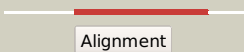

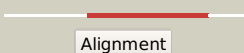

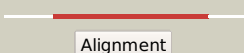
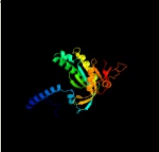
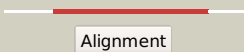

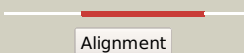

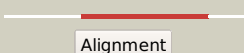

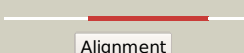





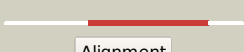

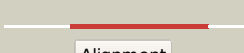



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1647_(-)_1856781_1857731
Date	Fri Aug 2 13:30:24 BST 2019
Unique Job ID	a7f3dd48b77b74e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fhtB_	 Alignment		100.0	27	PDB header: lyase Chain: B; PDB Molecule: bacteriophytochrome,adenylate cyclase; PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
2	c1y10C_	 Alignment		100.0	25	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenyllyl cyclase rv1264, holoenzyme, inhibited state
3	c4yusA_	 Alignment		100.0	19	PDB header: lyase Chain: A; PDB Molecule: family 3 adenylate cyclase; PDBTitle: crystal structure of photoactivated adenyllyl cyclase of a2 cyanobacteriaosillatoria acuminata in hexagonal form
4	c5nbyA_	 Alignment		100.0	18	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenyllyl cyclase; PDBTitle: structure of a bacterial light-regulated adenyllyl cyclase
5	c6r4oA_	 Alignment		100.0	23	PDB header: membrane protein Chain: A; PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a truncated adenyllyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
6	d1fx2a_	 Alignment		100.0	24	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyllyl and guanylyl cyclase catalytic domain
7	d1fx4a_	 Alignment		100.0	26	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyllyl and guanylyl cyclase catalytic domain
8	c6r4pA_	 Alignment		100.0	26	PDB header: membrane protein Chain: A; PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a soluble domain of adenyllyl cyclase bound to an2 activated stimulatory g protein
9	c3mr7B_	 Alignment		100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: adenylate/guanylate cyclase/hydrolase, alpha/beta fold PDBTitle: crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
10	c1wc6B_	 Alignment		100.0	30	PDB header: lyase Chain: B; PDB Molecule: adenylate cyclase; PDBTitle: soluble adenyllyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
11	c4cIIA_	 Alignment		100.0	19	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenyllyl cyclase in complex with2 bicarbonate

12	c3uvjC_	Alignment		100.0	21	PDB header: lyase Chain: C: PDB Molecule: guanylate cyclase soluble subunit alpha-3; PDBTitle: crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
13	c4wp3E_	Alignment		100.0	31	PDB header: lyase Chain: E: PDB Molecule: ma1120; PDBTitle: crystal structure of adenyl cyclase from mycobacterium avium ma11202 wild type
14	d1wc1a_	Alignment		100.0	29	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
15	c5o5kC_	Alignment		100.0	20	PDB header: membrane protein Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenyl cyclase soluble domain
16	c1cjkA_	Alignment		100.0	20	PDB header: lyase/lyase/signaling protein Chain: A: PDB Molecule: adenylate cyclase, type v; PDBTitle: complex of gs-alpha with the catalytic domains of mammalian adenyl cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
17	c1ybuA_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenyl cyclase rv1900c chd, in complex2 with a substrate analog.
18	d1azsa_	Alignment		100.0	20	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
19	c2w01C_	Alignment		100.0	26	PDB header: lyase Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
20	c3r5gB_	Alignment		100.0	26	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenyl cyclase cyab from p. aeruginosa
21	c2wz1B_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: structure of the catalytic domain of human soluble guanylate cyclase 12 beta 3.
22	d1azsb_	Alignment	not modelled	100.0	19	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
23	c3et6A_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
24	c1yk9A_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenyl cyclase rv1625c
25	c6aoaA_	Alignment	not modelled	100.0	26	PDB header: lyase Chain: A: PDB Molecule: bacterio-rhodopsin/guanylyl cyclase 1 fusion protein; PDBTitle: 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	c1w25B_	Alignment	not modelled	97.8	14	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
27	c4zmuD_	Alignment	not modelled	97.5	13	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
						PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase (qqdef) domain-

