1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Annot	tator: Function:	Annotation		
5' end: 3' end: Le	ngth:	Start position?		
<ul> <li>Is there coding potential based on Genemarks? (Y/N and description).</li> <li>Are there homologous genes based on a Blast search? (Answer)</li> <li>Is it longer than 120 bp (Y/N)</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> <li>Direction: (Fwd/Rev)</li> </ul>	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?	<ul> <li>Glimmer:</li> <li>Glimmer Score:</li> <li>GeneMark:</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)</li> <li>Is it the longest ORF? (Y/N)</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description)</li> </ul>		
- Notes:				

INUICS.



<mark>1<sup>st</sup> Annotato</mark> Gisselle Treje		2 <sup>nd</sup> Annotator:		Function: Not a Gene	]	Feature X Annotation		
<b>5' end:</b>	3' end:	Lei	ngth:			<b>Start position?</b>		
Is it a gene?			🗅 Likel	Function? ly function from nerator (Answer)		Glimmer Score: 1.71 GeneMark: Starterator MAs for selected and for alt options (number, number alt MAs)		
Are there homologou	Genemarks? (Y/N and description). No because there wasn't another EG cluster hat 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)		Likel (Ansv or bo	ly function from Blastp? wer using phagesDB, NCBI, oth)		Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)		
□ Is it longer than a			-	: ces DB: ly Function from HHpred? served domains and	<ul> <li>Alignment agreem Source)</li> <li>Does it include all</li> </ul>	Is it the longest ORF? (Y/N) Alignment agreement from Blast? (Y/N, Source) Does it include all of the functional region		
			funct	tional regions)		(HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description)		
- C TRNA				brane binding domain? \?		Sap, overlap, and spacing. (description)		
Notes:						- A A A A A A A A A A A A A A A A A A A		

<mark>1<sup>st</sup> Annotator:</mark> Daniel	2 <sup>nd</sup> Anno Nir		Function: Hypothetical protein	Feature 1 Annotation	1
	nd: L	ength: 369		Start position?	
<ul> <li>Is there coding potential Genemarks? (Y/N and do Yes, bumpy but potential goe sequence</li> <li>Are there homologous g Blast search? (Answer) Yes</li> <li>Are there homologous g Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp (Yes)</li> <li>Do other related phages (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev) <ul> <li>Reverse</li> </ul> </li> <li>Notes:</li> </ul>	based on escription). s along with enes based on a Y/N)	Like (Ans or bo Hy Blas Phag Un Like (con func NKF C Men	pothetical protein t: pothetical protein ges DB: known function ly Function from HHpred? served domains and tional regions) function	<ul> <li>Glimmer: 1079</li> <li>Glimmer Score: 10.51</li> <li>GeneMark 1019</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>1040 14 MA'S, 1079 1 MA</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, N</li> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) Y, 98%</li> <li>Does it include all of the functional region (HHpred)? No</li> <li>SD Score? Is there one higher? (number, Y/N) Y, -1.907</li> <li>Gap, overlap, and spacing? (description)</li> </ul>	



1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Annot Trenton Shappee			ator:	Function: hypothetical protein	<b>Feature 2 Annotation</b>				
<b>5' end:</b> 1225	<b>3' end:</b> 1037		ngth: <sup>189</sup>		<b>Start position?</b> Glimmer: 1225				
<ul> <li>Is there cod Genemarks</li> <li>Y</li> <li>Are there ho a Blast searce</li> <li>Is it longer t</li> </ul>	it a gene? ing potential based of (Y/N and description omologous genes bas ch? (Answer) Y han 120 bp (Y/N) lated phages agree r) (Y/N) Fwd/Rev)		<ul> <li>(Ansy both)</li> <li>Likel (Ansy both)</li> <li>Blast</li> <li>Phag prote</li> <li>Likel (cons regio)</li> <li>NKF</li> </ul>	<b>: Function unknown</b> res DB: merr-like hth dna binding in y Function from HHpred? served domains and functional ons) there is no known function brane binding domain?	<ul> <li>Glimmer Score: 5.91</li> <li>GeneMark1225</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>(Start: 13 @1225 has 6 MA's)</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) N,Y</li> <li>Is it the longest ORF? (Y/N) <ul> <li>N it is the second longest</li> </ul> </li> <li>Alignment agreement from Blast? (Y/N, Source) Y</li> <li>YDoes it include all of the functional region (HHpred)? No</li> <li>SD Score? Is there one higher? (number, Y/N)-2.845N</li> <li>Gap, overlap, and spacing? (description)</li> </ul>				
Notes:									

<mark>1<sup>st</sup> Annota</mark> Aisley All				2 <sup>nd</sup> Annotator: Function: Phoenix larsen		Function:	Feature 3 Annotation
<b>5' end:</b> 1704	<b>3' end:</b> 1225		Hypothetical protein 480		<b>Start position?</b>		
<ul> <li>Is there codi Genemarks? YES</li> <li>Are there ho a Blast searc YES</li> <li>Is it longer the search of th</li></ul>	ated phages agree r) (Y/N)		<ul> <li>Likel (Ansyboth)</li> <li>Blast</li> <li>Phag</li> <li>Likel (construction)</li> <li>NKF</li> <li>Mem</li> </ul>	tes DB: Function Unknown by Function from HHpred? Served domains and functional ons) Zinc-binding domain of ation initiation factor 2 beta	<ul> <li>Glimmer: 1704</li> <li>Glimmer Score: 10.99</li> <li>GeneMark 1704</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 1</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES, YES</li> <li>Is it the longest ORF? (Y/N) NO</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>Does it include all of the functional region (HHpred)? 18.239</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) gap: -4 spacer: 12</li> </ul>		



1 <sup>st</sup> Annotator: Phoenix		Annot sley Al		Function: PnuC-like	]	Feature 4 Annotation
<b>5' end:</b> 2408 3' en 170			<mark>gth</mark> : <sup>08</sup>	Nicotinamide riboside transporter		Start position?
<ul> <li>Is there coding potentia Genemarks? (Y/N and de Are there homologous g a Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp ( yes</li> <li>Do other related phages (Phamerator) (Y/N) yes</li> <li>Direction: (Fwd/Rev) - Reverse</li> </ul>	l based on escription enes based ) (Y/N)	d on	<ul> <li>Likel (Ansy or bo</li> <li>Blast</li> <li>Phag</li> <li>Likel (cons funct</li> <li>NKF</li> </ul>	: es DB: y Function from HHpred? erved domains and tional regions) brane binding domain?		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:						

<mark>1<sup>st</sup> Annota</mark> Nina	1 <sup>st</sup> Annotator: Nina Madal				<b>Function</b> : Membrane Protein	]	Feature 5 Annotation
<b>5' end:</b> 2647	<b>3' er</b> 240		Leng 242			0	<b>Start position?</b> Glimmer: 2647 Glimmer Score: 0.64
Is there codi Genemarks?	mologous g h? (Answer han 120 bp ated phages ) (Y/N)	l based on escription). renes based or ) (Y/N)		I Likel (Ans' or bo Fui Blast Me Phag Fui Likel (cons funct Fui NKF Yes No	nction unknown t: mbrane protein ges DB: nction Unknown ly Function from HHpred? served domains and tional regions) nction Unknown		Glimmer Score: 9.64 GeneMark: 2647 Starterator MAs for selected and for alt options (number, number alt MAs) MAs Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) es 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:					A? No		Ant



	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Madison Renn		otator:Function:Unknown		]	Feature 6 Annotation			
	<b>5' end:</b> 2832	<b>3' end:</b> 2644		ngth: (Hypothetical Protein)			Start position?		
	Is there codin Genemarks? Yes Are there hon a Blast search Is it longer th Do other rela (Phamerator	t a gene? ng potential based (Y/N and descript mologous genes b h? (Answer): Yes nan 120 bp (Y/N): Yes nted phages agree ) (Y/N): Yes wd/Rev): Revers	ased on Zes	(Answ Likely Likely Blast: Blast: Phage Likely (consi region NKF:	brane binding domain?: No		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:		
N	otes: Start (	Codon ATG							

