Pham 96862

1: BirdInFrench_101 + 2

2: Marcie_107

3: CandC_102 + 6

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 96862 Report

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

Pham number 96862 has 11 members, 3 are drafts.

Phages represented in each track:
• Track 1 : BirdInFrench_101, Pepe25_100, Wilca_101
• Track 2 : Marcie_107
• Track 3 : CandC_102, Tempo_104, RobinRose_106, Romm_106, Kelcole_102, Fregley_103, OneinaGillian_100

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

The start number called the most often in the published annotations is 1, it was called in 8 of the 8 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• BirdInFrench_101, CandC_102, Fregley_103, Kelcole_102, Marcie_107, OneinaGillian_100, Pepe25_100, RobinRose_106, Romm_106, Tempo_104, Wilca_101,

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 1:
• Found in 11 of 11 (100.0%) of genes in pham
• Manual Annotations of this start: 8 of 8
• Called 100.0% of time when present
• Phage (with cluster) where this start called: BirdInFrench_101 (EG), CandC_102 (EG), Fregley_103 (EG), Kelcole_102 (EG), Marcie_107 (EG), OneinaGillian_100 (EG), Pepe25_100 (EG), RobinRose_106 (EG), Romm_106 (EG), Tempo_104 (EG), Wilca_101 (EG),

Summary by clusters:

There is one cluster represented in this pham: EG

Info for manual annotations of cluster EG:
•Start number 1 was manually annotated 8 times for cluster EG.

Gene Information:

Gene: BirdInFrench_101 Start: 60396, Stop: 60130, Start Num: 1
Candidate Starts for BirdInFrench_101:
(Start: 1 @60396 has 8 MA's), (3, 60348), (4, 60339), (6, 60315), (7, 60291),

Gene: CandC_102 Start: 60668, Stop: 60396, Start Num: 1
Candidate Starts for CandC_102:
(Start: 1 @60668 has 8 MA's), (3, 60620), (6, 60587),

Gene: Fregley_103 Start: 60615, Stop: 60343, Start Num: 1
Candidate Starts for Fregley_103:
(Start: 1 @60615 has 8 MA's), (3, 60567), (6, 60534),

Gene: Kelcole_102 Start: 61136, Stop: 60864, Start Num: 1
Candidate Starts for Kelcole_102:
(Start: 1 @61136 has 8 MA's), (3, 61088), (6, 61055),

Gene: Marcie_107 Start: 61023, Stop: 60751, Start Num: 1
Candidate Starts for Marcie_107:
(Start: 1 @61023 has 8 MA's), (2, 60978), (5, 60945),

Gene: OneinaGillian_100 Start: 60027, Stop: 59755, Start Num: 1
Candidate Starts for OneinaGillian_100:
(Start: 1 @60027 has 8 MA's), (3, 59979), (6, 59946),

Gene: Pepe25_100 Start: 59327, Stop: 59058, Start Num: 1
Candidate Starts for Pepe25_100:
(Start: 1 @59327 has 8 MA's), (3, 59279), (4, 59270), (6, 59246), (7, 59222),

Gene: RobinRose_106 Start: 61335, Stop: 61063, Start Num: 1
Candidate Starts for RobinRose_106:
(Start: 1 @61335 has 8 MA's), (3, 61287), (6, 61254),

Gene: Romm_106 Start: 61332, Stop: 61060, Start Num: 1
Candidate Starts for Romm_106:
(Start: 1 @61332 has 8 MA's), (3, 61284), (6, 61251),

Gene: Tempo_104 Start: 61193, Stop: 60921, Start Num: 1
Candidate Starts for Tempo_104:
(Start: 1 @61193 has 8 MA's), (3, 61145), (6, 61112),

Gene: Wilca_101 Start: 60396, Stop: 60130, Start Num: 1
Candidate Starts for Wilca_101:
(Start: 1 @60396 has 8 MA's), (3, 60348), (4, 60339), (6, 60315), (7, 60291),