Feature Template Annotation

1st Annotator:

2nd Annotator:

Function:

5’ end:

3’ end:

Length:

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
- ☐ Is it longer than 120 bp (Y/N)
- ☐ Do other related phages agree (Phamerator) (Y/N)
- ☐ Direction: (Fwd/Rev)

Function?

- ☐ Likely function from Phamerator (Answer)
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast:
- ☐ Phages DB:
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer:
- ☐ Glimmer Score:
- ☐ GeneMark:
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:

Feature X Annotation

1st Annotator:
Gisselle Trejo

2nd Annotator:

Function:
Not a Gene

5’ end:

3’ end:

Length:

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).**

No because there wasn’t another EG cluster that matched up with Rowlf.

Are there homologous genes based on a Blast search? (Answer)

- ☐ **Is it longer than 120 bp (Y/N)**
- ☐ **Do other related phages agree (Phamerator) (Y/N)**
- ☐ **Direction: (Fwd/Rev)**

-

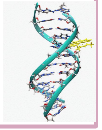
Function?

- ☐ **Likely function from Phamerator (Answer)**
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both)**
- ☐ **Blast:**
- ☐ **Phages DB:**
- ☐ **Likely Function from HHpred? (conserved domains and functional regions)**
- ☐ **NKF**
- ☐ **Membrane binding domain?**
- ☐ **tRNA?**

Start position?

- ☐ **Glimmer: 12**
- ☐ **Glimmer Score: 1.71**
- ☐ **GeneMark:**
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs)**
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)**
- ☐ **Is it the longest ORF? (Y/N)**
- ☐ **Alignment agreement from Blast? (Y/N, Source)**
- ☐ **Does it include all of the functional region (HHpred)?**
- ☐ **SD Score? Is there one higher? (number, Y/N)**
- ☐ **Gap, overlap, and spacing? (description)**

Notes:



Feature 1 Annotation

1st Annotator:
Daniel

2nd Annotator:
Nina

Function:
Hypothetical protein

5’ end:
1040

3’ end:
672

Length:
369

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes, bumpy but potential goes along with sequence

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

- Reverse

Function?

☐ Likely function from Phamerator (Answer)
Hypothetical protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Hypothetical protein

☐ Blast:
Hypothetical protein

☐ Phages DB:
Unknown function

☐ Likely Function from HHpred? (conserved domains and functional regions)
No function

☐ NKF
Yes

☐ Membrane binding domain?
No

☐ tRNA? No

Start position?

☐ Glimmer: 1079

☐ Glimmer Score: 10.51

☐ GeneMark 1019

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
1040 14 MA’s, 1079 1 MA

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, N

☐ Is it the longest ORF? (Y/N) No

☐ Alignment agreement from Blast? (Y/N, Source) Y, 98%

☐ Does it include all of the functional region (HHpred)? No

☐ SD Score? Is there one higher? (number, Y/N) Y, -1.907

☐ Gap, overlap, and spacing? (description)

Notes:

Feature 2 Annotation

1st Annotator:
Trenton Shappee

2nd Annotator:

Function:
hypothetical protein

5’ end:
1225

3’ end:
1037

Length:
189

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Y

☐ Are there homologous genes based on a Blast search? (Answer) Y

☐ Is it longer than 120 bp (Y/N)
Y

☐ Do other related phages agree (Phamerator) (Y/N)
Y

☐ Direction: (Fwd/Rev)
Rev

-

Function?

☐ Likely function from Phamerator (Answer) No

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) No

☐ Blast: Function unknown

☐ Phages DB: merr-like hth dna binding protein

☐ Likely Function from HHpred? (conserved domains and functional regions)

☐ NKF there is no known function

☐ Membrane binding domain?
No

☐ tRNA?
No

Start position?

☐ Glimmer: 1225

☐ Glimmer Score: 5.91

☐ GeneMark1225

☐ Starterator MAs for selected and for alt options (number, number alt MAs)

(Start: 13 @1225 has 6 MA's)

Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)

N,Y

☐ Is it the longest ORF? (Y/N)
N it is the second longest

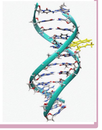
☐ Alignment agreement from Blast? (Y/N, Source) Y

☐ YDoes it include all of the functional region (HHpred)? No

☐ SD Score? Is there one higher? (number, Y/N)-2.845N

☐ Gap, overlap, and spacing? (description)

Notes:



1st Annotator:
Aisley Allen

2nd Annotator:
Phoenix larsen

Function:

Hypothetical protein

Feature 3 Annotation

5’ end:
1704

3’ end:
1225

Length:
480

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
YES
- ☐ Are there homologous genes based on a Blast search? (Answer)
YES
- ☐ Is it longer than 120 bp (Y/N)
YES
- ☐ Do other related phages agree (Phamerator) (Y/N)
YES
- ☐ Direction: (Fwd/Rev)
REV

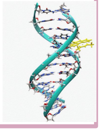
Function?

- ☐ Likely function from Phamerator (Answer) UNKNOWN
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Hypothetical protein
- ☐ Blast:
- ☐ Phages DB: Function Unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Zinc-binding domain of translation initiation factor 2 beta
- ☐ NKF YES
- ☐ Membrane binding domain? NO
- ☐ tRNA? NO

Start position?

- ☐ Glimmer: 1704
- ☐ Glimmer Score: 10.99
- ☐ GeneMark 1704
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 1
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES, YES
- ☐ Is it the longest ORF? (Y/N) NO
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)? 18.239
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description) gap: -4 spacer: 12

Notes:



Feature 4 Annotation

1st Annotator:
Phoenix

2nd Annotator:
Aisley Allen

Function:
PnuC-like Nicotinamide riboside transporter

5’ end:
2408

3’ end:
1701

Length:
708

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)

Yes

- ☐ Is it longer than 120 bp (Y/N)

yes

- ☐ Do other related phages agree (Phamerator) (Y/N)

yes

- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast:
- ☐ Phages DB:
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 2408
- ☐ Glimmer Score: 8.17
- ☐ GeneMark 2408
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  - -4, 12

Notes:

Feature 5 Annotation

1st Annotator: Nina

2nd Annotator: Madalyne

Function: Membrane Protein

5’ end: 2647

3’ end: 2405

Length: 242

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)
Reverse

Function?

☐ Likely function from Phamerator (Answer)
Function unknown

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Function unknown

☐ Blast:
Membrane protein

☐ Phages DB:
Function Unknown

☐ Likely Function from HHpred? (conserved domains and functional regions)
Function Unknown

☐ NKF
Yes

☐ Membrane binding domain?
No

☐ tRNA? No

Start position?

☐ Glimmer: 2647

☐ Glimmer Score: 9.64

☐ GeneMark: 2647

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
11 MAs

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
Yes and Yes

☐ Is it the longest ORF? (Y/N)
No

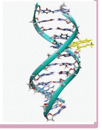
☐ Alignment agreement from Blast? (Y/N, Source)
Yes

☐ Does it include all of the functional region (HHpred)?
Yes

☐ SD Score? Is there one higher? (number, Y/N)

☐ Gap, overlap, and spacing? (description)
Gap= -10, Space= 10

Notes:



Feature 6 Annotation

1st Annotator: Madison Renn

2nd Annotator:

Function: Unknown (Hypothetical Protein)

5’ end: 2832

3’ end: 2644

Length: 189

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).: Yes
- ☐ Are there homologous genes based on a Blast search? (Answer): Yes
- ☐ Is it longer than 120 bp (Y/N): Yes
- ☐ Do other related phages agree (Phamerator) (Y/N): Yes
- ☐ Direction: (Fwd/Rev): Reverse

Function?

- ☐ Likely function from Phamerator (Answer): Unknown Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both): Function Unknown
- ☐ Blast: Hypothetical Protein
- ☐ Phages DB: Function Unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions): Nitroreductase
- ☐ NKF: Yes
- ☐ Membrane binding domain?: No
- ☐ tRNA?: No

Start position?

- ☐ Glimmer: 2832
- ☐ Glimmer Score: 8.48
- ☐ GeneMark: 2832
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs): 4 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes, Yes
- ☐ Is it the longest ORF? (Y/N): No
- ☐ Alignment agreement from Blast? (Y/N, Source): 100%
- ☐ Does it include all of the functional region (HHpred)?: 24.193%
- ☐ SD Score? Is there one higher? (number, Y/N): Shine Delgarno Score
- ☐ Gap, overlap, and spacing? (description): Gap: -4, Spacer: 10, Overlap:

Notes: Start Codon ATG

Feature 7 Annotation

1st Annotator: Madalyne

2nd Annotator:

Function: DprA-like DNA processing chain

5’ end: 3344

3’ end: 2829

Length: 516

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description). yes

☐ Are there homologous genes based on a Blast search? (Answer) Yes

☐ Is it longer than 120 bp (Y/N) Yes

☐ Do other related phages agree (Phamerator) (Y/N) Yes

☐ Direction: (Fwd/Rev)

- Reverse

Function?

☐ Likely function from Phamerator (Answer) DprA-like ssDNA binding protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

☐ Blast: DprA-like DNA processing chain

☐ Phages DB: DprA-like DNA processing chain

☐ Likely Function from HHpred? (conserved domains and functional regions) Hypothetical Protein or DNA processing Protein

☐ NKF ???

☐ Membrane binding domain?

☐ tRNA? No

Start position?

☐ Glimmer: 3344

☐ Glimmer Score: 13.43

☐ GeneMark: 3353

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
Alt start: 3353 both starts have 1 MA

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes it includes all coding potential but genemark and glimmer do not agree

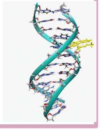
☐ Is it the longest ORF? (Y/N) No

☐ Alignment agreement from Blast? (Y/N, Source) Yes 100%

☐ SD Score? Is there one higher? (number, Y/N)

☐ Gap, overlap, and spacing? (description)
-4 gap, 13 space

Notes:



Feature 8 Annotation

1st Annotator: Alex

2nd Annotator: Madison

Function: Hypothetical Protein

5’ end: 3583

3’ end: 3341

Length: 243

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer) function unknown
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) function unknown
- ☐ Blast: function unknown
- ☐ Phages DB: function unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Helix-turn-helix Domain
- ☐ NKF Yes
- ☐ Membrane binding domain? No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 3583
- ☐ Glimmer Score: 7.22
- ☐ GeneMark: 3583
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 24 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes 100%
- ☐ SD Score? Is there one higher? (number, Y/N) -3.766
- ☐ Gap, overlap, and spacing? (description) -4

Notes:

Feature 9 Annotation

1st Annotator:
Daniel

2nd Annotator:

Function:
helix-turn-helix DNA binding domain

5’ end:
3936

3’ end:
3580

Length:
357

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  helix-turn-helix DNA binding domain
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast:
  helix-turn-helix DNA binding domain
- ☐ Phages DB:
  helix-turn-helix DNA binding domain
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  helix-turn-helix DNA binding domain
- ☐ NKF
  No
- ☐ Membrane binding domain?
  No
- ☐ tRNA? No

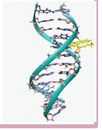
Start position?

- ☐ Glimmer: 3936
- ☐ Glimmer Score: 6.23
- ☐ GeneMark: 3936
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)

36 MA’s

- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y
- ☐ Is it the longest ORF? (Y/N) Y
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N) Y, -3.105
- ☐ Gap, overlap, and spacing? (description)
  -8,

Notes:



Feature 10 Annotation

1st Annotator:
Trenton

2nd Annotator:

Function:
helix-turn-helix DNA binding domain protein

5’ end:
4144

3’ end:
3929

Length:
216

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
YES on DNA master it says that it contains all coding potential

☐ Are there homologous genes based on a Blast search? (Answer)

Yes

☐ Is it longer than 120 bp (Y/N)

Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

Rev

Function?

☐ Likely function from Phamerator (Answer)
  ☐ helix-turn-helix DNA binding domain protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

☐ Blast: helix-turn-helix DNA binding domain protein

☐ Phages DB: helix-turn-helix dna binding domain

☐ Likely Function from HHpred? (conserved domains and functional regions) helix-turn-helix DNA binding domain protein

☐ NKF
No

☐ Membrane binding domain?
no

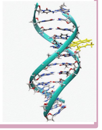
☐ tRNA?
No

Start position?

☐ Glimmer: 4144
☐ Glimmer Score: 7.44
☐ GeneMarkPeccan said 4144 DNA master siad 4087
☐ Starterator MAs for selected and for alt options (number, number alt MAs)
Start: 50 @4144 has 28 MA's
That's the only one

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, N
☐ Is it the longest ORF? (Y/N)Y
☐ Alignment agreement from Blast? (Y/N, Source)Y
☐ Does it include all of the functional region (HHpred)?yes
☐ SD Score? Is there one higher? (number, Y/N) N SD is the best score
☐ Gap, overlap, and spacing? (description)
There is some overlap between gene 10 on the 5’ end.

Notes:



Feature 11 Annotation

1st Annotator:
Aisley Allen

2nd Annotator:

Function:
Ribbon helix-helix DNA binding domain protein

5' end:
4248

3' end:
4361

Length:
113

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). YES,
- ☐ Are there homologous genes based on a Blast search? (Answer) YES
- ☐ Is it longer than 120 bp (Y/N) NO
- ☐ Do other related phages agree (Phamerator) (Y/N) YES
- ☐ Direction: (Fwd/Rev) fwd

Function?

- ☐ Likely function from Phamerator (Answer) ribbon-helix-helix DNA binding domain protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) ribbon-helix-helix DNA binding domain protein
- ☐ Blast: ribbon-helix-helix DNA binding domain protein
- ☐ Phages DB: ribbon-helix-helix DNA binding domain protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions) DNA binding protein
- ☐ NKF
- ☐ Membrane binding domain? NO
- ☐ tRNA? NO

Start position?

- ☐ Glimmer: 4248
- ☐ Glimmer Score: 12.13
- ☐ GeneMark 4248
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 6 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES, NO
- ☐ Is it the longest ORF? (Y/N) NO
- ☐ Alignment agreement from Blast? (Y/N, Source) 100%
- ☐ Does it include all of the functional region (HHpred)? 88.9%
- ☐ SD Score? Is there one higher? (number, Y/N) -2.839
- ☐ Gap, overlap, and spacing? (description) Gap = 103, Space = 10

Notes: Check start position! There are more MAs for 4206

Feature 12 Annotation

1st Annotator:
Phoenix

2nd Annotator:

Function:
helix-turn-helix DNA binding domain

5' end:
4358

3' end:
5116

Length:
651

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
yes
- ☐ Is it longer than 120 bp (Y/N)
yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
yes
- ☐ Direction: (Fwd/Rev)
Forward

-

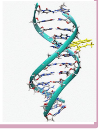
Function?

