
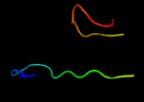

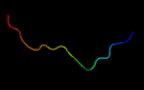











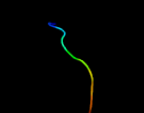

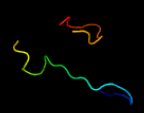

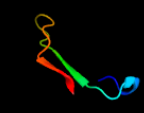

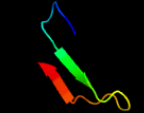
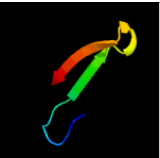
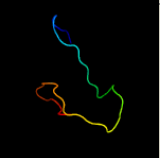
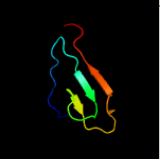
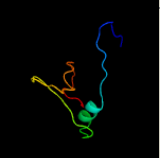
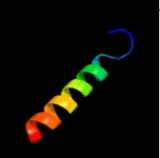
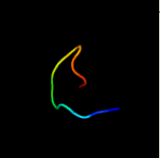
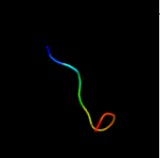
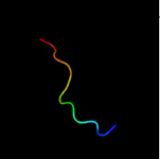
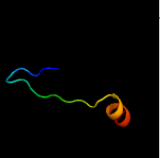


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0495c_(- )_585427_586317
Date	Fri Jul 26 01:50:04 BST 2019
Unique Job ID	283e2405f390b9f2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6chgC_</a>	 Alignment		51.4	35	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-4 specific; <b>PDBTitle:</b> crystal structure of the yeast compass catalytic module
2	<a href="#">c5uz9B_</a>	 Alignment		40.8	30	<b>PDB header:</b> immune system/rna <b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated protein csy2; <b>PDBTitle:</b> cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
3	<a href="#">c4rg6S_</a>	 Alignment		33.7	37	<b>PDB header:</b> protein binding <b>Chain:</b> S: <b>PDB Molecule:</b> anaphase-promoting complex subunit 16; <b>PDBTitle:</b> crystal structure of apc3-apc16 complex
4	<a href="#">c4rg9S_</a>	 Alignment		33.4	37	<b>PDB header:</b> protein binding <b>Chain:</b> S: <b>PDB Molecule:</b> anaphase-promoting complex subunit 16; (selenomethionine derivative) <b>PDBTitle:</b> crystal structure of apc3-apc16 complex
5	<a href="#">c4ui9E_</a>	 Alignment		29.5	37	<b>PDB header:</b> cell cycle <b>Chain:</b> E: <b>PDB Molecule:</b> anaphase-promoting complex subunit 16; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
6	<a href="#">c4whnB_</a>	 Alignment		25.7	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> apxc; <b>PDBTitle:</b> structure of toxin-activating acyltransferase (taat)
7	<a href="#">c5iiaH_</a>	 Alignment		21.6	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> H: <b>PDB Molecule:</b> vitelline envelope sperm lysin receptor; <b>PDBTitle:</b> crystal structure of red abalone egg ver1 repeat 3 in complex with2 sperm lysin at 1.7 a resolution (crystal form i)
8	<a href="#">d1uyra2</a>	 Alignment		19.2	45	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
9	<a href="#">c6agoA_</a>	 Alignment		18.2	22	<b>PDB header:</b> transferase/gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase ash1; <b>PDBTitle:</b> crystal structure of mrg15-ash1 histone methyltransferase complex
10	<a href="#">d2fbae1</a>	 Alignment		17.0	23	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> SPRY domain
11	<a href="#">c4n7uA_</a>	 Alignment		16.4	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> butyrophilin subfamily 3 member a1; <b>PDBTitle:</b> crystal structure of intracellular b30.2 domain of btn3a1 in complex2 with chdmapp

