Pham 106799

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 106799 Report

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

Pham number 106799 has 10 members, 0 are drafts.

Phages represented in each track:
• Track 1 : Alvin_1
• Track 2 : Scowl_1, GageAP_1
• Track 3 : Kanely_1, Altman_1
• Track 4 : Marsha_1, Blue_1, Makemake_1, Traft412_1, Niza_1

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

The start number called the most often in the published annotations is 2, it was called in 10 of the 10 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• Altman_1, Alvin_1, Blue_1, GageAP_1, Kanely_1, Makemake_1, Marsha_1, Niza_1, Scowl_1, Traft412_1,

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 2:
• Found in 10 of 10 (100.0%) of genes in pham
• Manual Annotations of this start: 10 of 10
• Called 100.0% of time when present
• Phage (with cluster) where this start called: Altman_1 (A1), Alvin_1 (A1), Blue_1 (A1), GageAP_1 (A1), Kanely_1 (A1), Makemake_1 (A1), Marsha_1 (A1), Niza_1 (A1), Scowl_1 (A1), Traft412_1 (A1),

Summary by clusters:

There is one cluster represented in this pham: A1

Info for manual annotations of cluster A1:
•Start number 2 was manually annotated 10 times for cluster A1.

Gene Information:

Gene: Altman_1 Start: 540, Stop: 1013, Start Num: 2
Candidate Starts for Altman_1:
(1, 510), (Start: 2 @540 has 10 MA's), (6, 654), (8, 804), (9, 837), (11, 855), (13, 882), (14, 951),

Gene: Alvin_1 Start: 540, Stop: 1067, Start Num: 2
Candidate Starts for Alvin_1:
(1, 510), (Start: 2 @540 has 10 MA's), (8, 804), (9, 837), (14, 951), (15, 1035), (16, 1044),

Gene: Blue_1 Start: 538, Stop: 1011, Start Num: 2
Candidate Starts for Blue_1:
(1, 508), (Start: 2 @538 has 10 MA's), (8, 802), (9, 835), (14, 949),

Gene: GageAP_1 Start: 540, Stop: 989, Start Num: 2
Candidate Starts for GageAP_1:
(1, 510), (Start: 2 @540 has 10 MA's), (3, 609), (4, 621), (5, 645), (7, 738), (9, 837), (10, 846), (12, 870), (14, 951),

Gene: Kanely_1 Start: 540, Stop: 1013, Start Num: 2
Candidate Starts for Kanely_1:
(1, 510), (Start: 2 @540 has 10 MA's), (6, 654), (8, 804), (9, 837), (11, 855), (13, 882), (14, 951),

Gene: Makemake_1 Start: 540, Stop: 1013, Start Num: 2
Candidate Starts for Makemake_1:
(1, 510), (Start: 2 @540 has 10 MA's), (8, 804), (9, 837), (14, 951),

Gene: Marsha_1 Start: 539, Stop: 1012, Start Num: 2
Candidate Starts for Marsha_1:
(1, 509), (Start: 2 @539 has 10 MA's), (8, 803), (9, 836), (14, 950),

Gene: Niza_1 Start: 540, Stop: 1013, Start Num: 2
Candidate Starts for Niza_1:
(1, 510), (Start: 2 @540 has 10 MA's), (8, 804), (9, 837), (14, 951),

Gene: Scowl_1 Start: 540, Stop: 989, Start Num: 2
Candidate Starts for Scowl_1:
(1, 510), (Start: 2 @540 has 10 MA's), (3, 609), (4, 621), (5, 645), (7, 738), (9, 837), (10, 846), (12, 870), (14, 951),

Gene: Traft412_1 Start: 539, Stop: 1012, Start Num: 2
Candidate Starts for Traft412_1:
(1, 509), (Start: 2 @539 has 10 MA's), (8, 803), (9, 836), (14, 950),