



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 8635 Report

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

Pham number 8635 has 5 members, 0 are drafts.

Phages represented in each track:

- Track 1 : TZGordon_5, Huff_5, DinoDaryn_5
- Track 2 : Banquo_5
- Track 3 : Dardanus_5

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

The start number called the most often in the published annotations is 6, it was called in 3 of the 5 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- DinoDaryn_5, Huff_5, TZGordon_5,

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:

- Banquo_5, Dardanus_5,

Summary by start number:

Start 3:

- Found in 1 of 5 (20.0%) of genes in pham
- Manual Annotations of this start: 1 of 5
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Dardanus_5 (CU3),

Start 6:

- Found in 3 of 5 (60.0%) of genes in pham
- Manual Annotations of this start: 3 of 5
- Called 100.0% of time when present
- Phage (with cluster) where this start called: DinoDaryn_5 (CU1), Huff_5 (CU1), TZGordon_5 (CU1),

Start 7:

- Found in 5 of 5 (100.0%) of genes in pham
- Manual Annotations of this start: 1 of 5
- Called 20.0% of time when present
- Phage (with cluster) where this start called: Banquo_5 (CU1),

Summary by clusters:

There are 2 clusters represented in this pham: CU3, CU1,

Info for manual annotations of cluster CU1:

- Start number 6 was manually annotated 3 times for cluster CU1.
- Start number 7 was manually annotated 1 time for cluster CU1.

Info for manual annotations of cluster CU3:

- Start number 3 was manually annotated 1 time for cluster CU3.

Gene Information:

Gene: Banquo_5 Start: 1988, Stop: 1686, Start Num: 7

Candidate Starts for Banquo_5:

(1, 2102), (2, 2075), (5, 2024), (Start: 7 @1988 has 1 MA's), (9, 1892), (11, 1826), (12, 1784), (13, 1727),

Gene: Dardanus_5 Start: 2243, Stop: 1875, Start Num: 3

Candidate Starts for Dardanus_5:

(Start: 3 @2243 has 1 MA's), (4, 2222), (5, 2219), (Start: 7 @2183 has 1 MA's), (8, 2177), (9, 2087), (10, 2027), (11, 2021), (12, 1979), (13, 1922), (14, 1910),

Gene: DinoDaryn_5 Start: 1685, Stop: 1371, Start Num: 6

Candidate Starts for DinoDaryn_5:

(Start: 6 @1685 has 3 MA's), (Start: 7 @1679 has 1 MA's), (8, 1673), (9, 1583), (11, 1517), (12, 1475), (13, 1418), (14, 1406),

Gene: Huffy_5 Start: 1685, Stop: 1371, Start Num: 6

Candidate Starts for Huffy_5:

(Start: 6 @1685 has 3 MA's), (Start: 7 @1679 has 1 MA's), (8, 1673), (9, 1583), (11, 1517), (12, 1475), (13, 1418), (14, 1406),

Gene: TZGordon_5 Start: 1600, Stop: 1286, Start Num: 6

Candidate Starts for TZGordon_5:

(Start: 6 @1600 has 3 MA's), (Start: 7 @1594 has 1 MA's), (8, 1588), (9, 1498), (11, 1432), (12, 1390), (13, 1333), (14, 1321),