



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 87698 Report

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

Pham number 87698 has 9 members, 0 are drafts.

Phages represented in each track:

- Track 1 : LilhomieP_139, Glaske16_141, Auspice_140, Dulcita_139, Bricole_141, PegLeg_142, IPhane7_137, Skinny_145, Diminimus_139

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:

- Auspice_140, Bricole_141, Diminimus_139, Dulcita_139, Glaske16_141, IPhane7_137, LilhomieP_139, PegLeg_142, Skinny_145,

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: Auspice_140 (M1), Bricole_141 (M1), Diminimus_139 (M1), Dulcita_139 (M1), Glaske16_141 (M1), IPhane7_137 (M1), LilhomieP_139 (M1), PegLeg_142 (M1), Skinny_145 (M1),

Summary by clusters:

There is one cluster represented in this pham: M1

Info for manual annotations of cluster M1:

- Start number 1 was manually annotated 9 times for cluster M1.

Gene Information:

Gene: Auspice_140 Start: 72290, Stop: 72201, Start Num: 1

Candidate Starts for Auspice_140:

(Start: 1 @72290 has 9 MA's), (2, 72242),

Gene: Bricole_141 Start: 72055, Stop: 71966, Start Num: 1

Candidate Starts for Bricole_141:

(Start: 1 @72055 has 9 MA's), (2, 72007),

Gene: Diminimus_139 Start: 71726, Stop: 71637, Start Num: 1

Candidate Starts for Diminimus_139:

(Start: 1 @71726 has 9 MA's), (2, 71678),

Gene: Dulcita_139 Start: 71727, Stop: 71638, Start Num: 1

Candidate Starts for Dulcita_139:

(Start: 1 @71727 has 9 MA's), (2, 71679),

Gene: Glaske16_141 Start: 72845, Stop: 72756, Start Num: 1

Candidate Starts for Glaske16_141:

(Start: 1 @72845 has 9 MA's), (2, 72797),

Gene: IPhone7_137 Start: 71906, Stop: 71817, Start Num: 1

Candidate Starts for IPhone7_137:

(Start: 1 @71906 has 9 MA's), (2, 71858),

Gene: LilhomieP_139 Start: 72756, Stop: 72667, Start Num: 1

Candidate Starts for LilhomieP_139:

(Start: 1 @72756 has 9 MA's), (2, 72708),

Gene: PegLeg_142 Start: 72640, Stop: 72551, Start Num: 1

Candidate Starts for PegLeg_142:

(Start: 1 @72640 has 9 MA's), (2, 72592),

Gene: Skinny_145 Start: 73757, Stop: 73668, Start Num: 1

Candidate Starts for Skinny_145:

(Start: 1 @73757 has 9 MA's), (2, 73709),