



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 87667 Report

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

Pham number 87667 has 10 members, 1 are drafts.

Phages represented in each track:

- Track 1 : Katyusha_51, Benczkowski14_51
- Track 2 : Tredge_52, Teatealatte_52, Niagara_51, Teech_51
- Track 3 : Demosthenes_50, ASerpRocky_50
- Track 4 : Hollow_51
- Track 5 : Kvothe_50

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

The start number called the most often in the published annotations is 2, it was called in 9 of the 9 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- ASerpRocky_50, Benczkowski14_51, Demosthenes_50, Hollow_51, Katyusha_51, Kvothe_50, Niagara_51, Teatealatte_52, Teech_51, Tredge_52,

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 2:

- Found in 10 of 10 (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: ASerpRocky_50 (CS4), Benczkowski14_51 (CS4), Demosthenes_50 (CS4), Hollow_51 (CS4), Katyusha_51 (CS4), Kvothe_50 (CS4), Niagara_51 (CS4), Teatealatte_52 (CS4), Teech_51 (CS4), Tredge_52 (CS4),

Summary by clusters:

There is one cluster represented in this pham: CS4

Info for manual annotations of cluster CS4:

•Start number 2 was manually annotated 9 times for cluster CS4.

Gene Information:

Gene: ASerpRocky_50 Start: 49820, Stop: 49563, Start Num: 2

Candidate Starts for ASerpRocky_50:

(1, 49910), (Start: 2 @49820 has 9 MA's), (3, 49748),

Gene: Benczkowski14_51 Start: 50091, Stop: 49834, Start Num: 2

Candidate Starts for Benczkowski14_51:

(Start: 2 @50091 has 9 MA's), (3, 50019), (5, 49899),

Gene: Demosthenes_50 Start: 49796, Stop: 49539, Start Num: 2

Candidate Starts for Demosthenes_50:

(1, 49886), (Start: 2 @49796 has 9 MA's), (3, 49724),

Gene: Hollow_51 Start: 50272, Stop: 50015, Start Num: 2

Candidate Starts for Hollow_51:

(Start: 2 @50272 has 9 MA's), (3, 50200), (4, 50128), (5, 50080),

Gene: Katyusha_51 Start: 50091, Stop: 49834, Start Num: 2

Candidate Starts for Katyusha_51:

(Start: 2 @50091 has 9 MA's), (3, 50019), (5, 49899),

Gene: Kvothe_50 Start: 49990, Stop: 49733, Start Num: 2

Candidate Starts for Kvothe_50:

(Start: 2 @49990 has 9 MA's), (3, 49918), (4, 49846), (5, 49798),

Gene: Niagara_51 Start: 50081, Stop: 49824, Start Num: 2

Candidate Starts for Niagara_51:

(1, 50171), (Start: 2 @50081 has 9 MA's), (3, 50009), (4, 49937), (5, 49889),

Gene: Teatealatte_52 Start: 49993, Stop: 49736, Start Num: 2

Candidate Starts for Teatealatte_52:

(1, 50083), (Start: 2 @49993 has 9 MA's), (3, 49921), (4, 49849), (5, 49801),

Gene: Teech_51 Start: 49794, Stop: 49537, Start Num: 2

Candidate Starts for Teech_51:

(1, 49884), (Start: 2 @49794 has 9 MA's), (3, 49722), (4, 49650), (5, 49602),

Gene: Tredge_52 Start: 49993, Stop: 49736, Start Num: 2

Candidate Starts for Tredge_52:

(1, 50083), (Start: 2 @49993 has 9 MA's), (3, 49921), (4, 49849), (5, 49801),