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		<sup>t</sup> Annotator: 2 <sup>nd</sup> Anno Madalyne		Madalyne DprA-like DNA		]	Feature 7 Annotation
	<b>5' end:</b> 3344	<b>3' end:</b> 2829		<mark>ngth</mark> : <sup>516</sup>	processing chain		Start position?
	Is it a gene?			🗆 Likel	Function?		Glimmer: 3344 Glimmer Score: 13.43 GeneMark: 3353 Starterator MAs for selected and for alt
D	Is there codi Genemarks? ves	there coding potential based on nemarks? (Y/N and description).			y function from Phamerator ver) DprA-like ssDNA binding in		<b>options (number, number alt MAs)</b> Alt start: 3353 both starts have 1 MA
	J	mologous genes based on ch? (Answer) Yes		using	t: DprA-like DNA processing chain ges DB: DprA-like DNA processing n ly Function from HHpred? served domains and functional		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,
D	Is it longer tl	han 120 bp (Y/N) Ye	·				
٩	Do other rela (Phamerator	lated phages agree r) (Y/N) Yes		regio			
	Direction: (F	wd/Rev)					Y/N) Gap, overlap, and spacing? (description)
	- Reverse			<ul><li>Mem</li><li>tRNA</li></ul>	brane binding domain? ? No		-4 gap, 13 space
Ň	otes:						

1 <sup>st</sup> Annot Alex	74		otator: son	Function: Hypothetical Protein	Featu	re 8 Annotation
<b>5' end:</b> 3583	<b>3' en</b> 3341		ength: 243		Start position?	
<ul> <li>Is there cod Genemarks Yes</li> <li>Are there he a Blast sear Yes</li> <li>Is it longer t Yes</li> </ul>	than 120 bp ( lated phages r) (Y/N) Fwd/Rev)	l based on escription). enes based on Y/N)	<ul> <li>Likel (Ans both</li> <li>Blast</li> <li>Phag</li> <li>Likel (cons regit Fiel</li> <li>NKF</li> </ul>	ix-turn-helix Domain Yes Ibrane binding domain? No	<ul> <li>GeneMar</li> <li>Starterate options (n 24 MA<sup>2</sup></li> <li>Does it in and do Ga (Y/N, Y/N)</li> <li>Is it the log Alignmer Source) Y</li> <li>SD Score Y/N) -3.76</li> </ul>	Score: 7.22 k: 3583 or MAs for selected and for alt number, number alt MAs) 's iclude all of the coding potential enemark and Glimmer agree? ) Yes and Yes ongest ORF? (Y/N) Yes it agreement from Blast? (Y/N, Yes 100% ? Is there one higher? (number,

S.

1 <sup>st</sup> Annotator: 2 <sup>nd</sup> An Daniel	iel helix-turn-helix DNA		Feature 9 Annotation			
5' end:     3' end:       3936     3580	Length: 357	binding domain	Start position?			
<ul> <li>Is there coding potential based on Genemarks? (Y/N and description).</li> <li>Are there homologous genes based of a Blast search? (Answer)</li> <li>Are thore than 120 bp (Y/N)</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> <li>Direction: (Fwd/Rev)</li> <li>Reverse</li> </ul>	(An Lika (An Dot An Dot An Dot An Dot An Dot An An An An An An An An An An An An An	st: elix-turn-helix DNA binding main ages DB: elix-turn-helix DNA binding omain ely Function from HHpred? nserved domains and functional ions) elix-turn-helix DNA binding omain	<ul> <li>Glimmer: 3936</li> <li>Glimmer Score: 6.23</li> <li>GeneMark: 3936</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>36 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y</li> <li>Is it the longest ORF? (Y/N) Y</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N) Y, -3.105</li> <li>Gap, overlap, and spacing? (description) -8,</li> </ul>			
Notes:						

	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Trenton		Annot	ator:	Function: helix-turn-helix DNA binding domain	Feature 10 Annotation		
	<b>5' end:</b> 4144	<b>3' end:</b> 3929		<mark>ngth</mark> : 216	protein		Start position?	
	<ul> <li>Is there coding (Y/N and descrives)</li> <li>YES on DNA master in potential</li> <li>Are there homonon search? (Answer Yes)</li> <li>Is it longer than Yes</li> </ul>	d phages agree (Phamerat	Blast	<ul> <li>(Ansy helix)</li> <li>Likel using</li> <li>Blast protei</li> <li>Phag doma</li> <li>Likel (consy region protei</li> <li>NKF No</li> </ul>	ix-turn-helix DNA binding domain protein ly function from Blastp? (Answer g phagesDB, NCBL, or both) t: helix-turn-helix DNA binding domain in ges DB: helix-turn-helix dna binding ain ly Function from HHpred? served domains and functional ons) helix-turn-helix DNA binding domain in		Glimmer Score: 7.44 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.	
1	NT - 4						hourse	



	<mark>1<sup>st</sup> Annota</mark> Aisley All		Anno	tator:	<b>Function</b> : Ribbon helix-helix	Feature 11 Annotation		
	<b>5' end:</b> 4248 <b>3' end:</b> 4361			Length: <sup>113</sup> DNA binding domain protein			Start position?	
	Is it	t a gene?		<b>Function?</b> <ul> <li>Likely function from Phamerator (Answer)ribbon-helix-helix DNA binding domain protein</li> </ul>			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	
•	Is there cod Genemarks description		d on	<ul> <li>Likely function from Blastp? (Answer using phagesDB, NCBI, or both) ribbon-helix-helix DNA binding domain protein</li> <li>Blast: ribbon-helix-helix DNA binding domain protein</li> </ul>			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,	
		omologous genes h earch? (Answer)¥H		<ul> <li>domain protein</li> <li>Phages DB: ribbon-helix-helix DNA binding domain protein</li> </ul>			Source)100% Does it include all of the functional region (HHpred)?88.9%	
	Is it longer t	han 120 bp (Y/N)	NO	Likely (conse region	Function from HHpred? erved domains and functional ns) DNA binding protein	D	SD Score? Is there one higher? (number, Y/N)-2.839	
		lated phages agree r) (Y/N) YES	;	<ul><li>NKF</li><li>Membrane binding domain? NO</li></ul>			Gap, overlap, and spacing? (description) Gap = 103, Space = 10	
		Fwd/Rev) fwd	Thoras				10-1	

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



<mark>1<sup>st</sup> Annotato</mark> Phoenix	<b>Dr:</b> 2 <sup>nd</sup>	2 <sup>nd</sup> Annotator:		Function: helix-turn-helix DNA binding domain		Feature 12 Annotation	
<b>5' end:</b> 4358	<b>3' end:</b> 5116		ngth: <sup>651</sup>			Start position?	
<ul> <li>Is there coding Genemarks? (Y yes</li> <li>Are there hom a Blast search? yes</li> <li>Is it longer that yes</li> </ul>	ed phages agree Y/N)		<ul> <li>Likel (Ansy both) doma</li> <li>Blast</li> <li>Phag term</li> <li>Likel (cons regio</li> <li>NKF</li> </ul>	Function? by function from Phamerator wer) terminase small subunit by function from Blastp? wer using phagesDB, NCBI, or helix-turn-helix DNA binding in (both NCBI and phagesDB) t: small subunit terminase res DB: small subunit inase by Function from HHpred? served domains and functional ons) not informative brane binding domain? no A? no		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



		1st Annotator: Gigi Trejo2nd Anno Josh				Function: Unknown function		Feature 13 Annotation
	5' end: 5118					ength: 162		Start position?
	Is there codi Genemarks? No coding Are there ho a Blast searc Hypothet Is it longer th Yes Do other rela (Phamerator Yes Direction: (F Forward	mologous g h? (Answer ical protein han 120 bp ( ated phages ) (Y/N)	l based o escriptio enes bas ) Y/N)		(Answ No k Likely Using No k Blast: No k Phage No k Likely (conso region No NKF Yes	chówn function y function from Blastp? (Answer phagesDB, NCBI, or both) known function es DB: known function y Function from HHpred? erved domains and functional ns)		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
N	lotes:							

			1st Annotator:2nd AnnoDanielAisley					Feature 14 Annotation
	5' end:     3' end:     L       5276     5449				ength: <sup>174</sup>			Start position?
	Is there codi Genemarks? Yes Are there hor a Blast searc Yes Is it longer th Yes Do other rela (Phamerator Yes Direction: (F Forward	mologous g h? (Answer han 120 bp ( ated phages ) (Y/N)	l based o escriptio enes bas ) Y/N)		<ul> <li>(Answing Hyp)</li> <li>Likely using Hyp)</li> <li>Blast: Hyp)</li> <li>Phage Unic</li> <li>Likely (conserve)</li> <li>Likely (conserve)</li> <li>NKF Yes</li> </ul>	othetical protein / function from Blastp? (Answer phagesDB, NCBI, or both) othetical protein othetical protein as DB: nown function y Function from HHpred? erved domains and functional ns) prane binding domain?		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 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
Ν	otes:							

