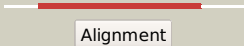

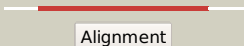

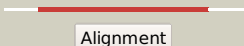







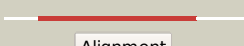











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1359_(-)_1530179_1530931
Date	Wed Jul 31 22:05:46 BST 2019
Unique Job ID	0f37c538111bd345

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	d1fx2a_	 Alignment		100.0	27	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
3	d1fx4a_	 Alignment		100.0	29	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
4	c1y10C_	 Alignment		100.0	17	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
5	c4yusA_	 Alignment		100.0	19	PDB header: lyase Chain: A; PDB Molecule: family 3 adenylate cyclase; PDBTitle: crystal structure of photoactivated adenylyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
6	c4wp3E_	 Alignment		100.0	27	PDB header: lyase Chain: E; PDB Molecule: ma1120; PDBTitle: crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type
7	c5nbyA_	 Alignment		100.0	16	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenylyl cyclase; PDBTitle: structure of a bacterial light-regulated adenylyl cyclase
8	c3mr7B_	 Alignment		100.0	26	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
9	c4cIIA_	 Alignment		100.0	17	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenylyl cyclase in complex with2 bicarbonate
10	c1ybuA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A; PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
11	c1wc6B_	 Alignment		100.0	19	PDB header: lyase Chain: B; PDB Molecule: adenylate cyclase; PDBTitle: soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate

12	c3et6A_	Alignment		100.0	20	PDB header: lyase Chain: A; PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
13	c6r4oA_	Alignment		100.0	18	PDB header: membrane protein Chain: A; PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a truncated adenylyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
14	d1wc1a_	Alignment		100.0	20	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
15	c6r4pA_	Alignment		100.0	18	PDB header: membrane protein Chain: A; PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a soluble domain of adenylyl cyclase bound to an2 activated stimulatory g protein
16	c3r5gB_	Alignment		100.0	23	PDB header: lyase Chain: B; PDB Molecule: cyab; PDBTitle: crystal structure of the adenylyl cyclase cyab from p. aeruginosa
17	c2w01C_	Alignment		100.0	25	PDB header: lyase Chain: C; PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
18	c5o5kC_	Alignment		100.0	16	PDB header: membrane protein Chain: C; PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenylyl cyclase soluble domain
19	c1cjkA_	Alignment		100.0	16	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 adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
20	c3uvjC_	Alignment		100.0	18	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.
21	d1azsa_	Alignment	not modelled	100.0	18	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
22	c2wz1B_	Alignment	not modelled	100.0	19	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.
23	c1yk9A_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
24	d1azsb_	Alignment	not modelled	99.9	15	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
25	c6aooA_	Alignment	not modelled	99.9	18	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	85.3	17	PDB header: signaling protein Chain: B; PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
27	c3ezuA_	Alignment	not modelled	74.4	19	PDB header: signaling protein Chain: A; PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
28	c2ov6D_	Alignment	not modelled	72.7	13	PDB header: hydrolase Chain: D; PDB Molecule: gtp cyclohydrolase iii;

