Abstract of the changes/no changes:

a) Gene 17: Deleted. Not called by GeneMark, it has no coding potential. and it has not been annotated after its overlapping a forward gene.

b) Gene 18: Changed from 9738 start to 9477, doesn’t show any start on Starterator.

c) Gene 32: GeneMark and Glimmer disagreed on the start; however , no changes were made following Starterator and RBS score; this matched the original start from Glimmer.

d) Gene 40: Changed from 29645 to 29681, reason is due to GeneMark and Starterator calling the start on 29681 gene.

e) Gene 46: Changed from 34067 to 34052 due GeneMark calling it and not Glimmer and Starterator stating that 34052 is the start.

f) Gene 59: Changed from 38953 to 38971 due to GeneMark and Glimmer having different starts and Starterator calls 38971 as the start.

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/24/24

Gene # 1	Original 5' End Start 1	Original 3' End Stop 519	Original Length 519	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 1

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start:1

Ribosome Binding Site

RBS Final Score -6.600	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.711 Start #: 325 ORF Length: 195

Starterator

Starterator Start 1	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes

No

Conserved Start:

served?

Annotation Documentation

Phage Name: **GreenIvy**	
Student Name: **Lance Mejia**	
Date: **1/24/24**	

Gene # 2	Original 5’ End Start 512	Original 3’ End Stop 1960	Original Length 1449	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	Yes	Start:
	No	Glimmer Start: 512 heMark Start: 521
Does this Gene have Coding Potential	Yes No	

Estimated Start: 521

Ribosome Binding Site

RBS Final Score -3.733	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.544 Start #: 941 ORF Length: 1020

Starterator

Starterator Start 512	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date:01/24/24

Gene # 3	Original 5’ End Start 1963	Original 3’ End Stop 2109	Original Length 147	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start:1963
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start:1963

Ribosome Binding Site

RBS Final Score -3.820	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 1963	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/24/24

Gene # 4	Original 5' End Start 2113	Original 3' End Stop 3543	Original Length 1431	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start:2113
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 2113

Ribosome Binding Site

RBS Final Score -2.605	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 2113	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date:01/24/24

Gene # 5	Original 5’ End Start 3546	Original 3’ End Stop 3755	Original Length 210	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 3546
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start:3546

Ribosome Binding Site

RBS Final Score -5.650	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -4.003 Start #: 3663 ORF Length:93

Starterator

Starterator Start 3546	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/24/24

Gene # 6	Original 5’ End Start 3755	Original 3’ End Stop 4468	Original Length 714	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 3755
	No	Glimmer Start:
		neMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 3755

Ribosome Binding Site

RBS Final Score -4.192	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0:
		Start #:
		ORF Length:

Starterator

Starterator Start 3755	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/24/24

Gene # 7	Original 5' End Start 4583	Original 3' End Stop 5149	Original Length 567	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 4583

Glimmer Start:

heMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 4583

Ribosome Binding Site

RBS Final Score -3.709	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 4583	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera

Yes

No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy	
Student Name: William Morales	
Date: 01/24/24	

Gene # 8	Original 5’ End Start 5188	Original 3’ End Stop 6168	Original Length 981	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 5188
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 5188

Ribosome Binding Site

RBS Final Score -2.095	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0:
		Start #:
		ORF Length:

Starterator

Starterator Start 5188	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/31/2024

Gene # 9	Original 5’ End Start 6171	Original 3’ End Stop 6461	Original Length 291	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 6171
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 6171

Ribosome Binding Site

RBS Final Score -4.258	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 6171	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date:01/31/24

Gene # 10	Original 5’ End Start 6539	Original 3’ End Stop 6964	Original Length 426	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 6539

Glimmer Start:

heMark Start:

Estimated Start: 6539

Does this Gene have Coding Potential [✓ Yes] No

Ribosome Binding Site

RBS Final Score -2.708	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 6539	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes
No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/31/2024

Gene # 11	Original 5' End Start 6936	Original 3' End Stop 7346	Original Length 411	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 6936

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 6936

Ribosome Binding Site

RBS Final Score -3.812	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.679 Start #: 7230 ORF Length: 117

Starterator

Starterator Start 6936	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera

Yes

No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/31/2024

Gene # 12	Original 5' End Start 7343	Original 3' End Stop 7687	Original Length 345	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No
Start: 7343
Glimmer Start:
heMark Start:

Estimated Start: 7343

Does this Gene have Coding Potential [✓ Yes] No

Ribosome Binding Site

RBS Final Score -2.584	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 7343	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes
No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/31/2024

Gene # 13	Original 5’ End Start 7684	Original 3’ End Stop 8034	Original Length 351	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 7684
	No	Glimmer Start: neMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 7684

Ribosome Binding Site

RBS Final Score [✓ -3.593]	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 7684	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/31/2024

Gene # 14	Original 5’ End Start 8034	Original 3’ End Stop 8366	Original Length 333	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 8034

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 8034

Ribosome Binding Site

RBS Final Score -2.505	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 8034	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera

Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/31/24

Gene # 15	Original 5’ End Start 8369	Original 3’ End Stop 8863	Original Length 495	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 8369

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 8369

Ribosome Binding Site

RBS Final Score -3.649	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 8369	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes
No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/31/24

Gene # 17	Original 5' End Start 9471	Original 3' End Stop 9632	Original Length 162	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? Yes / [✓ No] (if no, answer below)			
	Revised 5' End Start DELETE GENE		New Length DELETE GENE	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? Yes [✓ No]

Start:

Glimmer Start: 9632

neMark Start:

Does this Gene have Coding Potential Yes [✓ No]

Estimated Start:

Ribosome Binding Site

RBS Final Score -4.024	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.115 Start #: 9626 ORF Length: 152

Starterator

Starterator Start 9632	Is the starterator Start called on by other phages in this cluster/subcluster? Yes / [✓ No] (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/31/24

Gene # 18	Original 5' End Start 9738	Original 3' End Stop 9851	Original Length 114	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? Yes / [✓ No] (if no, answer below)			
	Revised 5' End Start 9477		New Length 375	New Start Codon [✓ ATG] / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? Yes [✓ No]

Start:

Glimmer Start: 9738

heMark Start: 9477

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 9477

Ribosome Binding Site

RBS Final Score -6.242	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.891 Start #: 9738 ORF Length: 114

Starterator

Starterator Start N/A	Is the starterator Start called on by other phages in this cluster/subcluster? Yes / [✓ No] (if no)

Is the s cluster Genera served? Yes No

Conserved Start:

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 19	Original 5' End Start 9872	Original 3' End Stop 12313	Original Length 2442	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 9872
	No	Glimmer Start: neMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 9872

Ribosome Binding Site

RBS Final Score -1.954	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 9872	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 20	Original 5’ End Start 12306	Original 3’ End Stop 14549	Original Length 2244	Original Start Codon ATG / GTG / [✓ TTG]
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 12306

Glimmer Start:

heMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 12306

Ribosome Binding Site

RBS Final Score -4.022	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 12306	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes

No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 21	Original 5' End Start 14549	Original 3' End Stop 16297	Original Length 1749	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 14549

Glimmer Start:

heMark Start:

