




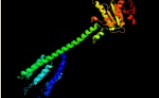


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1318c_(-)_1479205_1480830
Date	Wed Jul 31 22:05:41 BST 2019
Unique Job ID	98a6c05f894ffc1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fhtB_	 Alignment		100.0	30	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	c4yusA_	 Alignment		100.0	24	PDB header: lyase Chain: A; PDB Molecule: family 3 adenylate cyclase; PDBTitle: crystal structure of photoactivated adenyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
3	c6r4oA_	 Alignment		100.0	16	PDB header: membrane protein Chain: A; PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a truncated adenyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
4	c5nbyA_	 Alignment		100.0	23	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenyl cyclase; PDBTitle: structure of a bacterial light-regulated adenyl cyclase
5	c4cliA_	 Alignment		100.0	24	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenyl cyclase in complex with2 bicarbonate
6	c5o5kC_	 Alignment		100.0	26	PDB header: membrane protein Chain: C; PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenyl cyclase soluble domain
7	c6r4pA_	 Alignment		100.0	19	PDB header: membrane protein Chain: A; PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a soluble domain of adenyl cyclase bound to an2 activated stimulatory g protein
8	c1y10C_	 Alignment		100.0	20	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenyl cyclase rv1264, holoenzyme, inhibited state
9	c2w01C_	 Alignment		100.0	30	PDB header: lyase Chain: C; PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
10	c1wc6B_	 Alignment		100.0	32	PDB header: lyase Chain: B; PDB Molecule: adenylate cyclase; PDBTitle: soluble adenyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
11	d1wc1a_	 Alignment		100.0	33	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain

12	c3r5gB_	Alignment		100.0	25	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenyl cyclase cyab from p. aeruginosa
13	c1cjkA_	Alignment		100.0	17	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
14	d1azsa_	Alignment		100.0	17	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
15	d1fx2a_	Alignment		100.0	18	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
16	c3uvjC_	Alignment		100.0	19	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.
17	d1fx4a_	Alignment		100.0	19	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
18	c3et6A_	Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
19	c3mr7B_	Alignment		100.0	23	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
20	c2wz1B_	Alignment		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.
21	c1ybuA_	Alignment	not modelled	99.9	29	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenyl cyclase rv1900c chd, in complex2 with a substrate analog.
22	d1azsb_	Alignment	not modelled	99.9	19	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
23	c1yk9A_	Alignment	not modelled	99.9	26	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenyl cyclase rv1625c
24	c4wp3E_	Alignment	not modelled	99.9	28	PDB header: lyase Chain: E: PDB Molecule: ma1120; PDBTitle: crystal structure of adenyl cyclase from mycobacterium avium ma11202 wild type
25	c6aoaA_	Alignment	not modelled	99.9	24	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	c5jefA_	Alignment	not modelled	98.9	19	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
27	c4gn0D_	Alignment	not modelled	98.8	11	PDB header: signaling protein Chain: D: PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
28	c3lnrA_	Alignment	not modelled	98.4	16	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p.

