	Alignment	not modelled	6.9	25	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> e1 envelope glycoprotein; <b>PDBTitle:</b> modeling barmah forest virus structural proteins
62	<a href="#">c3nuhB</a>	Alignment	not modelled	6.7	57	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
63	<a href="#">d2alaa2</a>	Alignment	not modelled	6.6	63	<b>Fold:</b> Viral glycoprotein, central and dimerisation domains <b>Superfamily:</b> Viral glycoprotein, central and dimerisation domains <b>Family:</b> Viral glycoprotein, central and dimerisation domains
64	<a href="#">c4exnF</a>	Alignment	not modelled	6.4	62	<b>PDB header:</b> cytokine <b>Chain:</b> F: <b>PDB Molecule:</b> interleukin-34; <b>PDBTitle:</b> crystal structure of mouse interleukin-34
65	<a href="#">c6eezC</a>	Alignment	not modelled	6.4	22	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> dsba-like disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of the thiol-disulfide exchange protein alpha-dsba22 from wolbachia pipientis
66	<a href="#">c1kmhA</a>	Alignment	not modelled	6.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atpase alpha subunit; <b>PDBTitle:</b> crystal structure of spinach chloroplast f1-atpase complexed with 2 tentoxin
67	<a href="#">c5d50E</a>	Alignment	not modelled	6.2	42	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> anti-repressor protein; <b>PDBTitle:</b> crystal structure of rep-ant complex from salmonella-temperate phage
68	<a href="#">c1na6B</a>	Alignment	not modelled	6.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> restriction endonuclease ecorii; <b>PDBTitle:</b> crystal structure of restriction endonuclease ecorii mutant2 r88a
69	<a href="#">d1u0bb1</a>	Alignment	not modelled	6.0	32	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
70	<a href="#">d1t1ua2</a>	Alignment	not modelled	5.9	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
71	<a href="#">c3h0gL</a>	Alignment	not modelled	5.9	33	<b>PDB header:</b> transcription <b>Chain:</b> L: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc4; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
72	<a href="#">d1iv8a2</a>	Alignment	not modelled	5.6	50	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
73	<a href="#">c6o55B</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila
74	<a href="#">c2zkr9</a>	Alignment	not modelled	5.6	38	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l32; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
75	<a href="#">d1vaea</a>	Alignment	not modelled	5.4	18	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
76	<a href="#">d3etja1</a>	Alignment	not modelled	5.4	43	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
77	<a href="#">c6a5eD</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> gpi-anchored protein llg2; <b>PDBTitle:</b> crystal structure of plant peptide ralf23 in complex with fer and llg2
78	<a href="#">d1alna2</a>	Alignment	not modelled	5.3	20	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
79	<a href="#">c1l6jA</a>	Alignment	not modelled	5.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-9; <b>PDBTitle:</b> crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
80	<a href="#">c2of6C</a>	Alignment	not modelled	5.3	42	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein e;

						<b>PDBTitle:</b> structure of immature west Nile virus
81	<a href="#">c4lh9A_</a>	Alignment	not modelled	5.2	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> heterocyst differentiation control protein; <b>PDBTitle:</b> crystal structure of the refolded hood domain (asp256-gly295) of hetr
82	<a href="#">c1d6gA_</a>	Alignment	not modelled	5.2	55	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> cholecystokinin type a receptor; <b>PDBTitle:</b> molecular complex of cholecystokinin-8 and n-terminus of2 the cholecystokinin a receptor by nmr spectroscopy
83	<a href="#">c4k90A_</a>	Alignment	not modelled	5.2	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular metalloproteinase mep; <b>PDBTitle:</b> extracellular metalloproteinase from aspergillus
84	<a href="#">c2xznQ_</a>	Alignment	not modelled	5.1	27	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> ribosomal protein s17 containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
85	<a href="#">c4cbfE_</a>	Alignment	not modelled	5.1	25	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> envelope protein e; <b>PDBTitle:</b> near-atomic resolution cryo-em structure of dengue serotype 4 virus