ı <sup>st</sup> Annota Nina		Anno Madiso		<b>Function:</b> Ribbon Helix-Helix DNA		Feature 15 Annotation
<b>5' end:</b> 5449	<b>3' end:</b> 5823		ength: 375 Binding Domair			<b>Start position?</b> Glimmer: 5449
<ul> <li>Is there codi Genemarks?</li> <li>Yes</li> <li>Are there hor a Blast searc</li> <li>Yes</li> <li>Is it longer the Yes</li> </ul>	<b>t a gene?</b> ng potential based o (Y/N and description mologous genes bas h? (Answer) nan 120 bp (Y/N) nted phages agree ) (Y/N) wd/Rev)		<ul> <li>(Anservice)</li> <li>(Anservice)</li> <li>Like (Anservice)</li> <li>Blass Bind</li> <li>Pha DNA</li> <li>Like (con reginged)</li> <li>NKH</li> </ul>	swer) boon Helix-Helix DNA Binding by function from Blastp? swer using phagesDB, NCBI, or n) Ribbon Helix DNA Binding hain t: Ribbon Helix-Helix DNA ling Domain ges DB: Ribbon Helix-Helix A Binding Domain ely Function from HHpred? Iserved domains and functional ons)		Glimmer Score: 9.19 GeneMark: 5449 Starterator MAs for selected and for alt options (number, number alt MAs) 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:						

<mark>1<sup>st</sup> Annota</mark> Madison F		Annot Nina	notator: ina		<b>Function</b> : Terminase	]	Feature 16 Annotation
5798 7309			ength: 1512		<b>Start position?</b> <ul> <li>Glimmer: 5798</li> </ul>		
<ul> <li>Is there codi Genemarks? Yes</li> <li>Are there ho a Blast searc</li> <li>Is it longer the Do other relation</li> </ul>	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? unction from Phamerator r): Terminase unction from Blastp? (Answer hagesDB, NCBI, or both): mase Verminase DB: Terminase DB: Terminase Sunction from HHpred? ved domains and functional ): Large Subunit Terminase 0 ane binding domain? : No No		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; fun	ction c	hang	ed fr	om terminase, large su	ıbu	init (see pecaan for notes)

	1st Annotator: Madalyne2nd Ann Nin				tator:	Function: Hypothetical Protein		Feature 17 Annotation
	<b>5' end:</b> 7306 <b>3' end:</b> 7644				ength: 339			Start position?
	<ul> <li>Genemarks? (Y/N and description).</li> <li>Yes</li> <li>Are there homologous genes based on a Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp (Y/N) Yes</li> <li>Do other related phages agree (Phamerator) (Y/N) Yes</li> </ul>				(Answ Likel (Ansy both) Blast Phag Likel (cons regio	: Hypothetical Protein es DB: y Function from HHpred? erved domains and functional ns) Hypothetical Protein yes brane binding domain?		Glimmer Score: 8.62 GeneMark 7306 Starterator MAs for selected and for alt options (number, number alt MAs) 7 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
N	otes:							Es

	1st Annotator: Madalyne2nd Anno Alex			Annot Alex		Function: Portal Protein		Feature 18 Annotation
	, , , , , , , , , , , , , , , , , , , ,						00	<b>Start position?</b> Glimmer: 7897 Glimmer Score: 10.96
	Is there codin Genemarks? Yes Are there hold a Blast search Yes Is it longer the yes Do other rela (Phameratory Yes Direction: (F - Forwa	mologous g h? (Answer nan 120 bp ( nted phages ) (Y/N) wd/Rev)	l based o escriptio enes bas ) (Y/N)		(Ansv Por Likef (Ansv both) Blast Phag Likef (cons regio cover	tal Protein y function from Blastp? ver using phagesDB, NCBI, or : Portal Protein es DB: Portal Protein y Function from HHpred? erved domains and functional ns) Portal Protein about 63% age brane binding domain? No		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
No	otes:							

1 <sup>st</sup> Annotator: Alex		2 <sup>nd</sup> Annotator: Madalyne			Function: Major capsid and	F	eature 19 Annotation
<b>5' end:</b> 9723 3' en 1292				ngth: 203	Protease fusion protein		Start position?
Is there coding p Genemarks? (Y/ Yes Are there homol Blast search? (A Yes Is it longer than Yes Do other related (Phamerator) (Y Yes Direction: (Fwd Forward	logous gen nswer) 120 bp (Y/ 1 phages aş /N)	ased on cription). les based o N)	on a	<ul> <li>(Ansv Ca Likel using Cap</li> <li>Blast</li> <li>Phag Prot</li> <li>Likel (cons regio cove</li> <li>NKF No</li> </ul>	psid Maturation Protease y function from Blastp? (Answer phagesDB, NCBI, or both) sid Maturation Protease : Capsid Maturation Protease es DB: Capsid Maturation ease y Function from HHpred? erved domains and functional ns) Capsid Protein about 8% rage brane binding domain? ?		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



	<mark>1<sup>st</sup> Annota</mark> Phoenix		2 <sup>nd</sup>	2 <sup>nd</sup> Annotator: Trenton		Function: Hypothetical Protein		Feature 20 Annotation				
	<b>5' end:</b> 12930							<b>Start position?</b> Glimmer: 12930				
0 0 0	<ul> <li>Is there codin Genemarks?</li> <li>Are there hon a Blast search - yes</li> <li>Is it longer th - yes</li> <li>Do other rela (Phamerator) - yes</li> </ul>	Is it longer than 120 bp (Y/N) - yes Do other related phages agree (Phamerator) (Y/N)				Function? y function from Phamerator y function from Phamerator y function from Blastp? y function from Blastp? wer using phagesDB, NCBI, or : unknown es DB: terminase y Function from HHpred? erved domains and functional ns) ncharacterized protein; ribosome, otein-protein interaction brane binding domain? ? no		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:											

	1st Annotator: Gigi Trejo2nd Anno Josh				Function: major capsid		Feature 21 Annotation		
<b>5' en</b> 13250						D	<b>Start position?</b> Glimmer: 132520		
- Ye Are ti on a l - Ye I Is it I - Ye Do ot (Phar - Ye	here homologous Blast search? (An S onger than 120 bj S ther related phag merator) (Y/N)	ial based descripti genes ba swer) o (Y/N)		<ul> <li>mpi</li> <li>Likely using p</li> <li>mpi</li> <li>Blast:</li> <li>mpi</li> <li>Phage:</li> <li>Phage:</li> <li>pi</li> <li>Likely domai</li> <li>NKF</li> </ul>	ajor capsid hexamer cotein Function from HHpred? (conserved ns and functional regions) rane binding domain? No		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:									

<mark>1<sup>st</sup> Annota</mark> Josh	tor:	2 <sup>nd</sup>	Annot	ator:	Function: Hypothetical Protein	] ]	Feature 22 Annotation
<b>5' end:</b> 15147	<b>3' en</b> 1588	_		ength: 735		8	<b>Start position?</b> Glimmer: 15147 Glimmer Score: 11.82
Is there codin Genemarks? Y Are there hou a Blast search T Is it longer th Y Do other rela (Phamerator Y	mologous g h? (Answer 1an 120 bp ( ated phages ) (Y/N)	l based o escriptio renes bas ) (Y/N)		(Answ Unki Likely Unki Blast: Unki Phage Unki Likely (conso regior NKF Yes	nown function function from Blastp? (Answer phagesDB, NCBI, or both) nown function s DB: nown function Function from HHpred? reved domains and functional is)		Ginnmer Score. 11.02 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 Is it the longest ORF? (Y/N) Alignment agreement from Blast? (Y/N, Source) Y, hypothetical protein SEA_NIKE_26 Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) -3.153, N Gap, overlap, and spacing? (description) Gap: 64 Spacer: 10
Notes:			· · · · ·				

ı <sup>st</sup> Annotator: Sara	2 <sup>nd</sup> Annotator: Josh		Function:	Feature 23 Annotation
<b>5' end:</b> 15891 1639	d: Length:		Hypothetical Protein	Start position?
<ul> <li>Is there coding potentia Genemarks? (Y/N and d Y</li> <li>Are there homologous g a Blast search? (Answer Y</li> <li>Is it longer than 120 bp d Do other related phages (Phamerator) (Y/N) Y</li> <li>Direction: (Fwd/Rev) Fwd</li> <li>Notes:</li> </ul>	ll based on lescription). genes based on (Y/N)	<ul> <li>(Ansy Hype)</li> <li>Likel (Ansy both)</li> <li>Blast</li> <li>Phag</li> <li>Likel (consy region Non NKF</li> </ul>	othetical y function from Blastp? wer using phagesDB, NCBI, or ) : Hypothetical res DB: Hypothetical y Function from HHpred? served domains and functional ons) ne Yes brane binding domain? No	<ul> <li>Glimmer: 15891</li> <li>Glimmer Score: 17.64</li> <li>GeneMark 15891</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 4 @15891 has 36 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y.Y</li> <li>Is it the longest ORF? (Y/N) Y</li> <li>Alignment agreement from Blast? (Y/N, Source) Y, Hyperion 26</li> <li>Does it include all of the functional region (HHpred)? N</li> <li>SD Score? Is there one higher? (number, Y/N) -1.290 N</li> <li>Gap, overlap, and spacing? (description) 9</li> </ul>



ı <sup>st</sup> Annota Group						] ]	Feature 24 Annotation
<b>5' end:</b> 16422	<b>3' en</b> 1736	9	ngth: 948	Function?	0000	<b>Start position?</b> Glimmer: 16422 Glimmer Score: 13.07 GeneMark: 16446 Starterator MAs for selected and for alt	
<ul> <li>Is there codi Genemarks? Yes</li> <li>Are there ho a Blast searc Yes</li> <li>Is it longer the Yes</li> <li>Do other relation (Phamerator Yes</li> <li>Direction: (Fer the search of th</li></ul>	ng potentia (Y/N and d mologous g h? (Answer han 120 bp ( ated phages r) (Y/N)	l based or escription renes base ) (Y/N)	<ul> <li>Blas</li> <li>Phag</li> <li>Like HHI and</li> <li>Men</li> </ul>	ly function from merator (Answer) jor Tail Protein ly function from Blastp? wer using phagesDB, it, or both) t: NCBI ges DB: Major Tail Protein ly Function from ored? (conserved domains functional regions) nbrane binding domain? A? No		<ul> <li>Starterator MAS for selected and for all options (number, number alt MAS) 221 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree?</li> <li>(Y/N, Y/N) Yes- Includes all coding potential. No- genemark and glimmer do not agree Is it the longest ORF? (Y/N)</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description)</li> <li>There is a gap of 30 and a space of 10</li> </ul>	
Notos:						10-5	



<mark>1<sup>st</sup> Annotator:</mark> Aisley Allen	2 <sup>nd</sup> AI	<mark>motator:</mark>	Function:	Feature 25 Annotation
<b>5' end:</b> 3 17495	<b>s' end:</b> 18358	Length: 864	Hypothetical protein	Start position?
<ul> <li>Is there coding pote Genemarks? (Y/N a YES</li> <li>Are there homology a Blast search? (An YES</li> <li>Is it longer than 120 YES</li> <li>Do other related ph (Phamerator) (Y/N) YES</li> <li>Direction: (Fwd/Re FORWARD</li> </ul>	ential based on nd description). ous genes based ( swer) o bp (Y/N) nages agree	ON ON ON ON ON ON ON ON ON ON ON ON ON O	ges DB: Hypothetical Protein ely Function from HHpred? aserved domains and functional ions) Phage Tail Repeat	<ul> <li>Glimmer: 17495</li> <li>Glimmer Score: 9.56</li> <li>GeneMark 17495</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 25</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES YES</li> <li>Is it the longest ORF? (Y/N) YES</li> <li>Alignment agreement from Blast? (Y/N, Source) YES</li> <li>Does it include all of the functional region (HHpred)? 12.2%</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) Gap: 125 space: 10</li> </ul>
Notes:				



1 <sup>st</sup> Annotator Phoenix			tator:	Function:	]	Feature 26 Annotation	
<b>5' end:</b> 18355	3' end: 20409 gene?	Le: 2	ngth: 2055 Likel (Answ	Function? y function from Phamerator wer) phosphoesterase	Start position?          Glimmer: 18355         Glimmer Score: 7.1         GeneMark: 18355         Starterator MAs for selected and for all options (number, number alt MAs)		
Genemarks? (Y/ yes Are there homol a Blast search? ( yes Is it longer than Yes Do other related (Phamerator) (Y) yes Direction: (Fwd/ Forward	ogous genes ba Answer) 120 bp (Y/N) I phages agree /N) Possibly		<ul> <li>Blast</li> <li>Phag</li> <li>Likel (cons regio</li> <li>NKF</li> </ul>	y function from Blastp? wer using phagesDB, NCBI, or purple acid phosphotase : purple acid phosphotase es DB: pap y Function from HHpred? erved domains and functional ns) alkaline phosphotase brane binding domain? no ? no		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:		,					

<mark>1<sup>st</sup> Annotator:</mark> Daniel	2 <sup>nd</sup> Anno Madis	tator: on	Function: head-to-tail adaptor	Feature 27 Annotation
5' end:     3' end       20430     21278		e <mark>ngth</mark> : 849		Start position?
<ul> <li>Is there coding potential Genemarks? (Y/N and de Yes)</li> <li>Are there homologous ge a Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp (Yes)</li> <li>Do other related phages (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev) <ul> <li>Forward</li> </ul> </li> </ul>	based on escription). enes based on Y/N)	Lika (Ans or b He Blas He Pha He Lika (con fund He NKH	ad-to-tail adaptor ges DB: ad-to-tail adaptor ely Function from HHpred? served domains and ctional regions) ad completion protein	<ul> <li>Glimmer: 20430</li> <li>Glimmer Score: 9</li> <li>GeneMark 20430</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) No MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y</li> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes, 99%</li> <li>Does it include all of the functional region (HHpred)? Yes</li> <li>SD Score? Is there one higher? (number, Y/N) No, -2.071</li> <li>Gap, overlap, and spacing? (description)</li> </ul>





1st Annotator:2nd AnnoTrentonMadaly					Feature 28 Annotation		
	21808	Leng 531			Start position?		
Is it a g Is there coding pote Genemarks? (Y/N a Y there is not dip on the Are there homologo a Blast search? (And No Is it longer than 120 Yes Do other related ph (Phamerator) (Y/N) Direction: (Fwd/Ree Fwd	ential based on nd description). e Graph ous genes based ( swer) o bp (Y/N) aages agree		(Ansv No Likel (Ansv both) Blast Phag Likel (cons regio NKF VCS	y function from Blastp? wer using phagesDB, NCBI, or oothetical Protien : Hypothetical Protien es DB: None y Function from HHpred? served domains and functional ms) brane binding domain? No	<ul> <li>Glimmer: 21278</li> <li>Glimmer Score: 8.83</li> <li>GeneMark21278</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>(Start: 20 @21278 has 36 MA's),</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) N,Y</li> <li>Is it the longest ORF? (Y/N) <ul> <li>N second longest</li> </ul> </li> <li>Alignment agreement from Blast? (Y/N, Source) Y</li> <li>Does it include all of the functional region (HHpred)? No</li> <li>SD Score? Is there one higher? (number, Y/N)-5.541 N</li> <li>Gap, overlap, and spacing? (description) No</li> </ul>		



	<sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Madalyne Madis				<b>Function</b> :	]	Feature 29 Annotation
<ul> <li><b>5' end:</b> 21810</li> <li><b>Is</b> there codin Genemarks?</li> <li>Are there hor Blast search?</li> <li>Is it longer the Do other rela (Phamerator)</li> <li>Direction: (Further of the search)</li> <li>-</li> </ul>	nologous ger ' (Answer) Yes an 120 bp (Y/ ted phages a ) (Y/N)	23 e? eased on cription). Ye ues based on N) Yes	es	<ul> <li>Likely (Ansv both)</li> <li>Blast:</li> <li>Phage chape</li> <li>Likely (cons regio</li> <li>NKF</li> </ul>	: Hypothetical Protein es DB: tail assembly erone y Function from HHpred? erved domains and functional ns) Minor Capsid/ Unknown brane binding domain?		Start position? Simmer: 21810 Minner Score: 4.81 Gimmer Score: 4.81 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? VN, V/N Yes and yes is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Yes Does overlap, and spacing? (description) -56 gap, 9 space
Notes:				-			