- ☐ Likely function from Phamerator (Answer) terminase small subunit
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) helix-turn-helix DNA binding domain (both NCBI and phagesDB)
- ☐ Blast: small subunit terminase
- ☐ Phages DB: small subunit terminase
- ☐ Likely Function from HHpred? (conserved domains and functional regions) not informative
- ☐ NKF
- ☐ Membrane binding domain? no
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 4358
- ☐ Glimmer Score: 12.24
- ☐ GeneMark 4358
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 23,0
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? -4 gap

Notes: changed from terminase, small subunit; see pecaan for notes



Feature 13 Annotation

1st Annotator:
Gigi Trejo

2nd Annotator:
Josh B.

Function:
Unknown function

5’ end:
5118

3’ end:
5279

Length:
162

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  No coding potential
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Hypothetical protein
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Forward

Function?

- ☐ Likely function from Phamerator (Answer)
  No known function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  No known function
- ☐ Blast:
  No known function
- ☐ Phages DB:
  No known function
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  No
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  Yes
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer:
- ☐ Glimmer Score:
- ☐ GeneMark: 5118
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  26 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  No, No
- ☐ Is it the longest ORF? (Y/N)
  Yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes, hypothetical protein
- ☐ Does it include all of the functional region (HHpred)?
  No
- ☐ SD Score? Is there one higher? (number, Y/N)
  2.996, No
- ☐ Gap, overlap, and spacing? (description)
  Gap: 1
  No overlap
  Spacing: 11

Notes:

Feature 14 Annotation

1st Annotator:
Daniel

2nd Annotator:
Aisley Allen

Function:
Hypothetical protein

5’ end:
5276

3’ end:
5449

Length:
174

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Forward

Function?

- ☐ Likely function from Phamerator (Answer)
  Hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Hypothetical protein
- ☐ Blast:
  Hypothetical protein
- ☐ Phages DB:
  Unknown function
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  No
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 5276
- ☐ Glimmer Score: 3.13
- ☐ GeneMark: 5276
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  5276 16 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y, Y
- ☐ Is it the longest ORF? (Y/N)
  Yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes, 100%
- ☐ Does it include all of the functional region (HHpred)?
  No
- ☐ SD Score? Is there one higher? (number, Y/N)
  -5.180, Yes, -2.934
- ☐ Gap, overlap, and spacing? (description)
  -4 gap

Notes:

Feature 15 Annotation

1st Annotator: Nina

2nd Annotator: Madison

Function: Ribbon Helix-Helix DNA Binding Domain

5’ end: 5449

3’ end: 5823

Length: 375

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)
Forward

-

Function?

☐ Likely function from Phamerator (Answer)
Ribbon Helix-Helix DNA Binding Domain

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Ribbon Helix DNA Binding Domain

☐ Blast: Ribbon Helix-Helix DNA Binding Domain

☐ Phages DB: Ribbon Helix-Helix DNA Binding Domain

☐ Likely Function from HHpred? (conserved domains and functional regions)

☐ NKF No

☐

☐ Membrane binding domain? Yes

☐ tRNA? No

Start position?

☐ Glimmer: 5449

☐ Glimmer Score: 9.19

☐ GeneMark: 5449

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
29 Ma’s

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
Yes- includes coding potential, Yes- genemark and glimmer agree

☐ Is it the longest ORF? (Y/N)

☐ Alignment agreement from Blast? (Y/N, Source)
Yes

☐ Does it include all of the functional region (HHpred)?

☐ SD Score? Is there one higher? (number, Y/N)
Yes, -3.662

☐ Gap, overlap, and spacing? (description)
Gap = -1, space = 14, overlap of 1 nucleotide

Notes:

Feature 16 Annotation

1st Annotator:
Madison Renn

2nd Annotator:
Nina

Function:
Terminase

5’ end:
5798

3’ end:
7309

Length:
1512

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).: Yes
- ☐ Are there homologous genes based on a Blast search? (Answer): Yes
- ☐ Is it longer than 120 bp (Y/N): Yes
- ☐ Do other related phages agree (Phamerator) (Y/N): Yes
- ☐ Direction: (Fwd/Rev): Forward

Function?

- ☐ Likely function from Phamerator (Answer): Terminase
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both): Terminase
- ☐ Blast: Terminase
- ☐ Phages DB: Terminase
- ☐ Likely Function from HHpred? (conserved domains and functional regions): Large Subunit Terminase
- ☐ NKF: No
- ☐ Membrane binding domain? : No
- ☐ tRNA?: No

Start position?

- ☐ Glimmer: 5798
- ☐ Glimmer Score: 9.76
- ☐ GeneMark: 5798
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs): 36 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes, Yes
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source): Yes
- ☐ Does it include all of the functional region (HHpred)?: 86%
- ☐ SD Score? Is there one higher? (number, Y/N):
- ☐ Gap, overlap, and spacing? (description) : Gap: -26, Spacing: 11

Notes: Start Codon ATG; function changed from terminase, large subunit (see pecaan for notes)

Feature 17 Annotation

1st Annotator:
Madalyne

2nd Annotator:
Nina

Function:
Hypothetical Protein

5’ end:
7306

3’ end:
7644

Length:
339

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev) Forward

-

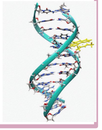
Function?

- ☐ Likely function from Phamerator (Answer) Hypothetical Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: Hypothetical Protein
- ☐ Phages DB:
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Hypothetical Protein
- ☐ NKF yes
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 7306
- ☐ Glimmer Score: 8.62
- ☐ GeneMark 7306
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  27 MA’s and an alt start of 7315 with 44 ma’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes they agree
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)? 76.7857%
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  -4 gap, 10 space

Notes:



Feature 18 Annotation

1st Annotator:
Madalyne

2nd Annotator:
Alex

Function:
Portal Protein

5’ end:
7897

3’ end:
9723

Length:
1827

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

- Forward

Function?

☐ Likely function from Phamerator (Answer)
Portal Protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

☐ Blast: Portal Protein

☐ Phages DB: Portal Protein

☐ Likely Function from HHpred? (conserved domains and functional regions) Portal Protein about 63% coverage

☐ Membrane binding domain? No

☐ tRNA? No

Start position?

☐ Glimmer: 7897
☐ Glimmer Score: 10.96
☐ GeneMark: 7897
☐ Starterator MAs for selected and for alt options (number, number alt MAs)
There are 35 MA’s

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes
☐ Is it the longest ORF? (Y/N) Yes
☐ Alignment agreement from Blast? (Y/N, Source) Yes 100%
☐ SD Score? Is there one higher? (number, Y/N) -2.422 yes there is a higher one
☐ Gap, overlap, and spacing? (description)
There is a gap where 18 stops at 7644 and 19 starts at 7897

Notes:

Feature 19 Annotation

1st Annotator:
Alex

2nd Annotator:
Madalyne

Function:
Major capsid and Protease fusion protein

5' end:
9723

3' end:
12926

Length:
3203

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Forward

-

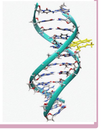
Function?

- ☐ Likely function from Phamerator (Answer)
  Capsid Maturation Protease
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Capsid Maturation Protease
- ☐ Blast: Capsid Maturation Protease
- ☐ Phages DB: Capsid Maturation Protease
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Capsid Protein about 8% coverage
- ☐ NKF
  No
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 9723
- ☐ Glimmer Score: 9.89
- ☐ GeneMark: 9723
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  33 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes 99.25%
- ☐ SD Score? Is there one higher? (number, Y/N) -3.912, yes there is on at -0.818
- ☐ Gap, overlap, and spacing? (description)
- ☐ No gap, 19 ends at 9723 and 20 starts at 9723

Notes: function change from Capsid Maturation Protease; see pecaan for notes



Feature 20 Annotation

1st Annotator:
Phoenix

2nd Annotator:
Trenton

Function:
Hypothetical Protein

5’ end:
12930

3’ end:
13112

Length:
183

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
  - yes
- ☐ Is it longer than 120 bp (Y/N)
  - yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  - yes
- ☐ Direction: (Fwd/Rev)
  - Forward

Function?

- ☐ Likely function from Phamerator (Answer)
  - Hypothetical
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: unknown
- ☐ Phages DB: terminase
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  - Uncharacterized protein; ribosome, protein-protein interaction
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 12930
- ☐ Glimmer Score: 5.79
- ☐ GeneMark 12963
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) no
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  - 3, 13

Notes:

Feature 21 Annotation

1st Annotator:
Gigi Trejo

2nd Annotator:
Josh B.

Function:
major capsid hexamer protein

5' end:
13250

3' end:
15082

Length:
1833

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  - Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  - Yes
- ☐ Is it longer than 120 bp (Y/N)
  - Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  - Yes
- ☐ Direction: (Fwd/Rev)
  - Forward

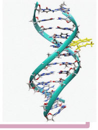
Function?

- ☐ Likely function from Phamerator (Answer)
  - major capsid hexamer protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  - major capsid hexamer protein
- ☐ Blast:
  - major capsid hexamer protein
- ☐ Phages DB:
  - major capsid hexamer protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain? No
- ☐ tRNA? - No

Start position?

- ☐ Glimmer: 132520
- ☐ Glimmer Score: 12.34
- ☐ GeneMark- 13250
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  - 24
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  - Yes, gene and glinmark agree
- ☐ Is it the longest ORF? (Y/N)
  - Yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
  - Yes, 99.8%
- ☐ Does it include all of the functional region (HHpred)?
  - No, 3.2%
- ☐ SD Score? Is there one higher? (number, Y/N)
  - -1.767, not a higher score
- ☐ Gap, overlap, and spacing? (description)
  - Gap: 137
  - Spacer: 11
  - No overlap

Notes:



Feature 22 Annotation

1st Annotator:
Josh

2nd Annotator:

Function:
Hypothetical Protein

5’ end:
15147

3’ end:
15881

Length:
735

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Y
- ☐ Are there homologous genes based on a Blast search? (Answer)
  T
- ☐ Is it longer than 120 bp (Y/N)
  Y
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Y
- ☐ Direction: (Fwd/Rev)
  - FWD

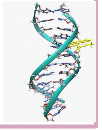
Function?

- ☐ Likely function from Phamerator (Answer)
  Unknown function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Unknown function
- ☐ Blast:
  Unknown function
- ☐ Phages DB:
  Unknown function
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?

Start position?

- ☐ Glimmer: 15147
- ☐ Glimmer Score: 11.82
- ☐ GeneMark: 15147
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  36 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y, Y
- ☐ Is it the longest ORF? (Y/N)
  Y
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Y, hypothetical protein SEA_NIKE_26
- ☐ Does it include all of the functional region (HHpred)?
  N
- ☐ SD Score? Is there one higher? (number, Y/N)
  -3.153, N
- ☐ Gap, overlap, and spacing? (description)
  Gap: 64
  Spacer: 10

Notes:



Feature 23 Annotation

1st Annotator: Sara

2nd Annotator: Josh

Function:

Hypothetical Protein

5’ end: 15891

3’ end: 16391

Length: 501

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Y
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Y
- ☐ Is it longer than 120 bp (Y/N)
  Y
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Y
- ☐ Direction: (Fwd/Rev)
  Fwd

-

Function?

- ☐ Likely function from Phamerator (Answer)
- ☐ Hypothetical
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: Hypothetical
- ☐ Phages DB: Hypothetical
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  None
- ☐ NKF Yes
- ☐ Membrane binding domain? No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 15891
- ☐ Glimmer Score: 17.64
- ☐ GeneMark 15891
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  4 @15891 has 36 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y, Y
- ☐ Is it the longest ORF? (Y/N) Y
- ☐ Alignment agreement from Blast? (Y/N, Source) Y, Hyperion_26
- ☐ Does it include all of the functional region (HHpred)? N
- ☐ SD Score? Is there one higher? (number, Y/N) -1.290 N
- ☐ Gap, overlap, and spacing? (description)
  9

Notes:

Feature 24 Annotation

1st Annotator: Group

2nd Annotator: Madison

Function: Major Tail Protein

5' end: 16422

3' end: 17369

Length: 948

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)
Forward

Function?

☐ Likely function from Phamerator (Answer)
Major Tail Protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

☐ Blast: NCBI

☐ Phages DB: Major Tail Protein

☐ Likely Function from HHpred? (conserved domains and functional regions)

☐ Membrane binding domain?

☐ tRNA? No

Start position?

☐ Glimmer: 16422

☐ Glimmer Score: 13.07

☐ GeneMark: 16446

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
221 MA's

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes- Includes all coding potential. No- genemark and glimmer do not agree

☐ Is it the longest ORF? (Y/N)

☐ Alignment agreement from Blast? (Y/N, Source)

☐ Does it include all of the functional region (HHpred)?

☐ SD Score? Is there one higher? (number, Y/N)

☐ Gap, overlap, and spacing? (description)
There is a gap of 30 and a space of 10

Notes:

Feature 25 Annotation

1st Annotator:
Aisley Allen

2nd Annotator:

Function:

Hypothetical protein

5’ end:
17495

3’ end:
18358

Length:
864

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  YES
- ☐ Are there homologous genes based on a Blast search? (Answer)
  YES
- ☐ Is it longer than 120 bp (Y/N)
  YES
- ☐ Do other related phages agree (Phamerator) (Y/N)
  YES
- ☐ Direction: (Fwd/Rev)
  FORWARD

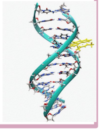
Function?

- ☐ Likely function from Phamerator (Answer) N/A
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Function Unknown
- ☐ Blast:
- ☐ Phages DB: Hypothetical Protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Phage Tail Repeat
- ☐ NKF
- ☐ Membrane binding domain? NO
- ☐ tRNA? NO

Start position?

- ☐ Glimmer: 17495
- ☐ Glimmer Score: 9.56
- ☐ GeneMark 17495
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 25
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES YES
- ☐ Is it the longest ORF? (Y/N) YES
- ☐ Alignment agreement from Blast? (Y/N, Source) YES
- ☐ Does it include all of the functional region (HHpred)? 12.2%
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap: 125 space: 10

Notes:



Feature 26 Annotation

1st Annotator:
Phoenix

2nd Annotator:
Nina

Function:
purple acid phosphatase

5’ end:
18355

3’ end:
20409

Length:
2055

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Possibly
  yes
- ☐ Direction: (Fwd/Rev)
  Forward

-

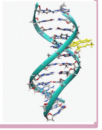
Function?

