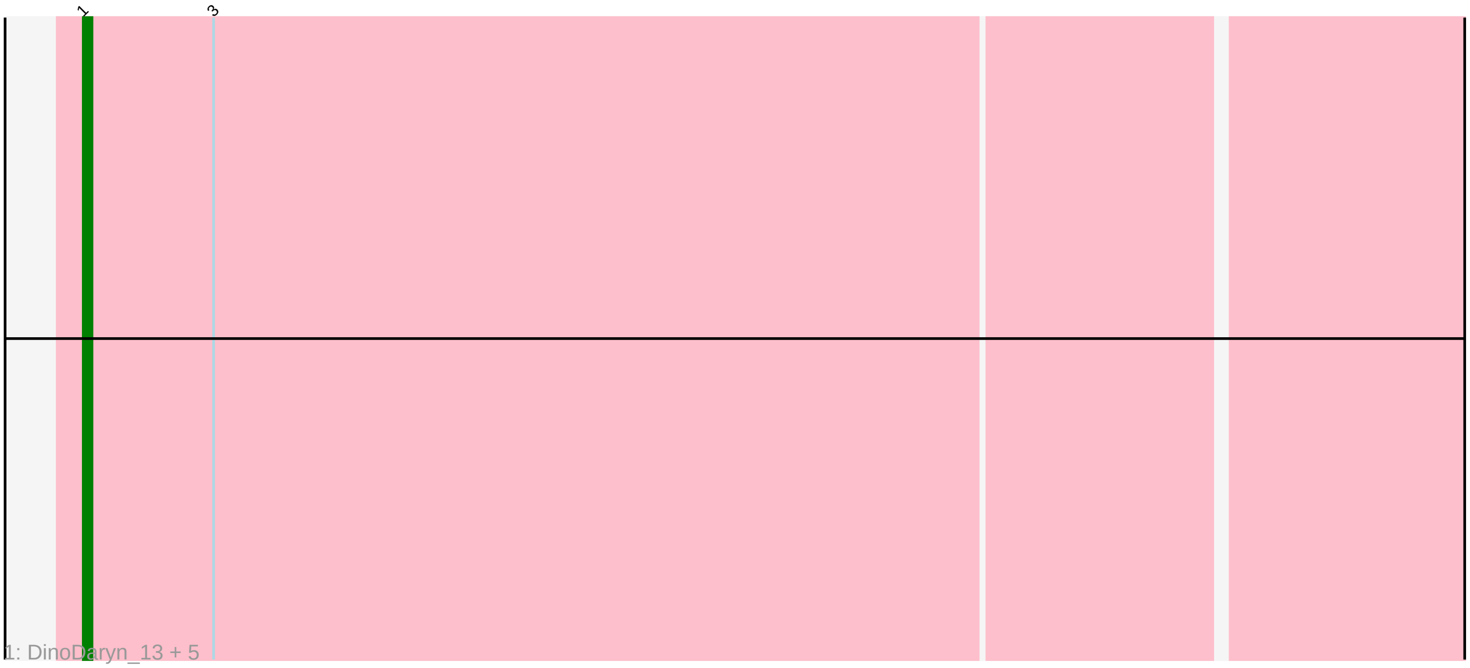
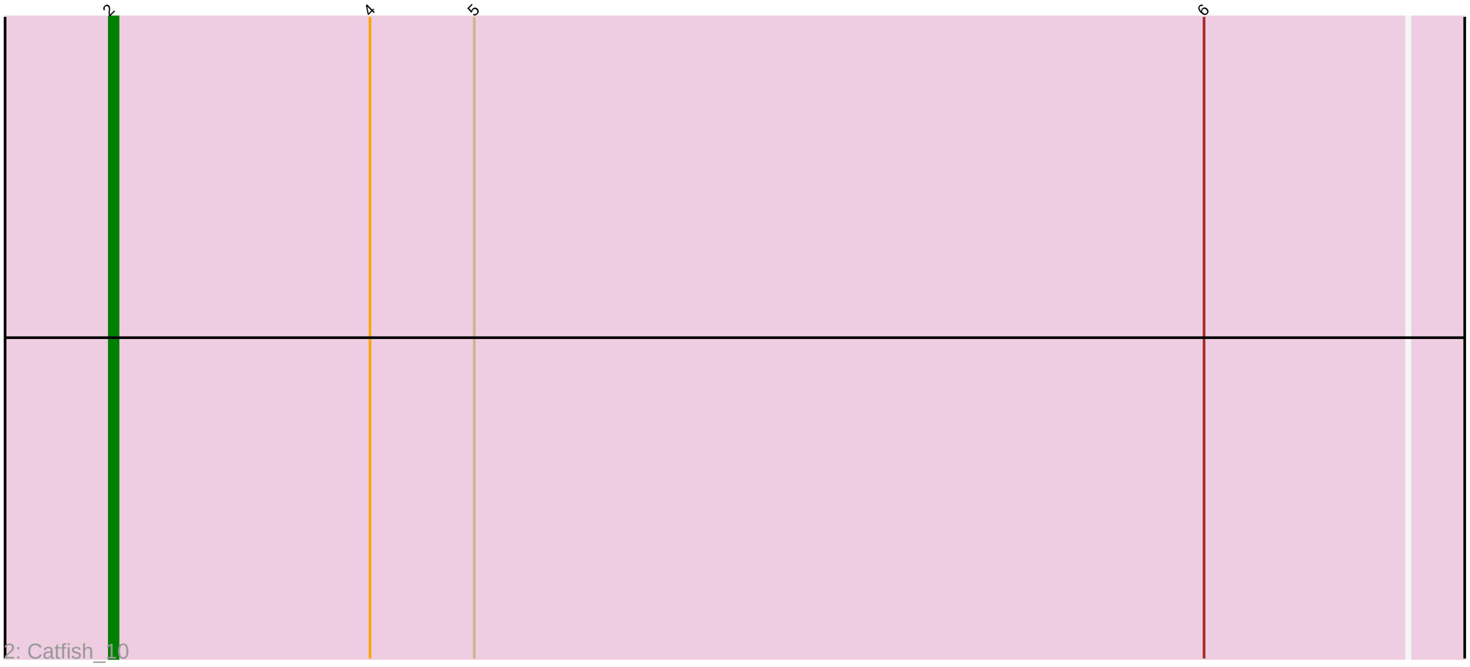
Pham 300603





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 300603 Report

This analysis was run 06/08/26 on database version 649.

Pham number 300603 has 7 members, 0 are drafts.

Phages represented in each track:
- Track 1 : DinoDaryn_13, Huffy_13, Vendetta_11, TZGordon_13, Splinter_11, Goib_12
- Track 2 : Catfish_10

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:
- DinoDaryn_13, Goib_12, Huffy_13, Splinter_11, TZGordon_13, Vendetta_11,

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

Genes that do not have the "Most Annotated" start:
- Catfish_10,

Summary by start number:

Start 1:
- Found in 6 of 7 (85.7%) 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: DinoDaryn_13 (CU1), Goib_12 (CU1), Huffy_13 (CU1), Splinter_11 (CU1), TZGordon_13 (CU1), Vendetta_11 (CU1),

Start 2:
- Found in 1 of 7 (14.3%) of genes in pham
- Manual Annotations of this start: 1 of 7
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Catfish_10 (CU5),

Summary by clusters:

There are 2 clusters represented in this pham: CU5, CU1,

Info for manual annotations of cluster CU1:
- Start number 1 was manually annotated 6 times for cluster CU1.

Info for manual annotations of cluster CU5:
- Start number 2 was manually annotated 1 time for cluster CU5.

Gene Information:

Gene: Catfish_10 Start: 7651, Stop: 7947, Start Num: 2
Candidate Starts for Catfish_10:
(Start: 2 @7651 has 1 MA's), (4, 7681), (5, 7693), (6, 7777),

Gene: DinoDaryn_13 Start: 8801, Stop: 9109, Start Num: 1
Candidate Starts for DinoDaryn_13:
(Start: 1 @8801 has 6 MA's), (3, 8816),

Gene: Goib_12 Start: 8576, Stop: 8884, Start Num: 1
Candidate Starts for Goib_12:
(Start: 1 @8576 has 6 MA's), (3, 8591),

Gene: Huffy_13 Start: 8801, Stop: 9109, Start Num: 1
Candidate Starts for Huffy_13:
(Start: 1 @8801 has 6 MA's), (3, 8816),

Gene: Splinter_11 Start: 8576, Stop: 8884, Start Num: 1
Candidate Starts for Splinter_11:
(Start: 1 @8576 has 6 MA's), (3, 8591),

Gene: TZGordon_13 Start: 8718, Stop: 9026, Start Num: 1
Candidate Starts for TZGordon_13:
(Start: 1 @8718 has 6 MA's), (3, 8733),

Gene: Vendetta_11 Start: 8576, Stop: 8884, Start Num: 1
Candidate Starts for Vendetta_11:
(Start: 1 @8576 has 6 MA's), (3, 8591),