						aeruginosa soluble2 receptor aer2
29	c3zx6A	Alignment	not modelled	98.0	13	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
30	d2asxa1	Alignment	not modelled	98.0	14	Fold: HAMP domain-like Superfamily: HAMP domain-like Family: HAMP domain
31	c3zrwB	Alignment	not modelled	97.8	15	PDB header: signaling protein Chain: B: PDB Molecule: af1503 protein, osmolarity sensor protein envz; PDBTitle: the structure of the dimeric hamp-dhp fusion a291v mutant
32	c4i5sA	Alignment	not modelled	97.5	23	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
33	c4biuB	Alignment	not modelled	96.9	23	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
34	c2qv6D	Alignment	not modelled	96.9	19	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
35	c4ctiA	Alignment	not modelled	96.8	14	PDB header: signaling protein Chain: A: PDB Molecule: osmolarity sensor protein envz, af1503; PDBTitle: escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
36	c5llxB	Alignment	not modelled	96.0	17	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
37	c3i5cA	Alignment	not modelled	95.5	13	PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wspir response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspir from pseudomonas aeruginosa
38	c1w25B	Alignment	not modelled	94.5	15	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
39	c2rm8A	Alignment	not modelled	94.3	20	PDB header: signaling protein Chain: A: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
40	c3breA	Alignment	not modelled	94.2	13	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
41	c4zmuD	Alignment	not modelled	93.8	12	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
42	c3ungC	Alignment	not modelled	93.7	24	PDB header: unknown function Chain: C: PDB Molecule: cmr2dhd; PDBTitle: structure of the cmr2 subunit of the crispr rna silencing complex
43	c4wxoA	Alignment	not modelled	93.3	11	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
44	c3i5aA	Alignment	not modelled	93.3	15	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wspir from pseudomonas syringae
45	c6d9mA	Alignment	not modelled	92.8	17	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
46	c3mtkA	Alignment	not modelled	92.7	11	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
47	c3ezuA	Alignment	not modelled	92.0	20	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
48	c4w8yA	Alignment	not modelled	91.6	22	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)
49	c5euhA	Alignment	not modelled	88.7	11	PDB header: membrane protein Chain: A: PDB Molecule: putative ggdef domain membrane protein; PDBTitle: crystal structure of the c-di-gmp-bound ggdef domain of p. fluorescens2 gcbs
50	c3hvwA	Alignment	not modelled	88.0	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
51	c3ignA	Alignment	not modelled	87.9	10	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
						Fold: Ferredoxin-like

52	d1w25a3	Alignment	not modelled	84.9	13	Superfamily: Nucleotide cyclase Family: GGDEF domain
53	c4zvvhB	Alignment	not modelled	84.5	19	PDB header: signaling protein Chain: B: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of ggdef domain of the e. coli dosc - form iv
54	c3i5bA	Alignment	not modelled	84.4	12	PDB header: signaling protein Chain: A: PDB Molecule: wspr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wspir from2 pseudomonas aeruginosa
55	c5m3cB	Alignment	not modelled	84.2	20	PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: 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
56	c4h54B	Alignment	not modelled	83.2	14	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase ydeh; PDBTitle: crystal structure of the diguanylate cyclase dgcz
57	c3hvaA	Alignment	not modelled	82.7	13	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas aeruginosa
58	c3icIA	Alignment	not modelled	81.9	14	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
59	c4ymeA	Alignment	not modelled	81.8	16	PDB header: lyase Chain: A: PDB Molecule: sensory box/ggdef family protein; PDBTitle: crystal structure of a sensory box/ggdef family protein (cc_0091) from2 caulobacter crescentus cb15 at 1.40 a resolution (psi community3 target, shapiro)
60	c3pjwA	Alignment	not modelled	79.4	10	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
61	c4dmzB	Alignment	not modelled	78.6	6	PDB header: nucleotide-binding protein Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo form
62	c4urgB	Alignment	not modelled	77.6	20	PDB header: lyase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from t.maritima (active-like dimer)
63	c6eibC	Alignment	not modelled	76.9	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.
64	c3qyvB	Alignment	not modelled	76.1	15	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
65	c4iobA	Alignment	not modelled	75.9	17	PDB header: lyase Chain: A: PDB Molecule: diguanylate cyclase tpbb; PDBTitle: crystal structure of the ggdef domain of pa1120 (yfin or tpbb) from2 pseudomonas aeruginosa at 2.7 ang.
66	c5xgdA	Alignment	not modelled	74.7	16	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
67	c4zmmB	Alignment	not modelled	65.1	13	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: ggdef domain of dcsbis complexed with c-di-gmp
68	c4euvA	Alignment	not modelled	62.8	11	PDB header: signaling protein Chain: A: PDB Molecule: peld; PDBTitle: crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
69	c3tvkA	Alignment	not modelled	62.7	15	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase dgcz; PDBTitle: diguanylate cyclase domain of dgcz
70	c6ifnA	Alignment	not modelled	44.5	17	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
71	c3dcaC	Alignment	not modelled	40.5	11	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: rpa0582; PDBTitle: crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
72	c2w6bA	Alignment	not modelled	37.4	22	PDB header: signaling protein Chain: A: PDB Molecule: rho guanine nucleotide exchange factor 7; PDBTitle: crystal structure of the trimeric beta-pix coiled-coil2 domain
73	c4biyD	Alignment	not modelled	36.6	19	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
74	c3hlsE	Alignment	not modelled	36.3	18	PDB header: signaling protein Chain: E: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: crystal structure of the signaling helix coiled-coil domain2 of the beta-1 subunit of the soluble guanylyl cyclase
75	c4rnhA	Alignment	not modelled	34.3	21	PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
76	c2x5eA	Alignment	not modelled	33.5	10	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
77	d2dfaa1	Alignment	not modelled	32.0	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase

						Family: LamB/YcsF-like
78	c5n9jB_	Alignment	not modelled	30.8	10	PDB header: transcription Chain: B: PDB Molecule: mediator of rna polymerase ii transcription subunit 10; PDBTitle: core mediator of transcriptional regulation
79	c5buzC_	Alignment	not modelled	30.6	23	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 chaetomium thermophilum
80	d1v6ta_	Alignment	not modelled	29.0	7	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
81	c4rndC_	Alignment	not modelled	23.2	18	PDB header: hydrolase Chain: C: PDB Molecule: v-type proton atpase subunit d; PDBTitle: crystal structure of the subunit df-assembly of the eukaryotic v-2 atpase.
82	c3w3aO_	Alignment	not modelled	23.1	12	PDB header: hydrolase Chain: O: PDB Molecule: v-type atp synthase subunit d; PDBTitle: crystal structure of v1-atpase at 3.9 angstrom resolution
83	c5bw9G_	Alignment	not modelled	20.6	14	PDB header: hydrolase Chain: G: PDB Molecule: v-type proton atpase subunit d; PDBTitle: crystal structure of yeast v1-atpase in the autoinhibited form
84	c6b87C_	Alignment	not modelled	15.8	25	PDB header: membrane protein Chain: C: PDB Molecule: tmhc2_e; PDBTitle: crystal structure of transmembrane protein tmhc2_e
85	d1h41a2	Alignment	not modelled	15.5	16	Fold: Zincin-like Superfamily: beta-N-acetylhexosaminidase-like domain Family: alpha-D-glucuronidase, N-terminal domain
86	c6iu3A_	Alignment	not modelled	15.1	21	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
87	c3a5dG_	Alignment	not modelled	14.9	12	PDB header: hydrolase Chain: G: PDB Molecule: v-type atp synthase subunit d; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
88	c4axkB_	Alignment	not modelled	14.4	29	PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
89	c3j9vM_	Alignment	not modelled	13.2	18	PDB header: hydrolase Chain: M: PDB Molecule: v-type proton atpase subunit d; PDBTitle: yeast v-atpase state 3
90	c3nvbA_	Alignment	not modelled	12.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
91	d1veha_	Alignment	not modelled	12.2	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
92	c6iqwA_	Alignment	not modelled	11.6	17	PDB header: rna binding protein/rna Chain: A: PDB Molecule: csm1; PDBTitle: cryo-em structure of csm effector complex
93	c5xu1M_	Alignment	not modelled	11.3	11	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
94	d2hwna1	Alignment	not modelled	10.7	23	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
95	c3lmbA_	Alignment	not modelled	10.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein olei01261 with unknown function2 from chlorobaculum tepidum t1s
96	c2f7ta_	Alignment	not modelled	10.5	6	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
97	c5cw9A_	Alignment	not modelled	10.5	24	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed ferredoxin-ferredoxin domain insertion PDBTitle: crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
98	c2kjaA_	Alignment	not modelled	10.4	17	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s6; PDBTitle: solution structure and backbone dynamics of the permutant p54-55
99	d1q8ka2	Alignment	not modelled	10.0	13	Fold: Ferredoxin-like Superfamily: eIF-2-alpha, C-terminal domain Family: eIF-2-alpha, C-terminal domain