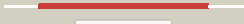



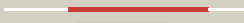

























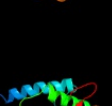


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0891c (-) _992601_993458
Date	Fri Jul 26 01:50:48 BST 2019
Unique Job ID	65cf1c649a4e5dba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6fhtB_</a>	 Alignment		100.0	20	<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="#">d1fx2a_</a>	 Alignment		100.0	34	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
3	<a href="#">d1fx4a_</a>	 Alignment		100.0	37	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
4	<a href="#">c1y10C_</a>	 Alignment		100.0	18	<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
5	<a href="#">c4yusA_</a>	 Alignment		100.0	22	<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
6	<a href="#">c5nbyA_</a>	 Alignment		100.0	20	<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
7	<a href="#">c4wp3E_</a>	 Alignment		100.0	29	<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
8	<a href="#">c3mr7B_</a>	 Alignment		100.0	27	<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
9	<a href="#">c6r4oA_</a>	 Alignment		100.0	19	<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
10	<a href="#">c4cIIA_</a>	 Alignment		100.0	20	<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
11	<a href="#">c5o5kC_</a>	 Alignment		100.0	20	<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

12	<a href="#">c1ybuA</a>	Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipj; <b>PDBTitle:</b> mycobacterium tuberculosis adenyllyl cyclase rv1900c chd, in complex2 with a substrate analog.
13	<a href="#">c1wc6B</a>	Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> soluble adenyllyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
14	<a href="#">d1wc1a</a>	Alignment		100.0	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenyllyl and guanylyl cyclase catalytic domain
15	<a href="#">c3r5gB</a>	Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cyab; <b>PDBTitle:</b> crystal structure of the adenyllyl cyclase cyab from p. aeruginosa
16	<a href="#">c6r4pA</a>	Alignment		100.0	19	<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 adenyllyl cyclase bound to an2 activated stimulatory g protein
17	<a href="#">c3uviC</a>	Alignment		100.0	22	<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.
18	<a href="#">c1cjkA</a>	Alignment		100.0	15	<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 adenyllyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
19	<a href="#">c3et6A</a>	Alignment		100.0	20	<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
20	<a href="#">c2w01C</a>	Alignment		100.0	25	<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
21	<a href="#">d1azsa</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenyllyl and guanylyl cyclase catalytic domain
22	<a href="#">c2wz1B</a>	Alignment	not modelled	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.
23	<a href="#">c1yk9A</a>	Alignment	not modelled	100.0	24	<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 adenyllyl cyclase rv1625c
24	<a href="#">d1azsb</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenyllyl and guanylyl cyclase catalytic domain
25	<a href="#">c6a0aA</a>	Alignment	not modelled	100.0	22	<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="#">c2qv6D</a>	Alignment	not modelled	96.9	17	<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
27	<a href="#">c4zmuD</a>	Alignment	not modelled	88.4	13	<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
28	<a href="#">c1w25B</a>	Alignment	not modelled	88.1	14	<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 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ggdef domain protein;
29	<a href="#">c3ezuA</a>	Alignment	not modelled	87.9	22	<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
30	<a href="#">c6d9mA</a>	Alignment	not modelled	87.4	17	<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
31	<a href="#">c3ignA</a>	Alignment	not modelled	85.7	12	<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
32	<a href="#">c3mtkA</a>	Alignment	not modelled	79.5	14	<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
33	<a href="#">c4wxoA</a>	Alignment	not modelled	78.2	13	<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
34	<a href="#">c5llxB</a>	Alignment	not modelled	76.8	12	<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
35	<a href="#">c3breA</a>	Alignment	not modelled	76.0	22	<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
36	<a href="#">c3i5aA</a>	Alignment	not modelled	75.3	20	<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
37	<a href="#">c3hvwA</a>	Alignment	not modelled	73.9	10	<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
38	<a href="#">c4w8yA</a>	Alignment	not modelled	73.8	13	<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)
39	<a href="#">c4h54B</a>	Alignment	not modelled	71.2	16	<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
40	<a href="#">c3hvaA</a>	Alignment	not modelled	70.0	17	<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
41	<a href="#">c3ungC</a>	Alignment	not modelled	67.3	14	<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
42	<a href="#">c3qyyB</a>	Alignment	not modelled	59.8	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
43	<a href="#">c3icIA</a>	Alignment	not modelled	58.5	14	<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
44	<a href="#">c4urgB</a>	Alignment	not modelled	56.1	15	<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)
45	<a href="#">c4zvhB</a>	Alignment	not modelled	49.7	15	<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
46	<a href="#">c4euvA</a>	Alignment	not modelled	49.0	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
47	<a href="#">c4dmzB</a>	Alignment	not modelled	43.8	14	<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
48	<a href="#">c6eibC</a>	Alignment	not modelled	43.4	11	<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.
49	<a href="#">c4iobA</a>	Alignment	not modelled	42.9	18	<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.
50	<a href="#">c5euhA</a>	Alignment	not modelled	42.3	19	<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="#">c4ymeA</a>	Alignment	not modelled	36.3	16	<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)
52	<a href="#">c3i5cA</a>	Alignment	not modelled	35.6	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 wspr from pseudomonas aeruginosa
53	<a href="#">c4zmmB</a>	Alignment	not modelled	35.3	12	<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
54	<a href="#">d1w25a3</a>	Alignment	not modelled	30.8	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> GGDEF domain
55	<a href="#">d1ufwa</a>	Alignment	not modelled	23.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
56	<a href="#">c2vg2C</a>	Alignment	not modelled	21.8	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthetase; <b>PDBTitle:</b> rv2361 with ipp
57	<a href="#">d2coha2</a>	Alignment	not modelled	21.4	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
58	<a href="#">c3tvkA</a>	Alignment	not modelled	16.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase dgcz; <b>PDBTitle:</b> diguanylate cyclase domain of dgcz
59	<a href="#">c3k1qA</a>	Alignment	not modelled	15.8	50	<b>PDB header:</b> <b>PDB COMPND:</b>
60	<a href="#">c5apgA</a>	Alignment	not modelled	15.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tsr3; <b>PDBTitle:</b> structure of the sam-dependent rrna:acp-transferase tsr32 from vulcanisaeta distributa
61	<a href="#">c2cseU</a>	Alignment	not modelled	15.0	29	<b>PDB header:</b> virus <b>Chain:</b> U: <b>PDB Molecule:</b> guanylyltransferase; <b>PDBTitle:</b> features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
62	<a href="#">c3i5bA</a>	Alignment	not modelled	12.5	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> wspr response regulator; <b>PDBTitle:</b> crystal structure of the isolated ggdef domain of wspr from2 pseudomonas aeruginosa
63	<a href="#">c5m3cB</a>	Alignment	not modelled	12.3	11	<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
64	<a href="#">c6acsA</a>	Alignment	not modelled	11.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ditrans,polycis-undecaprenyl-diphosphate synthase ((2e,6e)- <b>PDBTitle:</b> poly-cis-prenyltransferase
65	<a href="#">c4h8eA</a>	Alignment	not modelled	10.4	8	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthase; <b>PDBTitle:</b> structure of s. aureus undecaprenyl diphosphate synthase in complex2 with fpp and sulfate
66	<a href="#">c1yvrA</a>	Alignment	not modelled	9.4	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 60-kda ss-a/ro ribonucleoprotein; <b>PDBTitle:</b> ro autoantigen
67	<a href="#">d1veha</a>	Alignment	not modelled	8.8	12	<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
68	<a href="#">c2hncC</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sam-dependent o-methyltransferase; <b>PDBTitle:</b> crystal structure of sam-dependent o-methyltransferase from pathogenic2 bacterium leptospira interrogans
69	<a href="#">c4q9mA</a>	Alignment	not modelled	8.1	12	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> isoprenyl transferase; <b>PDBTitle:</b> crystal structure of upps in complex with fpp and an allosteric2 inhibitor
70	<a href="#">c5a4aA</a>	Alignment	not modelled	7.7	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maternal effect protein oskar; <b>PDBTitle:</b> crystal structure of the osk domain of drosophila oskar
71	<a href="#">c6f0kD</a>	Alignment	not modelled	7.0	10	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> actd; <b>PDBTitle:</b> alternative complex iii
72	<a href="#">c5hc7A</a>	Alignment	not modelled	6.9	8	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> prenyltransferase for protein; <b>PDBTitle:</b> crystal structure of lavandulyl diphosphate synthase from lavandula x2 intermedia in complex with s-thio- isopentenylidiphosphate
73	<a href="#">d2qtva1</a>	Alignment	not modelled	6.8	21	<b>Fold:</b> ERP29 C domain-like <b>Superfamily:</b> Helical domain of Sec23/24 <b>Family:</b> Helical domain of Sec23/24
74	<a href="#">c4lrvL</a>	Alignment	not modelled	6.7	54	<b>PDB header:</b> dna binding protein <b>Chain:</b> L: <b>PDB Molecule:</b> dna sulfur modification protein dnde; <b>PDBTitle:</b> crystal structure of dnde from escherichia coli b7a involved in dna2 phosphorothioation modification
75	<a href="#">c3dmyA</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein fdra; <b>PDBTitle:</b> crystal structure of a predicated acyl-coa synthetase from e.coli
76	<a href="#">d1r31a1</a>	Alignment	not modelled	6.3	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> NAD-binding domain of HMG-CoA reductase <b>Family:</b> NAD-binding domain of HMG-CoA reductase
77	<a href="#">c2y0fD</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> structure of gcpe (ispq) from thermus thermophilus hb27
						<b>PDB header:</b> transferase

