
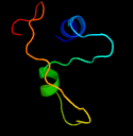


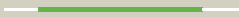
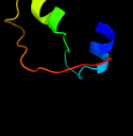
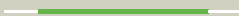






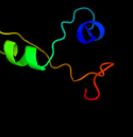










# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1119c_(-)_1242869_1243018
Date	Wed Jul 31 22:05:20 BST 2019
Unique Job ID	ea2d74b54d24632e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1y10C_</a>	 Alignment		62.6	26	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> mycobacterial adenyl cyclase rv1264, holoenzyme, inhibited state
2	<a href="#">d1fx4a_</a>	 Alignment		57.9	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenyl and guanyl cyclase catalytic domain
3	<a href="#">c3et6A_</a>	 Alignment		57.3	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> soluble guanyl cyclase beta; <b>PDBTitle:</b> the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
4	<a href="#">d1fx2a_</a>	 Alignment		53.2	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenyl and guanyl cyclase catalytic domain
5	<a href="#">c4wp3E_</a>	 Alignment		52.6	53	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> ma1120; <b>PDBTitle:</b> crystal structure of adenyl cyclase from mycobacterium avium ma11202 wild type
6	<a href="#">c3mr7B_</a>	 Alignment		48.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylate/guanyl cyclase/hydrolase, alpha/beta fold <b>PDBTitle:</b> crystal structure of adenylate/guanyl cyclase/hydrolase from2 silicibacter pomeroyi
7	<a href="#">c3r5gB_</a>	 Alignment		45.7	17	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> cyab; <b>PDBTitle:</b> crystal structure of the adenyl cyclase cyab from p. aeruginosa
8	<a href="#">c2wz1B_</a>	 Alignment		43.7	17	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> guanyl cyclase soluble subunit beta-1; <b>PDBTitle:</b> structure of the catalytic domain of human soluble guanyl cyclase 12 beta 3.
9	<a href="#">c5o5kC_</a>	 Alignment		33.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> adenyl cyclase; <b>PDBTitle:</b> x-ray structure of a bacterial adenyl cyclase soluble domain
10	<a href="#">d1wc1a_</a>	 Alignment		32.2	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenyl and guanyl cyclase catalytic domain
11	<a href="#">d1azsa_</a>	 Alignment		28.6	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenyl and guanyl cyclase catalytic domain

12	<a href="#">c1wc6B_</a>	Alignment		27.6	24	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
13	<a href="#">c3uvjC_</a>	Alignment		27.2	19	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> guanylate cyclase soluble subunit alpha-3; <b>PDBTitle:</b> crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
14	<a href="#">d1azsb_</a>	Alignment		24.0	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
15	<a href="#">c1yk9A_</a>	Alignment		20.8	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
16	<a href="#">c1cjkA_</a>	Alignment		19.8	9	<b>PDB header:</b> lyase/lyase/signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase, type v; <b>PDBTitle:</b> complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
17	<a href="#">c4qamB_</a>	Alignment		16.9	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> x-linked retinitis pigmentosa gtpase regulator-interacting <b>PDBTitle:</b> crystal structure of the rpgr rcc1-like domain in complex with the2 rpgr-interacting domain of rpgr1p1
18	<a href="#">c2w01C_</a>	Alignment		13.4	21	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of the guanylyl cyclase cya2
19	<a href="#">c6fhtB_</a>	Alignment		13.1	23	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> bacteriophytochrome,adenylate cyclase; <b>PDBTitle:</b> crystal structure of an artificial phytochrome regulated2 adenylyl/guanylate cyclase in its dark adapted pr form
20	<a href="#">c2a45L_</a>	Alignment		11.3	86	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> L; <b>PDB Molecule:</b> fibrinogen gamma chain; <b>PDBTitle:</b> crystal structure of the complex between thrombin and the central "e"2 region of fibrin
21	<a href="#">c1ybuA_</a>	Alignment	not modelled	10.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipj; <b>PDBTitle:</b> mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
22	<a href="#">c6a0aA_</a>	Alignment	not modelled	8.7	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> bacterio-rhodopsin/guanylyl cyclase 1 fusion protein; <b>PDBTitle:</b> 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	<a href="#">c5c5zA_</a>	Alignment	not modelled	8.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamyl-trna amidotransferase; <b>PDBTitle:</b> crystal structure analysis of c4763, a uropathogenic e. coli-specific2 protein
24	<a href="#">c4ktbA_</a>	Alignment	not modelled	7.9	32	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of posible asymmetric diadenosine tetraphosphate2 (ap(4)a) hydrolases from jonesia denitrificans dsm 20603
25	<a href="#">c2jorA_</a>	Alignment	not modelled	7.0	44	<b>PDB header:</b> blood clotting <b>Chain:</b> A; <b>PDB Molecule:</b> fibrinogen alpha chain; <b>PDBTitle:</b> nmr solution structure, stability, and interaction of the2 recombinant bovine fibrinogen alphac-domain fragment
26	<a href="#">c5aj8B_</a>	Alignment	not modelled	6.8	40	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> tubulin binding cofactor c; <b>PDBTitle:</b> tubulin binding cofactor c from leishmania major
27	<a href="#">c5ituB_</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B; <b>PDB Molecule:</b> endonuclease 8-like 1; <b>PDBTitle:</b> crystal structure of human neil1(242k) bound to duplex dna containing2 thf
						<b>Fold:</b> EF Hand-like

28	<a href="#">d1eg3a1</a>	Alignment	not modelled	5.4	33	<b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
29	<a href="#">d1qmg1</a>	Alignment	not modelled	5.3	50	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Acetohydroxy acid isomeroeductase (ketol-acid reductoisomerase, KARI)