Estimated Start: 14549

Does this Gene have Coding Potential [✓ Yes] No

Ribosome Binding Site

RBS Final Score -3.739	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 14549	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 22	Original 5’ End Start 16294	Original 3’ End Stop 17061	Original Length 768	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 16294

Glimmer Start:

heMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 16294

Ribosome Binding Site

RBS Final Score -3.509	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 16294	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 23	Original 5’ End Start 17076	Original 3’ End Stop 17333	Original Length 258	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 17076
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 17076

Ribosome Binding Site

RBS Final Score -2.523	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0:
		Start #:
		ORF Length:

Starterator

Starterator Start 17076	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 24	Original 5’ End Start 17333	Original 3’ End Stop 18202	Original Length 870	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 17333

Glimmer Start:

heMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 17333

Ribosome Binding Site

RBS Final Score -5.092	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -2.794 Start #: 17849 ORF Length: 354

Starterator

Starterator Start
17333

Is the starterator Start called on by other phages in this cluster/subcluster?
[✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes
No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 25	Original 5’ End Start 18265	Original 3’ End Stop 18813	Original Length 549	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 18265
	No	Glimmer Start: heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 18265

Ribosome Binding Site

RBS Final Score -3.545	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 18265	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 26	Original 5’ End Start 18810	Original 3’ End Stop 19172	Original Length 363	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 18810
	No	Glimmer Start: heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 18810

Ribosome Binding Site

RBS Final Score -3.782	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.328 Start #: 19005 ORF Length: 168

Starterator

Starterator Start [✓ 18810]	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 27	Original 5’ End Start 19176	Original 3’ End Stop 19523	Original Length 348	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 19176

Glimmer Start:

neMark Start:

Estimated Start: 19176

Does this Gene have Coding Potential [✓ Yes] No

Ribosome Binding Site

RBS Final Score -2.443	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 19176	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 28	Original 5' End Start 19688	Original 3' End Stop 19873	Original Length 186	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes] No	Start: 19873 Glimmer Start: heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 19873

Ribosome Binding Site

RBS Final Score -2.072	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 19873	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/24/24

Gene # 29	Original 5' End Start 19886	Original 3' End Stop 20071	Original Length 186	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 20071
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 20071

Ribosome Binding Site

RBS Final Score -5.512	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -5.348 Start #: 19951 ORF Length: 66

Starterator

Starterator Start 20071	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/31/24

Gene # 30	Original 5’ End Start 20091	Original 3’ End Stop 20273	Original Length 183	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 20273
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] / No	

Estimated Start: 20273

Ribosome Binding Site

RBS Final Score -5.709	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -4.699 Start #: 20135 ORF Length: 45

Starterator

Starterator Start 20273	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	

Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/31/24

Gene # 31	Original 5' End Start 20273	Original 3' End Stop 20785	Original Length 513	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 20785

Glimmer Start:

heMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 20785

Ribosome Binding Site

RBS Final Score -2.443	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 20785	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes
No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Lance Mejia
Date: 1/31/24

Gene # 32	Original 5’ End Start 20863	Original 3’ End Stop 22530	Original Length 1668	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	Yes	Start:
	[✓ No]	Glimmer Start: 22530 neMark Start: 22461
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 22530

Ribosome Binding Site

RBS Final Score -2.433	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 22530	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: William Morales
Date: 01/31/2024

Gene # 33	Original 5’ End Start 22506	Original 3’ End Stop 22799	Original Length 294	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 22799
	No	Glimmer Start:
		neMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 22799

Ribosome Binding Site

RBS Final Score -6.601	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.120 Start #: 22535 ORF Length: 30

Starterator

Starterator Start 22799	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date: 1/24/24

Gene # 34	Original 5’ End Start 22799	Original 3’ End Stop 23662	Original Length 864	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 23662

Glimmer Start:

neMark Start

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start:23662

Ribosome Binding Site

RBS Final Score -2.589	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 23662	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera

Yes

No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/24/24

Gene # 35	Original 5’ End Start 23694	Original 3’ End Stop 24389	Original Length 696	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:24389

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 24389

Ribosome Binding Site

RBS Final Score -5.622	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.999 Start #: 24521 ORF Length:828

Starterator

Starterator Start 24389	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera

Yes

No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/24/24

Gene # 36	Original 5’ End Start 24386	Original 3’ End Stop 25564	Original Length 1179	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:25564

Glimmer Start:

heMark Start:

Estimated Start:25564

Does this Gene have Coding Potential [✓ Yes] No

Ribosome Binding Site

RBS Final Score -5.211	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.028 Start #: 24700 ORF Length:315

Starterator

Starterator Start 25564	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera Yes No served?

Conserved Start:

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/24/24

Gene # 37	Original 5' End Start 25564	Original 3' End Stop 25728	Original Length 165	Original Start Codon ATG / GTG / [✓ TTG]
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	Yes [✓ No]	Start: Glimmer Start: 25728 heMark Start:N/A
Does this Gene have Coding Potential	Yes [✓ No]	

Estimated Start:

Ribosome Binding Site

RBS Final Score -4.518	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.058 Start #: 25800 ORF Length:237

Starterator

Starterator Start 25728	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Note: Was not called by GeneMark only by Glimmer. Its shows to have little to non-coding potential.

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/24/24

Gene # 38	Original 5' End Start 25715	Original 3' End Stop 27580	Original Length 1866	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes] No	Start:27580 Glimmer Start: heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start:27580

Ribosome Binding Site

RBS Final Score -2.837	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 27580	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Note: Was not called by GeneMark only by Glimmer. Its shows to have little to non-coding potential.

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/24/24

Gene # 39	Original 5' End Start 27770	Original 3' End Stop 28165	Original Length 396	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes] No	Start:28165 Glimmer Start: heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start:28165

Ribosome Binding Site

RBS Final Score -2.725	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 28165	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Note: Was not called by GeneMark only by Glimmer. Its shows to have little to non-coding potential.

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/24/24

Gene # 40	Original 5' End Start 28254	Original 3' End Stop 29645	Original Length 1392	Original Start Codon ATG / GTG / [✓ TTG]
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? Yes / [✓ No] (if no, answer below)			
	Revised 5' End Start 29681		New Length 1428	New Start Codon ATG / [✓ GTG] / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	Yes [✓ No]	Start: Glimmer Start:29645 neMark rt:29681
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start:29681

Ribosome Binding Site

RBS Final Score -5.111	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.633 Start #: 28976 ORF Length:723

Starterator

Starterator Start 29681	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Note: The start was changed from 29645 to 29681. The reason is due to Genemark and Starterator calling 29681 as the start for the gene

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/24/24

Gene # 41	Original 5’ End Start 29678	Original 3’ End Stop 29908	Original Length 231	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:29908

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start:29908

Ribosome Binding Site

RBS Final Score -4.124	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 29908	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/24/24

Gene # 42	Original 5’ End Start 29908	Original 3’ End Stop 30783	Original Length 876	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start:30783
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start:30783

Ribosome Binding Site

RBS Final Score -2.701	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 30783	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/25/24

Gene # 43	Original 5’ End Start 30780	Original 3’ End Stop 31562	Original Length 783	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:31562