28	c2qv0D	Alignment	not modelled	72.7	13	PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions PDB header: lyase
29	c4zmuD	Alignment	not modelled	55.5	13	Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
30	c3ignA	Alignment	not modelled	53.2	17	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of the ggdef domain from marinobacter aquaeolei2 diguanylate cyclase complexed with c-di-gmp - northeast structural3 genomics consortium target mqr89a
31	c4h54B	Alignment	not modelled	49.6	13	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase ydeh; PDBTitle: crystal structure of the diguanylate cyclase dgcz
32	c6d9mA	Alignment	not modelled	38.3	13	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
33	c3ungC	Alignment	not modelled	31.2	16	PDB header: unknown function Chain: C: PDB Molecule: cmr2dh; PDBTitle: structure of the cmr2 subunit of the crispr rna silencing complex
34	c3mtkA	Alignment	not modelled	26.8	18	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase; PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
35	c3i5aA	Alignment	not modelled	26.2	17	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
36	c3breA	Alignment	not modelled	25.7	16	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
37	d2al1a1	Alignment	not modelled	19.8	18	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
38	d1r31a1	Alignment	not modelled	12.9	11	Fold: Ferredoxin-like Superfamily: NAD-binding domain of HMG-CoA reductase Family: NAD-binding domain of HMG-CoA reductase
39	c4lrVL	Alignment	not modelled	12.7	54	PDB header: dna binding protein Chain: L: PDB Molecule: dna sulfur modification protein dnde; PDBTitle: crystal structure of dnde from escherichia coli b7a involved in dna2.phosphorothioation modification
40	c6eibC	Alignment	not modelled	11.5	12	PDB header: transferase Chain: C: PDB Molecule: sensory box/ggdef family protein; PDBTitle: structure of the active ggeef domain of a diguanylate cyclase from2 vibrio cholerae.
41	c6f0kD	Alignment	not modelled	11.5	17	PDB header: membrane protein Chain: D: PDB Molecule: actd; PDBTitle: alternative complex iii
42	c3abdA	Alignment	not modelled	11.3	11	PDB header: cell cycle/replication Chain: A: PDB Molecule: mitotic spindle assembly checkpoint protein mad2b; PDBTitle: structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
43	c3hvaA	Alignment	not modelled	11.1	15	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas aeruginosa
44	c3hvwA	Alignment	not modelled	11.0	13	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567 protein from2 pseudomonas aeruginosa, northeast structural genomics consortium3 target par365c
45	d1nija2	Alignment	not modelled	11.0	13	Fold: Hypothetical protein YjiA, C-terminal domain Superfamily: Hypothetical protein YjiA, C-terminal domain Family: Hypothetical protein YjiA, C-terminal domain
46	c4aezB	Alignment	not modelled	10.6	11	PDB header: cell cycle Chain: B: PDB Molecule: mitotic spindle checkpoint component mad2; PDBTitle: crystal structure of mitotic checkpoint complex
47	c3icIA	Alignment	not modelled	10.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium target mcr174c
48	c5a4aA	Alignment	not modelled	10.4	25	PDB header: rna binding protein Chain: A: PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the osk domain of drosophila oskar
49	d2ptza1	Alignment	not modelled	10.4	20	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
50	c4dmzB	Alignment	not modelled	10.2	12	PDB header: nucleotide-binding protein Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo form
51	c5llxB	Alignment	not modelled	9.5	9	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase (ggdef) domain-containing protein; PDBTitle: bacteriophytochrome activated diguanylyl cyclase from idiomarina2 species a28l with gtp bound
52	d1go4a	Alignment	not modelled	8.9	13	Fold: The spindle assembly checkpoint protein mad2 Superfamily: The spindle assembly checkpoint protein mad2 Family: The spindle assembly checkpoint protein mad2
						Fold: Ferredoxin-like

53	d1w25a3	Alignment	not modelled	7.3	17	Superfamily: Nucleotide cyclase Family: GGDEF domain
54	c4w8yA	Alignment	not modelled	7.2	12	PDB header: rna binding protein Chain: A: PDB Molecule: crispr system cmr subunit cmr2; PDBTitle: structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
55	d2irfg	Alignment	not modelled	7.0	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Interferon regulatory factor
56	c4urgB	Alignment	not modelled	6.8	12	PDB header: lyase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from t.maritima (active-like dimer)
57	d1mbma	Alignment	not modelled	6.4	57	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
58	d1p42a1	Alignment	not modelled	6.2	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
59	d1dl5a2	Alignment	not modelled	6.1	20	Fold: Protein-L-isoaspartyl O-methyltransferase, C-terminal domain Superfamily: Protein-L-isoaspartyl O-methyltransferase, C-terminal domain Family: Protein-L-isoaspartyl O-methyltransferase, C-terminal domain
60	c4wxoA	Alignment	not modelled	5.5	18	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
61	c6btmD	Alignment	not modelled	5.5	7	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
62	c2y0fD	Alignment	not modelled	5.4	26	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
63	c2d35A	Alignment	not modelled	5.4	24	PDB header: cell cycle Chain: A: PDB Molecule: cell division activator ceda; PDBTitle: solution structure of cell division reactivation factor,2 ceda
64	c2dIIA	Alignment	not modelled	5.3	0	PDB header: cytokine Chain: A: PDB Molecule: interferon regulatory factor 4; PDBTitle: solution structure of the irf domain of human interferon2 regulator factors 4