



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 8205 Report

This analysis was run 04/28/24 on database version 559.

Pham number 8205 has 9 members, 3 are drafts.

Phages represented in each track:

- Track 1 : CandC_76, Fregley_79
- Track 2 : BirdInFrench_78, Wilca_78
- Track 3 : Tempo_79
- Track 4 : Romm_80, RobinRose_80, Kelcole_77
- Track 5 : Pepe25_76

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

Genes that call this "Most Annotated" start:

- BirdInFrench_78, CandC_76, Fregley_79, Kelcole_77, Pepe25_76, RobinRose_80, Romm_80, Tempo_79, Wilca_78,

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 9 of 9 (100.0%) of genes in pham
- Manual Annotations of this start: 6 of 6
- Called 100.0% of time when present
- Phage (with cluster) where this start called: BirdInFrench_78 (EG), CandC_76 (EG), Fregley_79 (EG), Kelcole_77 (EG), Pepe25_76 (EG), RobinRose_80 (EG), Romm_80 (EG), Tempo_79 (EG), Wilca_78 (EG),

Summary by clusters:

There is one cluster represented in this pham: EG

Info for manual annotations of cluster EG:

- Start number 3 was manually annotated 6 times for cluster EG.

Gene Information:

Gene: BirdInFrench_78 Start: 50998, Stop: 50666, Start Num: 3

Candidate Starts for BirdInFrench_78:

(1, 51190), (2, 51157), (Start: 3 @50998 has 6 MA's), (4, 50836), (5, 50803), (6, 50704),

Gene: CandC_76 Start: 50364, Stop: 50032, Start Num: 3

Candidate Starts for CandC_76:

(Start: 3 @50364 has 6 MA's), (4, 50202),

Gene: Fregley_79 Start: 50713, Stop: 50381, Start Num: 3

Candidate Starts for Fregley_79:

(Start: 3 @50713 has 6 MA's), (4, 50551),

Gene: Kelcole_77 Start: 50936, Stop: 50604, Start Num: 3

Candidate Starts for Kelcole_77:

(Start: 3 @50936 has 6 MA's), (4, 50774), (6, 50642),

Gene: Pepe25_76 Start: 49917, Stop: 49585, Start Num: 3

Candidate Starts for Pepe25_76:

(Start: 3 @49917 has 6 MA's), (4, 49755), (5, 49722), (6, 49623),

Gene: RobinRose_80 Start: 51120, Stop: 50788, Start Num: 3

Candidate Starts for RobinRose_80:

(Start: 3 @51120 has 6 MA's), (4, 50958), (6, 50826),

Gene: Romm_80 Start: 51117, Stop: 50785, Start Num: 3

Candidate Starts for Romm_80:

(Start: 3 @51117 has 6 MA's), (4, 50955), (6, 50823),

Gene: Tempo_79 Start: 51060, Stop: 50728, Start Num: 3

Candidate Starts for Tempo_79:

(Start: 3 @51060 has 6 MA's), (4, 50898),

Gene: Wilca_78 Start: 50998, Stop: 50666, Start Num: 3

Candidate Starts for Wilca_78:

(1, 51190), (2, 51157), (Start: 3 @50998 has 6 MA's), (4, 50836), (5, 50803), (6, 50704),