12	<a href="#">c4cg4D_</a>	Alignment		15.7	18	<b>PDB header:</b> actin-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> pyrin; <b>PDBTitle:</b> crystal structure of the chs-b30.2 domains of trim20
13	<a href="#">c3opeA_</a>	Alignment		15.1	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable histone-lysine n-methyltransferase ash1l; <b>PDBTitle:</b> structural basis of auto-inhibitory mechanism of histone2 methyltransferase
14	<a href="#">c3uv0B_</a>	Alignment		14.9	19	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> mutator 2, isoform b; <b>PDBTitle:</b> crystal structure of the drosophila mu2 fha domain
15	<a href="#">c4z4pA_</a>	Alignment		14.8	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase 2d; <b>PDBTitle:</b> structure of the ml14 set domain
16	<a href="#">d1rj9b1</a>	Alignment		14.4	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain of the SRP/SRP receptor G-proteins <b>Family:</b> Domain of the SRP/SRP receptor G-proteins
17	<a href="#">c2l7sA_</a>	Alignment		14.2	50	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> adrenomedullin; <b>PDBTitle:</b> determination of the three-dimensional structure of adrenomedullin, a2 first step towards the analysis of its interactions with receptors3 and small molecules
18	<a href="#">c1uzqA_</a>	Alignment		13.9	60	<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
19	<a href="#">c5cskB_</a>	Alignment		12.9	55	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
20	<a href="#">c3dalA_</a>	Alignment		12.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pr domain zinc finger protein 1; <b>PDBTitle:</b> methyltransferase domain of human pr domain-containing protein 1
21	<a href="#">c5gkeB_</a>	Alignment	not modelled	12.8	40	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease endoms; <b>PDBTitle:</b> structure of endoms-dsdna1 complex
22	<a href="#">c2of6C_</a>	Alignment	not modelled	12.5	50	<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
23	<a href="#">c6g2dC_</a>	Alignment	not modelled	12.3	55	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa carboxylase 1; <b>PDBTitle:</b> citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
24	<a href="#">c6epkA_</a>	Alignment	not modelled	11.9	60	<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
25	<a href="#">c4jdxB_</a>	Alignment	not modelled	11.9	33	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> slr1964 protein; <b>PDBTitle:</b> structure of the fluorescence recovery protein from synechocystis sp2 pcc 6803
26	<a href="#">c5cslA_</a>	Alignment	not modelled	11.9	55	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
27	<a href="#">c2wl1A_</a>	Alignment	not modelled	11.9	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> pyrin; <b>PDBTitle:</b> pyrin pryspry domain
28	<a href="#">c3ff6D_</a>	Alignment	not modelled	11.8	64	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> human acc2 ct domain with cp-640186
						<b>PDB header:</b> transferase

29	<a href="#">c2w5zA</a>	Alignment	not modelled	11.4	28	<b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase hrx; <b>PDBTitle:</b> ternary complex of the mixed lineage leukaemia (ml1) set2 domain with the cofactor product s-adenosylhomocysteine3 and histone peptide.
30	<a href="#">d1ok8a2</a>	Alignment	not modelled	11.2	50	<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
31	<a href="#">c3mqiA</a>	Alignment	not modelled	10.9	8	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor coe1; <b>PDBTitle:</b> human early b-cell factor 1 (ebf1) ipt/tig domain
32	<a href="#">d1svba2</a>	Alignment	not modelled	10.4	40	<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
33	<a href="#">c1od4C</a>	Alignment	not modelled	10.4	50	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase; <b>PDBTitle:</b> acetyl-coa carboxylase carboxyltransferase domain
34	<a href="#">c1p58C</a>	Alignment	not modelled	10.3	50	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> major envelope protein e; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
35	<a href="#">c5wsnC</a>	Alignment	not modelled	10.2	50	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> e protein; <b>PDBTitle:</b> structure of japanese encephalitis virus
36	<a href="#">c4b03A</a>	Alignment	not modelled	10.2	50	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> dengue virus 1 e protein; <b>PDBTitle:</b> 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
37	<a href="#">c3uajA</a>	Alignment	not modelled	10.2	50	<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
38	<a href="#">c4qeoA</a>	Alignment	not modelled	10.1	29	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-9 specific <b>PDBTitle:</b> crystal structure of kryptonite in complex with mchh dna, h3(1-15)2 peptide and sah
39	<a href="#">c4xb6D</a>	Alignment	not modelled	9.9	71	<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
40	<a href="#">c5o6vC</a>	Alignment	not modelled	9.8	40	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
41	<a href="#">c5i6hA</a>	Alignment	not modelled	9.6	50	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase-like protein; <b>PDBTitle:</b> crystal structure of cd-ct domains of chaetomium thermophilum acetyl-2 coa carboxylase
42	<a href="#">c5ujgA</a>	Alignment	not modelled	9.5	33	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> granulin; <b>PDBTitle:</b> ovgrn12-35_3s
43	<a href="#">c5ireA</a>	Alignment	not modelled	9.4	50	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> e protein; <b>PDBTitle:</b> the cryo-em structure of zika virus
44	<a href="#">d1z21a1</a>	Alignment	not modelled	9.3	17	<b>Fold:</b> Type III secretion system domain <b>Superfamily:</b> Type III secretion system domain <b>Family:</b> YopR Core
45	<a href="#">c4b8eA</a>	Alignment	not modelled	9.3	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin/isg15 ligase trim25; <b>PDBTitle:</b> pry-spry domain of trim25
46	<a href="#">c5ii5A</a>	Alignment	not modelled	9.3	50	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,vitelline envelope <b>PDBTitle:</b> crystal structure of red abalone verl repeat 1 at 1.8 a resolution
47	<a href="#">c3ukwC</a>	Alignment	not modelled	9.2	41	<b>PDB header:</b> protein transport/inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> bimax1 peptide; <b>PDBTitle:</b> mouse importin alpha: bimax1 peptide complex
48	<a href="#">c4ntwB</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> transport protein/toxin <b>Chain:</b> B: <b>PDB Molecule:</b> neurotoxin mitx-alpha; <b>PDBTitle:</b> structure of acid-sensing ion channel in complex with snake toxin
49	<a href="#">c2kgyA</a>	Alignment	not modelled	9.0	78	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> possible exported protein; <b>PDBTitle:</b> solution structure of rv0603 protein from mycobacterium2 tuberculosis h37rv
50	<a href="#">c2ormA</a>	Alignment	not modelled	9.0	31	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tautomerase hp0924; <b>PDBTitle:</b> crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
51	<a href="#">d1g2914</a>	Alignment	not modelled	9.0	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
52	<a href="#">c3c6dB</a>	Alignment	not modelled	8.9	50	<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
53	<a href="#">c1urzC</a>	Alignment	not modelled	8.9	40	<b>PDB header:</b> virus/viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus
54	<a href="#">c4cbfE</a>	Alignment	not modelled	8.8	50	<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