28	c5llxB_	Alignment	not modelled	97.2	13	containing protein; PDBTitle: bacteriophytochrome activated diguanylyl cyclase from <i>idiomarina2</i> species a28l with gtp bound PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein;
29	c3ezuA_	Alignment	not modelled	97.1	18	PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from <i>geobacter sulfurreducens</i> at 1.95 a3 resolution PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator;
30	c3breA_	Alignment	not modelled	97.1	24	PDBTitle: crystal structure of <i>p.aeruginosa</i> pa3702 PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein;
31	c3i5aA_	Alignment	not modelled	97.0	20	PDBTitle: crystal structure of full-length <i>wpsr</i> from <i>pseudomonas syringae</i> PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor
32	c6d9mA_	Alignment	not modelled	97.0	13	PDBTitle: t4-lysozyme fusion to <i>geobacter</i> ggdef PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii;
33	c2qv6D_	Alignment	not modelled	97.0	17	PDBTitle: gtp cyclohydrolase iii from <i>m. jannaschii</i> (mj0145)2 complexed with gtp and metal ions PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein <i>gcn4</i> and <i>wpsr</i> response
34	c3i5cA_	Alignment	not modelled	96.7	19	PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 <i>gcn4</i> and the ggdef domain of <i>wpsr</i> from <i>pseudomonas aeruginosa</i> PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase;
35	c3ignA_	Alignment	not modelled	96.6	13	PDBTitle: crystal structure of the ggdef domain from <i>marinobacter aquaeolei2</i> diguanylate cyclase complexed with c-di-gmp - northeast structural3 genomics consortium target <i>mqr89a</i> PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase;
36	c3mtkA_	Alignment	not modelled	96.2	12	PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from2 <i>caldicellulosiruptor saccharolyticus</i> , northeast structural genomics3 consortium target <i>clr27c</i> PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein;
37	c4wxoA_	Alignment	not modelled	96.1	15	PDBTitle: <i>sadc</i> (300-487) from <i>pseudomonas aeruginosa</i> <i>pao1</i> PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc);
38	c3hvwA_	Alignment	not modelled	95.7	12	PDBTitle: crystal structure of the ggdef domain of the <i>pa2567</i> protein from2 <i>pseudomonas aeruginosa</i> , northeast structural genomics consortium3 target <i>par365c</i> PDB header: membrane protein Chain: A: PDB Molecule: putative ggdef domain membrane protein;
39	c5euhA_	Alignment	not modelled	95.2	16	PDBTitle: crystal structure of the c-di-gmp-bound ggdef domain of <i>p. fluorescens2</i> <i>gcbc</i> PDB header: transferase Chain: A: PDB Molecule: protein <i>fimx</i> ;
40	c3hvaA_	Alignment	not modelled	94.9	18	PDBTitle: crystal structure of <i>fimx</i> ggdef domain from <i>pseudomonas aeruginosa</i> PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase <i>ydeh</i> ;
41	c4h54B_	Alignment	not modelled	94.8	17	PDBTitle: crystal structure of the diguanylate cyclase <i>dgcz</i> PDB header: transferase Chain: C: PDB Molecule: sensory box/ggdef family protein;
42	c6eibC_	Alignment	not modelled	94.6	12	PDBTitle: structure of the active ggeef domain of a diguanylate cyclase from2 <i>vibrio cholerae</i> . PDB header: lyase Chain: A: PDB Molecule: sensory box/ggdef family protein;
43	c4ymeA_	Alignment	not modelled	94.0	17	PDBTitle: crystal structure of a sensory box/ggdef family protein (cc_0091) from2 <i>caulobacter crescentus</i> <i>cb15</i> at 1.40 a resolution (psi community3 target, shapiro) PDB header: signaling protein Chain: A: PDB Molecule: <i>wpsr</i> response regulator;
44	c3i5bA_	Alignment	not modelled	93.9	24	PDBTitle: crystal structure of the isolated ggdef domain of <i>wpsr</i> from2 <i>pseudomonas aeruginosa</i> PDB header: signaling protein Chain: B: PDB Molecule: diguanylate cyclase <i>dosc</i> ;
45	c4zvhB_	Alignment	not modelled	93.7	15	PDBTitle: crystal structure of ggdef domain of the <i>e. coli</i> <i>dosc</i> - form iv PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein;
46	c3icIA_	Alignment	not modelled	93.6	20	PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 <i>m.capsulatus</i> , northeast structural genomics consortium target <i>mcr174c</i> PDB header: rna binding protein Chain: A: PDB Molecule: crispr system <i>cmr</i> subunit <i>cmr2</i> ;
47	c4w8yA_	Alignment	not modelled	93.5	11	PDBTitle: structure of full length <i>cmr2</i> from <i>pyrococcus furiosus</i> (manganese2 bound form) PDB header: signaling protein Chain: A: PDB Molecule: <i>peld</i> ;
48	c4euvA_	Alignment	not modelled	92.9	10	PDBTitle: crystal structure of <i>peld</i> 158-ct from <i>pseudomonas aeruginosa</i> <i>pao1</i> , in2 complex with c-di-gmp, form 1 PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase;
49	c4zmmB_	Alignment	not modelled	92.5	13	PDBTitle: ggdef domain of <i>dcsbis</i> complexed with c-di-gmp Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
50	d1w25a3	Alignment	not modelled	92.5	13	PDB header: unknown function Chain: C: PDB Molecule: <i>cmr2dh</i> d;
51	c3ungC_	Alignment	not modelled	92.3	14	PDBTitle: structure of the <i>cmr2</i> subunit of the crispr rna silencing complex PDB header: lyase

