

Dear Phage Annotation Quality Control Team,

Thank you for reviewing the genome of Refuge. We request that you pay extra attention to the genes listed below.

1. gp 2: Peptidase

* Blast alignment 77:77 to DarthPhader gp 2 seems odd
* Has large overlap with previous gene, but this is arrangement also occurs in DarthPhader Phamerator map

1. gp 36: NKF

* Added ORF (not called by Glimmer or GeneMark)
* Does not show BLAST hit to DarthPhader, but does have nt alignment with EagleEye (A16), and has BLAST hit (but 38:38) to EagleEye gp 37.

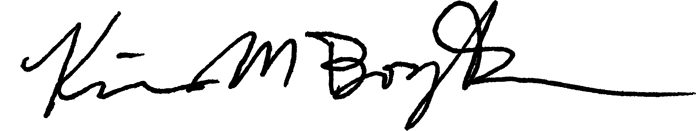
1. gp 57: DNA primase

* Added ORF (not called by Glimmer or GeneMark)
* Overlaps preceding DNA primase gene by 167 bp, yet both primases have different and strong Blastp alignments along full length
* DarthPhader has a DNA primase orpham at this location, but the alignment does not begin until residue 55 in Refuge, which corresponds to the second “M” in the product sequence.

1. gp 91: NKF

* Last gene
* Not the longest ORF, but extending length does not improve BLAST alignment to DarthPhader gp 92
* Does not include all coding potential shown on GeneMark-Smeg output
* Did not find evidence of another ORF in this region

Best regards,



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