55	<a href="#">d1ls1a1</a>	Alignment	not modelled	8.8	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain of the SRP/SRP receptor G-proteins <b>Family:</b> Domain of the SRP/SRP receptor G-proteins
56	<a href="#">c3h0jA</a>	Alignment	not modelled	8.6	55	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of 2 acetyl-coenzyme a carboxylase in complex with compound 2
57	<a href="#">d1mjea2</a>	Alignment	not modelled	8.6	27	<b>Fold:</b> BRCA2 tower domain <b>Superfamily:</b> BRCA2 tower domain <b>Family:</b> BRCA2 tower domain
58	<a href="#">d1bjpa</a>	Alignment	not modelled	8.4	29	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
59	<a href="#">c5i6fB</a>	Alignment	not modelled	8.4	55	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase-like protein; <b>PDBTitle:</b> crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase
60	<a href="#">c2lm3A</a>	Alignment	not modelled	8.3	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tripartite motif-containing protein 5; <b>PDBTitle:</b> structure of the rhesus monkey trim5alpha pryspry domain
61	<a href="#">c5i6fA</a>	Alignment	not modelled	8.2	55	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase-like protein; <b>PDBTitle:</b> crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase
62	<a href="#">c1uytC</a>	Alignment	not modelled	7.9	55	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> acetyl-coa carboxylase carboxyltransferase domain
63	<a href="#">c3ctoE</a>	Alignment	not modelled	7.8	63	<b>PDB header:</b> toxin inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein rv3357/mt3465; <b>PDBTitle:</b> crystal structure of m. tuberculosis yefm antitoxin
64	<a href="#">c2x4kB</a>	Alignment	not modelled	7.5	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase; <b>PDBTitle:</b> crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
65	<a href="#">c4rvqA</a>	Alignment	not modelled	7.3	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna splicing helicase-like protein; <b>PDBTitle:</b> pwi-like domain of chaetomium thermophilum brr2
66	<a href="#">c3h6lA</a>	Alignment	not modelled	7.2	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase setd2; <b>PDBTitle:</b> methyltransferase domain of human set domain-containing protein 2
67	<a href="#">c1ebpC</a>	Alignment	not modelled	6.9	43	<b>PDB header:</b> complex (cytokine receptor/peptide) <b>Chain:</b> C: <b>PDB Molecule:</b> epo mimetics peptide 1; <b>PDBTitle:</b> complex between the extracellular domain of erythropoietin2 (epo) receptor [ebp] and an agonist peptide [emp1]
68	<a href="#">c1ebpD</a>	Alignment	not modelled	6.9	43	<b>PDB header:</b> complex (cytokine receptor/peptide) <b>Chain:</b> D: <b>PDB Molecule:</b> epo mimetics peptide 1; <b>PDBTitle:</b> complex between the extracellular domain of erythropoietin2 (epo) receptor [ebp] and an agonist peptide [emp1]
69	<a href="#">d1qzxa1</a>	Alignment	not modelled	6.9	24	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain of the SRP/SRP receptor G-proteins <b>Family:</b> Domain of the SRP/SRP receptor G-proteins
70	<a href="#">c2x24B</a>	Alignment	not modelled	6.8	64	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> bovine acc2 ct domain in complex with inhibitor
71	<a href="#">c3rayA</a>	Alignment	not modelled	6.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pr domain-containing protein 11; <b>PDBTitle:</b> crystal structure of methyltransferase domain of human pr domain-2 containing protein 11
72	<a href="#">c6bx3E</a>	Alignment	not modelled	6.6	30	<b>PDB header:</b> gene regulation/transferase <b>Chain:</b> E: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-4 specific; <b>PDBTitle:</b> structure of histone h3k4 methyltransferase
73	<a href="#">c5xyiv</a>	Alignment	not modelled	6.6	33	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein s21; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
74	<a href="#">c2op8A</a>	Alignment	not modelled	6.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tautomerase ywhb; <b>PDBTitle:</b> crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
75	<a href="#">c4wyoB</a>	Alignment	not modelled	6.5	55	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of human-yeast chimera acetyl coa carboxylase ct2 domain bound to compound 1
76	<a href="#">d2fxta1</a>	Alignment	not modelled	6.5	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> TIM44-like
77	<a href="#">c2yjtD</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> hydrolase inhibitor/hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase srmb; <b>PDBTitle:</b> crystal structure of e. coli dead-box protein srmb bound to regulator2 of ribonuclease activity a (rraa)
78	<a href="#">d1z3xa1</a>	Alignment	not modelled	6.5	20	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> GUN4-associated domain
79	<a href="#">d1xm0a1</a>	Alignment	not modelled	6.4	13	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> SelR domain
80	<a href="#">c4rz0B</a>	Alignment	not modelled	6.4	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pfi0690c; <b>PDBTitle:</b> crystal structure of plasmodium falciparum putative histone2 methyltransferase pfi0690c <b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> protein aal3:

81	<a href="#">c3v2uC_</a>	Alignment	not modelled	6.3	16	<b>PDBTitle:</b> crystal structure of the yeast gal regulon complex of the repressor, gal80p, and the transducer, gal3p, with galactose and atp
82	<a href="#">c5a53A_</a>	Alignment	not modelled	6.2	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of ribosome biosynthesis; <b>PDBTitle:</b> crystal structure of the rpf2-rrs1 complex
83	<a href="#">c6a5mA_</a>	Alignment	not modelled	6.2	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-9 specific <b>PDBTitle:</b> crystal structure of arabidopsis thaliana suvh6 in complex with sam,2 form 2
84	<a href="#">c4y7iB_</a>	Alignment	not modelled	6.2	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> myotubularin-related protein 8; <b>PDBTitle:</b> crystal structure of mtmr8
85	<a href="#">c3hnaA_</a>	Alignment	not modelled	6.2	30	<b>PDB header:</b> hydrolase/hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-9 specific 5; <b>PDBTitle:</b> crystal structure of catalytic domain of human euchromatic histone2 methyltransferase 1 in complex with sah and mono-methylated h3k93 peptide
86	<a href="#">c3lo9B_</a>	Alignment	not modelled	6.1	45	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (w26ahp mutant)
87	<a href="#">c3lo9A_</a>	Alignment	not modelled	6.1	45	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (w26ahp mutant)
88	<a href="#">c3lo6B_</a>	Alignment	not modelled	6.1	45	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (w26aba mutant)
89	<a href="#">d1otfa_</a>	Alignment	not modelled	6.0	31	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
90	<a href="#">c3lo6A_</a>	Alignment	not modelled	6.0	45	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (w26aba mutant)
91	<a href="#">d1zs3a1</a>	Alignment	not modelled	6.0	7	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
92	<a href="#">c3dzvB_</a>	Alignment	not modelled	5.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-methyl-5-(beta-hydroxyethyl)thiazole kinase; <b>PDBTitle:</b> crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole kinase2 (np_816404.1) from enterococcus faecalis v583 at 2.57 a resolution
93	<a href="#">c6e1IA_</a>	Alignment	not modelled	5.9	33	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> granulin; <b>PDBTitle:</b> grn3ala
94	<a href="#">d1v43a2</a>	Alignment	not modelled	5.9	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
95	<a href="#">c4fdxB_</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonase tautomerase isozyme; <b>PDBTitle:</b> kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
96	<a href="#">c3q9dB_</a>	Alignment	not modelled	5.7	55	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein cpn_0803/cp_1068/cpj0803/cpb0832; <b>PDBTitle:</b> crystal structure of cpn0803 from c. pneumoniae.
97	<a href="#">c2p4fA_</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> similar to sp p32453 saccharomyces cerevisiae ynl315c
98	<a href="#">c2lydA_</a>	Alignment	not modelled	5.7	19	<b>PDB header:</b> transcription/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> decapping protein 1; <b>PDBTitle:</b> the solution structure of the dm dcp1 evh1 domain in complex with the2 xrn1 dbm peptide
99	<a href="#">c3ry0A_</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tautomerase; <b>PDBTitle:</b> crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway