



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 216807 Report

This analysis was run 02/22/25 on database version 588.

Pham number 216807 has 9 members, 3 are drafts.

Phages represented in each track:

- Track 1 : Bartholomune\_160
- Track 2 : Shuckle\_163
- Track 3 : Bmoc\_164
- Track 4 : Anedea\_162, Riptide\_158
- Track 5 : PinkiePie\_157, Liandry\_160, Squillium\_160
- Track 6 : Marsus\_168

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

The start number called the most often in the published annotations is 5, it was called in 5 of the 6 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- Anedea\_162, Bmoc\_164, Liandry\_160, Marsus\_168, PinkiePie\_157, Riptide\_158, Shuckle\_163, Squillium\_160,

Genes that have the "Most Annotated" start but do not call it:

- Bartholomune\_160,

Genes that do not have the "Most Annotated" start:

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### **Summary by start number:**

Start 5:

- Found in 9 of 9 ( 100.0% ) of genes in pham
- Manual Annotations of this start: 5 of 6
- Called 88.9% of time when present
- Phage (with cluster) where this start called: Anedea\_162 (BE1), Bmoc\_164 (BE1), Liandry\_160 (BE1), Marsus\_168 (BE1), PinkiePie\_157 (BE1), Riptide\_158 (BE1), Shuckle\_163 (BE1), Squillium\_160 (BE1),

Start 6:

- Found in 4 of 9 ( 44.4% ) of genes in pham

- Manual Annotations of this start: 1 of 6
- Called 25.0% of time when present
- Phage (with cluster) where this start called: Bartholomune\_160 (BE1),

### **Summary by clusters:**

There is one cluster represented in this pham: BE1

Info for manual annotations of cluster BE1:

- Start number 5 was manually annotated 5 times for cluster BE1.
- Start number 6 was manually annotated 1 time for cluster BE1.

### **Gene Information:**

Gene: Anedea\_162 Start: 90647, Stop: 90805, Start Num: 5

Candidate Starts for Anedea\_162:

(Start: 5 @90647 has 5 MA's), (9, 90788),

Gene: Bartholomune\_160 Start: 90858, Stop: 90983, Start Num: 6

Candidate Starts for Bartholomune\_160:

(1, 90732), (2, 90753), (3, 90777), (4, 90783), (Start: 5 @90831 has 5 MA's), (Start: 6 @90858 has 1 MA's),

Gene: Bmoc\_164 Start: 91216, Stop: 91374, Start Num: 5

Candidate Starts for Bmoc\_164:

(Start: 5 @91216 has 5 MA's), (7, 91306), (9, 91357),

Gene: Liandry\_160 Start: 91574, Stop: 91726, Start Num: 5

Candidate Starts for Liandry\_160:

(1, 91475), (2, 91496), (3, 91520), (4, 91526), (Start: 5 @91574 has 5 MA's), (Start: 6 @91601 has 1 MA's),

Gene: Marsus\_168 Start: 91227, Stop: 91379, Start Num: 5

Candidate Starts for Marsus\_168:

(Start: 5 @91227 has 5 MA's), (8, 91344), (9, 91362),

Gene: PinkiePie\_157 Start: 91574, Stop: 91726, Start Num: 5

Candidate Starts for PinkiePie\_157:

(1, 91475), (2, 91496), (3, 91520), (4, 91526), (Start: 5 @91574 has 5 MA's), (Start: 6 @91601 has 1 MA's),

Gene: Riptide\_158 Start: 89287, Stop: 89445, Start Num: 5

Candidate Starts for Riptide\_158:

(Start: 5 @89287 has 5 MA's), (9, 89428),

Gene: Shuckle\_163 Start: 92264, Stop: 92416, Start Num: 5

Candidate Starts for Shuckle\_163:

(1, 92165), (2, 92186), (3, 92210), (4, 92216), (Start: 5 @92264 has 5 MA's),

Gene: Squillum\_160 Start: 91576, Stop: 91728, Start Num: 5

Candidate Starts for Squillum\_160:

(1, 91477), (2, 91498), (3, 91522), (4, 91528), (Start: 5 @91576 has 5 MA's), (Start: 6 @91603 has 1 MA's),