



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 87325 Report

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

Pham number 87325 has 11 members, 0 are drafts.

Phages represented in each track:

- Track 1 : Hannaconda_90, MiaZeal_99, Superphikiman_96, Squint_97, Lucky2013_96, Courthouse_94, Ariel_98, Porcelain_97, Omega_108
- Track 2 : LittleE_102, KashFlow_94

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

The start number called the most often in the published annotations is 4, it was called in 11 of the 11 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- Ariel_98, Courthouse_94, Hannaconda_90, KashFlow_94, LittleE_102, Lucky2013_96, MiaZeal_99, Omega_108, Porcelain_97, Squint_97, Superphikiman_96,

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 4:

- Found in 11 of 11 (100.0%) of genes in pham
- Manual Annotations of this start: 11 of 11
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Ariel_98 (J), Courthouse_94 (J), Hannaconda_90 (J), KashFlow_94 (J), LittleE_102 (J), Lucky2013_96 (J), MiaZeal_99 (J), Omega_108 (J), Porcelain_97 (J), Squint_97 (J), Superphikiman_96 (J),

Summary by clusters:

There is one cluster represented in this pham: J

Info for manual annotations of cluster J:

- Start number 4 was manually annotated 11 times for cluster J.

Gene Information:

Gene: Ariel_98 Start: 56193, Stop: 56570, Start Num: 4

Candidate Starts for Ariel_98:

(3, 56166), (Start: 4 @56193 has 11 MA's), (5, 56253), (6, 56409), (7, 56502),

Gene: Courthouse_94 Start: 55793, Stop: 56170, Start Num: 4

Candidate Starts for Courthouse_94:

(3, 55766), (Start: 4 @55793 has 11 MA's), (5, 55853), (6, 56009), (7, 56102),

Gene: Hannaconda_90 Start: 54744, Stop: 55121, Start Num: 4

Candidate Starts for Hannaconda_90:

(3, 54717), (Start: 4 @54744 has 11 MA's), (5, 54804), (6, 54960), (7, 55053),

Gene: KashFlow_94 Start: 56308, Stop: 56685, Start Num: 4

Candidate Starts for KashFlow_94:

(1, 56110), (2, 56122), (Start: 4 @56308 has 11 MA's), (5, 56368), (6, 56524), (7, 56617),

Gene: LittleE_102 Start: 59886, Stop: 60263, Start Num: 4

Candidate Starts for LittleE_102:

(1, 59688), (2, 59700), (Start: 4 @59886 has 11 MA's), (5, 59946), (6, 60102), (7, 60195),

Gene: Lucky2013_96 Start: 56209, Stop: 56586, Start Num: 4

Candidate Starts for Lucky2013_96:

(3, 56182), (Start: 4 @56209 has 11 MA's), (5, 56269), (6, 56425), (7, 56518),

Gene: MiaZeal_99 Start: 56865, Stop: 57242, Start Num: 4

Candidate Starts for MiaZeal_99:

(3, 56838), (Start: 4 @56865 has 11 MA's), (5, 56925), (6, 57081), (7, 57174),

Gene: Omega_108 Start: 61662, Stop: 62039, Start Num: 4

Candidate Starts for Omega_108:

(3, 61635), (Start: 4 @61662 has 11 MA's), (5, 61722), (6, 61878), (7, 61971),

Gene: Porcelain_97 Start: 56865, Stop: 57242, Start Num: 4

Candidate Starts for Porcelain_97:

(3, 56838), (Start: 4 @56865 has 11 MA's), (5, 56925), (6, 57081), (7, 57174),

Gene: Squint_97 Start: 56984, Stop: 57361, Start Num: 4

Candidate Starts for Squint_97:

(3, 56957), (Start: 4 @56984 has 11 MA's), (5, 57044), (6, 57200), (7, 57293),

Gene: Superphikiman_96 Start: 56075, Stop: 56452, Start Num: 4

Candidate Starts for Superphikiman_96:

(3, 56048), (Start: 4 @56075 has 11 MA's), (5, 56135), (6, 56291), (7, 56384),