- ☐ Likely function from Phamerator (Answer) phosphoesterase
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) purple acid phosphotase
- ☐ Blast: purple acid phosphotase
- ☐ Phages DB: pap
- ☐ Likely Function from HHpred? (conserved domains and functional regions) alkaline phosphotase
- ☐ NKF
- ☐ Membrane binding domain? no
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 18355
- ☐ Glimmer Score: 7.1
- ☐ GeneMark: 18355
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) yes and yes
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source) no
- ☐ Does it include all of the functional region (HHpred)? yes
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
- ☐ -4,13

Notes:



Feature 27 Annotation

1st Annotator:
Daniel

2nd Annotator:
Madison

Function:
head-to-tail adaptor

5’ end:
20430

3’ end:
21278

Length:
849

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Forward

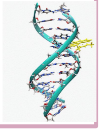
Function?

- ☐ Likely function from Phamerator (Answer)
  Head-to-tail adaptor
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Head-to-tail adaptor
- ☐ Blast:
  Head-to-tail adaptor
- ☐ Phages DB:
  Head-to-tail adaptor
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  Head completion protein
- ☐ NKF
  NO
- ☐ Membrane binding domain?
  No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 20430
- ☐ Glimmer Score: 9
- ☐ GeneMark 20430
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  No MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes, 99%
- ☐ Does it include all of the functional region (HHpred)? Yes
- ☐ SD Score? Is there one higher? (number, Y/N) No, -2.071
- ☐ Gap, overlap, and spacing? (description)

Notes:



Feature 28 Annotation

1st Annotator:
Trenton

2nd Annotator:
Madalyne

Function:
Hypothetical Protein

5’ end:
21278

3’ end:
21808

Length:
531

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Y there is not dip on the Graph

☐ Are there homologous genes based on a Blast search? (Answer)
No

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Y

☐ Direction: (Fwd/Rev)
Fwd

-

Function?

☐ Likely function from Phamerator (Answer)
No

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Hypothetical Protien

☐ Blast: Hypothetical Protien

☐ Phages DB: None

☐ Likely Function from HHpred? (conserved domains and functional regions)
No

☐ NKF
Yes

☐ Membrane binding domain? No

☐ tRNA?
No

Start position?

☐ Glimmer: 21278

☐ Glimmer Score: 8.83

☐ GeneMark21278

☐ Starterator MAs for selected and for alt options (number, number alt MAs)

(Start: 20 @21278 has 36 MA's),

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) N,Y

☐ Is it the longest ORF? (Y/N)
N second longest

☐ Alignment agreement from Blast? (Y/N, Source) Y

☐ Does it include all of the functional region (HHpred)? No

☐ SD Score? Is there one higher? (number, Y/N)-5.541 N

☐ Gap, overlap, and spacing? (description)
No

Notes:

Feature 29 Annotation

1st Annotator: Madalyne

2nd Annotator: Madison

Function:

5’ end: 21810

3’ end: 22223

Length: 414

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
- ☐ Direction: (Fwd/Rev) Forward

-

Function?

- ☐ Likely function from Phamerator (Answer) Hypothetical Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: Hypothetical Protein
- ☐ Phages DB: tail assembly chaperone
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Minor Capsid/ Unknown
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 21810
- ☐ Glimmer Score: 4.81
- ☐ GeneMark: 21810
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  28 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and yes
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  -56 gap, 9 space

Notes:

Feature 30 Annotation

1st Annotator:
Gigi Trejo

2nd Annotator:

Function:
tail assembly chaperone

5' end:
22,265

3' end:
22,723

Length:
459

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

- Forward

Function?

☐ Likely function from Phamerator (Answer)
tail assembly chaperone

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
tail assembly chaperone

☐ Blast:
tail assembly chaperone

☐ Phages DB:
tail assembly chaperone

☐ Likely Function from HHpred? (conserved domains and functional regions)

☐ NKF: There is no known function

☐ Membrane binding domain?
No

☐ tRNA?
No

Start position?

☐ Glimmer: 22,265
☐ Glimmer Score: 12.02
☐ GeneMark: 22,274
☐ Starterator MAs for selected and for alt options (number, number alt MAs)
25 Ma's

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
No, No

☐ Is it the longest ORF? (Y/N)
No

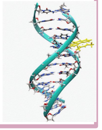
☐ Alignment agreement from Blast? (Y/N, Source)
Yes

☐ Does it include all of the functional region (HHpred)?
Yes

☐ SD Score? Is there one higher? (number, Y/N)
No, 5.3

☐ Gap, overlap, and spacing? (description)
Gap: 41
Overlap:
Spacing: 10

Notes:



Feature 31 Annotation

1st Annotator:
Trenton Shappee

2nd Annotator:

Function:
Tail Chaperone Protein

5' end:
22265

3' end:
22917

Length:
654

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

- Fwd

Function?

☐ Likely function from Phamerator (Answer)
Tail assembly Chaperone

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Tail assembly Chaperone

☐ Blast: Tail assembly Chaperone

☐

☐

☐ Phages DB: Tail assembly Chaperone

☐

☐

☐ Likely Function from HHpred? (conserved domains and functional regions)
Tail assembly Chaperone

☐ NKF no

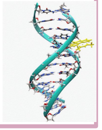
☐ Membrane binding domain?
No

☐ tRNA? no

Start position?

☐ Glimmer: None
☐ Glimmer Score: None
☐ GeneMark None
☐ Starterator MAs for selected and for alt options (number, number alt MAs)
There is none
☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)NN
☐ Is it the longest ORF? (Y/N)
Yes
☐ Alignment agreement from Blast? (Y/N, Source)
There is none
☐ Does it include all of the functional region (HHpred)?Yes
☐ SD Score? Is there one higher? (number, Y/N) -2.224 N
☐ Gap, overlap, and spacing? (description)
It overlaps with 31

Notes: There was a programmed translational frameshift



Feature 32 Annotation

1st Annotator:
Trenton

2nd Annotator:

Function:
Tape measure Protein

5’ end:
22926

3’ end:
26219

Length:
3294

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Fwd

-

Function?

- ☐ Likely function from Phamerator (Answer)
  Tape measure Protien
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Yes
- ☐ Blast: Tape measure protien
- ☐ Phages DB: Tape measure protien
- ☐
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  - ☐ Tape measure protien
- ☐ NKF
  No
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

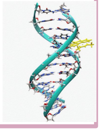
Start position?

- ☐ Glimmer: 22926
- ☐ Glimmer Score: 9.17
- ☐ GeneMark22926
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)

(Start: 2 @22926 has 28 MA's),

- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YY
- ☐ Is it the longest ORF? (Y/N)Y
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Y
- ☐ Does it include all of the functional region (HHpred)?
  Coverage is 79%
- ☐ SD Score? Is there one higher? (number, Y/N) SD is the best N
- ☐ Gap, overlap, and spacing? (description)
  There
  There is a small gap on both ends

Notes:



Feature 33 Annotation

1st Annotator: Nina

2nd Annotator:

Function: Minor Tail Protein

5’ end: 26252

3’ end: 27568

Length: 1316

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Forward

Function?

- ☐ Likely function from Phamerator (Answer)
  Major tail protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Major tail protein
- ☐ Blast:
  Major tail protein
- ☐ Phages DB:
  Major tail protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  Major tail protein
- ☐ NKF
  No
- ☐ Membrane binding domain? No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 26252
- ☐ Glimmer Score: 5.51
- ☐ GeneMark: 26228
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  26 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y, N= genemark and glimmer do not agree
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
  Yes
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap= 32, Space= 13

Notes:

Feature 34 Annotation

1st Annotator:
Madison Renn

2nd Annotator:
Trenton

Function:
Minor Tail Protein

5’ end:
27588

3’ end:
30509

Length:
2922

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).: Yes
- ☐ Are there homologous genes based on a Blast search? (Answer): Yes
- ☐ Is it longer than 120 bp (Y/N): Yes
- ☐ Do other related phages agree (Phamerator) (Y/N): Yes
- ☐ Direction: (Fwd/Rev): Forward

Function?

- ☐ Likely function from Phamerator (Answer): Minor Tail Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both): Minor Tail Protein
- ☐ Blast: Minor Tail Protein
- ☐ Phages DB: Minor Tail Protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions): Titin Myosin/Muscle Filament
- ☐ NKF: No
- ☐ Membrane binding domain?: No
- ☐ tRNA?: No

Start position?

- ☐ Glimmer: 27588
- ☐ Glimmer Score: 7.28
- ☐ GeneMark: 27588
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs): 33 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes, Yes
- ☐ Is it the longest ORF? (Y/N): No
- ☐ Alignment agreement from Blast? (Y/N, Source): Yes
- ☐ Does it include all of the functional region (HHpred)?: No – HHpred says Titin
- ☐ SD Score? Is there one higher? (number, Y/N): DNA Master
- ☐ Gap, overlap, and spacing? (description): Gap: 19, Overlap: DNA Master, Spacing: 12,

Notes: Start Codon ATG

Feature 35 Annotation

1st Annotator: Alex

2nd Annotator: Phoenix

Function: Minor tail protein

5’ end: 30509

3’ end: 31660

Length: 1151

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Forward

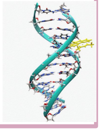
Function?

- ☐ Likely function from Phamerator (Answer) Minor tail protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Minor tail protein
- ☐ Blast: Minor tail protein
- ☐ Phages DB: Minor tail protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Tail protein
- ☐ NKF
  No
- ☐ Membrane binding domain?
  No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 30509
- ☐ Glimmer Score: 8.57
- ☐ GeneMark 30509
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  81 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes 100%
- ☐ SD Score? Is there one higher? (number, Y/N) -3.394, yes -3.262
- ☐ Gap, overlap, and spacing? (description)
  -1

Notes:



Feature 36 Annotation

1st Annotator:
Aisley Allen

2nd Annotator:

Function:

Hypothetical protein

5’ end:
31660

3’ end:
32421

Length:
762

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
YES
- ☐ Are there homologous genes based on a Blast search? (Answer)
- ☐ Is it longer than 120 bp (Y/N)
YES
- ☐ Do other related phages agree (Phamerator) (Y/N)
YES
- ☐ Direction: (Fwd/Rev)
FORWARD

Function?

- ☐ Likely function from Phamerator (Answer) N/A
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) hypothetical protein
- ☐ Blast:
- ☐ Phages DB: function unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Leucine zipper Dimerization domain of transcription factor
- ☐ NKF
- ☐ Membrane binding domain? NO
- ☐ tRNA? NO

Start position?

- ☐ Glimmer: 31660
- ☐ Glimmer Score: 6.35
- ☐ GeneMark 31660
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 33
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES YES
- ☐ Is it the longest ORF? (Y/N) YES
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)? 5.93%
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
Gap: -1 space: 12

Notes:

Feature 37 Annotation

1st Annotator:
Phoenix

2nd Annotator:
Nina

Function:
Hypothetical Protein

5’ end:
32370

3’ end:
32693

Length:
324

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).

yes

- ☐ Are there homologous genes based on a Blast search? (Answer)

yes

- ☐ Is it longer than 120 bp (Y/N)

yes

- ☐ Do other related phages agree (Phamerator) (Y/N)
- ☐ Direction: (Fwd/Rev)
  - Forward

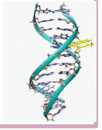
Function?

- ☐ Likely function from Phamerator (Answer)
  - Hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  - Hypothetical protein
- ☐ Blast: unknown
- ☐ Phages DB: unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  - Hypothetical protein
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 32433
- ☐ Glimmer Score: 11.05
- ☐ GeneMark: 32433
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source)yes
- ☐ Does it include all of the functional region (HHpred)?yes
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  -52, 10

Notes:



Feature 38 Annotation

1st Annotator:
Daniel

2nd Annotator:
Aisley Allen

Function:
Hypothetical protein

5’ end:
32698

3’ end:
33081

Length:
384

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
No

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
No

☐ Direction: (Fwd/Rev)

- Forward

Function?

☐ Likely function from Phamerator (Answer)
Unknown function

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
No

☐ Blast:
Hypothetical protein

☐ Phages DB:
Hypothetical protein

☐ Likely Function from HHpred? (conserved domains and functional regions)
No

☐ NKF
Yes

☐ Membrane binding domain?
No

☐ tRNA? No

Start position?

☐ Glimmer: No call

☐ Glimmer Score: No score

☐ GeneMark 32698

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
32968 5 MA’s

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, N

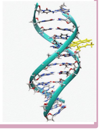
☐ Is it the longest ORF? (Y/N) Yes

☐ Alignment agreement from Blast? (Y/N, Source)
N

☐ SD Score? Is there one higher? (number, Y/N) Y, -3.342

☐ Gap, overlap, and spacing? (description)

Notes:



Feature 39 Annotation

1st Annotator:
Trenton

2nd Annotator:

Function:
Hypothetical Protien

5’ end:
33081

3’ end:
33272

Length:
192

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Kinda Theres just not alot of activity

☐ Are there homologous genes based on a Blast search? (Answer) No

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Y

☐ Direction: (Fwd/Rev)
Fwd

-

Function?

☐ Likely function from Phamerator (Answer)
No

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
No

☐ Blast: Hypothetical protein

☐ Phages DB: Hypothetical protein

☐ Likely Function from HHpred? (conserved domains and functional regions)

☐ NKF Yes

☐ Membrane binding domain?
No

☐ tRNA?
No

Start position?

☐ Glimmer: 33081

☐ Glimmer Score: 8.73

☐ GeneMark33081

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
(Start: 5 @33081 has 4 MA's),

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY

☐ Is it the longest ORF? (Y/N)
Y

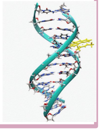
☐ Alignment agreement from Blast? (Y/N, Source)Yes

☐ Does it include all of the functional region (HHpred)? No

☐ SD Score? Is there one higher? (number, Y/N)-2.828Y

☐ Gap, overlap, and spacing? (description)
No

Notes:



Feature 40 Annotation

1st Annotator:
Nina

2nd Annotator:
Phoenix

Function:
Membrane Protein

5’ end:
33275

3’ end:
33964

Length:
689

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
  yes
- ☐ Is it longer than 120 bp (Y/N)
  yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  yes
- ☐ Direction: (Fwd/Rev)
  forward

Function?

