



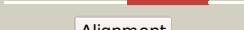

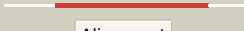
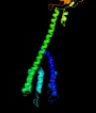





















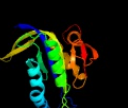



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3645 (- )_4082986_4084635
Date	Fri Aug 9 18:20:33 BST 2019
Unique Job ID	275a4a82e2a98f1d

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6fhtB_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> bacteriophytochrome,adenylate cyclase; <b>PDBTitle:</b> crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
2	<a href="#">c4yusA_</a>	 Alignment		100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> family 3 adenylate cyclase; <b>PDBTitle:</b> crystal structure of photoactivated adenylyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
3	<a href="#">c5nbyA_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> beta subunit of photoactivated adenylyl cyclase; <b>PDBTitle:</b> structure of a bacterial light-regulated adenylyl cyclase
4	<a href="#">c6r4oA_</a>	 Alignment		100.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase 9; <b>PDBTitle:</b> structure of a truncated adenylyl cyclase bound to mant- gtp, forskolin2 and an activated stimulatory galphas protein
5	<a href="#">c4cliA_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase type 10; <b>PDBTitle:</b> crystal structure of human soluble adenylyl cyclase in complex with2 bicarbonate
6	<a href="#">c5o5kC_</a>	 Alignment		100.0	26	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> x-ray structure of a bacterial adenylyl cyclase soluble domain
7	<a href="#">c6r4pA_</a>	 Alignment		100.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase 9; <b>PDBTitle:</b> structure of a soluble domain of adenylyl cyclase bound to an2 activated stimulatory g protein
8	<a href="#">c1y10C_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
9	<a href="#">c2w01C_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of the guanylyl cyclase cya2
10	<a href="#">c1wc6B_</a>	 Alignment		100.0	33	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
11	<a href="#">d1wclA_</a>	 Alignment		100.0	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain

12	<a href="#">c1cjkA</a>	Alignment		100.0	19	<b>PDB header:</b> lyase/lyase/signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase, type v; <b>PDBTitle:</b> complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
13	<a href="#">c3r5gB</a>	Alignment		100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> cyab; <b>PDBTitle:</b> crystal structure of the adenylyl cyclase cyab from p. aeruginosa
14	<a href="#">d1azsa</a>	Alignment		100.0	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
15	<a href="#">d1fx2a</a>	Alignment		100.0	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
16	<a href="#">c3uvjC</a>	Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> guanylate cyclase soluble subunit alpha-3; <b>PDBTitle:</b> crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
17	<a href="#">d1fx4a</a>	Alignment		100.0	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
18	<a href="#">c3et6A</a>	Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> soluble guanylyl cyclase beta; <b>PDBTitle:</b> the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
19	<a href="#">c3mr7B</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylate/guanylate cyclase/hydrolase, alpha/beta fold <b>PDBTitle:</b> crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
20	<a href="#">c2wz1B</a>	Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> guanylate cyclase soluble subunit beta-1; <b>PDBTitle:</b> structure of the catalytic domain of human soluble guanylate cyclase 12 beta 3.
21	<a href="#">c1ybuA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipj; <b>PDBTitle:</b> mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
22	<a href="#">d1azsb</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
23	<a href="#">c1yk9A</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
24	<a href="#">c4wp3E</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> ma1120; <b>PDBTitle:</b> crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type
25	<a href="#">c6aoaA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> bacterio-rhodopsin/guanylyl cyclase 1 fusion protein; <b>PDBTitle:</b> monomeric crystal structure of the e497/c566d double mutant of the2 guanylyl cyclase domain of the rhogc fusion protein from the aquatic3 fungus blastocladiella emersonii
26	<a href="#">c5jefA</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> nitrate/nitrite sensor protein narq; <b>PDBTitle:</b> fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
27	<a href="#">c4gn0D</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> signaling protein <b>Chain:</b> D; <b>PDB Molecule:</b> hamp domain of af1503; <b>PDBTitle:</b> de novo phasing of a hamp-complex using an improved arcimboldo method
28	<a href="#">c3lnrA</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> aerotaxis transducer aer2; <b>PDBTitle:</b> crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2

29	<a href="#">c3zx6A</a>	Alignment	not modelled	98.4	23	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hamp, methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
30	<a href="#">d2asxa1</a>	Alignment	not modelled	98.4	24	<b>Fold:</b> HAMP domain-like <b>Superfamily:</b> HAMP domain-like <b>Family:</b> HAMP domain
31	<a href="#">c3zrwB</a>	Alignment	not modelled	98.1	24	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> af1503 protein, osmolarity sensor protein envz; <b>PDBTitle:</b> the structure of the dimeric hamp-dhp fusion a291v mutant
32	<a href="#">c4i5sA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative histidine kinase covs; vick-like protein; <b>PDBTitle:</b> structure and function of sensor histidine kinase
33	<a href="#">c4ctiA</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> osmolarity sensor protein envz, af1503; <b>PDBTitle:</b> escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
34	<a href="#">c4biuB</a>	Alignment	not modelled	97.3	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein cpxa; <b>PDBTitle:</b> crystal structure of cpxahdc (orthorhombic form 1)
35	<a href="#">c2qv6D</a>	Alignment	not modelled	96.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> gtp cyclohydrolase iii; <b>PDBTitle:</b> gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
36	<a href="#">c2rm8A</a>	Alignment	not modelled	96.1	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory rhodopsin ii transducer; <b>PDBTitle:</b> the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
37	<a href="#">c5llxB</a>	Alignment	not modelled	95.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase (ggdef) domain-containing protein; <b>PDBTitle:</b> bacteriophytochrome activated diguanylyl cyclase from idiomarina2 species a28l with gtp bound
38	<a href="#">c1w25B</a>	Alignment	not modelled	95.6	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stalked-cell differentiation controlling protein; <b>PDBTitle:</b> response regulator pled in complex with c-digmp
39	<a href="#">c4wxoA</a>	Alignment	not modelled	95.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> sadc (300-487) from pseudomonas aeruginosa pao1
40	<a href="#">c4zmuD</a>	Alignment	not modelled	94.9	15	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
41	<a href="#">c3i5aA</a>	Alignment	not modelled	94.9	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator/ggdef domain protein; <b>PDBTitle:</b> crystal structure of full-length wpsr from pseudomonas syringae
42	<a href="#">c3mtkA</a>	Alignment	not modelled	94.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase/phosphodiesterase; <b>PDBTitle:</b> x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
43	<a href="#">c3ezuA</a>	Alignment	not modelled	94.1	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ggdef domain protein; <b>PDBTitle:</b> crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
44	<a href="#">c6d9mA</a>	Alignment	not modelled	94.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of endolysin,response receiver sensor <b>PDBTitle:</b> t4-lysozyme fusion to geobacter ggdef
45	<a href="#">c3breA</a>	Alignment	not modelled	92.4	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> crystal structure of p.aeruginosa pa3702
46	<a href="#">c3ignA</a>	Alignment	not modelled	92.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> crystal structure of the ggdef domain from marinobacter aquaeolei2 diguanylate cyclase complexed with c-di-gmp - northeast structural3 genomics consortium target mqr89a
47	<a href="#">c3i5cA</a>	Alignment	not modelled	91.8	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion of general control protein gcn4 and wpsr response <b>PDBTitle:</b> crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wpsr from pseudomonas aeruginosa
48	<a href="#">c3hvwA</a>	Alignment	not modelled	91.7	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate-cyclase (dgc); <b>PDBTitle:</b> crystal structure of the ggdef domain of the pa2567 protein from2 pseudomonas aeruginosa, northeast structural genomics consortium3 target par365c
49	<a href="#">c3ungC</a>	Alignment	not modelled	91.4	23	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> cmr2dhd; <b>PDBTitle:</b> structure of the cmr2 subunit of the crispr rna silencing complex
50	<a href="#">c5euhA</a>	Alignment	not modelled	89.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative ggdef domain membrane protein; <b>PDBTitle:</b> crystal structure of the c-di-gmp-bound ggdef domain of p. fluorescens2 gcbc
51	<a href="#">c3i5bA</a>	Alignment	not modelled	88.5	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> wpsr response regulator; <b>PDBTitle:</b> crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
52	<a href="#">c4h54B</a>	Alignment	not modelled	88.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase ydeh; <b>PDBTitle:</b> crystal structure of the diguanylate cyclase dgcz

