Actinobacteriophage Genome Annotation Submission Cover Sheet

This Cover Sheet will accompany each genome’s annotation file(s) submission and succinctly describe the work that your students and you have done. This document ensures that the work done was as complete and thorough as it could be. Most important to the QC reviewer, denote where the trouble spots were in your annotation and how they were resolved.

Phage Name. Faiyaz

Your Name. Allison Johnson

Your Institution. Virginia Commonwealth University

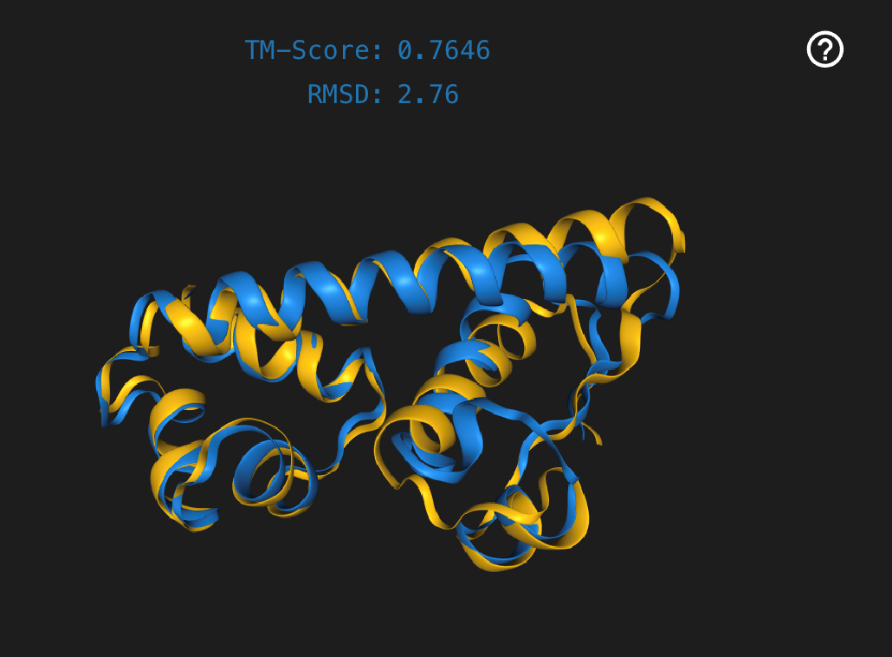
Your email. aajohnson@vcu.edu

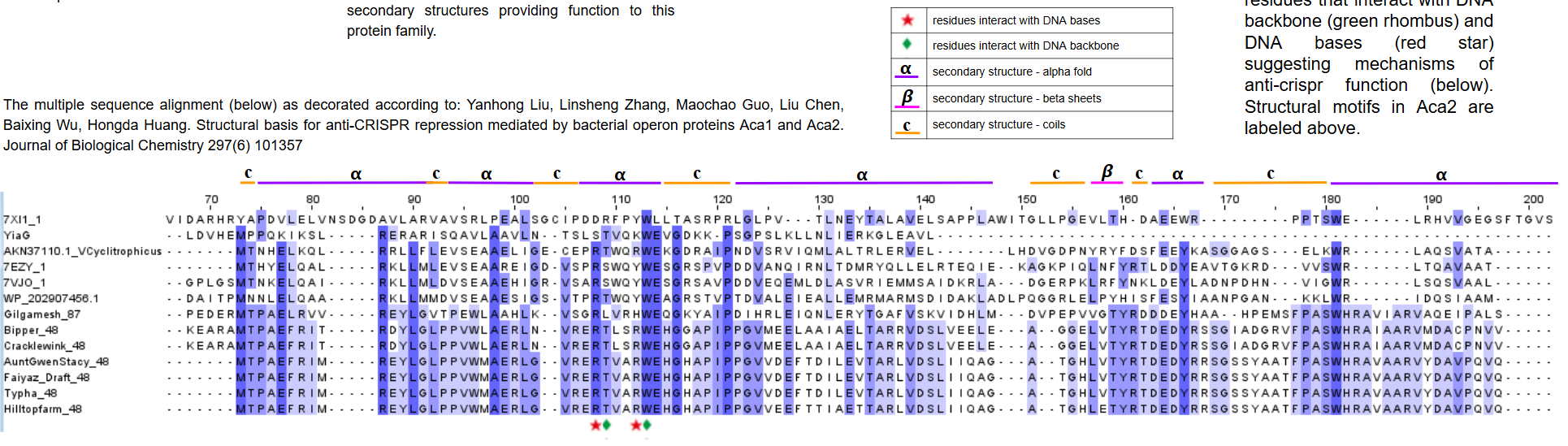
Additional emails. (for correspondence).

Describe any issues or specific genes that you would like to highlight for the QC reviewer. This includes any genes that you had questions about or received help with or that warrant further inspection in the QC review process. Include those genes that you deliberated on and/or want to strongly advocate for. If you contacted SMART, workshop facilitator, or a buddy school for help, please document.