- ☐ Likely function from Phamerator (Answer)
  Function Unkown
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Membrane Protein
- ☐ Blast:
  Membrane Protein
- ☐ Phages DB:
  Function Unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  Membrane Protein
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 33275
- ☐ Glimmer Score: 10.75
- ☐ GeneMark: 33275
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  N/A
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y,N= genermark and glimmer do not agree
- ☐ Is it the longest ORF? (Y/N)
  No
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap= 2, Space= 14

Notes:

Feature 41 Annotation

1st Annotator:
Aisley Allen

2nd Annotator:

Function:
endolysin

5’ end:
34067

3’ end:
34855

Length:
789

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
YES
- ☐ Are there homologous genes based on a Blast search? (Answer)
YES
- ☐ Is it longer than 120 bp (Y/N)
YES
- ☐ Do other related phages agree (Phamerator) (Y/N)
NO, there is a dip (?)
- ☐ Direction: (Fwd/Rev)
Forward

Function?

- ☐ Likely function from Phamerator (Answer) endolysin
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
endolysin
- ☐ Blast:
- ☐ Phages DB: endolysin
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Protein Structure Initiative
- ☐ NKF
- ☐ Membrane binding domain? NO
- ☐ tRNA? NO

Start position?

- ☐ Glimmer: 34067
- ☐ Glimmer Score: 10.47
- ☐ GeneMark34034
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 32
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) NO
- ☐ Is it the longest ORF? (Y/N) NO
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)? 29.771%
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
- ☐ Gap: 102 spacer: 7

Notes:

Feature 42 Annotation

1st Annotator:
Daniel

2nd Annotator:

Function:
Hypothetical protein

5' end:
35437

3' end:
34952

Length:
513 bp

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).

Y, but moderate

- ☐ Are there homologous genes based on a Blast search? (Answer)

Y

- ☐ Is it longer than 120 bp (Y/N)

Y

- ☐ Do other related phages agree (Phamerator) (Y/N)

Y

- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)

Unknown function

- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

Unknown function/Hypothetical protein

- ☐ Blast:

Hypothetical protein

- ☐ Phages DB:

Unknown function

- ☐ Likely Function from HHpred? (conserved domains and functional regions)

Unknown function

- ☐ NKF

Yes

- ☐ Membrane binding domain?

No

- ☐ tRNA? No

Start position?

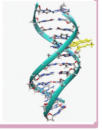
- ☐ Glimmer: 35287
- ☐ Glimmer Score: 7.59
- ☐ GeneMark: 35332
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)

33 MA's

- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y (moderate), No
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N) Y, -1.907
- ☐ Gap, overlap, and spacing? (description)

-32,

Notes:



Feature 43 Annotation

1st Annotator: Madalyne

2nd Annotator: Aisley Allen

Function: Hypothetical Protein

5’ end: 35708

3’ end: 35406

Length: 303

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev) Reverse

-

Function?

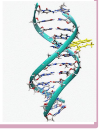
- ☐ Likely function from Phamerator (Answer) Hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: Hypothetical Protein
- ☐ Phages DB: binding protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Hypothetical Protein
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer: 35708
- ☐ Glimmer Score: 5
- ☐ GeneMark: 35708
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) No alt start 27 MA’s

- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) yes and yes
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:



Feature 44 Annotation

1st Annotator:
Madison Renn

2nd Annotator:
Daniel

Function:
DNAJ Like Chaperonin

5’ end:
36367

3’ end:
35705

Length:
663

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).:** Yes
- ☐ **Are there homologous genes based on a Blast search? (Answer):** Yes
- ☐ **Is it longer than 120 bp (Y/N):** Yes
- ☐ **Do other related phages agree (Phamerator) (Y/N):** Yes, SallyK
- ☐ **Direction: (Fwd/Rev):** Reverse

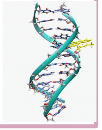
Function?

- ☐ **Likely function from Phamerator (Answer):** DNAJ Like Chaperonin
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both):** No NCBI data available - check on this
- ☐ **Blast:** DNAJ Like Chaperonin
- ☐ **Phages DB:** DNAJ Like Chaperonin
- ☐ **Likely Function from HHpred? (conserved domains and functional regions):** DNAJ Homolog Subfamily
- ☐ **NKF:** No
- ☐ **Membrane binding domain?:** Unknown
- ☐ **tRNA?:** No

Start position?

- ☐ **Glimmer:** 36262
- ☐ **Glimmer Score:** 8.02
- ☐ **GeneMark:** 36367
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs):** 9 for 36367
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N):** Genemark and Glimmer do not agree
- ☐ **Is it the longest ORF? (Y/N):** No
- ☐ **Alignment agreement from Blast? (Y/N, Source):** 82%
- ☐ **Does it include all of the functional region (HHpred)?:** 25% coverage
- ☐ **SD Score? Is there one higher? (number, Y/N):** Unknown
- ☐ **Gap, overlap, and spacing? (description):** Gap: -8, Overlap: No overlap, Spacing: 12

Notes: ***GTG START CODON***



Feature 45 Annotation

1st Annotator:
Phoenix

2nd Annotator:

Function:
hypothetical protein

5’ end:
36548

3’ end:
36360

Length:
306

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  - yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
- ☐ Is it longer than 120 bp (Y/N)
  yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  - Hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  - Hypoethetical
- ☐ Blast: function unknown
- ☐ Phages DB: no data
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  - rotein required for localization of TasA to extracellular matrix
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 36548
- ☐ Glimmer Score: 10.15
- ☐ GeneMark 36548
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source)yes
- ☐ Does it include all of the functional region (HHpred)?yes
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  - -125, 17

Notes:

Feature 46 Annotation

1st Annotator:
Gigi Trejo

2nd Annotator:
Daniel

Function:
Unknown function

5' end:
36750

3' end:
36,541

Length:
210

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  No
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  No
- ☐ Direction: (Fwd/Rev)
  - Reverse

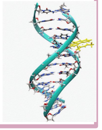
Function?

- ☐ Likely function from Phamerator (Answer)
  unknown function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  unknown function
- ☐ Blast:
  unknown function
- ☐ Phages DB:
  unknown function
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 36750
- ☐ Glimmer Score: 6.52
- ☐ GeneMark: 36,750
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  4 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes, Yes
- ☐ Is it the longest ORF? (Y/N)
  Yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
  No
- ☐ SD Score? Is there one higher? (number, Y/N)
  -4.421, Yes, -1.740
- ☐ Gap, overlap, and spacing? (description)
  Gap: -55
  Overlap:
  Spacing: 7

Notes:



Feature 47 Annotation

1st Annotator: Alex

2nd Annotator:

Function: Cas4 exonuclease

5’ end: 38966

3’ end: 36771

Length: 2196

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev) Reverse

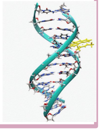
Function?

- ☐ Likely function from Phamerator (Answer) Cas4 exonuclease
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Cas4 exonuclease
- ☐ Blast: Cas4 exonuclease
- ☐ Phages DB: Cas4 exonuclease
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Cas4 exonuclease
- ☐ NKF no
- ☐ Membrane binding domain? no
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 38966
- ☐ Glimmer Score: 9.98
- ☐ GeneMark: 38966
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 25 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes 98.2%
- ☐ SD Score? Is there one higher? (number, Y/N) -3.709 and yes -1.907
- ☐ Gap, overlap, and spacing? (description) -1 gap

Notes:



Feature 48 Annotation

1st Annotator:
Daniel

2nd Annotator:
Aisley Allen

Function:
Hypothetical protein

5' end:
39958

3' end:
38966

Length:
993

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

- Reverse

Function?

☐ Likely function from Phamerator (Answer)
DNA recombinase

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

☐ Blast:
DNA recombinase

☐ Phages DB:
DNA recombinase

☐ Likely Function from HHpred? (conserved domains and functional regions)
Hypothetical protein

☐ NKF
No

☐ Membrane binding domain?
No

☐ tRNA? No

Start position?

☐ Glimmer: 39958

☐ Glimmer Score: 7.95

☐ GeneMark: 39958

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
25 MA's

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y

☐ Is it the longest ORF? (Y/N) No

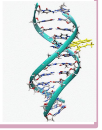
☐ Alignment agreement from Blast? (Y/N, Source) Yes

☐ Does it include all of the functional region (HHpred)? Yes

☐ SD Score? Is there one higher? (number, Y/N) Yes, -1.907

☐ Gap, overlap, and spacing? (description)

Notes:



Feature 49 Annotation

1st Annotator: Nina

2nd Annotator:

Function: HNH Endonuclease

5' end: 40488

3' end: 39955

Length: 533

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Reverse

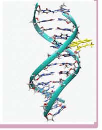
Function?

- ☐ Likely function from Phamerator (Answer)
  HNH Endonuclease
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  HNH Endonuclease
- ☐ Blast:
  HNH Endonuclease
- ☐ Phages DB:
  HNH Endonuclease
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  HNH Endonuclease
- ☐ NKF
  No
- ☐ Membrane binding domain?
  No
- ☐ tRNA?

Start position?

- ☐ Glimmer: 40488
- ☐ Glimmer Score: 9.37
- ☐ GeneMark: 40488
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)Yes
  36 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y, Y- genemark and glimmer agree
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap= -4, Space= 9

Notes:



Feature 50 Annotation

1st Annotator:
Trenton Shappee

2nd Annotator:
Madalyne

Function:
ruvc-like resolvase

5' end:
41057

3' end:
40485

Length:
573

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
Y there is potential for coding
- ☐ Are there homologous genes based on a Blast search? (Answer)
There are
- ☐ Is it longer than 120 bp (Y/N)
Y
- ☐ Do other related phages agree (Phamerator) (Y/N)
Y
- ☐ Direction: (Fwd/Rev)
  - Reverse

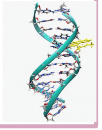
Function?

- ☐ Likely function from Phamerator (Answer)
  ruvc-like resolvase
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: ruvc-like resolvase
- ☐ Phages DB: ruvc-like resolvase
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF there is a known function
- ☐ Membrane binding domain?
  No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 41057
- ☐ Glimmer Score: 15.27
- ☐ GeneMark41057
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
, (Start: 190 @41057 has 30 MA's),
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY
- ☐ Is it the longest ORF? (Y/N)
  N i believe it is the second longest reading frame
- ☐ Alignment agreement from Blast? (Y/N, Source) There is an alignment agreement from blast
- ☐ Does it include all of the functional region (HHpred)? Y
- ☐ SD Score? Is there one higher? (number, Y/N)-3.976 N
- ☐ Gap, overlap, and spacing? (description)
- ☐ No gap

Notes:



Feature 51 Annotation

1st Annotator: Madison Renn

2nd Annotator: **Phoenix**

Function: Hypothetical Protein

5’ end: 41239

3’ end: 41054

Length: 186

Is it a gene?

☐ **Is there coding potential based on Genemarks? (Y/N and description).**
- Yes

☐ **Are there homologous genes based on a Blast search? (Answer)**
- Yes

☐ **Is it longer than 120 bp (Y/N)**
- Yes

☐ **Do other related phages agree (Phamerator) (Y/N)**
- Yes

☐ **Direction: (Fwd/Rev)**
- Reverse

Function?

☐ **Likely function from Phamerator (Answer)**
- Function Unknown

☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both):** Function Unknown

☐ **Blast:** Hypothetical Protein

☐ **Phages DB:** No Data Available

☐ **Likely Function from HHpred? (conserved domains and functional regions):** Several hits for different functions - look into this

☐ **NKF:** Yes

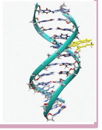
☐ **Membrane binding domain?:** Unknown

☐ **tRNA?:** No

Start position?

☐ **Glimmer:** 41239
☐ **Glimmer Score:** 41054
☐ **GeneMark:** 41239
☐ **Starterator MAs for selected and for alt options (number, number alt MAs):** 6 MA’s
☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N):** Yes
☐ **Is it the longest ORF? (Y/N):** No
☐ **Alignment agreement from Blast? (Y/N, Source):** Yes
☐ **Does it include all of the functional region (HHpred)?:** No
☐ **SD Score? Is there one higher? (number, Y/N):** DNA Master
☐ **Gap, overlap, and spacing? (description):** Gap: -4, Overlap: None, Spacing: 9

Notes: ATG Start Codon



Feature 52 Annotation

1st Annotator: Trenton

2nd Annotator: **Phoenix**

Function: Hypothetical Protein

5' end: 41508

3' end: 41236

Length: 273

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).

  Y
- ☐ Are there homologous genes based on a Blast search? (Answer)

  No
- ☐ Is it longer than 120 bp (Y/N)

  yes
- ☐ Do other related phages agree (Phamerator) (Y/N)

  Y
- ☐ Direction: (Fwd/Rev)

  - Rev

Function?

- ☐ Likely function from Phamerator (Answer)

  None
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

  No
- ☐ Blast: hypothetical protein
- ☐ Phages DB: Function unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF

  Yes
- ☐ Membrane binding domain?
- ☐ tRNA?

  No

Start position?

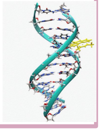
- ☐ Glimmer: 41508
- ☐ Glimmer Score: 11.91
- ☐ GeneMark 41508
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)

  (Start: 39 @41511 has 18 MA's), (Start: 40 @41508 has 13 MA's)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY
- ☐ Is it the longest ORF? (Y/N)N it is the second longest
- ☐ Alignment agreement from Blast? (Y/N, Source)

  Y
- ☐ Does it include all of the functional region (HHpred)? No
- ☐ SD Score? Is there one higher? (number, Y/N)Y yes but the starterator dosnt agree
- ☐ Gap, overlap, and spacing? (description)

  Little overlap on both ends

Notes:



Feature 53 Annotation

1st Annotator: Madalyne

2nd Annotator:

Function: MazG-like nucleotide pyrophosphohydrolase

5’ end: 41900

3’ end: 41508

Length: 393

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
- ☐ Direction: (Fwd/Rev) Reverse

-

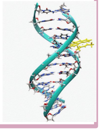
Function?