78	<a href="#">c3gczA_</a>	Alignment	not modelled	6.3	17	<b>Chain:</b> A: <b>PDB Molecule:</b> polyprotein; <b>PDBTitle:</b> yokose virus methyltransferase in complex with adomet
79	<a href="#">c6ifnA_</a>	Alignment	not modelled	5.9	14	<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
80	<a href="#">d2es7a1</a>	Alignment	not modelled	5.7	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> HyaE-like
81	<a href="#">d2fiua1</a>	Alignment	not modelled	5.6	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Atu0297-like
82	<a href="#">c3noyA_</a>	Alignment	not modelled	5.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> crystal structure of ispg (gcpe)
83	<a href="#">c2w3xE_</a>	Alignment	not modelled	5.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> cale7; <b>PDBTitle:</b> crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
84	<a href="#">d1bala_</a>	Alignment	not modelled	5.5	30	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
85	<a href="#">c4js0B_</a>	Alignment	not modelled	5.4	45	<b>PDB header:</b> signaling protein/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> brain-specific angiogenesis inhibitor 1-associated protein <b>PDBTitle:</b> complex of cdc42 with the crib-pr domain of irsp53
86	<a href="#">c3zi1A_</a>	Alignment	not modelled	5.3	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase domain-containing protein 4; <b>PDBTitle:</b> crystal structure of human glyoxalase domain-containing protein 42 (glod4)
87	<a href="#">c3cbgA_</a>	Alignment	not modelled	5.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> functional and structural characterization of a cationdependent o-2 methyltransferase from the cyanobacterium synechocystis sp. strain3 pcc 6803