Glimmer Start:

heMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start:31562

Ribosome Binding Site

RBS Final Score -3.485	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -2.725 Start #: 31376 ORF Length: 597

Starterator

Starterator Start 31562	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/25/24

Gene # 44	Original 5' End Start 31540	Original 3' End Stop 32133	Original Length 594	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:32133

Glimmer Start:

heMark Start:

Estimated Start:32133

Does this Gene have Coding Potential [✓ Yes] No

Ribosome Binding Site

RBS Final Score -3.344	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 32133	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera

Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/25/24

Gene # 45	Original 5’ End Start 32143	Original 3’ End Stop 33081	Original Length 939	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start:33081
	No	Glimmer Start:
		heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start:33081

Ribosome Binding Site

RBS Final Score -3.115	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0:
		Start #:
		ORF Length:

Starterator

Starterator Start 33081	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/25/24

Gene # 46	Original 5’ End Start 33078	Original 3’ End Stop 34067	Original Length 990	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? Yes / [✓ No] (if no, answer below)			
	Revised 5’ End Start 34052		New Length 975	New Start Codon ATG / [✓ GTG] / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? Yes [✓ No]

Start:

Glimmer Start:34067

neMark
rt:34052

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start:34052

Ribosome Binding Site

RBS Final Score -4.036	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.292 Start #: 33083 ORF Length:6

Starterator

Starterator Start 34052	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes
No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Kevin Ramos
Date:1/25/24

Gene # 47	Original 5' End Start 34045	Original 3' End Stop 34290	Original Length 246	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:34290

Glimmer Start:

heMark Start:

Estimated Start:34290

Does this Gene have Coding Potential [✓ Yes] No

Ribosome Binding Site

RBS Final Score -2.812	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 34290	Is the starterator Start called on by other phages in this cluster/subcluster? Yes / [✓ No] (if no)

Is the s
cluster
Genera

Yes
No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date: 1/24/24

Gene # 48	Original 5’ End Start 34350	Original 3’ End Stop 34490	Original Length 141	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 34490

Glimmer Start: 34490

GeneMark Start: 34490

Does this Gene have Coding Potential No

Estimated Start: 34490

Ribosome Binding Site

RBS Final Score -7.199	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -5.547 Start #: 34445 ORF Length: 96

Starterator

Starterator Start 34490	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera

Yes

No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy	
Student Name: Sandra Meesala	
Date:1/24/24	

Gene # 49	Original 5' End Start 34487	Original 3' End Stop 35242	Original Length 756	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 35242
	No	Glimmer Start:
		neMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 35242

Ribosome Binding Site

RBS Final Score -2.584	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 35242	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 50	Original 5’ End Start 35315	Original 3’ End Stop 35394	Original Length 180	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:35494

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 35494

Ribosome Binding Site

RBS Final Score -2.196	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 35494	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 51	Original 5’ End Start 35506	Original 3’ End Stop 35712	Original Length 207	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 35712

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 35712

Ribosome Binding Site

RBS Final Score -6.394	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 35712	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 52	Original 5’ End Start 35722	Original 3’ End Stop 35877	Original Length 156	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:35877

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 35877

Ribosome Binding Site

RBS Final Score -6.537	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -3.391 Start #: 35790 ORF Length: 69

Starterator

Starterator Start 35877	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera

Yes
No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 53	Original 5' End Start 35874	Original 3' End Stop 36740	Original Length 867	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:36740

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 36740

Ribosome Binding Site

RBS Final Score -2.523	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 36740	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s
cluster
Genera
served?

Yes
No

Conserved Start:

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 54	Original 5’ End Start 36737	Original 3’ End Stop 36988	Original Length 252	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:36988

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 36988

Ribosome Binding Site

RBS Final Score -3.368	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -2.601 Start #: 36823 ORF Length: 87

Starterator

Starterator Start 36988	Is the starterator Start called on by other phages in this cluster/subcluster? Yes / [✓ No] (if no)

Is the s
cluster
Genera

Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy	
Student Name: Sandra Meesala	
Date:1/24/24	

Gene # 55	Original 5' End Start 36981	Original 3' End Stop 37328	Original Length 348	Original Start Codon ATG / [✓ GTG] / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start:37328
	No	Glimmer Start: heMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 37328

Ribosome Binding Site

RBS Final Score -4.497	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -4.406 Start #: 37121 ORF Length: 141

Starterator

Starterator Start 37328	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 56	Original 5' End Start 37325	Original 3' End Stop 37573	Original Length 249	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 37573

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 37573

Ribosome Binding Site

RBS Final Score -4.573	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: - 3.703 Start #: 37441 ORF Length: 117

Starterator

Starterator Start 37573	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera Yes No served?

Conserved Start:

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 57	Original 5’ End Start 37573	Original 3’ End Stop 38238	Original Length 666	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start:38238
	No	Glimmer Start:
		neMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 38238

Ribosome Binding Site

RBS Final Score -2.505	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0:
		Start:
		ORF Length:

Starterator

Starterator Start 38238	Is the starterator Start called on by other phages in this cluster/subcluster? Yes / [✓ No] (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 58	Original 5' End Start 38235	Original 3' End Stop 38681	Original Length 447	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start:38681

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 38681

Ribosome Binding Site

RBS Final Score -7.327	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: -5.943 Start #: 38318 ORF Length: 84

Starterator

Starterator Start 38681	Is the starterator Start called on by other phages in this cluster/subcluster? Yes / [✓ No] (if no)

Is the s
cluster
Genera

Yes

No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy	
Student Name: Sandra Meesala	
Date:1/24/24	

Gene # 59	Original 5' End Start 38681	Original 3' End Stop 38953	Original Length 273	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction FWD / [✓ REV]	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? Yes / [✓ No] (if no, answer below)			
	Revised 5' End Start 38971		New Length 291	New Start Codon [✓ ATG] / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? Yes [✓ No]

Start:

Glimmer Start: 38953

heMark Start: 38971

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 38971

Ribosome Binding Site

RBS Final Score -2.523	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 38971	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)

Is the s cluster Genera

Yes No

Conserved Start:

served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 60	Original 5’ End Start 39358	Original 3’ End Stop 39603	Original Length 246	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5’ End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark?	[✓ Yes]	Start: 39358
	No	Glimmer Start:
		neMark Start:
Does this Gene have Coding Potential	[✓ Yes] No	

Estimated Start: 39358

Ribosome Binding Site

RBS Final Score -2.219	Is this Score the Closest to 0? [✓ Yes] / No (if no)	Score Closest to 0: Start #: ORF Length:

Starterator

Starterator Start 39358	Is the starterator Start called on by other phages in this cluster/subcluster? [✓ Yes] / No (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Annotation Documentation

Phage Name: GreenIvy
Student Name: Sandra Meesala
Date:1/24/24

Gene # 61	Original 5' End Start 39603	Original 3' End Stop 39938	Original Length 336	Original Start Codon [✓ ATG] / GTG / TTG
Gene Direction [✓ FWD] / REV	Gene Start, Length, and Start Codon Same as original (Auto Annotated) call? [✓ Yes] / No (if no, answer below)			
	Revised 5' End Start		New Length	New Start Codon ATG / GTG / TTG

Glimmer and GeneMark Calls

Start called by both Glimmer and GeneMark? [✓ Yes] No

Start: 39603

Glimmer Start:

neMark Start:

Does this Gene have Coding Potential [✓ Yes] No

Estimated Start: 39603

Ribosome Binding Site

RBS Final Score -5.318	Is this Score the Closest to 0? Yes / [✓ No] (if no)	Score Closest to 0: -4.602 Start #: 39861 ORF Length: 78

Starterator

Starterator Start 39603	Is the starterator Start called on by other phages in this cluster/subcluster? Yes / [✓ No] (if no)	Is the s cluster Genera	Yes No	Conserved Start: served?