- ☐ Likely function from Phamerator (Answer) MazG-like nucleotide pyrophosphohydrolase
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: MazG-like nucleotide pyrophosphohydrolase
- ☐ Phages DB: MazG-like nucleotide pyrophosphohydrolase
- ☐ Likely Function from HHpred? (conserved domains and functional regions) N/A
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer: 41903
- ☐ Glimmer Score: 12.84
- ☐ GeneMark: 41900
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 41903 has 7 MA’s 41900 has 15 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) No and No
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:



Feature 54 Annotation

1st Annotator: Gisselle Trejo

2nd Annotator: **Phoenix**

Function: Single-stranded DNA-binding protein

5’ end: 42,772

3’ end: 42,059

Length: 714

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)

  Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  ssdna binding protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  ssdna binding protein
- ☐ Blast:
  ssdna binding protein
- ☐ Phages DB:
  ssdna binding protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 42,772
- ☐ Glimmer Score: 7.73
- ☐ GeneMark: 42,772
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  22 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap: -1
  Spacer: 9
  Overlap:

Notes:

Feature 55 Annotation

1st Annotator: Alex

2nd Annotator: Aisley Allen

Function: Hypothetical protein

5’ end: 42906

3’ end: 42772

Length: 135

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

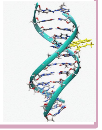
Function?

- ☐ Likely function from Phamerator (Answer) unknown function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) unknown function
- ☐ Blast: hypothetical protein
- ☐ Phages DB: hypothetical protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Nonstructural protein
- ☐ NKF No
- ☐ Membrane binding domain? No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 42906
- ☐ Glimmer Score: 20.96
- ☐ GeneMark: 42906
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 11 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes 100%
- ☐
- ☐ SD Score? Is there one higher? (number, Y/N) -1.748, no
- ☐ Gap, overlap, and spacing? (description) 1

Notes:



Feature 56 Annotation

1st Annotator:
Aisley Allen

2nd Annotator:

Function:
Hypothetical Protein
Function unknown

5’ end:
43093

3’ end:
42908

Length:
186

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). YES
- ☐ Are there homologous genes based on a Blast search? (Answer) YES
- ☐ Is it longer than 120 bp (Y/N) YES
- ☐ Do other related phages agree (Phamerator) (Y/N) YES
- ☐ Direction: (Fwd/Rev) rev

Function?

- ☐ Likely function from Phamerator (Answer) NONE
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) NCBI: uncharacterized protein
- ☐ Blast: hypothetical protein
- ☐ Phages DB: function unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions) uncharacterized protein, 89.19
- ☐ NKF Yes
- ☐ Membrane binding domain? NO
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 43093
- ☐ Glimmer Score: 9.28
- ☐ GeneMark 43093
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 1 MA
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES, YES
- ☐ Is it the longest ORF? (Y/N) NO
- ☐ Alignment agreement from Blast? (Y/N, Source) YES, 93.85%
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description) Gap: 8, Spacer: 8

Notes:

Feature 57 Annotation

1st Annotator:
Madalyne

2nd Annotator:
Madison

Function:
Hypothetical Protein

5’ end:
43338

3’ end:
43102

Length:
237

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description). yes

☐ Are there homologous genes based on a Blast search? (Answer) yes

☐ Is it longer than 120 bp (Y/N) Yes

☐ Do other related phages agree (Phamerator) (Y/N) Yes

☐ Direction: (Fwd/Rev) Reverse

-

Function?

☐ Likely function from Phamerator (Answer) Hypothetical Protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

☐ Blast: Hypothetical Protein

☐ Phages DB: Hypothetical Protein

☐ Likely Function from HHpred? (conserved domains and functional regions)

☐ NKF

☐ Membrane binding domain?

☐ tRNA?

Start position?

☐ Glimmer: 43338
☐ Glimmer Score: 12.42
☐ GeneMark 43338
☐ Starterator MAs for selected and for alt options (number, number alt MAs) 43338 has 24 MAs

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) yes and yes
☐ Is it the longest ORF? (Y/N) No
☐ Alignment agreement from Blast? (Y/N, Source) Yes
☐ Does it include all of the functional region (HHpred)?
☐ SD Score? Is there one higher? (number, Y/N)
☐ Gap, overlap, and spacing? (description)

Notes:

Feature 58 Annotation

1st Annotator:
Aisley Allen

2nd Annotator:
Nina

Function:
Unknown function

5' end:
43416

3' end:
43547

Length:
132

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
YES

☐ Are there homologous genes based on a Blast search? (Answer) YES

☐ Is it longer than 120 bp (Y/N)
YES

☐ Do other related phages agree (Phamerator) (Y/N)
NO

☐ Direction: (Fwd/Rev)
Forward

Function?

☐ Likely function from Phamerator (Answer)
None

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Function unknown

☐ Blast:
Function unknown

☐ Phages DB: function unknown

☐ Likely Function from HHpred? (conserved domains and functional regions)Protein of unknown function

☐ NKF
none

☐ Membrane binding domain? NO

☐ tRNA? NO

Start position?

☐ Glimmer: 43416

☐ Glimmer Score: 3.57

☐ GeneMark N/A

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
N/A

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) no genemark available.

☐ Is it the longest ORF? (Y/N) NO

☐ Alignment agreement from Blast? (Y/N, Source) YES

☐ Does it include all of the functional region (HHpred)? 41.86%

☐ SD Score? Is there one higher? (number, Y/N)

☐ Gap, overlap, and spacing? (description)
gap: 77 space: 18

Notes:

Feature 59 Annotation

1st Annotator:
Phoenix

2nd Annotator:

Function:
Hypothetical protein

5’ end:
43520

3’ end:
43410

Length:
111

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
- ☐ Is it longer than 120 bp (Y/N)
  - no
- ☐ Do other related phages agree (Phamerator) (Y/N)
  - yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

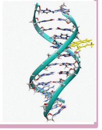
Function?

- ☐ Likely function from Phamerator (Answer)
  - Hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  - Hypothetical protein
- ☐ Blast: function unknown
- ☐ Phages DB: no data
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  - unknown function
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer:
- ☐ Glimmer Score:
- ☐ GeneMark 43520
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  - -4, 18

Notes:



Feature 60 Annotation

1st Annotator:
Gigi Trejo

2nd Annotator:
Daniel

Function:
Hypothetical protein

5’ end:
43,771

3’ end:
43,517

Length:
417

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  No
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

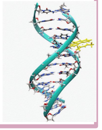
Function?

- ☐ Likely function from Phamerator (Answer)
  unknown function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  unknown function
- ☐ Blast:
  unknown function
- ☐ Phages DB:
  unknown function
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  unknown function
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 43771
- ☐ Glimmer Score: 6.65
- ☐ GeneMark: 43771
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  13 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes, Yes
- ☐ Is it the longest ORF? (Y/N)
  No
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
  No
- ☐ SD Score? Is there one higher? (number, Y/N)
  -5.421, Yes, -4.141
- ☐ Gap, overlap, and spacing? (description)
  Gap: -166
  Overlap:
  Spacing: 14

Notes:



Feature 62 Annotation

1st Annotator:
Alex

2nd Annotator:

Function:
Hypothetical protein

5’ end:
44046

3’ end:
43768

Length:
279

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).** Yes
- ☐ **Are there homologous genes based on a Blast search? (Answer)** Yes
- ☐ **Is it longer than 120 bp (Y/N)** Yes
- ☐ **Do other related phages agree (Phamerator) (Y/N)** Yes
- ☐ **Direction: (Fwd/Rev)**
  - Reverse

Function?

- ☐ **Likely function from Phamerator (Answer)** Unknown function
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both)** hypothetical protein
- ☐ **Blast:** hypothetical protein
- ☐ **Phages DB:** hypothetical protein
- ☐ **Likely Function from HHpred? (conserved domains and functional regions)** Transcription regulator
- ☐ **NKF** Yes
- ☐ **Membrane binding domain?** No
- ☐ **tRNA?** No

Start position?

- ☐ **Glimmer:** 44046
- ☐ **Glimmer Score:** 9.31
- ☐ **GeneMark:** 44046
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs)** 2 MA’s
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)** Yes and Yes
- ☐ **Is it the longest ORF? (Y/N)** No
- ☐ **Alignment agreement from Blast? (Y/N, Source)** Yes 100%
- ☐ **SD Score? Is there one higher? (number, Y/N)** -3.072 and no
- ☐ **Gap, overlap, and spacing? (description)** Gap of -4 and spacing of 16, no overlap

Notes:

Feature 62 Annotation

1st Annotator:
Nina

2nd Annotator:

Function:
Hypothetical Protein

5' end:
44135

3' end:
44043

Length:
92

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
No

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)
Reverse

Function?

☐ Likely function from Phamerator (Answer)
Function Unknown

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Function Unknown

☐ Blast:
Function Unknown

☐ Phages DB:
Function Unknown

☐ Likely Function from HHpred? (conserved domains and functional regions)

☐ NKF
Yes

☐ Membrane binding domain?
No

☐ tRNA? No

Start position?

☐ Glimmer: N/A

☐ Glimmer Score: N/A

☐ GeneMark: 44135

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
10 MA's

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
Y,Y

☐ Is it the longest ORF? (Y/N)
No

☐ Alignment agreement from Blast? (Y/N, Source)
Yes

☐ Does it include all of the functional region (HHpred)?
Yes

☐ SD Score? Is there one higher? (number, Y/N)

☐ Gap, overlap, and spacing? (description)
Gap = -1, space = 13

Notes:

Feature 63 Annotation

1st Annotator: Madison Renn

2nd Annotator: Gigi

Function: Hypothetical Protein

5’ end: 44419

3’ end: 44135

Length: 285

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).**
  - Yes
- ☐ **Are there homologous genes based on a Blast search? (Answer)**
  - Yes, SallyK
- ☐ **Is it longer than 120 bp (Y/N)**
  - Yes
- ☐ **Do other related phages agree (Phamerator) (Y/N)**
  - Yes
- ☐ **Direction: (Fwd/Rev)**
  - Reverse

Function?

- ☐ **Likely function from Phamerator (Answer):** Function Unknown
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both):** Function Unknown
- ☐ **Blast:** Function Unknown
- ☐ **Phages DB:** Function Unknown
- ☐ **Likely Function from HHpred? (conserved domains and functional regions):** Domain of Unknown Function
- ☐ **NKF:** Yes
- ☐ **Membrane binding domain?:** Unknown
- ☐ **tRNA?:** No

Start position?

- ☐ **Glimmer:** 44419
- ☐ **Glimmer Score:** 10.77
- ☐ **GeneMark:** 44419
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs):** 26 MA’s
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N):** Yes
- ☐ **Is it the longest ORF? (Y/N):** No
- ☐ **Alignment agreement from Blast? (Y/N, Source):** Yes
- ☐ **Does it include all of the functional region (HHpred)?** 34% Coverage
- ☐ **SD Score? Is there one higher? (number, Y/N):** DNA Master
- ☐ **Gap, overlap, and spacing? (description):** Gap: -4, Overlap: None, Spacing: 10

Notes: Start Codon GTG

Feature 64 Annotation

1st Annotator:
Aisley Allen

2nd Annotator:
Phoenix

Function:

Hypothetical Protein

5’ end:
44865

3’ end:
44416

Length:
450

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes, it is a little suspicious though
- ☐ Are there homologous genes based on a Blast search? (Answer)
Yes
- ☐ Is it longer than 120 bp (Y/N)
Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
No
- ☐ Direction: (Fwd/Rev)
Reverse

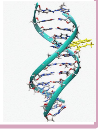
Function?

- ☐ Likely function from Phamerator (Answer) N/A, no synteny
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) hypothetical protein
- ☐ Blast: function unknown
- ☐ Phages DB: function unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Quinohemoprotein amine dehydrogenase
- ☐ NKF YES
- ☐ Membrane binding domain? NO
- ☐ tRNA? NO

Start position?

- ☐ Glimmer: N/A
- ☐ Glimmer Score: N/A
- ☐ GeneMark 44865
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 1 MA
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description) gap: -4 spacer: 11

Notes:



Feature 65 Annotation

1st Annotator: Madison Renn

2nd Annotator:

Function: Membrane Protein

5’ end: 44975

3’ end: 44862

Length: 114

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).:** Yes
- ☐ **Are there homologous genes based on a Blast search? (Answer):** Yes, Zagie and Nike
- ☐ **Is it longer than 120 bp (Y/N):** No
- ☐ **Do other related phages agree (Phamerator) (Y/N):** Yes
- ☐ **Direction: (Fwd/Rev):** Reverse

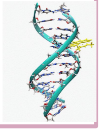
Function?

- ☐ **Likely function from Phamerator (Answer):** Function Unknown
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both):** Function Unknown
- ☐ **Blast:** Function Unknown
- ☐ **Phages DB:** No Data
- ☐ **Likely Function from HHpred? (conserved domains and functional regions):** Updated, shows signs of membrane protein
- ☐ **NKF:** Yes
- ☐ **Membrane binding domain?:** Yes according to DEEP search
- ☐ **tRNA?:** No

Start position?

- ☐ **Glimmer:** None
- ☐ **Glimmer Score:** None
- ☐ **GeneMark:** 44975
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs):** 5 MA’s
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N):** No
- ☐ **Is it the longest ORF? (Y/N):** No
- ☐ **Alignment agreement from Blast? (Y/N, Source):** Yes
- ☐ **Does it include all of the functional region (HHpred)?:** No
- ☐ **SD Score? Is there one higher? (number, Y/N):** -2.071, No
- ☐ **Gap, overlap, and spacing? (description):** Gap: -4, Space: 9

Notes: Start Codon ATG



Feature 66 Annotation

1st Annotator: Madalyne

2nd Annotator: Nina

Function: Hypothetical Protein

5' end: 45079

3' end: 44972

Length: 108

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
no

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

- Reverse

Function?

☐ Likely function from Phamerator (Answer) Hypothetical Protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

☐ Blast: Hypothetical Protein

☐ Phages DB: Hypothetical Protein

☐ Likely Function from HHpred? (conserved domains and functional regions) Hypothetical Protein

☐ NKF Yes

☐ Membrane binding domain?

☐ tRNA? No

Start position?

☐ Glimmer: N/A
☐ Glimmer Score: N/A
☐ GeneMark 45079
☐ Starterator MAs for selected and for alt options (number, number alt MAs)
7 MA's
☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) There is no Glimmer but Genemark does include all the coding potential.
☐ Is it the longest ORF? (Y/N) True
☐ Alignment agreement from Blast? (Y/N, Source) Yes 100%

☐ SD Score? Is there one higher? (number, Y/N)N 4.857
☐ Gap, overlap, and spacing? (description)
n

Notes:

Feature 67 Annotation

1st Annotator: Phoenix

2nd Annotator:

Function: helix-turn-helix DNA binding domain protein

5’ end: 45300

3’ end: 45076

Length: 225

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

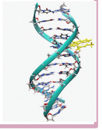
Function?

- ☐ Likely function from Phamerator (Answer)
  helix-turn-helix DNA binding domain protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  helix-turn-helix DNA binding domain protein
- ☐ Blast:
  helix-turn-helix DNA binding domain protein
- ☐ Phages DB:
  helix-turn-helix DNA binding domain protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  helix-turn-helix DNA binding domain protein
- ☐ NKF
  No
- ☐ Membrane binding domain?
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: None
- ☐ Glimmer Score: None
- ☐ GeneMark: 45,300
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  7 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  No, No
- ☐ Is it the longest ORF? (Y/N)
  No
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
  Yes
- ☐ SD Score? Is there one higher? (number, Y/N)
  -1.748, No
- ☐ Gap, overlap, and spacing? (description)
  Gap: 522
  Spacing: 10
  Overlap:

Notes:



Feature 68 Annotation

1st Annotator: Gigi Trejo

2nd Annotator:

Function: helix-turn-helix DNA binding domain

5' end: 45,300

3' end: 45,076

Length: 225

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  helix-turn-helix DNA binding domain
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast:
  helix-turn-helix DNA binding domain
- ☐ Phages DB:
  helix-turn-helix DNA binding domain
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  helix-turn-helix DNA binding domain
- ☐ NKF
  No
- ☐ Membrane binding domain?
  No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 47691
- ☐ Glimmer Score: 9.16
- ☐ GeneMark: 47691
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  47691 36 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes 100%
- ☐ Does it include all of the functional region (HHpred)? Yes
- ☐ SD Score? Is there one higher? (number, Y/N) Y, -2.377
- ☐ Gap, overlap, and spacing? (description)
  Gap: 522
  Overlap: 10

Notes:

Feature 69 Annotation

1st Annotator: Daniel

2nd Annotator: **Madison**

Function: DNA primase/helicase

5’ end: 47691

3’ end: 45823

Length: 1869

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).**
  Yes
- ☐ **Are there homologous genes based on a Blast search? (Answer)**
  Yes
- ☐ **Is it longer than 120 bp (Y/N)**
  Yes
- ☐ **Do other related phages agree (Phamerator) (Y/N)**
  Yes
- ☐ **Direction: (Fwd/Rev)**
  - Reverse

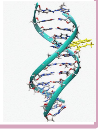
Function?

- ☐ **Likely function from Phamerator (Answer)**
  DNA primase/helicase
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both)**
  DNA primase/helicase
- ☐ **Blast:**
  DNA primase/helicase
- ☐ **Phages DB:**
  DNA primase/helicase
- ☐ **Likely Function from HHpred? (conserved domains and functional regions)**
  DNA primase/helicase
- ☐ **NKF**
  No
- ☐ **Membrane binding domain?**
  No
- ☐ **tRNA?** No

Start position?

- ☐ **Glimmer:** 47691
- ☐ **Glimmer Score:** 9.16
- ☐ **GeneMark:** 47691
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs)**
  47691 has 36 MA’s
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)** Yes, Yes
- ☐ **Is it the longest ORF? (Y/N)** Yes
- ☐ **Alignment agreement from Blast? (Y/N, Source)** Yes,
- ☐ **Does it include all of the functional region (HHpred)?** Yes
- ☐ **SD Score? Is there one higher? (number, Y/N)** -5.414, Yes, -2.377
- ☐ **Gap, overlap, and spacing? (description)**
  178 gap (lowest)

Notes:



Feature 70 Annotation

1st Annotator: Alex

2nd Annotator: Madison

Function: hypothetical protein

5’ end: 49363

3’ end: 47870

Length: 1493

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev) Reverse

-

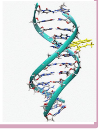
Function?

- ☐ Likely function from Phamerator (Answer) Function unknown
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Function unknown
- ☐ Blast: Function unknown
- ☐ Phages DB: Function unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Cell Wall Surface Anchor Protein, about 14% coverage
- ☐ NKF No
- ☐ Membrane binding domain? No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 49363
- ☐ Glimmer Score: 8.92
- ☐ GeneMark: 49363
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 11 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes 93.4%
- ☐ SD Score? Is there one higher? (number, Y/N) -1.951, no there is not
- ☐ Gap, overlap, and spacing? (description) 133

Notes:



Feature 71 Annotation

1st Annotator:
Nina

2nd Annotator:

Function:
Ribbon-Helix-Helix DNA Binding Protein Domain

5' end:
49755

3' end:
49497

Length:
258

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
  yes
- ☐ Is it longer than 120 bp (Y/N)
  yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  yes
- ☐ Direction: (Fwd/Rev)
  Reverse

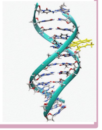
Function?

- ☐ Likely function from Phamerator (Answer)
  Ribbon-Helix-Helix Binding Domain
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Ribbon-Helix-Helix DNA Binding Domain
- ☐ Blast:
  Ribbon-Helix-Helix DNA Binding Domain
- ☐ Phages DB:
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  Ribbon-Helix-Helix DNA Binding Domain
- ☐ NKF
  No
- ☐ Membrane binding domain? yes
- ☐ tRNA?

Start position?

- ☐ Glimmer: 49724
- ☐ Glimmer Score: 15.08
- ☐ GeneMark: 49775
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  23 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y,N-Genemark does not agree with Glimmer
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap= 4, Space= 9

Notes:



Feature 72 Annotation

1st Annotator: Trenton

2nd Annotator:

Function: Hypothetical Protein

5’ end: 49942

3’ end: 49772

Length: 171

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Y

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Y

☐ Direction: (Fwd/Rev)

- Reverse

Function?

☐ Likely function from Phamerator (Answer)
No

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

☐ Blast: Hypothetical protein

☐ Phages DB: Hypothetical protein

☐ Likely Function from HHpred? (conserved domains and functional regions)

☐ NKF Yes

☐ Membrane binding domain?
No

☐ tRNA?
NO

Start position?

☐ Glimmer: 49942

☐ Glimmer Score: 15.59

☐ GeneMark49942

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
(Start: 10 @50044 has 15 MA's),

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY

☐ Is it the longest ORF? (Y/N)Y

☐ Alignment agreement from Blast? (Y/N, Source)Y

☐ Does it include all of the functional region (HHpred)? Yes

☐ SD Score? Is there one higher? (number, Y/N)Y-7.830

☐ Gap, overlap, and spacing? (description)
No

Notes:

Feature 73 Annotation

1st Annotator:
Gisselle Trejo

2nd Annotator:
Josh B.

Function:
Membrane Protein

5’ end:
50,207

3’ end:
50,028

Length:
180

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  - Yes
- ☐ Is it longer than 120 bp (Y/N)
  - Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

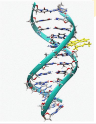
Function?

- ☐ Likely function from Phamerator (Answer)
  No known function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  No known function
- ☐ Blast: No known function
- ☐ Phages DB: No known function
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  87.2
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  Yes
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 50,207
- ☐ Glimmer Score: 4.78
- ☐ GeneMark: 50,207
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  - 18
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes, Yes
- ☐ Is it the longest ORF? (Y/N)
  Yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
  100%
- ☐ Does it include all of the functional region (HHpred)?
  No
- ☐ SD Score? Is there one higher? (number, Y/N)
  Yes
- ☐ Gap, overlap, and spacing? (description)
  Gap: -17
  Spacer: 12
  No overlap

Notes:



Feature 74 Annotation

1st Annotator:
Madison Renn

2nd Annotator:

Function:

Hypothetical Protein

5' end: 50532

3' end: 50191

Length: 516

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).: Yes

☐ Are there homologous genes based on a Blast search? (Answer): Yes, SallyK, AluminumJesus, BabyDotz

☐ Is it longer than 120 bp (Y/N): Yes

☐ Do other related phages agree (Phamerator) (Y/N): Yes

☐ Direction: (Fwd/Rev): Reverse

Function?

☐ Likely function from Phamerator (Answer): Unknown function/Hypothetical Protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both): Function unknown

☐ Blast: Function unknown

☐ Phages DB: Unknown function

☐ Likely Function from HHpred? (conserved domains and functional regions): Hypothetical protein

☐ NKF: Yes

☐ Membrane binding domain?: Unknown

☐ tRNA?: No

Start position?

☐ Glimmer: 50532

☐ Glimmer Score: 17.06

☐ GeneMark: 50532

☐ Starterator MAs for selected and for alt options (number, number alt MAs): 36

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes

☐ Is it the longest ORF? (Y/N): No

☐ Alignment agreement from Blast? (Y/N, Source): Yes

☐ Does it include all of the functional region (HHpred)?: 27% coverage

☐ SD Score? Is there one higher? (number, Y/N): DNA Master

☐ Gap, overlap, and spacing? (description): Gap: -8, Overlap: None , Spacing: 8

Notes: Start Codon ATG

1st Annotator:
Madison Renn

2nd Annotator:
Nina

Function:
Hypothetical Protein

Feature 75 Annotation

5’ end:
50836

3’ end:
50525

Length:
312

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).:** Yes
- ☐ **Are there homologous genes based on a Blast search? (Answer):** Yes, SallyK
- ☐ **Is it longer than 120 bp (Y/N):** Yes
- ☐ **Do other related phages agree (Phamerator) (Y/N):** Yes, SallyK
- ☐ **Direction: (Fwd/Rev):** Reverse

Function?

- ☐ **Likely function from Phamerator (Answer):** Function Unknown
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both):** Function Unknown
- ☐ **Blast:** Hypothetical Protein
- ☐ **Phages DB:** Function Unknown
- ☐ **Likely Function from HHpred? (conserved domains and functional regions):** No data for HHPRED
- ☐ **NKF:** Yes
- ☐ **Membrane binding domain?:** Unknown
- ☐ **tRNA?:** No

Start position?

- ☐ **Glimmer:** 50836
- ☐ **Glimmer Score:** 12.61
- ☐ **GeneMark:** 50836
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs):** No Phamerator Report available, check on this
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N):** Yes
- ☐ **Is it the longest ORF? (Y/N):** No
- ☐ **Alignment agreement from Blast? (Y/N, Source):** No BLAST report available
- ☐ **Does it include all of the functional region (HHpred)?:** No - 28% coverage phospholipase
- ☐ **SD Score? Is there one higher? (number, Y/N):** DNA Master
- ☐ **Gap, overlap, and spacing? (description):** Gap: -8, Overlap: , Spacer: 11

Notes: Start Codon ATG

Feature 76 Annotation

1st Annotator: Nina

2nd Annotator: Aisley Allen

Function: Hypothetical Function

5’ end: 51092

3’ end: 50829

Length: 200

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)

Yes

- ☐ Is it longer than 120 bp (Y/N)

Yes

- ☐ Do other related phages agree (Phamerator) (Y/N)

Yes

- ☐ Direction: (Fwd/Rev)

reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  Function Unknown
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Function Unknown
- ☐ Blast:
  Function Unknown
- ☐ Phages DB:
  Function Unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  Hypothetical Function
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?

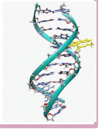
Start position?

- ☐ Glimmer: 51092
- ☐ Glimmer Score: 11.68
- ☐ GeneMark: 51092
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)

33 MAs

- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y,Y- Genemark and Glimmer agree
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap= -4, Space= 15

Notes:



Feature 77 Annotation

1st Annotator:
Alex

2nd Annotator:

Function:
Hypothetical protein

5' end:
51553

3' end:
51089

Length:
465

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  No
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Reverse

-

Function?

- ☐ Likely function from Phamerator (Answer) unknown
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Unknown function
- ☐ Blast: Unknown function
- ☐ Phages DB: No data
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Heparinase II C-terminal domain
- ☐ NKF Yes
- ☐ Membrane binding domain? Unknown
- ☐ tRNA? None

Start position?

- ☐ Glimmer: 51553
- ☐ Glimmer Score: 14.41
- ☐ GeneMark: 51544
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  1 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and No
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes 97%
- ☐ Does it include all of the functional region (HHpred)? 49%
- ☐ SD Score? Is there one higher? (number, Y/N) -1.748
- ☐ Gap, overlap, and spacing? (description)
  Gap: -1, Overlap: None Spacing: 15

Notes:

Feature 78 Annotation

1st Annotator:
Madison Renn

2nd Annotator:
Trenton

Function:
Hypothetical Protein

5’ end:
51825

3’ end:
51553

Length:
273

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).:** Yes
- ☐ **Are there homologous genes based on a Blast search? (Answer):** Yes, AluminumJesus
- ☐ **Is it longer than 120 bp (Y/N):** Yes
- ☐ **Do other related phages agree (Phamerator) (Y/N):** Yes
- ☐ **Direction: (Fwd/Rev):** Reverse

Function?

- ☐ **Likely function from Phamerator (Answer):** Hypothetical Protein
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both):** Unknown Function
- ☐ **Blast:** Function Unknown
- ☐ **Phages DB:** Function Unknown
- ☐ **Likely Function from HHpred? (conserved domains and functional regions):** Hypothetical Protein
- ☐ **NKF:** Yes
- ☐ **Membrane binding domain?:** Unknown
- ☐ **tRNA?:** No

Start position?

- ☐ **Glimmer:** 51825
- ☐ **Glimmer Score:** 10.62
- ☐ **GeneMark:** 51825
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs):** 3 MA’s
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N):** Yes
- ☐ **Is it the longest ORF? (Y/N):** No
- ☐ **Alignment agreement from Blast? (Y/N, Source):** Yes
- ☐ **Does it include all of the functional region (HHpred)?:** No
- ☐ **SD Score? Is there one higher? (number, Y/N):** DNA Master
- ☐ **Gap, overlap, and spacing? (description) :** Gap: -4, Overlap: No overlap Spacing: 9

Notes: Start Codon GTG

Feature 79 Annotation

1st Annotator: Madalyne Sisk

2nd Annotator: Phoenix

Function: Hypothetical Protein

5’ end: 52154

3’ end: 51825

Length: 330

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev) Reverse

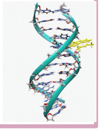
Function?

- ☐ Likely function from Phamerator (Answer) Hypothetical Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: Hypothetical Protein
- ☐ Phages DB: Hypothetical Protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Hypothetical Protein
- ☐ NKF yes
- ☐ Membrane binding domain? no
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 52154
- ☐ Glimmer Score: 12.95
- ☐ GeneMark 52154
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 36 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:



Feature 80 Annotation

1st Annotator:
Gigi Trejo

2nd Annotator:
Madalyne

Function:
hypothetical protein

5’ end:
52,433

3’ end:
52,179

Length:
255

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

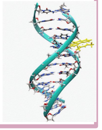
Function?

- ☐ Likely function from Phamerator (Answer)
  hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  hypothetical protein
- ☐ Blast:
  hypothetical protein
- ☐ Phages DB:
  hypothetical protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 52433
- ☐ Glimmer Score: 12.44
- ☐ GeneMark: 52433
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  21 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes, Yes
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
  Yes
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐
- ☐ Gap, overlap, and spacing? (description)
  Gap: -4
  Spacing: 12

Notes:



Feature 81 Annotation

1st Annotator: Daniel

2nd Annotator: Madalyne

Function: hypothetical protein

5' end: 52930

3' end: 52430

Length: 501

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  hypothetical protein
- ☐ Blast:
  hypothetical protein
- ☐ Phages DB:
  hypothetical protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  No
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 52930
- ☐ Glimmer Score: 10.91
- ☐ GeneMark: 52930
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  52930 12 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes, Yes
- ☐ Is it the longest ORF? (Y/N)
  No
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes, 99.39%
- ☐ Does it include all of the functional region (HHpred)?
  No
- ☐ SD Score? Is there one higher? (number, Y/N)
  -1.784, No
- ☐ Gap, overlap, and spacing? (description)
  Gap 2

Notes:

Feature 82 Annotation

1st Annotator: Madalyne

2nd Annotator:

Function: Hypothetical Protein

5’ end: 53466

3’ end: 52933

Length: 534

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). Yes
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev) Reverse

-

Function?

- ☐ Likely function from Phamerator (Answer) Hypothetical Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: Hypothetical protein
- ☐ Phages DB: Major capsid hexamer
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Hypothetical Protein
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer: 53466
- ☐ Glimmer Score: 14.66
- ☐ GeneMark 5366
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 28 MA’s no alt start
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes
- ☐ Is it the longest ORF? (Y/N) No
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:

Feature 83 Annotation

1st Annotator:
Phoenix

2nd Annotator:

Function:
Hypothetical protein

5’ end:
53765

3’ end:
53463

Length:
303

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
- ☐ Is it longer than 120 bp (Y/N)
  - yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  - no
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  - hypothetical
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  - Hypothetical
- ☐ Blast: function unknown
- ☐ Phages DB: hnh endonuclease
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  - Transcription repair
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 53651
- ☐ Glimmer Score: 8.26
- ☐ GeneMark 53651
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) no
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  - -118, 9

Notes:

Feature 84 Annotation

1st Annotator:
Trenton

2nd Annotator:
Nina

Function:
Hypothetical protein

5’ end:
53971

3’ end:
53648

Length:
324

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes there is coding potential
- ☐ Are there homologous genes based on a Blast search? (Answer)
Yes
- ☐ Is it longer than 120 bp (Y/N)
Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
Yes
- ☐ Direction: (Fwd/Rev)
  - Reversed

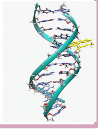
Function?

- ☐ Likely function from Phamerator (Answer)
None
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Nd
- ☐ Blast: unknown Function
- ☐ Phages DB: hypothetical protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
No
- ☐ NKF there is no known function
- ☐ Membrane binding domain? No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 53971
- ☐ Glimmer Score: 13.23
- ☐ GeneMark53980
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
(Start: 3 @53971 has 18 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YN
- ☐ Is it the longest ORF? (Y/N)
It has the Second longest ORF
- ☐ Alignment agreement from Blast? (Y/N, Source) Y
- ☐ Does it include all of the functional region (HHpred)? yes
- ☐ SD Score? Is there one higher? (number, Y/N)-4.062
- ☐ Gap, overlap, and spacing? (description)
No significant gaps or overlaps

Notes:



Feature 85 Annotation

1st Annotator:
Aisley Allen

2nd Annotator:
Madison

Function:
Unknown function

5’ end:
54288

3’ end:
53968

Length:
321

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
yes

☐ Are there homologous genes based on a Blast search? (Answer)
yes

☐ Is it longer than 120 bp (Y/N)
yes

☐ Do other related phages agree (Phamerator) (Y/N)
yes

☐ Direction: (Fwd/Rev)
Reverse

Function?

☐ Likely function from Phamerator (Answer)
No known function
☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Function unknown
☐ Blast:
Function unknown
☐ Phages DB:
Function unknown
☐ Likely Function from HHpred? (conserved domains and functional regions)
Ribosomal protein
☐ NKF
no
☐ Membrane binding domain?
no
☐ tRNA?

No

Start position?

☐ Glimmer: 54288
☐ Glimmer Score: 11.04
☐ GeneMark 54288
☐ Starterator MAs for selected and for alt options (number, number alt MAs)
3587
☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
Yes, yes
☐ Is it the longest ORF? (Y/N) yes
☐ Alignment agreement from Blast? (Y/N, Source) yes
☐ Does it include all of the functional region (HHpred)? yes
☐ SD Score? Is there one higher? (number, Y/N) no
☐ Gap, overlap, and spacing? (description)
Gap: 8, spacer: 8

Notes:

Feature 86 Annotation

1st Annotator:
Madalyne Sisk

2nd Annotator:

Function:
Hypothetical Protein

5' end:
54869

3' end:
54297

Length:
573

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
Yes
- ☐ Is it longer than 120 bp (Y/N)
Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
Yes
- ☐ Direction: (Fwd/Rev)
Reverse

-

Function?

- ☐ Likely function from Phamerator (Answer) Hypothetical Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: Hypothetical Protein
- ☐ Phages DB: Hypothetical Protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer: 54869
- ☐ Glimmer Score: 13.51
- ☐ GeneMark 54869
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 15 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:

Feature 87 Annotation

1st Annotator: Nina

2nd Annotator:

Function: Hypothetical Protein

5’ end: 55483

3’ end: 54866

Length: 617

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  Hypothetical Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Hypothetical Protein
- ☐ Blast:
  Hypothetical Protein
- ☐ Phages DB:
  Hypothetical Protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  Hypothetical Protein
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?

Start position?

- ☐ Glimmer: 55483
- ☐ Glimmer Score: 9.95
- ☐ GeneMark: 55444
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  7 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y,N= genemark and glimmer do not agree
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap= -4, Space= 10

Notes:

Feature 88 Annotation

1st Annotator:
Alex

2nd Annotator:
Phoenix

Function:
Hypothetical protein

5’ end:
55728

3’ end:
55460

Length:
249

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
No

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

- Reverse

Function?

☐ Likely function from Phamerator (Answer) unknown function

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Hypothetical protein

☐ Blast: unknown function

☐ Phages DB: Unknown function

☐ Likely Function from HHpred? (conserved domains and functional regions) Structural and Functional Protein

☐ NKF Yes

☐ Membrane binding domain?
No

☐ tRNA? No

Start position?

☐ Glimmer: 55728

☐ Glimmer Score: 10.22

☐ GeneMark: 55728

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
25 MA’s

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes

☐ Is it the longest ORF? (Y/N) No

☐ Alignment agreement from Blast? (Y/N, Source) Yes

☐ Does it include all of the functional region (HHpred)? Yes

☐ SD Score? Is there one higher? (number, Y/N) -4.705, yes -3.072

☐ Gap, overlap, and spacing? (description)
Gap: -1 Overlap: None Spacing: 9

Notes:

Feature 89 Annotation

1st Annotator:
Gigi Trejo

2nd Annotator:
Madalyne

Function:
Hypothetical Protein

5’ end:
56,210

3’ end:
55,728

Length:
483

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  Hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Hypothetical protein
- ☐ Blast:
  Hypothetical protein
- ☐ Phages DB:
  Hypothetical protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 56210
- ☐ Glimmer Score: 13.35
- ☐ GeneMark: 56210
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  23 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes, Yes
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
  Yes
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap: -4
  Spacing: 12

Notes:

Feature 90 Annotation

1st Annotator:
Daniel

2nd Annotator:

Function:
Hypothetical Protein

5' end:
56773

3' end:
56207

Length:
567

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  Hypothetical protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Hypothetical protein
- ☐ Blast:
  Hypothetical protein
- ☐ Phages DB:
  Hypothetical protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  No
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?
  No

Start position?

- ☐ Glimmer: 56773
- ☐ Glimmer Score: 11.49
- ☐ GeneMark: 56773
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  56773 19 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes, Yes
- ☐ Is it the longest ORF? (Y/N)
  Yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes, 100%
- ☐ Does it include all of the functional region (HHpred)?
  No
- ☐ SD Score? Is there one higher? (number, Y/N)
  -1.784, Yes but 3 other starts with same sd
- ☐ Gap, overlap, and spacing? (description)
  112 gap

Notes:

Feature 91 Annotation

1st Annotator:
Madalyne

2nd Annotator:

Function:
Hypothetical Protein

5’ end:
57059

3’ end:
56886

Length:
174

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
Yes
- ☐ Is it longer than 120 bp (Y/N)
Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
Yes
- ☐ Direction: (Fwd/Rev)
Reverse

-

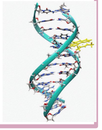
Function?

- ☐ Likely function from Phamerator (Answer) Hypothetical Protein
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast: Hypothetical Protein
- ☐ Phages DB: Hypothetical Protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer: 57059
- ☐ Glimmer Score: 7.22
- ☐ GeneMark 57059
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 20 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:



Feature 92 Annotation

1st Annotator:
Phoenix

2nd Annotator:
Nina

Function:
Hypothetical protein

5’ end:
57383

3’ end:
57056

Length:
228

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  - yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  - no
- ☐ Is it longer than 120 bp (Y/N)
  - yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  - yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

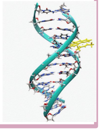
- ☐ Likely function from Phamerator (Answer)
  -
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  - Hypothetical protein
- ☐ Blast: function unknown
- ☐ Phages DB: tape measure protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  - hypothetical
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA? no

Start position?

- ☐ Glimmer: 57283
- ☐ Glimmer Score: 12.08
- ☐ GeneMark: 57283
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)

- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source) yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  - -8, 11

Notes:



Feature 93 Annotation

1st Annotator: Alex

2nd Annotator: Madalyne

Function: Hypothetical protein

5’ end: 57440

3’ end: 57276

Length: 165

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description). No
- ☐ Are there homologous genes based on a Blast search? (Answer) Yes
- ☐ Is it longer than 120 bp (Y/N) Yes
- ☐ Do other related phages agree (Phamerator) (Y/N) Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer) **Function unknown**
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) hypothetical protein
- ☐ Blast: hypothetical protein
- ☐ Phages DB: unknown function
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Ribosomal protein
- ☐ NKF Yes
- ☐ Membrane binding domain? No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 57440
- ☐ Glimmer Score: 13.28
- ☐ GeneMark: 57440
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs) 24 MA’s
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) No and No
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source) Yes 98%
- ☐ SD Score? Is there one higher? (number, Y/N) -1.748, no
- ☐ Gap, overlap, and spacing? (description) Gap: 51, no overlap, spacing: 12

Notes:

Feature 94 Annotation

1st Annotator:
AIsley Allen

2nd Annotator:
Phoenix

Function:
Hypothetical protein

5’ end:
57851

3’ end:
57492

Length:
360

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes sallyK 97

☐ Direction: (Fwd/Rev)
reverse

Function?

☐ Likely function from Phamerator (Answer)
Unknown

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Hypothetical protein

☐ Blast:
Unknown function

☐ Phages DB:
Function unknown

☐ Likely Function from HHpred? (conserved domains and functional regions)
Hypothetical protein

☐ NKF
no

☐ Membrane binding domain?
no

☐ tRNA? no

Start position?

☐ Glimmer: 57852
☐ Glimmer Score: 10.02
☐ GeneMark 57836
☐ Starterator MAs for selected and for alt options (number, number alt MAs)

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
No

☐ Is it the longest ORF? (Y/N) yes
☐ Alignment agreement from Blast? (Y/N, Source) yes
☐ Does it include all of the functional region (HHpred)? Yes
☐ SD Score? Is there one higher? (number, Y/N) No
☐ Gap, overlap, and spacing? (description) \
Gap: -19, Spacer: 15

Notes:

Feature 95 Annotation

1st Annotator:
Madison Renn

2nd Annotator:

Function:

5’ end:
58090

3’ end:
57833

Length:
258

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).: Yes
- ☐ Are there homologous genes based on a Blast search? (Answer):
- ☐ Is it longer than 120 bp (Y/N):
- ☐ Do other related phages agree (Phamerator) (Y/N): No
- ☐ Direction: (Fwd/Rev):

Function?

- ☐ Likely function from Phamerator (Answer)
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast:
- ☐ Phages DB:
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer:
- ☐ Glimmer Score:
- ☐ GeneMark
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:

Feature 96 Annotation

1st Annotator:
Nina

2nd Annotator:
Aisley Allen

Function:
Hypothetical Protein

5’ end:
58224

3’ end:
58087

Length:
137

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Reverse

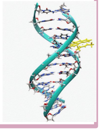
Function?

- ☐ Likely function from Phamerator (Answer) Function Unknown
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Function Unknown
- ☐ Blast: Function Unknown
- ☐ Phages DB: tape measure protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions) Function Unknown
- ☐ NKF Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA?

Start position?

- ☐ Glimmer: 58224
- ☐ Glimmer Score: 15.06
- ☐ GeneMark: 58224
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  34 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Y,Y= Genemakr and Glimmer agree
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap= -4, Space= 13

Notes:



Feature 97 Annotation

1st Annotator:
Alex

2nd Annotator:
Gigi

Function:
Hypothetical protein

5’ end:
58550

3’ end:
58221

Length:
330

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).**
  No, no matches found
- ☐ **Are there homologous genes based on a Blast search? (Answer)**
  no
- ☐ **Is it longer than 120 bp (Y/N)**
  Yes
- ☐ **Do other related phages agree (Phamerator) (Y/N)**
  No
- ☐ **Direction: (Fwd/Rev)**
  Reverse

-

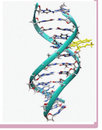
Function?

- ☐ **Likely function from Phamerator (Answer)** unknown function
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both)** unknown function
- ☐ **Blast:** hypothetical protein
- ☐ **Phages DB:** unknown function
- ☐ **Likely Function from HHpred? (conserved domains and functional regions)**
  Ribosome hibernator
- ☐ **NKF** Yes
- ☐ **Membrane binding domain?** No
- ☐ **tRNA?** No

Start position?

- ☐ **Glimmer:** 58490
- ☐ **Glimmer Score:** 10.6
- ☐ **GeneMark:** 58550
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs)**
  No MA’s
- ☐ **Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)** No and No
- ☐ **Is it the longest ORF? (Y/N)** No
- ☐ **Alignment agreement from Blast? (Y/N, Source)** Not really 64%
- ☐ **SD Score? Is there one higher? (number, Y/N)** -4.910, yes -2.934
- ☐ **Gap, overlap, and spacing? (description)**
  Gap: -4, Spacing: 12

Notes:



Feature 98 Annotation

1st Annotator:
Daniel

2nd Annotator:

Function:
Hypothetical Protein

5' end:
59011

3' end:
58547

Length:
465

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
Yes

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)

- Reverse

Function?

☐ Likely function from Phamerator (Answer)
Hypothetical protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
Hypothetical protein

☐ Blast:
Hypothetical protein

☐ Phages DB:
Hypothetical protein

☐ Likely Function from HHpred? (conserved domains and functional regions)
No

☐ NKF
Yes

☐ Membrane binding domain?
No

☐ tRNA?
No

Start position?

☐ Glimmer: 59011

☐ Glimmer Score: 14.87

☐ GeneMark: 59011

☐ Starterator MAs for selected and for alt options (number, number alt MAs)
59011 23 MA's

☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
Yes, Yes

☐ Is it the longest ORF? (Y/N)
Yes

☐ Alignment agreement from Blast? (Y/N, Source)
Yes, 96.7%

☐ Does it include all of the functional region (HHpred)?
No

☐ SD Score? Is there one higher? (number, Y/N)
-3.580, No

☐ Gap, overlap, and spacing? (description)
33 gap

Notes:

Feature 99 Annotation

1st Annotator:
Phoenix

2nd Annotator:

Function:
Hypothetical protein

5’ end:
59353

3’ end:
59045

Length:
309

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).
Yes

☐ Are there homologous genes based on a Blast search? (Answer)
Yes

☐ Is it longer than 120 bp (Y/N)
- yes

☐ Do other related phages agree (Phamerator) (Y/N) yes

☐ Direction: (Fwd/Rev)
- Reverse

Function?

☐ Likely function from Phamerator (Answer)
- Hypothetical protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- Hypothetical protein

☐ Blast: hypothetical

☐ Phages DB: Major tail protein

☐ Likely Function from HHpred? (conserved domains and functional regions)
- hypothetical

☐ NKF

☐ Membrane binding domain? no

☐ tRNA? no

Start position?

☐ Glimmer: 59326
☐ Glimmer Score: 13.77
☐ GeneMark 59326
☐ Starterator MAs for selected and for alt options (number, number alt MAs)
59326 23 MA’s
☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES
☐ Is it the longest ORF? (Y/N) YES
☐ Alignment agreement from Blast? (Y/N, Source) YES
☐ Does it include all of the functional region (HHpred)?
☐ SD Score? Is there one higher? (number, Y/N)
☐ Gap, overlap, and spacing? (description)
- 10, 10

Notes:

1st Annotator:
Aisley Allen

2nd Annotator:
Madalyne Sisk

Function:
hypothetical protein

Annotation

5' end:
59714

3' end:
59364

Length:
351

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  yes
- ☐ Is it longer than 120 bp (Y/N)
  yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  no
- ☐ Direction: (Fwd/Rev)
  Reverse

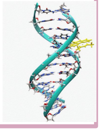
Function?

- ☐ Likely function from Phamerator (Answer)
  none
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Hypothetical protein
- ☐ Blast:
  Function unknown
- ☐ Phages DB:
  Function unknown
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  NICOTINATE PHOSPHORIBOSYLTRANSFERASE; TRANSFERASE
- ☐ NKF
  none
- ☐ Membrane binding domain?
  none
- ☐ tRNA? none

Start position?

- ☐ Glimmer: 59714
- ☐ Glimmer Score: 13.37
- ☐ GeneMark 59714
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) yes!
- ☐ Is it the longest ORF? (Y/N) yes
- ☐ Alignment agreement from Blast? (Y/N, Source) yes
- ☐ Does it include all of the functional region (HHpred)? no
- ☐ SD Score? Is there one higher? (number, Y/N) no
- ☐ Gap, overlap, and spacing? (description)
  Gap: -4, spacer: 11

Notes:



Feature 101 Annotation

1st Annotator: Madison Renn

2nd Annotator: **Trenton**

Function: Hypothetical Protein

5' end: 60142

3' end: 59711

Length: 432

Is it a gene?

- ☐ **Is there coding potential based on Genemarks? (Y/N and description).:** Yes
- ☐ **Are there homologous genes based on a Blast search? (Answer):** Yes, SallyK, AluminumJesus and BabyDotz
- ☐ **Is it longer than 120 bp (Y/N):** Yes
- ☐ **Do other related phages agree (Phamerator) (Y/N):** Yes
- ☐ **Direction: (Fwd/Rev):** Reverse

Function?

- ☐ **Likely function from Phamerator (Answer):** Hypothetical Protein
- ☐ **Likely function from Blastp? (Answer using phagesDB, NCBI, or both):** Function Unknown
- ☐ **Blast:** Function Unknown
- ☐ **Phages DB:** No data available
- ☐ **Likely Function from HHpred? (conserved domains and functional regions):** Function Unknown
- ☐ **NKF:** Yes
- ☐ **Membrane binding domain?:** No
- ☐ **tRNA?:** No

Start position?

- ☐ **Glimmer:** 60142
- ☐ **Glimmer Score:** 12.58
- ☐ **GeneMark:** 60142
- ☐ **Starterator MAs for selected and for alt options (number, number alt MAs):** 8 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? **(Y/N, Y/N):** Yes
- ☐ **Is it the longest ORF? (Y/N):** No
- ☐ **Alignment agreement from Blast? (Y/N, Source):** Yes
- ☐ **Does it include all of the functional region (HHpred)?:** No
- ☐ **SD Score? Is there one higher? (number, Y/N):** DNA Master
- ☐ **Gap, overlap, and spacing? (description):** Gap: 45, Spacer: 8

Notes: ATG Start Codon

Feature 102 Annotation

1st Annotator:
Nina

2nd Annotator:

Function:
Hypothetical Protein

5’ end:
60277

3’ end:
60188

Length:
89

Is it a gene?

☐ Is there coding potential based on Genemarks? (Y/N and description).

☐ Are there homologous genes based on a Blast search? (Answer)

☐ Is it longer than 120 bp (Y/N)
No

☐ Do other related phages agree (Phamerator) (Y/N)
Yes

☐ Direction: (Fwd/Rev)
Reverse

Function?

☐ Likely function from Phamerator (Answer) Hypothetical protein

☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Hypothetical Protein

☐ Blast: Function Unknown

☐ Phages DB: Unknown Function

☐ Likely Function from HHpred? (conserved domains and functional regions) function unknown

☐ NKF yes

☐ Membrane binding domain? no

☐ tRNA?

Start position?

☐ Glimmer: N/A
☐ Glimmer Score: N/A
☐ GeneMark: 60277
☐ Starterator MAs for selected and for alt options (number, number alt MAs)
23 MAs
☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
☐ Is it the longest ORF? (Y/N)
☐ Alignment agreement from Blast? (Y/N, Source)
☐ Does it include all of the functional region (HHpred)?
Y
☐ SD Score? Is there one higher? (number, Y/N)
☐ Gap, overlap, and spacing? (description)
Gap=-104, Space=10

Notes:

Feature 103 Annotation

1st Annotator:

2nd Annotator:

Function:

5’ end:

3’ end:

Length:

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
- ☐ Is it longer than 120 bp (Y/N)
- ☐ Do other related phages agree (Phamerator) (Y/N)
- ☐ Direction: (Fwd/Rev)

-

Function?

- ☐ Likely function from Phamerator (Answer)
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast:
- ☐ Phages DB:
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer:
- ☐ Glimmer Score:
- ☐ GeneMark:
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes:

Feature 104 Annotation

1st Annotator:
Nina

2nd Annotator:

Function:
Hypothetical Protein

5’ end:
60423

3’ end:
60277

Length:
146

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  Function Unknown
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  Function Unknown
- ☐ Blast:
  Hypothetical Protein
- ☐ Phages DB:
  Hypothetical Protein
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
  Yes
- ☐ Membrane binding domain? No
- ☐ tRNA?

Start position?

- ☐ Glimmer: 60423
- ☐ Glimmer Score: 6.72
- ☐ GeneMark: 6042
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  14 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y= genemark and glimmer agree
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap= 36, Space= 10

Notes:

Feature 105 Annotation

1st Annotator:
Alex

2nd Annotator:

Function:
hypothetical protein

5' end:
60762

3' end:
60460

Length:
303

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  No
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  Reverse

-

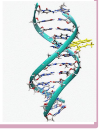
Function?

- ☐ Likely function from Phamerator (Answer) unknown function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both) unknown function
- ☐ Blast: hypothetical protein
- ☐ Phages DB: hypothetical function
- ☐ Likely Function from HHpred? (conserved domains and functional regions) unknown function
- ☐ NKF yes
- ☐ Membrane binding domain? no
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 60762
- ☐ Glimmer Score: 9.68
- ☐ GeneMark: 60735
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  25 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) no and no
- ☐ Is it the longest ORF? (Y/N)
  No
- ☐ Alignment agreement from Blast? (Y/N, Source) 93%
- ☐ SD Score? Is there one higher? (number, Y/N) -4.228, yes -3.440
- ☐ Gap, overlap, and spacing? (description)
  Gap of -4, no overlap. Spacing of 10

Notes:



Feature 107 Annotation

1st Annotator:
Gigi

2nd Annotator:

Function:
Unknown function

5’ end:
60974

3’ end:
60759

Length:
216

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

Function?

- ☐ Likely function from Phamerator (Answer)
  unknown function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  unknown function
- ☐ Blast:
  unknown function
- ☐ Phages DB:
  unknown function
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer: 60754
- ☐ Glimmer Score: 9.94
- ☐ GeneMark:
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  33 MAs
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)
  Gap: 186
  Overlap:
  Spacing: 9

Notes:

Annotation

1st Annotator:
Trenton Shappee

2nd Annotator:

Function:
Hypothetical Protein

5’ end:
60174

3’ end:
60308

Length:
135

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).

Y

- ☐ Are there homologous genes based on a Blast search? (Answer)

No

- ☐ Is it longer than 120 bp (Y/N)

Yes

- ☐ Do other related phages agree (Phamerator) (Y/N)

Yes

- ☐ Direction: (Fwd/Rev)

- Rev

Function?

- ☐ Likely function from Phamerator (Answer)
- ☐ No
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)

No

- ☐ Blast: None
- ☐ Phages DB: None
- ☐ Likely Function from HHpred? (conserved domains and functional regions)

Nothing with enough coverage

- ☐ NKF
- ☐ Yes
- ☐ Membrane binding domain?

No

- ☐ tRNA? No

Start position?

- ☐ Glimmer: 60308
- ☐ Glimmer Score: 3.58
- ☐ GeneMark:None
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)

Not displayed

- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY
- ☐ Is it the longest ORF? (Y/N) Y
- ☐ Alignment agreement from Blast? (Y/N, Source)No
- ☐ Does it include all of the functional region (HHpred)?Yes
- ☐ SD Score? Is there one higher? (number, Y/N)N
- ☐ Gap, overlap, and spacing? (description)

Notes:

Feature 107 Annotation

1st Annotator:
Daniel

2nd Annotator:

Function:
Hypothetical protein

5' end:
61856

3' end:
61161

Length:
696

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
  Yes
- ☐ Are there homologous genes based on a Blast search? (Answer)
  Yes
- ☐ Is it longer than 120 bp (Y/N)
  Yes
- ☐ Do other related phages agree (Phamerator) (Y/N)
  Yes
- ☐ Direction: (Fwd/Rev)
  - Reverse

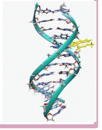
Function?

- ☐ Likely function from Phamerator (Answer)
  unknown function
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
  unknown function
- ☐ Blast:
  unknown function
- ☐ Phages DB:
  unknown function
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
  Unknown function
- ☐ NKF
  Yes
- ☐ Membrane binding domain?
  No
- ☐ tRNA? No

Start position?

- ☐ Glimmer: 61856
- ☐ Glimmer Score: 10.52
- ☐ GeneMark: 61775
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
  61856 30 MA's; 61775 1 MA's
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
  Yes, No
- ☐ Is it the longest ORF? (Y/N) Yes
- ☐ Alignment agreement from Blast? (Y/N, Source)
  Yes
- ☐ Does it include all of the functional region (HHpred)? No
- ☐ SD Score? Is there one higher? (number, Y/N) -4.177, Yes
- ☐ Gap, overlap, and spacing? (description) 0

Notes:



Feature 108 Annotation

1st Annotator:
Madison Renn

2nd Annotator:

Function:

5’ end:
61857

3’ end:

Length:

Is it a gene?

- ☐ Is there coding potential based on Genemarks? (Y/N and description).
- ☐ Are there homologous genes based on a Blast search? (Answer)
- ☐ Is it longer than 120 bp (Y/N)
- ☐ Do other related phages agree (Phamerator) (Y/N)
- ☐ Direction: (Fwd/Rev)

Function?

- ☐ Likely function from Phamerator (Answer)
- ☐ Likely function from Blastp? (Answer using phagesDB, NCBI, or both)
- ☐ Blast:
- ☐ Phages DB:
- ☐ Likely Function from HHpred? (conserved domains and functional regions)
- ☐ NKF
- ☐ Membrane binding domain?
- ☐ tRNA?

Start position?

- ☐ Glimmer:
- ☐ Glimmer Score:
- ☐ GeneMark:
- ☐ Starterator MAs for selected and for alt options (number, number alt MAs)
- ☐ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)
- ☐ Is it the longest ORF? (Y/N)
- ☐ Alignment agreement from Blast? (Y/N, Source)
- ☐ Does it include all of the functional region (HHpred)?
- ☐ SD Score? Is there one higher? (number, Y/N)
- ☐ Gap, overlap, and spacing? (description)

Notes: