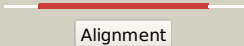

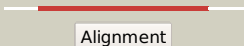

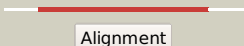







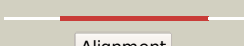











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1120c_(-)_1243015_1243509
Date	Wed Jul 31 22:05:20 BST 2019
Unique Job ID	a670518a64869552

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fhtB_	 Alignment		100.0	23	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	c5nbyA_	 Alignment		100.0	19	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenylyl cyclase; PDBTitle: structure of a bacterial light-regulated adenylyl cyclase
3	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 cyanobacteriaosillatoria acuminata in hexagonal form
4	c6r4oA_	 Alignment		100.0	15	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
5	c6r4pA_	 Alignment		99.9	15	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
6	c1y10C_	 Alignment		99.9	14	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
7	d1fx2a_	 Alignment		99.9	31	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
8	d1fx4a_	 Alignment		99.9	30	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
9	c4cIIA_	 Alignment		99.9	21	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenylyl cyclase in complex with2 bicarbonate
10	c5o5kC_	 Alignment		99.9	15	PDB header: membrane protein Chain: C; PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenylyl cyclase soluble domain
11	c1cjkA_	 Alignment		99.9	21	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

12	c4wp3E_	Alignment		99.9	76	PDB header: lyase Chain: E: PDB Molecule: ma1120; PDBTitle: crystal structure of adenyl cyclase from mycobacterium avium ma11202 wild type
13	c1wc6B_	Alignment		99.9	21	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
14	d1wc1a_	Alignment		99.9	24	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
15	d1azsa_	Alignment		99.9	20	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
16	c3mr7B_	Alignment		99.9	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
17	c3uvjC_	Alignment		99.8	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.
18	c3r5gB_	Alignment		99.8	22	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenyl cyclase cyab from p. aeruginosa
19	c2w01C_	Alignment		99.8	24	PDB header: lyase Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
20	c1ybuA_	Alignment		99.8	36	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenyl cyclase rv1900c chd, in complex2 with a substrate analog.
21	d1azsb_	Alignment	not modelled	99.8	16	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
22	c6a0aA_	Alignment	not modelled	99.7	22	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
23	c1yk9A_	Alignment	not modelled	99.7	17	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenyl cyclase rv1625c
24	c3et6A_	Alignment	not modelled	99.7	18	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
25	c2wz1B_	Alignment	not modelled	99.6	17	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.
26	c1w25B_	Alignment	not modelled	97.8	15	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	97.6	14	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
28	c2qv6D_	Alignment	not modelled	97.5	20	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
29	c3i5aA_	Alignment	not modelled	97.4	11	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
30	c3ezuA_	Alignment	not modelled	97.3	15	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
31	c3breA_	Alignment	not modelled	97.3	10	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	97.2	16	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
33	c5llxB_	Alignment	not modelled	97.2	16	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
34	c4h54B_	Alignment	not modelled	96.7	19	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase ydeh; PDBTitle: crystal structure of the diguanylate cyclase dgcZ
35	c6eibC_	Alignment	not modelled	96.7	15	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.
36	c3mtkA_	Alignment	not modelled	96.6	15	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
37	c3i5cA_	Alignment	not modelled	96.5	10	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	c3i5bA_	Alignment	not modelled	96.4	10	PDB header: signaling protein Chain: A: PDB Molecule: wpsr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
39	c4wxoA_	Alignment	not modelled	96.3	14	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
40	c5m3cB_	Alignment	not modelled	96.2	15	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
41	c3hvaA_	Alignment	not modelled	96.0	10	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas aeruginosa
42	d1w25a3	Alignment	not modelled	96.0	15	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
43	c5euhA_	Alignment	not modelled	95.8	19	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
44	c3hvwA_	Alignment	not modelled	95.8	11	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	c4ymeA_	Alignment	not modelled	95.8	10	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)
46	c4zvhB_	Alignment	not modelled	95.8	17	PDB header: signaling protein Chain: B: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of ggdef domain of the e. coli dosc - form iv
47	c3tvkA_	Alignment	not modelled	95.6	12	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase dgcZ; PDBTitle: diguanylate cyclase domain of dgcZ
48	c4w8yA_	Alignment	not modelled	95.2	16	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	c3icIA_	Alignment	not modelled	95.1	21	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
50	c3ignA_	Alignment	not modelled	94.6	11	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
51	c4zmmB_	Alignment	not modelled	94.3	17	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: ggdef domain of dcsbis complexed with c-di-gmp
						PDB header: unknown function

52	c3ungC	Alignment	not modelled	94.2	16	Chain: C; PDB Molecule: cmr2dhd; PDBTitle: structure of the cmr2 subunit of the crispr rna silencing complex
53	c3qyyB	Alignment	not modelled	94.2	13	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
54	c4iobA	Alignment	not modelled	94.1	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.
55	c4urgB	Alignment	not modelled	93.9	18	PDB header: lyase Chain: B; PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from t.maritima (active-like dimer)
56	c5xgdA	Alignment	not modelled	92.9	15	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
57	c4euvA	Alignment	not modelled	92.0	13	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
58	c3pjwA	Alignment	not modelled	91.1	16	PDB header: lyase Chain: A; PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
59	c4dmzB	Alignment	not modelled	87.3	9	PDB header: nucleotide-binding protein Chain: B; PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo form
60	c6ifnA	Alignment	not modelled	72.8	10	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
61	c4rnhA	Alignment	not modelled	69.7	16	PDB header: transferase, hydrolase Chain: A; PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
62	c3noyA	Alignment	not modelled	39.9	27	PDB header: oxidoreductase Chain: A; PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
63	c2y0fD	Alignment	not modelled	35.0	30	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
64	d1v6ta	Alignment	not modelled	31.9	5	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
65	c2x5eA	Alignment	not modelled	28.0	5	PDB header: unknown function Chain: A; PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
66	d2dfaa1	Alignment	not modelled	27.0	5	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
67	c6iqwA	Alignment	not modelled	27.0	14	PDB header: rna binding protein/rna Chain: A; PDB Molecule: csm1; PDBTitle: cryo-em structure of csm effector complex
68	d1veha	Alignment	not modelled	26.5	11	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
69	d1pnoa	Alignment	not modelled	23.9	25	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
70	d1d4oa	Alignment	not modelled	23.3	29	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
71	c1pt9B	Alignment	not modelled	21.7	30	PDB header: oxidoreductase Chain: B; PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
72	c4o9uB	Alignment	not modelled	20.9	18	PDB header: membrane protein Chain: B; PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
73	c2f7tA	Alignment	not modelled	19.5	9	PDB header: dna binding protein Chain: A; PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
74	c2bruC	Alignment	not modelled	18.8	25	PDB header: oxidoreductase Chain: C; PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
75	d1mbma	Alignment	not modelled	17.0	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
76	c3dcaC	Alignment	not modelled	12.2	14	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
77	c4ashB	Alignment	not modelled	10.3	24	PDB header: hydrolase Chain: B; PDB Molecule: ns6 protease; PDBTitle: crystal structure of the ns6 protease from murine norovirus 1
						PDB header: transferase

78	c3f2kB_	Alignment	not modelled	10.0	9	Chain: B: PDB Molecule: histone-lysine n-methyltransferase setmar; PDBTitle: structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
79	c4mwaA_	Alignment	not modelled	10.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
80	c2diuA_	Alignment	not modelled	9.4	14	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0430 protein; PDBTitle: solution structure of the rrm domain of kiaa0430 protein
81	c3hosA_	Alignment	not modelled	8.8	9	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
82	d2al1a1	Alignment	not modelled	8.6	20	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
83	c4uw2A_	Alignment	not modelled	7.3	14	PDB header: immune system Chain: A: PDB Molecule: csm1; PDBTitle: crystal structure of csm1 in t.onnurineus
84	d1m9dc_	Alignment	not modelled	6.9	17	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	d1xhja_	Alignment	not modelled	6.8	10	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
86	d2eiaa2	Alignment	not modelled	6.6	6	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	d1m9fd_	Alignment	not modelled	6.6	17	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
88	c2xgvA_	Alignment	not modelled	6.5	17	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)
89	c5cr4B_	Alignment	not modelled	6.5	13	PDB header: hydrolase Chain: B: PDB Molecule: sleeping beauty transposase, sb100x; PDBTitle: crystal structure of the sleeping beauty transposase catalytic domain
90	c1q01A_	Alignment	not modelled	6.3	46	PDB header: blood clotting Chain: A: PDB Molecule: lebetin 2 isoform alpha; PDBTitle: lebetin peptides, a new class of potent aggregation2 inhibitors
91	d2pxrc1	Alignment	not modelled	6.2	17	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
92	c2wlvA_	Alignment	not modelled	6.0	17	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal capsid domain of hiv-2
93	c2v4oB_	Alignment	not modelled	5.9	19	PDB header: hydrolase Chain: B: PDB Molecule: multifunctional protein sur e; PDBTitle: crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
94	c2phjA_	Alignment	not modelled	5.6	17	PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase sure; PDBTitle: crystal structure of sure protein from aquifex aeolicus
95	c5ocsB_	Alignment	not modelled	5.6	15	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-dependent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans