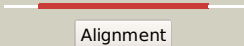

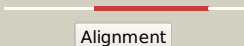

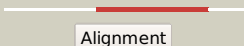







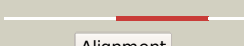











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2212 (-)_2477198_2478334
Date	Mon Aug 5 13:25:34 BST 2019
Unique Job ID	f5f61ea0f57ab5c9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y10C_	 Alignment		100.0	24	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenyllyl cyclase rv1264, holoenzyme, inhibited state
2	c6fhtB_	 Alignment		100.0	19	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	c4yusA_	 Alignment		100.0	20	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
4	c5nbyA_	 Alignment		100.0	21	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenyllyl cyclase; PDBTitle: structure of a bacterial light-regulated adenyllyl cyclase
5	d1fx2a_	 Alignment		100.0	32	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyllyl and guanylyl cyclase catalytic domain
6	c6r4oA_	 Alignment		100.0	18	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
7	d1fx4a_	 Alignment		100.0	34	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyllyl and guanylyl cyclase catalytic domain
8	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
9	c4wp3E_	 Alignment		100.0	30	PDB header: lyase Chain: E; PDB Molecule: ma1120; PDBTitle: crystal structure of adenyllyl cyclase from mycobacterium avium ma11202 wild type
10	c4cIIA_	 Alignment		100.0	17	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenyllyl cyclase in complex with2 bicarbonate
11	c5o5kC_	 Alignment		100.0	25	PDB header: membrane protein Chain: C; PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenyllyl cyclase soluble domain

12	c6r4pA_	Alignment		100.0	19	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
13	d1wc1a_	Alignment		100.0	30	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
14	c1wc6B_	Alignment		100.0	30	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	28	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
16	c3r5gB_	Alignment		100.0	28	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenylyl cyclase cyab from p. aeruginosa
17	c2w01C_	Alignment		100.0	21	PDB header: lyase Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
18	c1cjkA_	Alignment		100.0	25	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	c3uviC_	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.
20	d1lzas_	Alignment		100.0	24	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
21	c3et6A_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
22	d1lzasb_	Alignment	not modelled	100.0	21	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
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	c1yk9A_	Alignment	not modelled	100.0	27	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
25	c6aoaA_	Alignment	not modelled	100.0	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
26	c2ev2B_	Alignment	not modelled	99.9	21	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cyclase rv1264, at ph 8.5
27	c2qv6D_	Alignment	not modelled	96.3	18	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
28	c1w25B_	Alignment	not modelled	96.0	12	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein;

						PDBTitle: response regulator pled in complex with c-digmp
29	c5llxB_	Alignment	not modelled	95.9	14	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
30	c4zmuD_	Alignment	not modelled	95.1	18	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
31	c3breA_	Alignment	not modelled	94.3	13	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
32	c6d9mA_	Alignment	not modelled	93.4	17	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
33	c3ignA_	Alignment	not modelled	93.2	9	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
34	c3i5aA_	Alignment	not modelled	92.6	18	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
35	c4h54B_	Alignment	not modelled	91.5	15	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase ydeh; PDBTitle: crystal structure of the diguanylate cyclase dgcz
36	c3hvwA_	Alignment	not modelled	90.9	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
37	c3i5cA_	Alignment	not modelled	90.6	9	PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wpsr response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wpsr from pseudomonas aeruginosa
38	c3mtkA_	Alignment	not modelled	89.7	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
39	c4wxoA_	Alignment	not modelled	89.4	15	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
40	c5euhA_	Alignment	not modelled	87.9	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 gbc
41	c3hvaA_	Alignment	not modelled	87.4	15	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas aeruginosa
42	c3ungC_	Alignment	not modelled	82.5	17	PDB header: unknown function Chain: C: PDB Molecule: cmr2dhd; PDBTitle: structure of the cmr2 subunit of the crispr rna silencing complex
43	c3ezuA_	Alignment	not modelled	81.3	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
44	c6eibC_	Alignment	not modelled	77.3	10	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.
45	c4iobA_	Alignment	not modelled	77.0	14	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.
46	c3i5bA_	Alignment	not modelled	75.5	13	PDB header: signaling protein Chain: A: PDB Molecule: wpsr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
47	c4ymeA_	Alignment	not modelled	74.6	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)
48	d1w25a3	Alignment	not modelled	72.7	11	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
49	c4w8yA_	Alignment	not modelled	71.9	18	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)
50	c4zvhB_	Alignment	not modelled	71.2	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
51	c3qyyB_	Alignment	not modelled	62.8	7	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
52	c4urgB_	Alignment	not modelled	60.9	16	PDB header: lyase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from t.maritima (active-

						like dimer)
53	c4euvA_	Alignment	not modelled	60.0	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
54	c3icIA_	Alignment	not modelled	56.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: real/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium target mcr174c
55	d1v6ta_	Alignment	not modelled	50.3	24	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
56	c2x5eA_	Alignment	not modelled	47.8	17	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
57	d2dfaa1	Alignment	not modelled	47.4	27	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
58	c4dmzB_	Alignment	not modelled	47.1	7	PDB header: nucleotide-binding protein Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo form
59	c5xgdA_	Alignment	not modelled	41.1	20	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
60	c4zmmB_	Alignment	not modelled	40.0	18	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: ggdef domain of dcsbis complexed with c-di-gmp
61	c5m3cB_	Alignment	not modelled	35.4	16	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
62	c3pjwA_	Alignment	not modelled	31.2	15	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
63	c3tvkA_	Alignment	not modelled	31.2	12	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase dgcz; PDBTitle: diguanylate cyclase domain of dgcz
64	c3js3C_	Alignment	not modelled	25.8	18	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
65	c2yr1B_	Alignment	not modelled	23.2	20	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
66	d1gqna_	Alignment	not modelled	21.7	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
67	d1sfla_	Alignment	not modelled	16.2	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
68	c3l2iB_	Alignment	not modelled	15.5	18	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
69	c2kjaA_	Alignment	not modelled	11.5	21	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s6; PDBTitle: solution structure and backbone dynamics of the permutant p54-55
70	d1veha_	Alignment	not modelled	11.3	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
71	c4r24B_	Alignment	not modelled	11.0	10	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
72	c1ojhK_	Alignment	not modelled	10.7	22	PDB header: protein binding Chain: K: PDB Molecule: nbla; PDBTitle: crystal structure of nbla from pcc 7120
73	d1ojha_	Alignment	not modelled	10.3	22	Fold: NblA-like Superfamily: NblA-like Family: NblA-like
74	c4lrL_	Alignment	not modelled	9.3	55	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
75	c2aq4A_	Alignment	not modelled	8.7	17	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: ternary complex of the catalytic core of rev1 with dna and dctp.
76	c3dcaC_	Alignment	not modelled	8.5	23	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: rpa0582; PDBTitle: crystal structure of the rpa0582- protein of unknown2 function from rhodospseudomonas palustris- a structural3 genomics target
77	c4r4eA_	Alignment	not modelled	8.4	13	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
						Fold: Ferredoxin-like

78	d2fiua1	Alignment	not modelled	8.4	12	Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
79	d2nzca1	Alignment	not modelled	8.1	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: TM1266-like
80	c5c8eC	Alignment	not modelled	8.0	11	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
81	c2xgva	Alignment	not modelled	7.8	22	PDB header: viral protein Chain: A: PDB Molecule: psiv capsid n-terminal domain; PDBTitle: structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
82	c5nnyA	Alignment	not modelled	7.6	15	PDB header: hydrolase Chain: A: PDB Molecule: wipb; PDBTitle: crystal structure of the phosphatase domain from the legionella2 effector wipb
83	d1m9dc	Alignment	not modelled	7.6	39	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
84	d1m9fd	Alignment	not modelled	7.6	39	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
85	d2eiaa2	Alignment	not modelled	7.6	22	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
86	d2pxrc1	Alignment	not modelled	7.3	39	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
87	c2wlvA	Alignment	not modelled	7.1	33	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal capsid domain of hiv-2
88	c3uitA	Alignment	not modelled	6.7	22	PDB header: cell adhesion Chain: A: PDB Molecule: inad-like protein, maguk p55 subfamily member 5, protein PDBTitle: overall structure of patj/pals1/mals complex
89	c2y0fD	Alignment	not modelled	6.5	19	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
90	d2hrva	Alignment	not modelled	6.4	44	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
91	c5buzC	Alignment	not modelled	6.3	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
92	c5yqgE	Alignment	not modelled	6.2	42	PDB header: peptide binding protein Chain: E: PDB Molecule: peptide from protein numb homolog; PDBTitle: the structure of 14-3-3 and pnumb peptide
93	c4a1aH	Alignment	not modelled	6.2	24	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l10; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
94	c2f7tA	Alignment	not modelled	6.2	12	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
95	c3iwfA	Alignment	not modelled	6.1	18	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
96	d2fq4a1	Alignment	not modelled	6.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
97	c1z8rA	Alignment	not modelled	5.9	44	PDB header: hydrolase Chain: A: PDB Molecule: coxsackievirus b4 polyprotein; PDBTitle: 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschoten / new york / 51)
98	c5d1wD	Alignment	not modelled	5.9	22	PDB header: transcription Chain: D: PDB Molecule: rv3249c transcriptional regulator; PDBTitle: crystal structure of mycobacterium tuberculosis rv3249c2 transcriptional regulator.
99	c4l3uA	Alignment	not modelled	5.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf3571 family protein (abaye3784) from2 acinetobacter baumannii aye at 1.95 a resolution