**SESSION GUIDE:  
Collaborative Annotation Teams (CATs): CLUSTER-SPECIFIC ANNOTATION TIPS**

**PURPOSE**:   
To capture difficult gene calls for a given cluster and to begin drafting Cluster Specific Annotation Tips for those difficult gene calls to support a future annotator tasked with annotating a newly sequenced genome belonging to this cluster.

**INSTRUCTIONS:**

* Working in Collaborative Annotation Teams (CATs) and focused on a given cluster, gather all the genes that were difficult to call. Sort the list by what your group considers the most difficult gene calls (e.g. because most annotators were stumped by that gene).
* Compare the list you generated with the list of Cluster Specific Annotation Tips previously developed for that cluster and is available on the seaphages.org forums: <https://seaphages.org/forums/forum/32/>
* As a group, and guided by SMART members and Expedited Submitters, begin working to draft annotation tip for as many difficult gene calls, as possible. Keep in mind these tips are for a future annotator encountering these genes in newly sequenced genomes.
* At the end of the session,
  + The SMART/Expedited Submitter should copy and paste the list of difficult gene calls as a post in the CAT Forum specific for your cluster. Note, this is **not** the same as the Cluster Specific Annotation Tips forum.   
    Access the CAT forums here: <https://seaphages.org/forums/forum/228/>
  + The SMART/Expedited Submitter should also copy and paste any draft annotation tips developed during your session to the same CAT Forum:   
    Access the CAT forums here: <https://seaphages.org/forums/forum/228/>

Over the coming months, and in anticipation of the next Phage Genomics semester in Fall, SEA will work to further develop these draft annotation tips and post them to the Cluster Specific Annotation Tips Forum.