Function **(F)** Hypothetical protein	Gene No: 1			Student name: William Morales Date: 02/07/2024	
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 2e-119	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 100%	E-value (if < 10^{-7}) 7e-92	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All below 90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (183) of Pham 84998		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84998 (182)	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?
Transmembrane domains by TmHmm using Phamerator				N/A	

Notes :

Function **(F)** Terminase	Gene No: 2	Student name: William Morales Date: 02/07/2024			
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Terminase	% Query 99%	% Identity 99.79%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Terminase		% Identity 99%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Terminase	Name / Descr (incl DUF) Avs3 bound to phage PhiV-1 Terminase	Hit 8DGC_F	Probability (if > 90%) 100	E-value (if < 1) 3.3e-37
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Terminase	Pham number and number of members Members (246) of Pham 84823	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84998	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 145515	
Transmembrane domains by TmHmm using Phamerator	N/A				

Notes :

Function **(F)** Hypothetical Protein	Gene No: 3		Student name: William Morales Date: 02/14/2024		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 97%	% Identity 100%	E-value (if < 10^{-7}) 5e-25	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 3e-22	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All below 90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Pham number and number of members Members (115) of Pham 145515	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84823		Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 633
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Portal Protein	Gene No: 4		Student name: William Morales Date: 02/14/2024		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Portal Protein	% Query 99%	% Identity 98.95%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Portal Protein		% Identity 98%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Portal Protein	Name / Descr (incl DUF) Portal protein; Bacteriophage, SPP1, Portal Protein, Head completion proteins, Connector Complex, DNA Channel, VIRAL PRO	Hit 7Z4W_B	Probability (if > 90%) 99.92%	E-value (if < 1) 3.5e-22
Supporting Information for Function, from Syntney **(SIF-Syn)**	Function (or NKF) Portal Protein	Pham number and number of members Members (186) of Pham 633		upstream pham conserved ? [✓ Yes] or No	Downstream pham conserved ? [✓ Yes] or No

(All three lines of SIF evidence must be filled in)			If yes, what pham # or function ? 145515	If yes, what pham # or function ? 103828
Transmembrane domains by TmHmm using Phamerator			N/A	

Notes :

Function **(F)** Hypothetical Protein	Gene No: 5		Student name: William Morales Date: 02/14/2024		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 3e-44	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 3e-38	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Name / Descr (incl DUF) YjdM_Zn_Ribbon ; PhnA Zinc-Ribbon	Hit PF08274.16	Probability (if > 90%) 92.01	E-value (if < 1) 0.44
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Pham number and number of members Members (23) of Pham 103828	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 633	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Hypothetical Protein	Gene No: 6		Student name: William Morales Date: 02/14/2024		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 99%	% Identity 99.58%	E-value (if < 10^{-7}) 2e-170	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 99%	E-value (if < 10^{-7}) e-134	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor capsid protein	Name / Descr (incl DUF) Phage_min_cap2 ; Phage minor capsid protein 2	Hit PF06152.15	Probability (if > 90%) 99.55	E-value (if < 1) 4.8e-14
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Pham number and number of members Members (172) of Pham 146890		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 103828	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 67102
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Scaffolding Protein	Gene No: 7		Student name: William Morales Date: 02/14/2024		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Scaffolding Protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 9e-133	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Scaffolding Protein		% Identity 100%	E-value (if < 10^{-7}) e-104	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Scaffolding Protein	Name / Descr (incl DUF) Coronin-1A; coiled coil, coronin 1, PROTEIN BINDING; 1.2A {N/A}	Hit 2AKF_B	Probability (if > 90%) 93.14	E-value (if < 1) 0.25
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Scaffolding Protein	Pham number and number of members Members (186) of Pham 67102		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146890	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146738
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Major capsid protein	Gene No:8		Student name: William Morales Date:2/15/2024		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Major capsid protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Major capsid protein		% Identity 100%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Major capsid protein	Name / Descr (incl DUF) Major capsid protein; HK97-fold, T=9, tailed bacteriophage, VIRUS; 2.6A {Gordonia phage Ziko}	Hit 8EB4_B	Probability (if > 90%) 100	E-value (if < 1) 1.5e-31
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Major capsid protein	Pham number and number of members Members (453) of Pham 146738	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 67102	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 6606	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Hypothetical protein	Gene No:9	Student name: William Morales Date:2/15/24			
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 9e-57	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 100%	E-value (if < 10^{-7}) 7e-47	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All Under 90%	E-value (if < 1) All Over 1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (38) of Pham 66006	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146738	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 643	
Transmembrane domains by TmHmm using Phamerator	N/A				

Notes :

Function **(F)** Hypothetical protein	Gene No:10		Student name: William Morales Date:2/15/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 99.29%	E-value (if < 10^{-7}) 1e-94	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 99%	E-value (if < 10^{-7}) 1e-76	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1) All over 1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (186) of Pham 643	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 66006		Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 632
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Hypothetical protein	Gene No:11		Student name: William Morales Date:2/15/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 99.26%	E-value (if < 10^{-7}) 2e-90	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 99%	E-value (if < 10^{-7}) 1e-69	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Name / Descr (incl DUF) DUF6093 ; Family of unknown function (DUF6093)	Hit PF19586.3	Probability (if > 90%) 96.98%	E-value (if < 1) 0.0049
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (186) of Pham 632		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 643	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 104815
Transmembrane domains by TmHmm using Phamerator					

Notes :

Function **(F)** Hypothetical protein	Gene No:12		Student name: William Morales Date:2/15/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 99e-77	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 100%	E-value (if < 10^{-7}) 1e-58	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor capsid protein	Name / Descr (incl DUF) Minor_capsid_2 ; Minor capsid protein	Hit PF11114.12	Probability (if > 90%) 99.56	E-value (if < 1) 6.8e-14
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (186) of Pham 104815	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 632	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 640	
Transmembrane domains by TmHmm using Phamerator	N/A				

Notes :

