Pham 106859

1: ABCat_135 + 7

2: Pab3_134

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 106859 Report

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

Pham number 106859 has 9 members, 0 are drafts.

Phages represented in each track:
• Track 1 : ABCat_135, Glexan_138, Gator_136, TeardropMSU_135, Dusk_135, BadStone_135, Tuco_140, Harella_140
• Track 2 : Pat3_134

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 9 of the 9 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• ABCat_135, BadStone_135, Dusk_135, Gator_136, Glexan_138, Harella_140, Pat3_134, TeardropMSU_135, Tuco_140,

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 9 of 9 (100.0%) of genes in pham
• Manual Annotations of this start: 9 of 9
• Called 100.0% of time when present
• Phage (with cluster) where this start called: ABCat_135 (E), BadStone_135 (E), Dusk_135 (E), Gator_136 (E), Glexan_138 (E), Harella_140 (E), Pat3_134 (E), TeardropMSU_135 (E), Tuco_140 (E),

Summary by clusters:

There is one cluster represented in this pham: E

Info for manual annotations of cluster E:

•Start number 1 was manually annotated 9 times for cluster E.

Gene Information:

Gene: ABCat_135 Start: 72863, Stop: 72477, Start Num: 1
Candidate Starts for ABCat_135:
(Start: 1 @72863 has 9 MA's), (2, 72836), (3, 72824), (4, 72815), (5, 72743), (6, 72650), (7, 72644), (8, 72626), (9, 72611), (10, 72578),

Gene: BadStone_135 Start: 72411, Stop: 72025, Start Num: 1
Candidate Starts for BadStone_135:
(Start: 1 @72411 has 9 MA's), (2, 72384), (3, 72372), (4, 72363), (5, 72291), (6, 72198), (7, 72192), (8, 72174), (9, 72159), (10, 72126),

Gene: Dusk_135 Start: 72071, Stop: 71685, Start Num: 1
Candidate Starts for Dusk_135:
(Start: 1 @72071 has 9 MA's), (2, 72044), (3, 72032), (4, 72023), (5, 71951), (6, 71858), (7, 71852), (8, 71834), (9, 71819), (10, 71786),

Gene: Gator_136 Start: 72362, Stop: 71976, Start Num: 1
Candidate Starts for Gator_136:
(Start: 1 @72362 has 9 MA's), (2, 72335), (3, 72323), (4, 72314), (5, 72242), (6, 72149), (7, 72143), (8, 72125), (9, 72110), (10, 72077),

Gene: Glexan_138 Start: 72512, Stop: 72126, Start Num: 1
Candidate Starts for Glexan_138:
(Start: 1 @72512 has 9 MA's), (2, 72485), (3, 72473), (4, 72464), (5, 72392), (6, 72299), (7, 72293), (8, 72275), (9, 72260), (10, 72227),

Gene: Harella_140 Start: 73028, Stop: 72642, Start Num: 1
Candidate Starts for Harella_140:
(Start: 1 @73028 has 9 MA's), (2, 73001), (3, 72989), (4, 72980), (5, 72908), (6, 72815), (7, 72809), (8, 72791), (9, 72776), (10, 72743),

Gene: Pat3_134 Start: 71656, Stop: 71270, Start Num: 1
Candidate Starts for Pat3_134:
(Start: 1 @71656 has 9 MA's), (2, 71629), (4, 71608), (5, 71536), (6, 71443), (7, 71437), (8, 71419), (9, 71404), (10, 71371),

Gene: TeardropMSU_135 Start: 71617, Stop: 71231, Start Num: 1
Candidate Starts for TeardropMSU_135:
(Start: 1 @71617 has 9 MA's), (2, 71590), (3, 71578), (4, 71569), (5, 71497), (6, 71404), (7, 71398), (8, 71380), (9, 71365), (10, 71332),

Gene: Tuco_140 Start: 73676, Stop: 73290, Start Num: 1
Candidate Starts for Tuco_140:
(Start: 1 @73676 has 9 MA's), (2, 73649), (3, 73637), (4, 73628), (5, 73556), (6, 73463), (7, 73457), (8, 73439), (9, 73424), (10, 73391),