52	c4jobA	Alignment	not modelled	92.2	18	Chain: A: PDB Molecule: diguanylate cyclase tpbb; PDBTitle: crystal structure of the ggdef domain of pa1120 (yfin or tpbb) from <i>Pseudomonas aeruginosa</i> at 2.7 ang.
53	c4urgB	Alignment	not modelled	90.2	15	PDB header: lyase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from <i>t.maritima</i> (active-like dimer)
54	c3qyyB	Alignment	not modelled	90.0	14	PDB header: signaling protein/inhibitor Chain: B: PDB Molecule: response regulator; PDBTitle: a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
55	c5m3cB	Alignment	not modelled	88.7	17	PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575 from <i>Pseudomonas aeruginosa</i> pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
56	c4dmzB	Alignment	not modelled	86.4	13	PDB header: nucleotide-binding protein Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from <i>Pseudomonas aeruginosa</i> pa14, apo form
57	c3tvkA	Alignment	not modelled	82.7	16	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase dgcz; PDBTitle: diguanylate cyclase domain of dgcz
58	c5xgdA	Alignment	not modelled	78.4	20	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from <i>Pseudomonas aeruginosa</i> in complex with gtp
59	c3pjwA	Alignment	not modelled	69.1	15	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of <i>Pseudomonas fluorescence</i> lapd ggdef-eal dual domain, i23
60	d1v6ta	Alignment	not modelled	55.7	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
61	c2x5eA	Alignment	not modelled	51.4	20	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from <i>Pseudomonas aeruginosa</i>
62	d2dfaa1	Alignment	not modelled	50.8	22	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
63	c6ifnA	Alignment	not modelled	48.8	8	PDB header: rna binding protein Chain: A: PDB Molecule: type iii-a crispr-associated protein csm1; PDBTitle: crystal structure of type iii-a crispr csm complex
64	c4rnhA	Alignment	not modelled	30.8	18	PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
65	c2y0fD	Alignment	not modelled	26.4	25	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpc (ispg) from <i>Thermus thermophilus</i> hb27
66	d2fiua1	Alignment	not modelled	24.3	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
67	d1veha	Alignment	not modelled	23.3	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
68	c3lo3E	Alignment	not modelled	20.1	19	PDB header: structure genomics, unknown function Chain: E: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from <i>Colwellia psychrerythraea</i> 34h.
69	c5buzC	Alignment	not modelled	14.1	12	PDB header: transport protein Chain: C: PDB Molecule: snap receptor-like protein; PDBTitle: crystal structure of a complex between the snare vam3 and the hops2 vps33-vps16 subcomplex from <i>Chaetomium thermophilum</i>
70	c4lrvL	Alignment	not modelled	10.6	55	PDB header: dna binding protein Chain: L: PDB Molecule: dna sulfur modification protein dnde; PDBTitle: crystal structure of dnde from <i>Escherichia coli</i> b7a involved in dna2 phosphorothioation modification
71	c3a9qR	Alignment	not modelled	9.8	18	PDB header: oxidoreductase Chain: R: PDB Molecule: ; PDBTitle: crystal structure analysis of e173a variant of the soybean2 ferritin sfer4
72	c3bdkB	Alignment	not modelled	9.8	12	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
73	c3dcaC	Alignment	not modelled	9.7	14	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: rpa0582; PDBTitle: crystal structure of the rpa0582- protein of unknown2 function from <i>Rhodospseudomonas palustris</i> - a structural3 genomics target
74	c2dqxA	Alignment	not modelled	9.6	15	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0430 protein; PDBTitle: solution structure of the rna recognition motif in kiaa04302 protein
75	c6iqwA	Alignment	not modelled	8.9	7	PDB header: rna binding protein/rna Chain: A: PDB Molecule: csm1; PDBTitle: cryo-em structure of csm effector complex
76	d1p42a1	Alignment	not modelled	7.8	50	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
77	d1gmnbl	Alignment	not modelled	7.2	26	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain

78	c2diuA_	Alignment	not modelled	6.7	21	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0430 protein; PDBTitle: solution structure of the rrm domain of kiaa0430 protein
79	d1mbma_	Alignment	not modelled	6.6	57	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
80	d2a1a1	Alignment	not modelled	6.2	21	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
81	c6f0kD_	Alignment	not modelled	6.2	29	PDB header: membrane protein Chain: D: PDB Molecule: actd; PDBTitle: alternative complex iii
82	c3nzkB_	Alignment	not modelled	6.0	42	PDB header: hydrolase Chain: B: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine PDBTitle: structure of lpxc from yersinia enterocolitica complexed with chir0902 inhibitor
83	d1xhja_	Alignment	not modelled	5.9	14	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like