<table>
<tr><td>Function **(F)**
Tail terminator</td><td colspan="3">Gene No:13</td><td colspan="2">Student name: William Morales
Date:2/15/24</td></tr>
<tr><td>Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)**
(All three lines of SIF evidence must be filled in)</td><td>Function
(or NKF)
Tail terminator</td><td>% Query
99%</td><td>% Identity
100%</td><td>E-value
(if < 10^{-7})
4e-79</td><td>AA # conserved in first 10 hits?
[✓ Yes] or No</td></tr>
<tr><td>Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)**
(All three lines of SIF evidence must be filled in)</td><td>Function
(or NKF)
Tail terminator</td><td></td><td>% Identity
100%</td><td>E-value
(if < 10^{-7})
7e-63</td><td>AA # conserved in first 10 hits?
[✓ Yes] or No</td></tr>
<tr><td>Supporting Information for Function, from HHpred **(HHpred)**
(All three lines of SIF evidence must be filled in)</td><td>Function
(or NKF)
Tail terminator</td><td>Name / Descr (incl DUF)
Tail terminator protein Rcc01690; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus}</td><td>Hit
6TE9_F</td><td>Probability (if > 90%)
97.56%</td><td>E-value
(if < 1)
0.0015</td></tr>
<tr><td>Supporting Information for Function, from Syntney **(SIF-Syn)**
(All three lines of SIF evidence must be filled in)</td><td>Function
(or NKF)
Tail terminator</td><td colspan="2">Pham number and number of members
Members (186) of Pham 640</td><td>upstream pham conserved ?
[✓ Yes] or No
If yes, what pham # or function ?
104815</td><td>Downstream pham conserved ?
[✓ Yes] or No
If yes, what pham # or function ?
147236</td></tr>
<tr><td colspan="3">Transmembrane domains by TmHmm using Phamerator</td><td colspan="3"></td></tr>
</table>

Notes :

Function **(F)** Hypothetical protein	Gene No:14		Student name: William Morales Date:2/15/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 99.09%	E-value (if < 10^{-7}) 1e-71	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 99%	E-value (if < 10^{-7}) 2e-57	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1) All over 1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (43) of Pham 147236	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 640	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84983	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Major tail protein	Gene No:15		Student name: William Morales Date: 2/15/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Major tail protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 5e-113	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Major tail protein		% Identity 100%	E-value (if < 10^{-7}) 2e-91	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1) All over 1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Major tail protein	Pham number and number of members Members (185) of Pham 84983		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 147236	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84979
Transmembrane domains by TmHmm using Phamerator				N/A	

Notes :

Function **(F)** Tape measure protein	Gene No: 19		Student name: Lance Mejia Date: 2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Tape measure protein	% Query 99%	% Identity 99.51%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Tape measure protein		% Identity 100%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Tape measure protein	Name / Descr (incl DUF) Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alph	Hit 6V8I_BF	Probability (if > 90%) 99.95	E-value (if < 1) 3e-19
Supporting Information	Function (or NKF)	Pham number and number of members		upstream pham conserved ?	Downstream pham conserved ?

for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Tape measure protein	Members (186) of Pham 59270	Yes or [✓ No] If yes, what pham # or function ?	[✓ Yes] or No If yes, what pham # or function ? 4166 (26)
Transmembrane domains by TmHmm using Phamerator			N/A	

Notes :

Function **(F)** Minor tail protein	Gene No: 20		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein	% Query 99%	% Identity 97.72%	E-value (if < 10^{-7}) 0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein		% Identity 97%	E-value (if < 10^{-7}) 0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Interleukin-6 receptor subunit beta	Name / Descr (incl DUF) Interleukin-6 receptor subunit beta; Ig-like, FNIII, Cell membrane, Disulfide bond, Glycoprotein, Immunoglobulin domain,	Hit 3L5H_A	Probability (if > 90%) 99.87	E-value (if < 1) 1.1e10^{-16}
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein	Pham number and number of members Members (26) of Pham 4166	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 59270		Downstream pham conserved ? Yes or [✓ No] If yes, what pham # or function ?
Transmembrane domains by TmHmm using Phamerator			**N/A**		

Notes :

Function **(F)** Minor Tail Protein	Gene No: 21		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein	% Query 99	% Identity 76.59	E-value (if < 10^{-7}) 0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein		% Identity 98%	E-value (if < 10^{-7}) 0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein	Name / Descr (incl DUF) Prophage MuSo2, 43 kDa tail protein; MuSo2, Shewanella oneidensis MR-1, Structural Genomics, PSI-2, Protein Structure In	Hit 3CDD_C	Probability (if > 90%) 99.89	E-value (if < 1) 1.2e-19
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein	Pham number and number of members Members (2) of Pham 133067		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 4166	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 7779

Transmembrane domains by TmHmm using Phamerator	N/A

Notes :

Function **(F)** Minor tail protein	Gene No: 22		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein		% Identity 100%	E-value (if < 10^{-7}) e-142	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Name / Descr (incl DUF) DUF2577 ; Protein of unknown function (DUF2577)	Hit PF10844.12	Probability (if > 90%) 96.92	E-value (if < 1) 0.0059
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Minor tail protein	Pham number and number of members Members (13) of Pham 7779	upstream pham conserved ? Yes or [✓ No] If yes, what pham # or function ?	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 147382	
Transmembrane domains by TmHmm using Phamerator	**N/A**				

Notes :

Function **(F)** Hypothetical Protein	Gene No: 23	Student name: Lance Mejia Date: 2/14/24

Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 9e-54	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 8e-45	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All hits <90%	E-value (if < 1) All above > 1

Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) N/A	Pham number and number of members Members (25) of Pham 147382	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 7779	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 98619

Transmembrane domains by TmHmm using Phamerator	N/A

Notes :

Function **(F)** Lysin A	Gene No: 24		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Lysin A	% Query 99%	% Identity 99.31	E-value (if < 10^{-7}) 0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Lysin A		% Identity 99%	E-value (if < 10^{-7}) e-168	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) D,D-Hypothetical protein	Name / Descr (incl DUF) D,D-dipeptidase/ D,D-carboxypeptidase; CENTER FOR STRUCTURAL GENOMICS OF INFECTIOUS DISEASES, CSGID, NATIONAL INSTITUTE O	Hit 4MUQ_A	Probability (if > 90%) 99.45	E-value (if < 1) 2.6e-12
Supporting Information for Function, from Syntney **(SIF-Syn)**	Function (or NKF) Lysin A	Pham number and number of members Members (138) of Pham 98619	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	

(All three lines of SIF evidence must be filled in)			147382	135440
Transmembrane domains by TmHmm using Phamerator			N/A	

Notes :

Function **(F)** membrane protein	Gene No: 25		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Membrane Protein	% Query 99%	% Identity 99.45%	E-value (if < 10^{-7}) 1e-125	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 99%	E-value (if < 10^{-7}) e-102	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All hits <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Pham number and number of members Members (104) of Pham 135440		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 98619	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 2158
Transmembrane domains by TmHmm using Phamerator			transmembrane domains detected		

Notes :

Function **(F)** membrane Protein	Gene No: 26		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Membrane Protein	% Query 99%	% Identity 99.17%	E-value (if < 10^{-7}) 1e-80	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 1e-63	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%)	E-value (if < 1) All e-values >1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Pham number and number of members Members (63) of Pham 2158	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 135440		Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 147015
Transmembrane domains by TmHmm using Phamerator			transmembrane domain detected		

Notes :

Function **(F)** membrane protein	Gene No: 27		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Membrane Protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 4e-72	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 3e-58	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All hits <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Pham number and number of members Members (100) of Pham 147015	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 2158	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 686	
Transmembrane domains by TmHmm using Phamerator			transmembrane domain detected		

Notes : **Not enough evidence to call Holin protein on BLAST-PhagesDB**

Function **(F)** Hypothetical Protein	Gene No: 28		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 5e-35	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 3e-28	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All hits <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Pham number and number of members Members (177) of Pham 686	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 147015	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 6231	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Hypothetical Protein	Gene No: 29		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 2e-35	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 9e-28	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All hits <90%	E-value (if < 1) All hits >1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) N/A	Pham number and number of members Members (12) of Pham 6231	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 686	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 85118	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Hypothetical Protein	Gene No: 30		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 4e-36	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 5e-31	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All hits <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (141) of Pham 85118	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 6231	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 88242	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Hypothetical Protein	Gene No: 31			Student name: Lance Mejia Date: 2/14/24	
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 5e-121	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 1e-97	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All hits <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Pham number and number of members Members (9) of Pham 88242		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 85118	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84815
Transmembrane domains by TmHmm using Phamerator				N/A	

Notes :

Function **(F)** RecA-like DNA recombinase	Gene No: 32		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) RecA-like DNA recombinase	% Query 99%	% Identity 99.64%	E-value (if < 10^{-7}) 0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) RecA-like DNA recombinase		% Identity 100%	E-value (if < 10^{-7}) 0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Regulatory protein repA	Name / Descr (incl DUF) Regulatory protein repA; replicative DNA helicase structural changes, REPLICATION; HET: SO4; 1.95A {Escherichia coli} SC	Hit 1NLF_A	Probability (if > 90%) 99.87%	E-value (if < 1) 5.5e-20
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) RecA-like DNA recombinase	Pham number and number of members Members (253) of Pham 84815	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 88242	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 142246	

Transmembrane domains by TmHmm using Phamerator	N/A

Notes :

Function **(F)** Nuclease	Gene No: 33		Student name: Lance Mejia Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Nuclease	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 8e-67	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Nuclease		% Identity 100%	E-value (if < 10^{-7}) 9e-52	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Nuclease	Name / Descr (incl DUF) Nuclease; Nuclease, HYDROLASE; HET: SO4; 1.85A {Salmonella phage SETP3} SCOP: c.52.1.35	Hit 4QBN_A	Probability (if > 90%) 99.84%	E-value (if < 1) 7.7e-19
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) N/A	Pham number and number of members Members (255) of Pham 142246	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84815	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146891	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** Hypothetical protein	Gene No: 34		Student name:Kevin Ramos Date:2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 99.30%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 99%	E-value (if < 10^{-7}) e-163	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Name / Descr (incl DUF) Hypothetical protein	Hit 2HJQ_A	Probability (if > 90%) 96.96	E-value (if < 1) 0.0028
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (169) of Pham 146891		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 142246	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84985
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** AAA-ATPase	Gene No:35	Student name:Kevin Ramos Date:2/7/24

Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) AAA-ATPase	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 1e-167	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) AAA-ATPase		% Identity 100%	E-value (if < 10^{-7}) e-128	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) ATPase	Name / Descr (incl DUF) Crystal Structure of RecA superfamily ATPase PH0284 from Pyrococcus horikoshii OT3	Hit 2DR3_B	Probability (if > 90%) 99.11%	E-value (if < 1) 4.1e-9

Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) AAA-ATPase	Pham number and number of members Members (185) of Pham 84985	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146891	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 142179

Transmembrane domains by TmHmm using Phamerator	N/A

Notes :

Function **(F)** Cas4 exonuclease	Gene No:36		Student name:Kevin Ramos Date:2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Cas4 exonuclease	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Cas4 exonuclease		% Identity 100%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Cas4 exonuclease	Name / Descr (incl DUF) Human Exonuclease 5 crystal structure	Hit 7LW7_A	Probability (if > 90%) 99.8%	E-value (if < 1) 8.9e-18
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Cas4 exonuclease	Pham number and number of members Members (255) of Pham 142179		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 84985	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 86939
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** hypothetical protein	Gene No:37		Student name:Kevin Ramos Date:2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) hypothetical protein	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 2e-30	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) hypothetical protein		% Identity 100%	E-value (if < 10^{-7}) 8e-27	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1) All over 1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) hypothetical protein	Pham number and number of members Members (19) of Pham 86939		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function? 142179	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146703
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** DNA polymerase I	Gene No:38		Student name:Kevin Ramos Date:2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) DNA polymerase I	% Query 99%	% Identity 99.36%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) DNA polymerase I		% Identity 99%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) DNA polymerase I	Name / Descr (incl DUF) Binary complex of human polymerase nu and DNA with the finger domain closed	Hit 4XVK_A	Probability (if > 90%) 100%	E-value (if < 1) 2.2e-67
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) DNA polymerase I	Pham number and number of members Members (1713) of Pham 146703		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 86939	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 652

Transmembrane domains by TmHmm using Phamerator	N/A

Notes :

Function **(F)** Hypothetical protein	Gene No:39		Student name:Kevin Ramos Date:2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 98.47%	E-value (if < 10^{-7}) 2e-81	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 98%	E-value (if < 10^{-7}) 4e-66	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1) All over 1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (185) of Pham 652		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146703	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 142245
Transmembrane domains by TmHmm using Phamerator	N/A				

Notes :

Function **(F)** DNA helicase	Gene No:40			Student name:Kevin Ramos Date:2/7/24	
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) DNA helicase	% Query 99%	% Identity 99.79%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) DNA helicase		% Identity 99%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) complex subunit	Name / Descr (incl DUF) Transcription regulatory protein SNF2; SWI/SNF remodeling, Swi-Snf complex, nucleosome, DNA BINDING PROTEIN; 2.89A {Sacc	Hit 7C4J_H	Probability (if > 90%) 100%	E-value (if < 1) 3.4e-39
Supporting Information for Function, from Syntney **(SIF-Syn)**	Function (or NKF) DNA helicase	Pham number and number of members Members (255) of Pham 142245	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	

(All three lines of SIF evidence must be filled in)			652	147423
Transmembrane domains by TmHmm using Phamerator			N/A	

Notes :

Function **(F)** Hypothetical protein	Gene No:41		Student name:Kevin Ramos Date:2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Membrane protein	% Query 88%	% Identity 97.06%	E-value (if < 10^{-7}) 9e-38	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 94%	E-value (if < 10^{-7}) 3e-35	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Name / Descr (incl DUF) Cell wall surface anchor protein; Adhesins, cell adhesion; 1.89A {Streptococcus agalactiae}	Hit 4Z1P_A	Probability (if > 90%) 96.43%	E-value (if < 1) 0.013
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (21) of Pham 147423	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 142245	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146170	
Transmembrane domains by TmHmm using Phamerator			One transmembrane domain detected by SOSUI but not DeepTMHMM		

Notes : In the draft it showns no gene between 41 and 42, however against others there seems to be another gene inbetween 41 and 42 known as 7632 (9) as its pham and member number.

Function **(F)** MazG-like nucleotide pyrophosphohydrolase	Gene No:42		Student name:Kevin Ramos Date:2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) MazG-like nucleotide pyrophosphohydrolase	% Query 99%	% Identity 99.31%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) MazG-like nucleotide pyrophosphohydrolase		% Identity 99%	E-value (if < 10^{-7}) e-169	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) NTP pyrophosphohydrolase	Name / Descr (incl DUF) putative NTP pyrophosphohydrolase; Structural Genomics, Joint Center for Structural Genomics, JCSG, Protein Structure In	Hit 3NL9_A	Probability (if > 90%) 99.97%	E-value (if < 1) 6.6e-31
Supporting Information for Function,	Function (or NKF) MazG-like nucleotide	Pham number and number of members		upstream pham conserved ? [✓ Yes] or No	Downstream pham conserved ? [✓ Yes] or No

from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	pyrophosph ohydrolase	Members (10) of Pham 146170	If yes, what pham # or function ? 147423	If yes, what pham # or function ? 146877
Transmembrane domains by TmHmm using Phamerator			N/A	

Notes :

Function **(F)** Hypothetical protein	Gene No:43		Student name:Kevin Ramos Date:2/7/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 99.62%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 99%	E-value (if < 10^{-7}) e-146	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (185) of Pham 146877	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146170	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 657	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** thymidylate kinase	Gene No:44		Student name:Kevin Ramos Date:2/8/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) thymidylate kinase	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 2e-144	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) thymidylate kinase		% Identity 100%	E-value (if < 10^{-7}) e-114	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) thymidylate kinase	Name / Descr (incl DUF) THYMIDYLATE KINASE; TRANSFERASE, MALARIA, INHIBITOR; HET: 74X; 1.5A {PLASMODIUM FALCIPARUM } SCOP: c.37.1.0	Hit 2YOG_B	Probability (if > 90%) 99.41	E-value (if < 1) 2.7e-12
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) thymidylate kinase	Pham number and number of members Members (185) of Pham 657	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146877	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 127501	

Transmembrane domains by TmHmm using Phamerator	N/A

Notes :

Function **(F)** glycosyltransferase	Gene No:45		Student name:Kevin Ramos Date:2/8/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) glycosyltransferase	% Query 99%	% Identity 99.68%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) glycosyltransferase		% Identity 100%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) glycosyltransferase	Name / Descr (incl DUF) Putative glycosyltransferase protein; Glycosyltransferase, Protein Structure Initiative II, PSI-II, 12059a, NYSGXRC, Str	Hit 3BCV_A	Probability (if > 90%) 99.69%	E-value (if < 1) 5e-16
Supporting Information for Function, from Syntney **(SIF-Syn)**	Function (or NKF) glycosyltransferase	Pham number and number of members Members (175) of Pham 127501	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	

(All three lines of SIF evidence must be filled in)			657	127501

Transmembrane domains by TmHmm using Phamerator	N/A

Notes : Phamerator shows that gene 45 takes up two blocks this could that the may have broken up or because how much is needed it created second block.

Function **(F)** glycosyltransferase	Gene No:46		Student name:Kevin Ramos Date:2/8/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) glycosyltransferase	% Query 99%	% Identity 99.69%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) glycosyltransferase		% Identity 99%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) glycosyltransferase	Name / Descr (incl DUF) Putative glycosyltransferase protein	Hit 3BCV_A	Probability (if > 90%) 98.89%	E-value (if < 1) 3.8e-7
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) glycosyltransferase	Pham number and number of members Members (174) of Pham 127501		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 127501	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 139587
Transmembrane domains by TmHmm using Phamerator				N/A	

Notes : Both gene 46 and 45 have the same Phamerator number and also the same name being glycostransferase. They could be a gene broken up or just have the same function.

Function **(F)** Hypothetical protein	Gene No:47		Student name:Kevin Ramos Date:2/8/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 98%	% Identity 97.53%	E-value (if < 10^{-7}) 2e-52	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 97%	E-value (if < 10^{-7}) 1e-44	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1) All over 1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (147) of Pham 146926		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 127501	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 4923
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

Function **(F)** membrane protein	Gene No:48		Student name:Kevin Ramos Date:2/8/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) membrane protein	% Query 97%	% Identity 95.65%	E-value (if < 10^{-7}) 9e-20	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) hypothetical protein		% Identity 95%	E-value (if < 10^{-7}) 1e-17	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1) All over 1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) hypothetical protein	Pham number and number of members Members (20) of Pham 4923		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 146926	Downstream pham conserved ? Yes or No If yes, what pham # or function ? 654
Transmembrane domains by TmHmm using Phamerator				One transmebrane domain detected with SOSUI and DeepTMHMM	

Notes :

Function **(F)** thymidylate synthase	Gene No:49		Student name:Kevin Ramos Date:2/8/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) thymidylate synthase	% Query 99%	% Identity 98.80%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) thymidylate synthase		% Identity 98%	E-value (if < 10^{-7}) e-146	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) thymidylate synthase	Name / Descr (incl DUF) PROTEIN (DEOXYCYTIDYLATE HYDROXYMETHYLASE); HYDROXYMETHYLASE, DNTP SYNTHESIZING COMPLEX, TRANSFERASE; HET: DCM; 1.6A {En	Hit 1B5E_B	Probability (if > 90%) 100	E-value (if < 1) 2.6e-40
Supporting Information for Function, from Syntney **(SIF-Syn)**	Function (or NKF) thymidylate synthase	Pham number and number of members Members (185) of Pham 654	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ?	

(All three lines of SIF evidence must be filled in)			<u>4923</u>	<u>7069</u>

Transmembrane domains by TmHmm using Phamerator	N/A

Notes :

Function **(F)** Hypothetical protein	Gene No: 50		Student name: Sandra Meesala Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 98%	% Identity 98.31%	E-value (if < 10^{-7}) 1x10^-32	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 98%	E-value (if < 10^{-7}) 3x10^-25	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All below 90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members #7069, 11 members	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 654	Downstream pham conserved ? Yes or [✓ No] If yes, what pham # or function ?	
Transmembrane domains by TmHmm using Phamerator	N/A				

Notes :

50	MAHATLDQQIAAAAEVYKSGQTNSKKALAEVKRLIKRKVFSQELALSLAASEDAVPSCPZ

Function **(F)** Hypothetical protein	Gene No: 51		Student name: Sandra Meesala Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 98%	% Identity 98.53%	E-value (if < 10^{-7}) 2x10^-36	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 98%	E-value (if < 10^{-7}) 6x10^-29	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All under 90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members: 16 Pham: 5163	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 8815	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 7069	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

51	MNSTKALLLKAINEQDARVIRRLLNDAVELQVVTAAAAVKLGHLADVMYTGKAAARNSATTAALALVKZ

Function **(F)** Hypothetical protein	Gene No: 52	Student name: Sandra Meesala Date: 2/14/24			
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 98%	% Identity 100%	E-value (if < 10^{-7}) 3x10^-30	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 100%	E-value (if < 10^{-7}) 2x10^-26	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members 8815 Members: 9	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 86072	Downstream pham conserved ? Yes or [✓ No] If yes, what pham # or function ?	
Transmembrane domains by TmHmm using Phamerator	N/A				

Notes :

52	MSDGVRDTQWFAYWEGVHQAVQAWANGTPMSCPYPTPKEVEEKFAQMMNDVZ

Function **(F)** Hypothetical protein	Gene No: 53		Student name: Sandra Meesala Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 99.65%	E-value (if < 10^{-7}) 0.0	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 99%	E-value (if < 10^{-7}) e-166	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) 5-hmdU DNA kinase, helical domain	Name / Descr (incl DUF) 5-hmdU DNA kinase, helical domain	Hit PF18723.5	Probability (if > 90%) 100	E-value (if < 1) 4.9e-67
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members 86072 Members: 40		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 4886	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 8815
Transmembrane domains by TmHmm using Phamerator			N/A		

53	MKTIEDVVKFAKARHRLWEGKGTKSRILTTRKFTNVFRVLDRGSQYLLQLMDLHDDPLDRVALSYFYRQVNRPDTMDDIIEANDGYVPEAAEIFDPKWYDKVVRPVATARPGRFLSGAYMIVVSPNDPRPIVDKMQATFPAAANLLGHVAEVGDLATRVMLLQEVRGIAAFMAMQIATDLGYTRGEPDQENTYILPGPGAKRGAGYLVGKTYASEKEARDIIQNFPVELLPTLPGSNGRPASWMDVQNVFCEFSKYARFLEKPVPPTATPYRRNGDFETIIPAQFIRPZ

Function **(F)** Hypothetical protein	Gene No: 54		Student name: Sandra Meesala Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 98%	% Identity 95.18%	E-value (if < 10^{-7}) 4x10^-51	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 95%	E-value (if < 10^{-7}) 2x10^-40	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members 4886 Members: 20	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 731	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 86072	
Transmembrane domains by TmHmm using Phamerator			N/A		

Notes :

54	MPSYYTAAGSVIDAGIVPTVSQEEFRITREDWINATLEELRWLHDVPLYTNQEASVSEEMFSGDVKVRIRYRTPCITTLKEAAZ

Function **(F)** Hypothetical protein	Gene No: 55		Student name: Sandra Meesala Date: 2/14/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 99%	% Identity 100%	E-value (if < 10^{-7}) 4x10^-79	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 100%	E-value (if < 10^{-7}) 1x10^-60	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members 731 Members: 164	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 2778		Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 4886
Transmembrane domains by TmHmm using Phamerator			N/A		

55	MNADRRIAGKVVIELLNEGSINGEISDQAHAVIGETLAHMQKQEYHQLRAQEKFEGKNASTDKQIAICRVALPALETALHAYNSDDFQECITGVKLAIETDGTVPKPKRKGRRRAZ

Function **(F)** Hypothetical protein	Gene No: 56	Student name: Sandra Meesala Date: 2/14/24

Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 98%	% Identity 96.34%	E-value (if < 10^{-7}) 2x10^-51	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 96%	E-value (if < 10^{-7}) 1x10^-39	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All <90%	E-value (if < 1)

Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members 2778 Members: 39	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 87511	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 731

Transmembrane domains by TmHmm using Phamerator	N/A

Notes :

56	MAEAYTIVLVDADLWRTERSRFTQIAQQAADEKFERLAQENMKGLVTRNPEPREMSHEELRKYMPYAVLDGLVGLYFTADITZ

Function **(F)** Hypothetical protein	Gene No: 57			Student name: Sandra Meesala Date: 2/14/24	
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 79.19%	E-value (if < 10^{-7}) 7e-120	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 79%	E-value (if < 10^{-7}) 8e-93	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All <90%	E-value (if < 1) All >1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (13) of Pham 87511		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 87210	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 2778
Transmembrane domains by TmHmm using Phamerator				N/A	

57	MTESLGKAIERLQKAAHSWRGFRHAAARPGDITAVLDELERLRVESLNTVLREATREPAEGVQVATPGEFAAM WNLRDEAGKQAILDRIRSSQDAALACFQKDHDALEAQLEIARHVSSTDLNRLAQYLYEEIGSAKEISLTMAMTG

	KPELVAVLEKALGRIGIRRVQHPDNWKVWYGHEDCAECEDLAEQAISYAKAANSTSEQMVKSAFGGHAGSAVRVZ

Function **(F)** Hypothetical protein	Gene No: 58			Student name: Sandra Meesala Date: 2/21/24	
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 96%	% Identity 87.59%	E-value (if < 10^{-7}) 9X10^-86	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 87%	E-value (if < 10^{-7}) 4x^10^-66	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%)	E-value (if < 1) All <1
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members 87210 Member: 16		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 2038	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 87511
Transmembrane domains by TmHmm using Phamerator				N/A	

Notes :

58	MSLYECKVPNEDKWVECSAQHCARERRINKNMDAVLRLEQYKLKLEAGQQLGEMEQQDLEEIAAHVAAIVESFISALQEAFKPILESITAALHNLWDSLPESMKVELLKEAEPRLEFKLGDVATPYSEAQNRVFGSPYITPRIQGDLSZ

Function **(F)** Hypothetical Protein	Gene No: 59		Student name: Sandra Meesala Date: 2/21/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	% Query 92%	% Identity 100%	E-value (if < 10^{-7}) 4e-59	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein		% Identity 100%	E-value (if < 10^{-7}) 2e-46	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical Protein	Name / Descr (incl DUF) ; DUF6354 ; Family of unknown function (DUF6354)	Hit PF19881	Probability (if > 90%) 97.13%	E-value (if < 1) 0.0029
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (58) of Pham 2038	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 134000	Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 87210	
Transmembrane domains by TmHmm using Phamerator	N/A				

Notes :

Function **(F)** membrane protein	Gene No: 60		Student name: Sandra Meesala Date: 02/21/2024		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Membrane protein	% Query 97%	% Identity 68.75%	E-value (if < 10^{-7}) 2e-27	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 68%	E-value (if < 10^{-7}) 8e-26	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All hits below 90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members Members (26) of Pham 134000	upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 145842		Downstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 2038
Transmembrane domains by TmHmm using Phamerator			One transmebrane domain detected with SOSUI and DeepTMHMM		

Notes :

Function **(F)** Hypothetical protein	Gene No: 61		Student name: Sandra Meesala Date: 2/21/24		
Supporting Information for Function, from BLAST (Protein) **(BLAST-NCBI)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	% Query 99%	% Identity 92.79%	E-value (if < 10^{-7}) 2X10^-69	AA # conserved in first 10 hits? Yes or [✓ No]
Supporting Information for Function, from BLAST (Protein) **(BLAST-phagesDB)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein		% Identity 92%	E-value (if < 10^{-7}) 4x10^-54	AA # conserved in first 10 hits? [✓ Yes] or No
Supporting Information for Function, from HHpred **(HHpred)** (All three lines of SIF evidence must be filled in)	Function (or NKF)	Name / Descr (incl DUF)	Hit	Probability (if > 90%) All <90%	E-value (if < 1)
Supporting Information for Function, from Syntney **(SIF-Syn)** (All three lines of SIF evidence must be filled in)	Function (or NKF) Hypothetical protein	Pham number and number of members 145842 Members: 34		upstream pham conserved ? [✓ Yes] or No If yes, what pham # or function ? 134000	Downstream pham conserved ? Yes or [✓ No] If yes, what pham # or function ?
Transmembrane domains by TmHmm using Phamerator			N/A		