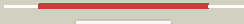























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1264 (-)_1411900_1413093
Date	Wed Jul 31 22:05:35 BST 2019
Unique Job ID	d1f2d28de7a30be8

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y10C_	 Alignment		100.0	100	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenyllyl cyclase rv1264, holoenzyme, inhibited state
2	c6fhtB_	 Alignment		100.0	18	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
3	c2ev2B_	 Alignment		100.0	100	PDB header: lyase Chain: B; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cyclase rv1264, at ph 8.5
4	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 cyanobacteriaoscillatoria acuminata in hexagonal form
5	d1fx2a_	 Alignment		100.0	22	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
6	d1fx4a_	 Alignment		100.0	23	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
7	c5nbyA_	 Alignment		100.0	19	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenyllyl cyclase; PDBTitle: structure of a bacterial light-regulated adenyllyl cyclase
8	c6r4oA_	 Alignment		100.0	20	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
9	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
10	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
11	c6r4pA_	 Alignment		100.0	21	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

12	c4wp3E_	Alignment		100.0	31	PDB header: lyase Chain: E: PDB Molecule: ma1120; PDBTitle: crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type
13	c5o5kC_	Alignment		100.0	28	PDB header: membrane protein Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenylyl cyclase soluble domain
14	c1wc6B_	Alignment		100.0	26	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
15	c1ybuA_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
16	d1wc1a_	Alignment		100.0	26	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
17	c3uviC_	Alignment		100.0	23	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.
18	c1cjkA_	Alignment		100.0	23	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
19	c3r5gB_	Alignment		100.0	23	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenylyl cyclase cyab from p. aeruginosa
20	c2w01C_	Alignment		100.0	20	PDB header: lyase Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
21	d1azsa_	Alignment	not modelled	100.0	21	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
22	c3et6A_	Alignment	not modelled	100.0	28	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
23	c2wz1B_	Alignment	not modelled	100.0	24	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.
24	d1azsb_	Alignment	not modelled	100.0	27	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
25	c1yk9A_	Alignment	not modelled	100.0	31	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
26	c6a0aA_	Alignment	not modelled	99.9	23	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
27	c4zmuD_	Alignment	not modelled	96.2	10	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
28	c5llxB_	Alignment	not modelled	95.7	11	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 PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
29	c5c8eC_	Alignment	not modelled	95.5	14	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
30	c2qv6D_	Alignment	not modelled	95.2	20	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
31	c1w25B_	Alignment	not modelled	94.4	12	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
32	c4r4eA_	Alignment	not modelled	94.1	10	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
33	c3ezuA_	Alignment	not modelled	93.8	16	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
34	c4r24B_	Alignment	not modelled	93.4	15	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
35	c5af3A_	Alignment	not modelled	93.2	11	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
36	c3hh0C_	Alignment	not modelled	91.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator rv1828; PDBTitle: crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
37	c5ydcA_	Alignment	not modelled	91.2	15	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
38	c6d9mA_	Alignment	not modelled	91.1	14	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
39	c3ignA_	Alignment	not modelled	89.6	10	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
40	c2zhhA_	Alignment	not modelled	89.4	14	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase ydeh; PDBTitle: crystal structure of the diguanylate cyclase dgcz
41	c4h54B_	Alignment	not modelled	89.4	10	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
42	c5i44E_	Alignment	not modelled	88.5	13	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
43	c3mtkA_	Alignment	not modelled	88.2	13	PDB header: metal binding protein Chain: A: PDB Molecule: mercuric resistance operon regulatory protein; PDBTitle: crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
44	c5crlA_	Alignment	not modelled	88.0	16	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
45	d1r8da_	Alignment	not modelled	87.4	18	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, merr-family; PDBTitle: crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
46	c5gpeB_	Alignment	not modelled	85.7	7	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
47	d1r8ea1	Alignment	not modelled	85.5	14	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
48	c2vz4A_	Alignment	not modelled	84.0	18	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)
49	c4ymeA_	Alignment	not modelled	83.5	16	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.
50	c6eibC_	Alignment	not modelled	82.8	15	PDB header: signaling protein Chain: B: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of ggdef domain of the e. coli dosc - form iv
51	c4zvhhB_	Alignment	not modelled	82.3	15	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567
52	c3hvwA_	Alignment	not modelled	81.4	12	

						protein from2 pseudomonas aeruginosa, northeast structural genomics consortium3 target par365c
53	c2jmlA_	Alignment	not modelled	80.3	25	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
54	c3hvaA_	Alignment	not modelled	80.0	16	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas aeruginosa
55	c4iobA_	Alignment	not modelled	79.9	13	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.
56	c4wxoA_	Alignment	not modelled	79.8	18	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
57	c3ucsB_	Alignment	not modelled	77.4	19	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
58	c3gp4B_	Alignment	not modelled	77.4	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
59	c3i5aA_	Alignment	not modelled	76.1	20	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
60	c4zmmB_	Alignment	not modelled	75.9	11	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: ggdef domain of dcsbis complexed with c-di-gmp
61	c3breA_	Alignment	not modelled	74.8	17	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
62	c4euvA_	Alignment	not modelled	72.8	8	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
63	d1q06a_	Alignment	not modelled	70.7	10	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
64	c3gpvA_	Alignment	not modelled	70.5	6	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
65	c3icIA_	Alignment	not modelled	67.4	15	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
66	c6amaO_	Alignment	not modelled	62.7	17	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. colorator/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
67	c4j2nB_	Alignment	not modelled	62.7	21	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
68	c4j2nA_	Alignment	not modelled	62.7	21	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
69	d1w25a3	Alignment	not modelled	62.1	11	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
70	c4urgB_	Alignment	not modelled	59.5	14	PDB header: lyase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from t.maritima (active-like dimer)
71	c3tvkA_	Alignment	not modelled	58.3	10	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase dgcz; PDBTitle: diguanylate cyclase domain of dgcz
72	d1v6ta_	Alignment	not modelled	57.9	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
73	c2x5eA_	Alignment	not modelled	54.8	20	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
74	c3qyvB_	Alignment	not modelled	51.6	11	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
75	c3ungC_	Alignment	not modelled	49.4	12	PDB header: unknown function Chain: C: PDB Molecule: cmr2dhd; PDBTitle: structure of the cmr2 subunit of the crispr rna silencing complex
76	d2dfaa1	Alignment	not modelled	44.7	23	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
77	c3iwfA_	Alignment	not modelled	43.1	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a PDB header: nucleotide-binding protein

78	c4dmzB_	Alignment	not modelled	41.6	8	Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo form
79	c4w8yA_	Alignment	not modelled	39.1	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)
80	c5euhA_	Alignment	not modelled	35.9	13	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 gcbc
81	c3i5cA_	Alignment	not modelled	35.2	15	PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wsp response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wsp from pseudomonas aeruginosa
82	c4ua2B_	Alignment	not modelled	29.6	16	PDB header: dna binding protein Chain: B: PDB Molecule: regulatory protein; PDBTitle: crystal structure of dual function transcriptional regulator merr from2 bacillus megaterium mb1
83	c3qaoA_	Alignment	not modelled	28.5	16	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
84	d2es9a1	Alignment	not modelled	27.9	11	Fold: YoaC-like Superfamily: YoaC-like Family: YoaC-like
85	c5m3cB_	Alignment	not modelled	24.9	17	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
86	c2y0fD_	Alignment	not modelled	22.9	9	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
87	c4ivnB_	Alignment	not modelled	22.2	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-6p
88	c5xgdA_	Alignment	not modelled	21.5	12	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
89	c3noyA_	Alignment	not modelled	21.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
90	d2p7vb1	Alignment	not modelled	20.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
91	c2dg6A_	Alignment	not modelled	19.3	14	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
92	c3pjwA_	Alignment	not modelled	16.7	10	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
93	c3i5bA_	Alignment	not modelled	16.0	13	PDB header: signaling protein Chain: A: PDB Molecule: wsp response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wsp from2 pseudomonas aeruginosa
94	c3t72o_	Alignment	not modelled	15.8	19	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
95	c5xqlA_	Alignment	not modelled	15.2	6	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
96	c2o3fC_	Alignment	not modelled	14.0	24	PDB header: transcription Chain: C: PDB Molecule: putative hth-type transcriptional regulator ybbh; PDBTitle: structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
97	d2o3fa1	Alignment	not modelled	14.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
98	d2tssa1	Alignment	not modelled	13.8	33	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
99	c2cwbA_	Alignment	not modelled	13.3	24	PDB header: protein binding Chain: A: PDB Molecule: chimera of immunoglobulin g binding protein g PDBTitle: solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin