



Note: Tracks are now grouped by subcluster and scaled. Switching in subcluster is indicated by changes in track color. Track scale is now set by default to display the region 30 bp upstream of start 1 to 30 bp downstream of the last possible start. If this default region is judged to be packed too tightly with annotated starts, the track will be further scaled to only show that region of the ORF with annotated starts. This action will be indicated by adding "Zoomed" to the title. For starts, yellow indicates the location of called starts comprised solely of Glimmer/GeneMark auto-annotations, green indicates the location of called starts with at least 1 manual gene annotation.

Pham 8139 Report

This analysis was run 04/05/24 on database version 557.

Pham number 8139 has 10 members, 3 are drafts.

Phages represented in each track:

- Track 1 : Marcie_108
- Track 2 : CandC_103, RobinRose_107, Romm_107, Kelcole_103
- Track 3 : BirdInFrench_102, Pepe25_101, Wilca_102
- Track 4 : Tempo_105
- Track 5 : Fregley_104

Summary of Final Annotations (See graph section above for start numbers):

The start number called the most often in the published annotations is 5, it was called in 7 of the 7 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- BirdInFrench_102, CandC_103, Fregley_104, Kelcole_103, Marcie_108, Pepe25_101, RobinRose_107, Romm_107, Tempo_105, Wilca_102,

Genes that have the "Most Annotated" start but do not call it:

-

Genes that do not have the "Most Annotated" start:

-

Summary by start number:

Start 5:

- Found in 10 of 10 (100.0%) of genes in pham
- Manual Annotations of this start: 7 of 7
- Called 100.0% of time when present
- Phage (with cluster) where this start called: BirdInFrench_102 (EG), CandC_103 (EG), Fregley_104 (EG), Kelcole_103 (EG), Marcie_108 (EG), Pepe25_101 (EG), RobinRose_107 (EG), Romm_107 (EG), Tempo_105 (EG), Wilca_102 (EG),

Summary by clusters:

There is one cluster represented in this pham: EG

Info for manual annotations of cluster EG:

- Start number 5 was manually annotated 7 times for cluster EG.

Gene Information:

Gene: BirdInFrench_102 Start: 60506, Stop: 60393, Start Num: 5

Candidate Starts for BirdInFrench_102:

(4, 60599), (Start: 5 @60506 has 7 MA's), (6, 60500), (7, 60428),

Gene: CandC_103 Start: 60778, Stop: 60665, Start Num: 5

Candidate Starts for CandC_103:

(2, 61111), (3, 60922), (Start: 5 @60778 has 7 MA's), (8, 60679),

Gene: Fregley_104 Start: 60725, Stop: 60612, Start Num: 5

Candidate Starts for Fregley_104:

(3, 60869), (Start: 5 @60725 has 7 MA's), (8, 60626),

Gene: Kelcole_103 Start: 61246, Stop: 61133, Start Num: 5

Candidate Starts for Kelcole_103:

(2, 61579), (3, 61390), (Start: 5 @61246 has 7 MA's), (8, 61147),

Gene: Marcie_108 Start: 61133, Stop: 61020, Start Num: 5

Candidate Starts for Marcie_108:

(Start: 5 @61133 has 7 MA's), (8, 61034), (9, 61031),

Gene: Pepe25_101 Start: 59431, Stop: 59324, Start Num: 5

Candidate Starts for Pepe25_101:

(4, 59524), (Start: 5 @59431 has 7 MA's), (6, 59425), (7, 59359),

Gene: RobinRose_107 Start: 61445, Stop: 61332, Start Num: 5

Candidate Starts for RobinRose_107:

(2, 61778), (3, 61589), (Start: 5 @61445 has 7 MA's), (8, 61346),

Gene: Romm_107 Start: 61442, Stop: 61329, Start Num: 5

Candidate Starts for Romm_107:

(2, 61775), (3, 61586), (Start: 5 @61442 has 7 MA's), (8, 61343),

Gene: Tempo_105 Start: 61303, Stop: 61190, Start Num: 5

Candidate Starts for Tempo_105:

(1, 61642), (2, 61636), (Start: 5 @61303 has 7 MA's), (8, 61204),

Gene: Wilca_102 Start: 60506, Stop: 60393, Start Num: 5

Candidate Starts for Wilca_102:

(4, 60599), (Start: 5 @60506 has 7 MA's), (6, 60500), (7, 60428),