53	<a href="#">c4dmzB</a>	Alignment	not modelled	87.7	9	<b>PDB header:</b> nucleotide-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein peld; <b>PDBTitle:</b> peld 156-455 from pseudomonas aeruginosa pa14, apo form
54	<a href="#">c4ymeA</a>	Alignment	not modelled	86.8	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sensory box/ggdef family protein; <b>PDBTitle:</b> crystal structure of a sensory box/ggdef family protein (cc_0091) from2 caulobacter crescentus cb15 at 1.40 a resolution (psi community3 target, shapiro)
55	<a href="#">c4zvhB</a>	Alignment	not modelled	86.2	13	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase dosc; <b>PDBTitle:</b> crystal structure of ggdef domain of the e. coli dosc - form iv
56	<a href="#">d1w25a3</a>	Alignment	not modelled	85.6	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> GGDEF domain
57	<a href="#">c5m3cB</a>	Alignment	not modelled	84.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> structure of the hybrid domain (ggdef-eal) of pa0575 from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
58	<a href="#">c3hvaA</a>	Alignment	not modelled	83.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein fimx; <b>PDBTitle:</b> crystal structure of fimx ggdef domain from pseudomonas aeruginosa
59	<a href="#">c3hlsE</a>	Alignment	not modelled	81.9	22	<b>PDB header:</b> signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> guanylate cyclase soluble subunit beta-1; <b>PDBTitle:</b> crystal structure of the signaling helix coiled-coil domain2 of the beta-1 subunit of the soluble guanylyl cyclase
60	<a href="#">c4w8yA</a>	Alignment	not modelled	81.8	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr2; <b>PDBTitle:</b> structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
61	<a href="#">c3pjwA</a>	Alignment	not modelled	81.6	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic dimeric gmp binding protein; <b>PDBTitle:</b> structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
62	<a href="#">c5xgdA</a>	Alignment	not modelled	81.5	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa0861; <b>PDBTitle:</b> crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
63	<a href="#">c3qyvB</a>	Alignment	not modelled	80.8	11	<b>PDB header:</b> signaling protein/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5 )-cyclic di-gmp
64	<a href="#">c4urgB</a>	Alignment	not modelled	80.2	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> crystal structure of ggdef domain from t.maritima (active-like dimer)
65	<a href="#">c3icIA</a>	Alignment	not modelled	79.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> eal/ggdef domain protein; <b>PDBTitle:</b> x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium target mcr174c
66	<a href="#">c6eibC</a>	Alignment	not modelled	79.3	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sensory box/ggdef family protein; <b>PDBTitle:</b> structure of the active ggeef domain of a diguanylate cyclase from2 vibrio cholerae.
67	<a href="#">c4iobA</a>	Alignment	not modelled	77.3	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase tpbb; <b>PDBTitle:</b> crystal structure of the ggdef domain of pa1120 (yfin or tpbb) from2 pseudomonas aeruginosa at 2.7 ang.
68	<a href="#">c3tvkA</a>	Alignment	not modelled	71.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase dgcz; <b>PDBTitle:</b> diguanylate cyclase domain of dgcz
69	<a href="#">c4zmmB</a>	Alignment	not modelled	54.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> ggdef domain of dcsbis complexed with c-di-gmp
70	<a href="#">c4euvA</a>	Alignment	not modelled	48.4	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> peld; <b>PDBTitle:</b> crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
71	<a href="#">c4b03D</a>	Alignment	not modelled	46.9	20	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> dengue virus 1 prm protein; <b>PDBTitle:</b> 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
72	<a href="#">c6ifnA</a>	Alignment	not modelled	34.3	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type iii-a crispr-associated protein csm1; <b>PDBTitle:</b> crystal structure of type iii-a crispr csm complex
73	<a href="#">c5buzC</a>	Alignment	not modelled	30.8	29	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> snap receptor-like protein; <b>PDBTitle:</b> crystal structure of a complex between the snare vam3 and the hops2 vps33-vps16 subcomplex from chaetomium thermophilum
74	<a href="#">c4rnhA</a>	Alignment	not modelled	30.7	19	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> motility regulator; <b>PDBTitle:</b> pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
75	<a href="#">c3j2pD</a>	Alignment	not modelled	29.0	17	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> cryoem structure of dengue virus envelope protein heterotetramer
76	<a href="#">c2x5eA</a>	Alignment	not modelled	25.0	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0271 protein pa4511; <b>PDBTitle:</b> crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
77	<a href="#">c6abeC</a>	Alignment	not modelled	23.1	26	<b>PDB header:</b> viral protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> polymerase pb2; <b>PDBTitle:</b> structure of influenza d virus polymerase bound to vrna promoter in2 mode b conformation (class b2)

78	<a href="#">c5wsnD_</a>	Alignment	not modelled	22.7	23	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> structure of japanese encephalitis virus
79	<a href="#">c5ireD_</a>	Alignment	not modelled	21.8	20	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> the cryo-em structure of zika virus
80	<a href="#">c5azdA_</a>	Alignment	not modelled	20.9	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriorhodopsin; <b>PDBTitle:</b> crystal structure of thermophilic rhodopsin.
81	<a href="#">c4biyD_</a>	Alignment	not modelled	20.2	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> sensor protein cpxa; <b>PDBTitle:</b> crystal structure of cpxahdc (monoclinic form 2)
82	<a href="#">c6abfC_</a>	Alignment	not modelled	18.2	26	<b>PDB header:</b> viral protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> polymerase pb2; <b>PDBTitle:</b> structure of influenza d virus polymerase bound to vrna promoter in2 mode b conformation (class b1)
83	<a href="#">c2d9dA_</a>	Alignment	not modelled	17.2	25	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> bag family molecular chaperone regulator 5; <b>PDBTitle:</b> solution structure of the bag domain (275-350) of bag-family2 molecular chaperone regulator-5
84	<a href="#">d1tlha_</a>	Alignment	not modelled	16.8	36	<b>Fold:</b> Anti-sigma factor AsIA <b>Superfamily:</b> Anti-sigma factor AsIA <b>Family:</b> Anti-sigma factor AsIA
85	<a href="#">c1p58E_</a>	Alignment	not modelled	16.1	14	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
86	<a href="#">c3dcaC_</a>	Alignment	not modelled	15.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> rpa0582; <b>PDBTitle:</b> crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
87	<a href="#">d1veha_</a>	Alignment	not modelled	15.4	31	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
88	<a href="#">c5b2nA_</a>	Alignment	not modelled	14.7	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chloride pumping rhodopsin; <b>PDBTitle:</b> crystal structure of the light-driven chloride ion-pumping rhodopsin,2 clp, from nonlabens marinus
89	<a href="#">c2w6bA_</a>	Alignment	not modelled	14.3	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rho guanine nucleotide exchange factor 7; <b>PDBTitle:</b> crystal structure of the trimeric beta-pix coiled-coil2 domain
90	<a href="#">d1q8ka2</a>	Alignment	not modelled	14.1	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eIF-2-alpha, C-terminal domain <b>Family:</b> eIF-2-alpha, C-terminal domain
91	<a href="#">d1u7la_</a>	Alignment	not modelled	13.5	30	<b>Fold:</b> Vacuolar ATP synthase subunit C <b>Superfamily:</b> Vacuolar ATP synthase subunit C <b>Family:</b> Vacuolar ATP synthase subunit C
92	<a href="#">d1zbx1</a>	Alignment	not modelled	12.1	7	<b>Fold:</b> ORC1-binding domain <b>Superfamily:</b> ORC1-binding domain <b>Family:</b> ORC1-binding domain
93	<a href="#">c4wrtC_</a>	Alignment	not modelled	11.9	26	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> pb2; <b>PDBTitle:</b> crystal structure of influenza b polymerase with bound vrna promoter2 (form flub2)
94	<a href="#">c6c5wA_</a>	Alignment	not modelled	11.5	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium uniporter; <b>PDBTitle:</b> crystal structure of the mitochondrial calcium uniporter
95	<a href="#">d2dfaa1</a>	Alignment	not modelled	11.3	22	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
96	<a href="#">c1z5sD_</a>	Alignment	not modelled	10.8	30	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> ran-binding protein 2; <b>PDBTitle:</b> crystal structure of a complex between ubc9, sumo-1,2 rangap1 and nup358/ranbp2
97	<a href="#">d1f6ga_</a>	Alignment	not modelled	10.7	15	<b>Fold:</b> Voltage-gated potassium channels <b>Superfamily:</b> Voltage-gated potassium channels <b>Family:</b> Voltage-gated potassium channels
98	<a href="#">d1v6ta_</a>	Alignment	not modelled	10.6	14	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
99	<a href="#">c2vg2C_</a>	Alignment	not modelled	10.5	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthetase; <b>PDBTitle:</b> rv2361 with ipp