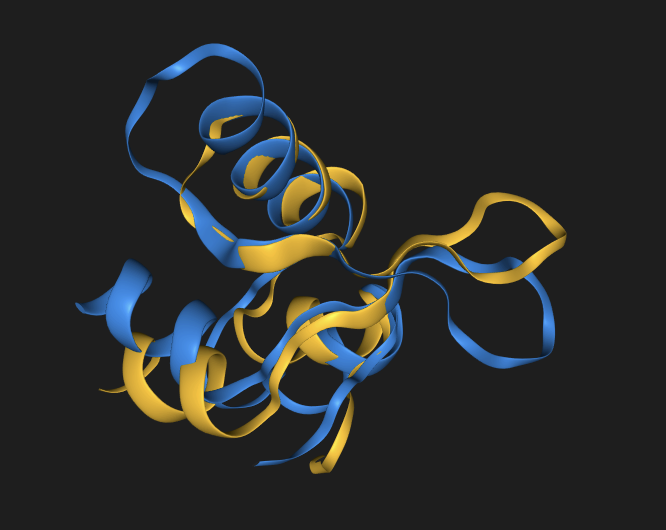
**Faiyaz gp40 has strong hits to brnt-like toxin but we didn’t find an antitoxin.**

**Faiyaz gp 46 matches** [**7VJO\_B in PDB**](https://www.rcsb.org/structure/7VJO)**, Aca2, an apo-Anti crispr associated protein from Pectobacterium phage ZF40. We used alpahfold/foldseek to show a nice overlay with Aca2 protein, with decent RMSD. A student also completed a multiple sequence alignment with sequences from the publication for 7VJO\_B to show secondary structures are conserved as well as conservation of residues important for Aca2 function (see green diamonds and red stars). Research poster is** [**here**](https://docs.google.com/presentation/d/1FH6qBv7V_ILLpQxhO84nNufrvJcMfnV5/edit?usp=sharing&ouid=109179460077108337879&rtpof=true&sd=true)**.**





**Faiyaz gp 96 used alphafold/foldseek to show evidence of wing in winged helix-turn-helix domain functional annotation. I’m sorry the student cropped out the RMSD value…but we’ve looked at these wings before, on the right in the image below.**



Please record yes/no for each of the questions below. If further explanation is needed, please add this item to the above box.

In the submitted DNA Master file (Yes/No):

Yes 1. Does the genome sequence in your submitted DNA Master file match the nucleotide fasta file posted on phagesDB (same number of bases, no N bases, etc.)?

Yes 2. Are all the genes ‘Valid” when you click the [Validation button](https://seaphagesbioinformatics.helpdocsonline.com/article-84)?

Yes 3. Are the genes (and matching LocusTag numbers) [sequential](https://seaphagesbioinformatics.helpdocsonline.com/article-77), starting with #1, counting by 1s.

Yes 4. Are the Locus Tags the “[SEA\_PHAGE NAME](https://seaphagesbioinformatics.helpdocsonline.com/article-77)” format?

Yes 5. Has the [documentation been recreated](https://seaphagesbioinformatics.helpdocsonline.com/article-86) from the Feature Table to match the latest file version?

Yes 6. Have tRNAs followed the [tRNA protocol](https://seaphagesbioinformatics.helpdocsonline.com/undefined), **COPYING** tRNA-AMINOACID type (DNA equivalent of the anti-codon) from Aragorn output - ﻿tRNA-Gln(ctg) - AND the ends been adjusted to match the Aragorn output?

Yes 7. Has the [frameshift in the tail assembly chaperone](https://seaphagesbioinformatics.helpdocsonline.com/article-54) been annotated correctly (if applicable)?

Yes 8. Have you cleared your Draft\_Blast data and have you [re-Blasted](https://seaphagesbioinformatics.helpdocsonline.com/article-57) the submitted DNA Master file?

Yes 9. Has every gene been [described and supported in your Supporting Data file](https://seaphagesbioinformatics.helpdocsonline.com/article-44)?

Yes 10. Did you investigate ‘[gaps](https://seaphagesbioinformatics.helpdocsonline.com/article-31)’?

Yes 11. Did you [delete the genes](https://seaphagesbioinformatics.helpdocsonline.com/article-65) that you meant to delete?

Now, [make a profile of the file](https://seaphagesbioinformatics.helpdocsonline.com/article-64) you plan to send. (And you can save this file for [Review to Improve!)](https://seaphagesbioinformatics.helpdocsonline.com/untitled-18)

Yes 1. Have any duplicate genes been deleted?

Yes 2. Has the Notes field been cleared (using the automated buttons)?

Yes 3. Do the gene numbers and locus tags match?

Yes 4. Are the correct Feature\_Types correctly selected (most will be ORFs, but check that tRNAs and tmRNAs are correctly labeled)?

Yes 5. Do the function names in the Product field either match the official function list or say “Hypothetical Protein”?

Yes 6. Has the Function field been cleared (using the automated buttons)?

How are you documenting your gene calls in class? Choose any/all that apply:

X PECAAN output- Pecaan output imported into DNA master documentation, parse, and save as Phage\_notes file

      DNA Master shorthand (previously used format)

      Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

X Other: Describe. We have an electronic notebook through a wiki system. Students do their work on their wiki and then transfer final call to Pecaan.

What is the file type (sort) submitted for QC to document your gene calls? Choose only one.:

      PECAAN output

X DNA Master shorthand (previously used format)

      Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

      Other: Describe.