

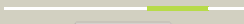


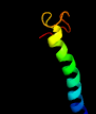











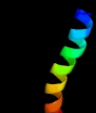




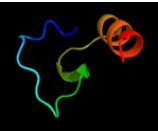

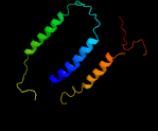
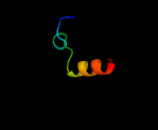
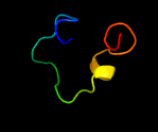

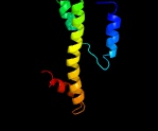




# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0017c\_rodA\_20231\_21640  
 Date Tue Jul 23 14:50:04 BST 2019  
 Unique Job ID 11892c3c4a7883ad

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c6basA_</a> |  Alignment   |    | 100.0      | 30     | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> peptidoglycan glycosyltransferase roda;<br><b>PDBTitle:</b> crystal structure of thermus thermophilus rod shape determining2 protein roda d255a mutant (q5six3_thet8)     |
| 2  | <a href="#">c6iedA_</a> |  Alignment   |    | 61.9       | 19     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> heme a synthase;<br><b>PDBTitle:</b> crystal structure of heme a synthase from bacillus subtilis   |
| 3  | <a href="#">c2jo1A_</a> |  Alignment   |    | 47.1       | 27     | <b>PDB header:</b> hydrolase regulator<br><b>Chain:</b> A; <b>PDB Molecule:</b> phospholemman;<br><b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxd1 in2 micelles  |
| 4  | <a href="#">c4mt1A_</a> |  Alignment   |    | 36.7       | 11     | <b>PDB header:</b> membrane protein, tranport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> drug efflux protein;<br><b>PDBTitle:</b> crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump                 |
| 5  | <a href="#">c6csxA_</a> |  Alignment |  | 35.4       | 17     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> multidrug efflux pump subunit acrb;<br><b>PDBTitle:</b> single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom             |
| 6  | <a href="#">c6dmoA_</a> |  Alignment |  | 30.7       | 11     | <b>PDB header:</b> protein binding<br><b>Chain:</b> A; <b>PDB Molecule:</b> protein patched homolog 1;<br><b>PDBTitle:</b> cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l   |
| 7  | <a href="#">c6owsB_</a> |  Alignment |  | 30.6       | 15     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> efflux pump membrane transporter;<br><b>PDBTitle:</b> cryo-em structure of an acinetobacter baumannii multidrug efflux pump  |
| 8  | <a href="#">c5ejdK_</a> |  Alignment |  | 30.6       | 20     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> K; <b>PDB Molecule:</b> tqaa;<br><b>PDBTitle:</b> the crystal structure of holo t3ct   |
| 9  | <a href="#">c2kncB_</a> |  Alignment |  | 28.6       | 26     | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B; <b>PDB Molecule:</b> integrin beta-3;<br><b>PDBTitle:</b> platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex   |
| 10 | <a href="#">c2v50A_</a> |  Alignment |  | 26.9       | 13     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> multidrug resistance protein mexb;<br><b>PDBTitle:</b> the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb |
| 11 | <a href="#">d2azea1</a> |  Alignment |  | 26.1       | 20     | <b>Fold:</b> E2F-DP heterodimerization region<br><b>Superfamily:</b> E2F-DP heterodimerization region<br><b>Family:</b> DP dimerization segment   |

|    |                         |           |   |      |    |   |
|----|-------------------------|-----------|---|------|----|---|
| 12 | <a href="#">c4pxhF_</a> | Alignment |     | 22.1 | 23 | <b>PDB header:</b> oxidoreductase/protein binding<br><b>Chain:</b> F; <b>PDB Molecule:</b> peptide synthetase;<br><b>PDBTitle:</b> structure of p450sky (cyp163b3), a cytochrome p450 from skllamycin2 biosynthesis in complex with a peptidyl carrier protein domain |
| 13 | <a href="#">c2mr7A_</a> | Alignment |    | 21.4 | 23 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> non-ribosomal peptide synthetase;<br><b>PDBTitle:</b> apo structure of the peptidyl carrier protein domain 7 of the2 teicoplanin producing non-ribosomal peptide synthetase          |
| 14 | <a href="#">c6nbxG_</a> | Alignment |    | 19.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j;<br><b>PDBTitle:</b> t.elongatus ndh (data-set 2)  |
| 15 | <a href="#">c5zk4D_</a> | Alignment |    | 18.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> D; <b>PDB Molecule:</b> disa protein;<br><b>PDBTitle:</b> the structure of dszs acyltransferase with carrier protein  |
| 16 | <a href="#">d2pnga1</a> | Alignment |    | 17.9 | 18 | <b>Fold:</b> Acyl carrier protein-like<br><b>Superfamily:</b> ACP-like<br><b>Family:</b> Acyl-carrier protein (ACP)   |
| 17 | <a href="#">d2gdwa1</a> | Alignment |    | 13.8 | 26 | <b>Fold:</b> Acyl carrier protein-like<br><b>Superfamily:</b> ACP-like<br><b>Family:</b> Peptidyl carrier domain  |
| 18 | <a href="#">d1iwga8</a> | Alignment |  | 13.4 | 11 | <b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain<br><b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain<br><b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain  |
| 19 | <a href="#">c4i4dA_</a> | Alignment |  | 13.3 | 25 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> peptide synthetase nrps type ii-pcp;<br><b>PDBTitle:</b> structure of blmi, a type-ii acyl-carrier-protein from streptomycetes2 verticillus involved in bleomycin biosynthesis       |
| 20 | <a href="#">c2jp3A_</a> | Alignment |  | 11.5 | 14 | <b>PDB header:</b> transcription<br><b>Chain:</b> A; <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4;<br><b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles   |
| 21 | <a href="#">c5zazA_</a> | Alignment | not modelled  | 11.4 | 21 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A; <b>PDB Molecule:</b> integrin beta-2;<br><b>PDBTitle:</b> solution structure of integrin b2 monomer tranmembrane domain in2 bicelle  |
| 22 | <a href="#">c5u3hA_</a> | Alignment | not modelled  | 11.3 | 23 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> hmwp2 nonribosomal peptide synthetase;<br><b>PDBTitle:</b> solution structure of apo pcp1 from yersiniabactin synthetase   |
| 23 | <a href="#">d2r6gf1</a> | Alignment | not modelled  | 10.6 | 18 | <b>Fold:</b> MalF N-terminal region-like<br><b>Superfamily:</b> MalF N-terminal region-like<br><b>Family:</b> MalF N-terminal region-like   |
| 24 | <a href="#">c5mtiA_</a> | Alignment | not modelled  | 9.9  | 27 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> phosphopantetheine-binding protein;<br><b>PDBTitle:</b> bamb_5917 acyl-carrier protein  |
| 25 | <a href="#">c2rmzA_</a> | Alignment | not modelled  | 8.9  | 21 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A; <b>PDB Molecule:</b> integrin beta-3;<br><b>PDBTitle:</b> bicelle-embedded integrin beta3 transmembrane segment  |
| 26 | <a href="#">c4pa5A_</a> | Alignment | not modelled  | 8.9  | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase;<br><b>PDBTitle:</b> tgl - a bacterial spore coat transglutaminase - cystamine complex  |
| 27 | <a href="#">c5msvB_</a> | Alignment | not modelled  | 8.5  | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B; <b>PDB Molecule:</b> thioester reductase domain-containing protein;<br><b>PDBTitle:</b> structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp    |
| 28 | <a href="#">c2mkvA_</a> | Alignment | not modelled  | 8.1  | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma;<br><b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in   |

|    |                         |           |              |     |    | micelles   |
|----|-------------------------|-----------|--------------|-----|----|--|
| 29 | <a href="#">c5zqbl_</a> | Alignment | not modelled | 6.3 | 46 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> I: <b>PDB Molecule:</b> psai;<br><b>PDBTitle:</b> cryo-em structure of the red algal psi-lhcr   |
| 30 | <a href="#">c5zghl_</a> | Alignment | not modelled | 6.3 | 46 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> I: <b>PDB Molecule:</b> psai;<br><b>PDBTitle:</b> cryo-em structure of the red algal psi-lhcr   |
| 31 | <a href="#">c4v19U_</a> | Alignment | not modelled | 6.1 | 13 | <b>PDB header:</b> ribosome<br><b>Chain:</b> U: <b>PDB Molecule:</b> mitoribosomal protein bl20m, mrpl20;<br><b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2   |
| 32 | <a href="#">d1wuua2</a> | Alignment | not modelled | 6.0 | 19 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> GHMP Kinase, C-terminal domain<br><b>Family:</b> Galactokinase   |
| 33 | <a href="#">c2cq8A_</a> | Alignment | not modelled | 5.7 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase;<br><b>PDBTitle:</b> solution structure of rsgi ruh-033, a pp-binding domain of 2 10-fthfdh from human cdna                         |
| 34 | <a href="#">c6fosl_</a> | Alignment | not modelled | 5.3 | 46 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> I: <b>PDB Molecule:</b> photosystem i reaction center subunit viii;<br><b>PDBTitle:</b> cyanidioschyzon merolae photosystem i   |
| 35 | <a href="#">d1q90g_</a> | Alignment | not modelled | 5.2 | 50 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> PetG subunit of the cytochrome b6f complex<br><b>Family:</b> PetG subunit of the cytochrome b6f complex   |
| 36 | <a href="#">c1q90G_</a> | Alignment | not modelled | 5.2 | 50 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome b6f complex subunit petg;<br><b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii |