



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 7205 Report

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

Pham number 7205 has 10 members, 3 are drafts.

Phages represented in each track:

- Track 1 : Nina_3, Cozz_3, Axym_3, Agatha_3, Quasar_3, Typhonomachy_4, GoldHunter_4
- Track 2 : Mayweather_4
- Track 3 : SheckWes_2, MAnor_3

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 6 of the 7 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- Agatha_3, Axym_3, Cozz_3, GoldHunter_4, MAnor_3, Nina_3, Quasar_3, SheckWes_2, Typhonomachy_4,

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

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

- Mayweather_4,

Summary by start number:

Start 1:

- Found in 9 of 10 (90.0%) of genes in pham
- Manual Annotations of this start: 6 of 7
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Agatha_3 (CT), Axym_3 (CT), Cozz_3 (CT), GoldHunter_4 (CT), MAnor_3 (CT), Nina_3 (CT), Quasar_3 (CT), SheckWes_2 (CT), Typhonomachy_4 (CT),

Start 2:

- Found in 8 of 10 (80.0%) of genes in pham
- Manual Annotations of this start: 1 of 7
- Called 12.5% of time when present

- Phage (with cluster) where this start called: Mayweather_4 (CT),

Summary by clusters:

There is one cluster represented in this pham: CT

Info for manual annotations of cluster CT:

- Start number 1 was manually annotated 6 times for cluster CT.
- Start number 2 was manually annotated 1 time for cluster CT.

Gene Information:

Gene: Agatha_3 Start: 879, Stop: 1073, Start Num: 1

Candidate Starts for Agatha_3:

(Start: 1 @879 has 6 MA's), (Start: 2 @885 has 1 MA's), (3, 909), (4, 999),

Gene: Axym_3 Start: 879, Stop: 1073, Start Num: 1

Candidate Starts for Axym_3:

(Start: 1 @879 has 6 MA's), (Start: 2 @885 has 1 MA's), (3, 909), (4, 999),

Gene: Cozz_3 Start: 879, Stop: 1073, Start Num: 1

Candidate Starts for Cozz_3:

(Start: 1 @879 has 6 MA's), (Start: 2 @885 has 1 MA's), (3, 909), (4, 999),

Gene: GoldHunter_4 Start: 879, Stop: 1073, Start Num: 1

Candidate Starts for GoldHunter_4:

(Start: 1 @879 has 6 MA's), (Start: 2 @885 has 1 MA's), (3, 909), (4, 999),

Gene: MAnor_3 Start: 666, Stop: 890, Start Num: 1

Candidate Starts for MAnor_3:

(Start: 1 @666 has 6 MA's), (4, 807),

Gene: Mayweather_4 Start: 1293, Stop: 1511, Start Num: 2

Candidate Starts for Mayweather_4:

(Start: 2 @1293 has 1 MA's), (4, 1428),

Gene: Nina_3 Start: 879, Stop: 1073, Start Num: 1

Candidate Starts for Nina_3:

(Start: 1 @879 has 6 MA's), (Start: 2 @885 has 1 MA's), (3, 909), (4, 999),

Gene: Quasar_3 Start: 1500, Stop: 1694, Start Num: 1

Candidate Starts for Quasar_3:

(Start: 1 @1500 has 6 MA's), (Start: 2 @1506 has 1 MA's), (3, 1530), (4, 1620),

Gene: SheckWes_2 Start: 666, Stop: 890, Start Num: 1

Candidate Starts for SheckWes_2:

(Start: 1 @666 has 6 MA's), (4, 807),

Gene: Typhonomachy_4 Start: 879, Stop: 1073, Start Num: 1

Candidate Starts for Typhonomachy_4:

(Start: 1 @879 has 6 MA's), (Start: 2 @885 has 1 MA's), (3, 909), (4, 999),

