



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 87471 Report

This analysis was run 03/30/24 on database version 556.

Pham number 87471 has 11 members, 2 are drafts.

Phages represented in each track:

- Track 1 : SummitAcademy\_31
- Track 2 : Pons\_32
- Track 3 : BigChungus\_30, Elinal\_33, KayGee\_31, Mayweather\_34, Feastonyeet\_30
- Track 4 : SheckWes\_31
- Track 5 : Vine\_32
- Track 6 : CherryonLim\_33
- Track 7 : PotPie\_32

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

The start number called the most often in the published annotations is 3, it was called in 9 of the 9 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- BigChungus\_30, CherryonLim\_33, Elinal\_33, Feastonyeet\_30, KayGee\_31, Mayweather\_34, Pons\_32, PotPie\_32, SheckWes\_31, SummitAcademy\_31, Vine\_32,

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 3:

- Found in 11 of 11 ( 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: BigChungus\_30 (CT), CherryonLim\_33 (CT), Elinal\_33 (CT), Feastonyeet\_30 (CT), KayGee\_31 (CT), Mayweather\_34 (CT), Pons\_32 (CT), PotPie\_32 (CT), SheckWes\_31 (CT), SummitAcademy\_31 (CT), Vine\_32 (CT),

## Summary by clusters:

There is one cluster represented in this pham: CT

Info for manual annotations of cluster CT:

- Start number 3 was manually annotated 9 times for cluster CT.

### ***Gene Information:***

Gene: BigChungus\_30 Start: 24836, Stop: 24675, Start Num: 3

Candidate Starts for BigChungus\_30:

(Start: 3 @24836 has 9 MA's),

Gene: CherryonLim\_33 Start: 26012, Stop: 25842, Start Num: 3

Candidate Starts for CherryonLim\_33:

(2, 26048), (Start: 3 @26012 has 9 MA's),

Gene: Elinal\_33 Start: 25223, Stop: 25068, Start Num: 3

Candidate Starts for Elinal\_33:

(Start: 3 @25223 has 9 MA's),

Gene: Feastonyeet\_30 Start: 24836, Stop: 24675, Start Num: 3

Candidate Starts for Feastonyeet\_30:

(Start: 3 @24836 has 9 MA's),

Gene: KayGee\_31 Start: 25223, Stop: 25068, Start Num: 3

Candidate Starts for KayGee\_31:

(Start: 3 @25223 has 9 MA's),

Gene: Mayweather\_34 Start: 25841, Stop: 25707, Start Num: 3

Candidate Starts for Mayweather\_34:

(Start: 3 @25841 has 9 MA's),

Gene: Pons\_32 Start: 25231, Stop: 25079, Start Num: 3

Candidate Starts for Pons\_32:

(Start: 3 @25231 has 9 MA's),

Gene: PotPie\_32 Start: 26158, Stop: 25997, Start Num: 3

Candidate Starts for PotPie\_32:

(1, 26194), (Start: 3 @26158 has 9 MA's),

Gene: SheckWes\_31 Start: 24168, Stop: 23998, Start Num: 3

Candidate Starts for SheckWes\_31:

(Start: 3 @24168 has 9 MA's),

Gene: SummitAcademy\_31 Start: 25113, Stop: 24952, Start Num: 3

Candidate Starts for SummitAcademy\_31:

(1, 25149), (Start: 3 @25113 has 9 MA's),

Gene: Vine\_32 Start: 25329, Stop: 25174, Start Num: 3

Candidate Starts for Vine\_32:  
(Start: 3 @25329 has 9 MA's),