Weekly PECAAN notes  
Please review and refer back to this information in the bioinformatics guide: <https://seaphagesbioinformatics.helpdocsonline.com/officialdocumentation>

Complete and submit all required items using the notes template below (excel file). See the next section for brief instructions.

* If you accept the autoannotation for “gene included”, and “selected gene” just write ‘OK’ in the gene included cell. If you delete a gene (uncheck gene included box) write “deleted” in the gene included cell and write a brief justification for deleting the gene. If you have any concerns about selecting this gene that are not covered in one of the other items below, **briefly** describe your thoughts and/or concerns in the cell.
* List the Starterator entry with a brief explanation if you choose NA (not applicable) or NI (not informative), or if the SS (suggested start) you chose is not the most annotated call.
* All GM coding capacity = ‘yes’ needs no explanation; = ‘no’ requires a brief explanation or flagging for further discussion.
* NCBI blast t:q for start. Must list the t:q ratio; if t:q is **not 1:1** write a short justification for using this start or flag for future discussion.
* RBS Z and final scores: either “both best” or “not best”. If not best, write a brief explanation. For example, the best scores are not shared by the same start, or other evidence supports using this start.
* List the gap. Add any comments or concerns you have.
* All function related analyses except SOSUI and synteny: type OK to indicate that you looked and checked a hit when appropriate.
* If you run a gene on SOSUI (<https://harrier.nagahama-i-bio.ac.jp/sosui/mobile/> ) write a summary of the result.
* For genes with a known function list the synteny.
* List the function (including NKF) and make sure you have selected that function on the PECAAN page. This is also the place to write any questions or concerns you have about assigning this function.