1 <sup>st</sup> Annota Gigi Tre				Function: tail assembly	] ]	Feature 30 Annotation			
5' end: 22,265	3' end: 22,723		ngth: 459	chaperone		Start position? Glimmer: 22,265 Glimmer Score: 12.02 GeneMark: 22,274 Starterator MAs for selected and for alt			
<ul> <li>Is there cod Genemarks Yes</li> <li>Are there ho a Blast searcy Yes</li> <li>Is it longer ty Yes</li> </ul>			(Ansv tail Likely using Blast: tail Phage tail Likely (consv region	aśsembly chaperone y function from Blastp? (Answer phagesDB, NCBI, or both) assembly chaperone assembly chaperone es DB: assembly chaperone y Function from HHpred? erved domains and functional ns) There is no known function prane binding domain?		Glimmer 22,209 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:									

1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Trenton Shappee			Tail Chaperone		Feature 31 Annotation		
<b>5' end:</b> 22265	3' end: 22917		ngth: 854	Protein	Start position?		
<ul> <li>Is there codin Genemarks?</li> <li>Are there hon a Blast search Yes</li> <li>Is it longer the Yes</li> <li>Do other rela (Phamerator) Yes</li> <li>Direction: (F</li> <li>Fwd</li> </ul>		ed on	Tail Likely using Tail Blast: Phage Likely domai Tail NKF n Memh No U tRNA?	orane binding domain? <sup>•</sup> no	<ul> <li>Glimmer Score: None</li> <li>GeneMark None</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>There is none</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)NN</li> <li>Is it the longest ORF? (Y/N) Yes</li> <li>Alignment agreement from Blast? (Y/N, Source) There is none</li> <li>Does it include all of the functional region (HHpred)?Yes</li> <li>SD Score? Is there one higher? (number, Y/N) -2.224 N</li> <li>Gap, overlap, and spacing? (description) It overlaps with 31</li> </ul>		
Notes There	was a nrogram	med ti	anglatio	nal frameshift	And the second s		

Notes: There was a programmed translational frameshift



1 <sup>st</sup> Annotator: Trenton		tator: Tape measure Protein		Feature 32 Annotation	
<b>5' end:</b> 22926	<b>3' end:</b> 26219	Lengt 3294			Start position?
<ul> <li>Is there coding podescription).</li> <li>Yes</li> <li>Are there homolog (Answer)</li> <li>Is it longer than 12 Yes</li> </ul>	hages agree (Phamerato	ast scarch?	Likely Using Yes Blast: Phage Likely domai Tapo	Function? function from Phamerator (Answer) measure Protien function from Blastp? (Answer phagesDB, NCBI, or both) Tape measure protien s DB: Tape measure protien s DB: Tape measure protien function from HHpred? (conserved ins and functional regions) e measure protien	<ul> <li>Glimmer Score: 9.17</li> <li>GeneMark22926</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>(Start: 2 @22926 has 28 MA's),</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YY</li> <li>Is it the longest ORF? (Y/N)Y</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>V</li> <li>Does it include all of the functional region (HHpred)?</li></ul>
Notes:					1-1



1 <sup>st</sup> Annotator: Nina	otator:	<b>Function</b> : Minor Tail Protein	Feature 33 Annotation
5' end:     3' end:     L       26252     27568	<mark>ength</mark> : 1316		<b>Start position?</b> <ul> <li>Glimmer: 26252</li> <li>Glimmer Score: 5.51</li> </ul>
<ul> <li>Is there coding potential based on Genemarks? (Y/N and description). Yes</li> <li>Are there homologous genes based on a Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp (Y/N) Yes</li> <li>Do other related phages agree (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev) Forward</li> <li>Notes:</li> </ul>	<ul> <li>Like (Ans or b</li> <li>Blas</li> <li>Blas</li> <li>Phay</li> <li>Phay</li> <li>Like</li> <li>(con func</li> <li>Mathematical (Construction)</li> <li></li></ul>	ajor tail protein ges DB: ajor tail protein ly Function from HHpred? served domains and ctional regions) ajor tail protein	<ul> <li>Glimmer Score: 5.51</li> <li>GeneMark: 26228</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>26 MAS</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)</li> <li>Y, N= genemark and glimmer do not agree</li> <li>Is it the longest ORF? (Y/N)</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>Yes</li> <li>Does it include all of the functional region (HHpred)? Yes</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) Gap= 32, Space= 13</li> </ul>



1st Annotator:2nd AnnoMadison RennTrento			<b>Function</b> : Minor Tail Protein	Feature 34 Annotation		
<b>5' end:</b> 27588	<b>3' e</b> 1 305			ngth: 2922		Start position?
<ul> <li>Is there codi Genemarks: Yes</li> <li>Are there ho on a Blast set</li> <li>Is it longer t</li> <li>Do other rel (Phamerato)</li> <li>Direction: (I</li> </ul>	? (Y/N and omologou earch? (A) than 120 h lated phag or) (Y/N): Y Fwd/Rev)	ntial base d descrip ns genes l nswer): Y op (Y/N): ges agree Yes : Forware	otion).: Dased Yes Yes	<ul> <li>(Ansv (Ansv both)</li> <li>Blast</li> <li>Phag</li> <li>Likel (cons regio Filam</li> <li>NKF:</li> </ul>	No brane binding domain?: No	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 C	Codon A'	ТG				

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			Annot Phoen		<b>Function</b> : Minor tail protein		Feature 35 Annotation		
	5' end: 30509 IS i Is there codi Genemarks? Ye Are there ho a Blast searc Ye Is it longer the Ye Do other rela (Phamerator	8 mologous g h? (Answer 8 han 120 bp ( 8 ated phages	50 I based o escriptio renes bas ) (Y/N)	n n).	(Ansv Likely (Ansv both) Blast Phage Likely (cons	Function? y function from Phamerator ver) Minor tail protein y function from Blastp? ver using phagesDB, NCBI, or Minor tail protein : Minor tail protein es DB: Minor tail protein y Function from HHpred? erved domains and functional ns) Tail protein	<ul> <li>Start position?</li> <li>Glimmer: 30509</li> <li>Glimmer Score: 8.57</li> <li>GeneMark 30509</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 81 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes</li> <li>Is it the longest ORF? (Y/N) Yes</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes 100%</li> <li>SD Score? Is there one higher? (number, Y/N) -3.394, Yes -3.262</li> <li>Gap, overlap, and spacing? (description)</li> </ul>		
D	<ul> <li>Direction: (Fwd/Rev)</li> <li>Forward</li> </ul>				<ul> <li>Memi No</li> <li>tRNA</li> </ul>	brane binding domain? ? No	4		
N	otes:				1				

<mark>1<sup>st</sup> Annotator:</mark> Aisley Allen	2 <sup>nd</sup> Anno	otator:	Function:	Feature 36 Annotation
<b>5' end: 3' en</b> 31660 3242		ength: 762	Hypothetical protein	Start position?
<ul> <li>Is there coding potential Genemarks? (Y/N and de YES</li> <li>Are there homologous g a Blast search? (Answer)</li> <li>Is it longer than 120 bp (YES</li> <li>Do other related phages (Phamerator) (Y/N) YES</li> <li>Direction: (Fwd/Rev) FORWARD</li> <li>Notes:</li> </ul>	l based on escription). enes based on ) Y/N)	(Ansy both) Blast Phag Likel (cons regio doma	Function? y function from Phamerator wer) N/A y function from Blastp? wer using phagesDB, NCBI, or ) hypothetical protein : res DB: function unknown y Function from HHpred? served domains and functional ons) Leucine zipper Dimerization in of transcription factor brane binding domain? NO .? NO	<ul> <li>Glimmer: 31660</li> <li>Glimmer Score: 6.35</li> <li>GeneMark 31660</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 33</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES YES</li> <li>Is it the longest ORF? (Y/N) YES</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>Does it include all of the functional region (HHpred)? 5.93%</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) Gap: -1 space: 12</li> </ul>



1 <sup>st</sup> Annotator: Phoenix		2 <sup>nd</sup> Annotator: Nina			<b>Function</b> : Hypothetical Protein	Feature 37 Annotation	
<b>5' end:</b> 32370	3' en 3269	_		<mark>ngth</mark> : 324		Start position?	
Is Is there coding p (Y/N and descrip) yes Are there homolo search? (Answer) yes Is it longer than p yes Do other related Direction: (Fwd/ - Forward	tion). ogous genes ba (20 bp (Y/N) phages agree ( Rev)	on Genemai ised on a Bla	ıst	(Ansv - H Likel (Ansv both) - H Blast Blast Phag Likel (cons regio H NKF	ypothetical protein y function from Blastp? wer using phagesDB, NCBI, or ypothetical protein : unknown es DB: unknown y Function from HHpred? werved domains and functional ms) ypothetical protein brane binding domain?	<ul> <li>Glimmer: 32433</li> <li>Glimmer Score: 11.05</li> <li>GeneMark: 32433</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes</li> <li>Is it the longest ORF? (Y/N) yes</li> <li>Alignment agreement from Blast? (Y/N, Source)yes</li> <li>Does it include all of the functional regio (HHpred)?yes</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) -52, 10</li> </ul>	Dn
Noto:							Ants



	1st Annotator:2nd AnDanielAisley		<mark>Annot</mark> sley Al		Function: Hypothetical protein	F	eature 38 Annotation	
	32698 33081 <b>Is it a gene?</b> Are 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 (Phanerator) (Y/N) NO Direction: (Fwd/Rev) - Forward				(Ansv Unk Likely (Ansv both) No Blast: Hyp Phage Hyp Likely (cons regio NKF Yes	mown function y function from Blastp? ver using phagesDB, NCBI, or othetical protein es DB: othetical protein y Function from HHpred? erved domains and functional ns) brane binding domain?		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)
N	- Forwa	rd						

ı <sup>st</sup> Annotator: Trenton		2 <sup>nd</sup> A	nnot	ator:	Function: Hypothetical Protien	]	Feature 39 Annotation
<b>5' end:</b> 33081	3' en 3327			<mark>1gth</mark> : 92			Start position?
<ul> <li>Is there codim Genemarks? ( Kinda Theres just)</li> <li>Are there hom search? (Answ</li> <li>Is it longer that Yes</li> <li>Do other relat (Y/N)</li> <li>Y</li> </ul>	<ul> <li>search? (Answer) No</li> <li>Is it longer than 120 bp (Y/N)</li> <li>Yes</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> <li>Y</li> </ul>			(Ansv No Likel (Ansv both) No Blast Denage Likel (cons regio	y function from Blastp? ver using phagesDB, NCBI, or : Hypothetical protein es DB: Hypothetical protein y Function from HHpred? erved domains and functional ns) Yes brane binding domain?		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:							

1 <sup>st</sup> Annotator: Nina		2 <sup>nd</sup> Annotator: Phoenix		or:	<b>Function</b> : Membrane Protein	]	Feature 40 Annotation	
<b>5' end:</b> 33275			U	ength: 689		<b>Start position?</b> <ul> <li>Glimmer: 33275</li> <li>Glimmer Score: 10.75</li> <li>GeneMark: 33275</li> </ul>		
<ul> <li>Is there codir Genemarks?</li> <li>Are there hor a Blast search yes</li> <li>Is it longer th yes</li> <li>Do other rela (Phamerator) yes</li> <li>Direction: (Further the search searc</li></ul>	nologous g 1? (Answer) an 120 bp ( ted phages ) (Y/N)	l based on escription). enes based on ) Y/N)		Like (Ans or bo Blast Blast Phag Fun Like: (con: func Me NKF Yes Mem NO	mbrane Protein t: mbrane Protein ges DB: nction Unknown ly Function from HHpred? served domains and tional regions) mbrane Protein		options (number, number alt MAs)	
Notos							hours	



	1 <sup>st</sup> Annotator: Aisley Allen		Annot	tator:	Function: endolysin		Feature 41 Annotation
<b>5' end:</b> 34067	<b>3' en</b> 3485			<mark>ngth</mark> : <sup>789</sup>			<b>Start position?</b>
Is it a gene?		n	Function?         Likely function from Phamerator (Answer) endolysin         Likely function from Blastp? (Answer using phagesDB, NCBI, or both) endolysin         Blast:         Phages DB: endolysin			<ul> <li>Glimmer Score: 10.47</li> <li>GeneMark34034</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 32</li> <li>Does it include all of the coding potential</li> </ul>	
Are there hon a Blast search YES	<ul> <li>Is there coding potential based on Genemarks? (Y/N and description). YES</li> <li>Are there homologous genes based on a Blast search? (Answer) YES</li> </ul>					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	
<ul> <li>Is it longer than 120 bp (Y/N) YES</li> <li>Do other related phages agree (Phamerator) (Y/N) NO, there is a dip (?)</li> <li>Direction: (Fwd/Rev) Forward</li> </ul>			<ul> <li>Like (con func Struc</li> <li>NKF</li> </ul>	ely Function from HHpred? Iserved domains and ctional regions)Protein cture Initiative		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)	
			<ul> <li>Membrane binding domain? NO</li> <li>tRNA? NO</li> </ul>		Gap: 102 spacer: 7		



	<b>notator:</b> 2 <sup>nd</sup> Daniel	Anno	tator:	Function: Hypothetical protein	Feature 42 Annotation		
-			ength: 513 bp		Start position?		
Y, but mod Are th a Blas Y Is it lo Y Do ot Y	<b>Is it a gene?</b> re coding potential based narks? (Y/N and descripti lerate ere homologous genes ba t search? (Answer) nger than 120 bp (Y/N) her related phages agree herator) (Y/N) tion: (Fwd/Rev) Reverse		(Ansy Likel (Ansy both) Blast Blast Phag Likel (consy regio	cnown function y function from Blastp? wer using phagesDB, NCBI, or chown function/Hypothetical tein tein bothetical protein ges DB: cnown function ly Function from HHpred? served domains and functional ons) cnown function	<ul> <li>Glimmer: 35287</li> <li>Glimmer Score: 7.59</li> <li>GeneMark: 35332</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>33 MA'8</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y (moderate), No</li> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N) Y, -1.907</li> <li>Gap, overlap, and spacing? (description) -32.</li> </ul>		



				<sup>d</sup> Annotator: Aisley Allen		Function: Hypothetical Protein	Feature 43 Annotation
	<b>5' end: 3' end: Le</b> 35708 35406			angth: 303		Start position?	
	Is there codi Genemarks? Yes Are there hor a Blast searc Is it longer th Do other rela (Phamerator Direction: (F	mologous g h? (Answer) 1an 120 bp (' ated phages ) (Y/N) Yes	based on escription enes base Yes Y/N) Yes agree		<ul> <li>Likely (Ansy both)</li> <li>Blast</li> <li>Phagy</li> <li>Likely (cons regio</li> <li>NKF</li> </ul>	: Hypothetical Protein es DB: binding protein y Function from HHpred? erved domains and functional ns) Hypothetical Protein brane binding domain?	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)
N	otes:						£5



	<mark>1<sup>st</sup> Annota</mark> Madison R		Anno Danio	el DNAJ Like		Feature 44 Annotation		
	<b>5' end:</b> 36367			<mark>ngth</mark> : 663	Chaperonin		Start position?	
	Is there cod Genemarks Yes Are there ho on a Blast so Is it longer t Do other rel (Phamerato	t a gene? ing potential base ? (Y/N and descrip omologous genes l earch? (Answer): Y than 120 bp (Y/N): han 120 bp (Y/N): lated phages agree r) (Y/N): Yes, Sally Fwd/Rev): Reverse	pased es Yes K	<ul> <li>(Ansyleta)</li> <li>Likel (Ansyleta)</li> <li>both check</li> <li>Blast</li> <li>Phag</li> <li>Likel (consyleta)</li> <li>NKF:</li> <li>Mem</li> </ul>	Function? y function from Phamerator wer): DNAJ Like Chaperonin y function from Blastp? wer using phagesDB, NCBI, or ? No NCBI data available - c on this : DNAJ Like Chaperonin tes DB: DNAJ Like Chaperonin y Function from HHpred? served domains and functional ons): DNAJ Homolog Subfamily No brane binding domain?: IOWN ?: No		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	
N	otes: *GTG :	START CODON	*					

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<mark>1<sup>st</sup> Annota</mark> Phoenix		Annotat	tor:	Function: hypothetical protein	Feature 4	5 Annotation	
5' end: 36548	3' end: 36360 t a gene?	<b>Leng</b> 306	6 I Likely (Answ	Function?	<ul> <li>Glimmer: 36548</li> <li>Glimmer Score: 1</li> <li>GeneMark 36548</li> <li>Starterator MAs</li> </ul>	2	
<ul> <li>yes</li> <li>Are there hom Blast search? (</li> <li>Is it longer that yes</li> </ul>	ed phages agree (Y/N) rd/Rev)		Likely Using Blast: Blast: Phage Likely (consc region - rot ex NKF Meml	y function from Blastp? (Answer phagesDB, NCBI, or both) ypoethetical function unknown es DB: no data y Function from HHpred? erved domains and functional ns) tein required for localization of TasA to tracellular matrix	<ul> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes</li> <li>Is it the longest ORF? (Y/N) yes</li> <li>Alignment agreement from Blast? (Y/N, Source)yes</li> <li>Does it include all of the functional region (HHpred)?yes</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description)125, 17</li> </ul>		
Notes:							

	1st Annotator: Gigi Trejo2nd Anno Danie				Feature 46 Annotation		
	5' end:       3' end:       Le         36750       36,541		<b>ngth:</b> 210		Start position?		
	<ul> <li>Is there codi Genemarks? Yes</li> <li>Are there ho a Blast searc No</li> <li>Is it longer the Yes</li> <li>Do other relation No</li> </ul>			(Ansv unk Likely (Ansv both) Blast: Blast: unk Phage Ink Cons regio NKF Yes Meml N0 TRNA	nown function y function from Blastp? ver using phagesDB, NCBI, or nown function es DB: nown function y Function from HHpred? erved domains and functional ns)		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
$\mathbf{F}$	Notes:			No			And S

No and Andrews

	1 <sup>st</sup> Annotator: Alex	2 <sup>nd</sup>	Annot	tator:	<b>Function</b> :	ł	Feature 47 Annotation
	5' end: 3	ential based o nd descriptio ous genes base swer) bp (Y/N) ages agree	n n).	<ul> <li>(Ansv Cas Likel (Ansv both)</li> <li>Blast</li> <li>Blast</li> <li>Phage Cas Cas</li> <li>Likel (cons regio</li> <li>Cas</li> <li>NKF1</li> <li>Mem no</li> </ul>	4 exonuclease y function from Blastp? ver using phagesDB, NCBI, or 4 exonuclease es DB: 4 exonuclease y Function from HHpred? erved domains and functional ns) 4 exonuclease no brane binding domain?		Start position? Glimmer: 38966 Glimmer Score: 9.98 GeneMark: 38966 Starterator MAs for selected and for alt options (number, number alt MAs) 25 MA'8 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
N	Reverse otes:			□ tRNA	. <sup>2</sup> No		

	Annotator: sley Allen	Function: Hypothetical protein	Feature 48 Annotation
<b>5' end:</b> 39958 <b>38966</b>	Length: 993		<b>Start position?</b> Glimmer: 30958
<ul> <li>Is there coding potential based of Genemarks? (Y/N and description Yes)</li> <li>Are there homologous genes base a Blast search? (Answer) Yes</li> <li>Are there homologous genes base a Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp (Y/N) Yes</li> <li>Do other related phages agree (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev)</li> <li>Reverse</li> </ul>	n). ed on ed on D Blast Phag D Like (Ans or bo D Phag D Like (cons func Hy M M M M M M M M M M M M M	t: A recombinase ges DB: A recombinase ly Function from HHpred? served domains and tional regions) pothetical protein	<ul> <li>Glimmer Score: 7.95</li> <li>GeneMark: 39958</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>25 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y</li> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes</li> <li>Does it include all of the functional region (HHpred)? Yes</li> <li>SD Score? Is there one higher? (number, Y/N) Yes, -1.907</li> <li>Gap, overlap, and spacing? (description)</li> </ul>
Notes:			

ı <sup>st</sup> Annotator: Nina	2 <sup>nd</sup> Anno	tator:	<b>Function</b> : HNH Endonuclease	Feature 49 Annotation
<b>5' end:</b> 40488 39955		<mark>ngth</mark> : <sup>533</sup>		<b>Start position?</b> Glimmer: 40488
<ul> <li>Is there coding potential backgenemarks? (Y/N and descrives)</li> <li>Are there homologous general a Blast search? (Answer) Yes</li> <li>Are though than 120 bp (Y/N Yes)</li> <li>Is it longer than 120 bp (Y/N Yes)</li> <li>Do other related phages ag (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev) Reverse</li> </ul>	ased on ription). es based on N)	<ul> <li>Like (Ans or bo H</li> <li>Blas H</li> <li>Phas H</li> <li>Like (con func</li> <li>NKF</li> </ul>	IH Endonuclease t: IH Endonuclease ges DB: IH Endonuclease Iy Function from HHpred? served domains and tional regions) IH Endonuclease	<ul> <li>Glimmer Score: 9.37</li> <li>GeneMark: 40488</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)Yes</li> <li>MAS</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)</li> <li>Y.Y- genemark and glimmer agree</li> <li>Is it the longest ORF? (Y/N)</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) Gap= -4, Space= 9</li> </ul>





1 <sup>st</sup> Annotator: Trenton Shapped		Annotato adalyne		Function: ruvc-like resolvase	Feature 50 Annotation		
	3' end: 40485 gene? otential based on and description r coding	Lengt 573	Likel (Ansv ruvc	<b>Function?</b> y function from Phamerator ver) -like resolvase y function from Blastp? ver using phagesDB, NCBI, or	<ul> <li>Start position?</li> <li>Glimmer: 41057</li> <li>Glimmer Score: 15.27</li> <li>GeneMark41057</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Start: 190 @41057 has 30 MA's),</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY</li> <li>Is it the longest ORF? (Y/N)</li> </ul>		
a Blast search? (A There are I Is it longer than 12 Y Do other related p (Phamerator) (Y/N Direction: (Fwd/R - Reverse	nswer) 20 bp (Y/N) phages agree N)		Phag Likel (cons regio NKF	t <mark>here is a known function</mark> brane binding domain?	<ul> <li>N i believe it is the second longest reading frame</li> <li>Alignment agreement from Blast? (Y/N, Source) There is an alignment agreement from blast</li> <li>Does it include all of the functional region (HHpred)? Y</li> <li>SD Score? Is there one higher? (number, Y/N)-3.976 N</li> <li>Gap, overlap, and spacing? (description)</li> <li>No gap</li> </ul>		
Notes:							

	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Madison Renn Phoer		Annot Phoen		<b>Function</b> : Hypothetical		Feature 51 Annotation
<b>5' end:</b> 41239	<b>3' en</b> 4105	_		<b>ngth:</b> 186	Protein		<b>Start position?</b> Glimmer: 41239 Glimmer Score: 41054
<ul> <li>Is there codi Genemarks: - Yes</li> <li>Are there ho on a Blast se - Yes</li> <li>Is it longer t - Yes</li> <li>Is it longer t - Yes</li> <li>Do other rel (Phamerato - Yes</li> <li>Direction: (I - Reverse</li> </ul>	omologous earch? (An han 120 bj ated phag r) (Y/N)	ial base descrip genes l swer) o (Y/N)	based	<ul> <li>(Ansv - Ft</li> <li>Likely (Ansv both)</li> <li>Blast:</li> <li>Phage</li> <li>Likely (constregio funct</li> <li>NKF:</li> </ul>	Inction Unknown y function from Blastp? ver using phagesDB, NCBI, or : Function Unknown : Hypothetical Protein es DB: No Data Available y Function from HHpred? erved domains and functional ns): Several hits for different ions - look into this Yes brane binding domain?: own		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 St	art Codo	n					

1st Annotator:2nd AnnoTrentonPhoen	tator: lix	Function: Hypothetical Protein	]	Feature 52 Annotation		
	<mark>ngth</mark> : 273	Function?		Start position?		
Is it a gene?				Glimmer Score: 11.91 GeneMark41508 Starterator MAs for selected and for alt options (number, number alt MAs) (Start: 39 @41511 has 18 MA's), (Start: 40		
<ul> <li>Is there coding potential based on Genemarks? (Y/N and description).</li> <li>Y</li> </ul>	<ul> <li>Likely function from Phamerator (Answer) None</li> <li>Likely function from Blastp? (Answer using phagesDB, NCBI, or both) No</li> <li>Blast: hypothetical protein</li> <li>Phages DB: Function unknown</li> </ul>		a	@41508 has 13 MA's)		
<ul> <li>Are there homologous genes based on a Blast search? (Answer)</li> <li>No</li> </ul>				(Y/N, Y/N)YY Is it the longest ORF? (Y/N)N it is the second longest		
<ul> <li>Is it longer than 120 bp (Y/N)</li> <li>Yes</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> </ul>	U	ly Function from HHpred? seryed domains and functional		Alignment agreement from Blast? (Y/N, Source) Does it include all of the functional region		
Y Direction: (Fwd/Rev)	□ NKF Yes	Yes		(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		
- Rev	<ul> <li>Mem</li> <li>tRNA</li> <li>No</li> </ul>	brane binding domain? .?		Little overlap on both ends		



	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Madalyne		2 <sup>nd</sup> Annotator: Function: MazG-like nucleotide			]	Feature 53 Annotation
	<b>5' end:</b> 41900	<b>3' end:</b> 41508		<mark>ngth</mark> : <sup>393</sup>	pyrophosphohydrolas e		Start position?
	Is it a gene?			<b>Function?</b> Likely function from Phamerator			Glimmer: 41903 Glimmer Score: 12.84 GeneMark: 41900 Starterator MAs for selected and for alt
	Is there codin Genemarks? (	g potential based on Y/N and description)	. Yes	(Ansy pyroj	<b>wer)</b> MazG-like nucleotide phosphohydrolase		<b>options (number, number alt MAs)</b> 41903 has 7 MA's 41900 has 15 MA's
D	Are there hon Blast search?	nologous genes based (Answer)	on a	Likely function from Blastp? (Answer using phagesDB, NCBI, or both)			Does it include all of the coding potential and do Genemark and Glimmer agree?
D	Is it longer th	an 120 bp (Y/N) <mark>Yes</mark>			<b>Blast:</b> MazG-like nucleotide pyrophosphohydrolase <b>Phages DB:</b> MazG-like nucleotide		(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
D	Do other related phages agree (Phamerator) (Y/N)				es DB: MazG-like nucleotide phosphohydrolase ly Function from HHpred? served domains and functional		
D	Direction: (Fv	vd/Rev) Reverse		regio	ns) N/A	D	(HHpred)? SD Score? Is there one higher? (number, Y/N)
	-				brane binding domain?		Gap, overlap, and spacing? (description)
	atacı				Λ.΄		h-∞





	1 <sup>st</sup> Annotator: Gisselle Trejo Phoen					Function: Single-stranded		Feature 54 Annotation
	<b>5' end:</b> 42,772	<b>3' en</b> 42,0			ngth: 714	DNA-binding protein		<b>Start position?</b> Glimmer: 42,772 Glimmer Score: 7.73
	Is there codin Genemarks? Yes Are there hon a Blast search Yes Is it longer th Yes Do other rela (Phamerator Yes Direction: (F Reverse	mologous g h? (Answer nan 120 bp ( nted phages ) (Y/N)	l based o escriptio enes bas ) (Y/N)		(Anss ssd Likel (Ansy both) Ssd Blast Ssd Phag Ssd Likel (cons regio	na binding protein y function from Blastp? wer using phagesDB, NCBI, or na binding protein : na binding protein es DB: na binding protein y Function from HHpred? served domains and functional ons)		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:
N	otes:							

	1 <sup>st</sup> Annota Alex	1 <sup>st</sup> Annotator: Alex 2 <sup>nd</sup> Anno Aisley A			Function: Hypothetical protein	Feature 55 Annotation	
	Is there codi Genemarks? Ye Are there ho a Blast searc Ye Is it longer th Ye Do other rela (Phamerator Ye	s mologous g h? (Answer) s nan 120 bp ( s ted phages ) (Y/N) s	2 e? l based o escriptio genes bas	on on).	<ul> <li>(Ansv unk Likel (Ansv both) unk</li> <li>Blast:</li> <li>Phage</li> <li>Likel (cons regio</li> <li>NKF No</li> </ul>	nown function y function from Blastp? ver using phagesDB, NCBI, or	Start position?Gimmer: 42906Gimmer Score: 20.96GeneMark: 42906Starterator MAs for selected and for alt options (number, number alt MAs)11 MA'sDoes it include all of the coding potential and do Genemark and Glimmer agree?(YN, YN) Yes and YesIs it the longest ORF? (Y/N) YesAlignment agreement from Blast? (Y/N, Source) Yes 100%SD Score? Is there one higher? (number, Y/N) -1.748, n0 Gap, overlap, and spacing? (description)
	- Rever	,			□ tRNA	? No	
]	Notes:						

	1 <sup>st</sup> Annotator Aisley Allen		Anno	tator:	Function:		Feature 56 Annotation
	<b>5' end:</b> 43093	<b>3' end:</b> 42908	Le	<mark>ngth</mark> : 186	Hypothetical Protein		Start position?
	Is there coding Genemarks? (Y YES Are there home on a Blast searce ES Is it longer that Do other relate (Phamerator) (	V/N and descrip plogous genes l ch? (Answer) n 120 bp (Y/N) ed phages agree Y/N)	otion). based YES	<ul> <li>(Ansv (Ansv both) prote</li> <li>Blast:</li> <li>Phage</li> <li>Likely (cons regio 89.19</li> <li>NKF V</li> </ul>	: hypothetical protein es DB: function unknown y Function from HHpred? erved domains and functional ns) uncharacterized protein, Yes brane binding domain? NO		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
N	otes:						

Ð

1 <sup>st</sup> Annotator: Madalyne	2 <sup>nd</sup> Annotato Madison	r: Function: Hypothetical Protein	Feature 57 Annotation
5' end:     3' end       43338     43102	: Lengtl 237	1:	Start position?
<ul> <li>Is there coding potential bas Genemarks? (Y/N and described of the second of</li></ul>	sed on iption). yes based on a ) Yes ee	<b>Function?</b> 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?	<ul> <li>Glimmer: 43338</li> <li>Glimmer Score: 12.42</li> <li>GeneMark 43338</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 43338 has 24 MAs</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) yes and yes</li> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description)</li> </ul>



<mark>1<sup>st</sup> Annotator:</mark> Aisley Allen			Function: Unknown function	Feature 58 Annotation		
<b>5' end: 3' en</b> 43416 4354		e <mark>ngth</mark> : 132		<b>Start position?</b>		
<ul> <li>Is there coding potentia Genemarks? (Y/N and d YES</li> <li>Are there homologous g a Blast search? (Answer</li> <li>Is it longer than 120 bp ( YES</li> <li>Do other related phages (Phamerator) (Y/N) NO</li> <li>Direction: (Fwd/Rev) Forward</li> </ul>	l based on escription). renes based on ) YES (Y/N)	(Ansy None Likel (Ansy both) Function Blast Function Phag Likel (cons regio	y function from Blastp? wer using phagesDB, NCBI, or unknown unknown es DB: function unknown y Function from HHpred? served domains and functional ons)Protein of unknown function	<ul> <li>Glimmer: 43416</li> <li>Glimmer Score: 3.57</li> <li>GeneMark N/A</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>N/A</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) no genemark available.</li> <li>Is it the longest ORF? (Y/N) NO</li> <li>Alignment agreement from Blast? (Y/N, Source) YES</li> <li>Does it include all of the functional region (HHpred)? 41.86%</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) gap: 77 space: 18</li> </ul>		





1 <sup>st</sup> Annotator: Phoenix	tator: Function: Hypothetical protein	Feature 59 Annotation
5' end:       3' end:       L         43520       43410       43410	ngth: 111	Start position?
<ul> <li>Is there coding potential based on Genemarks? (Y/N and description).</li> <li>Are there homologous genes based on a Blast search? (Answer)</li> <li>Is it longer than 120 bp (Y/N) <ul> <li>no</li> <li>Do other related phages agree (Phamerator) (Y/N) <ul> <li>yes</li> </ul> </li> <li>Direction: (Fwd/Rev) <ul> <li>Reverse</li> </ul> </li> </ul></li></ul>	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	<ul> <li>Glimmer:</li> <li>Glimmer Score:</li> <li>GeneMark 43520</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)</li> <li>Is it the longest ORF? (Y/N)</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description)4, 18</li> </ul>



	1st Annotator: Gigi Trejo2nd Annot Danie			Function: Hypothetical		Feature 60 Annotation		
	5' end:	3' en	d:		<mark>ngth</mark> :	protein		Start position?
	Is there codin Genemarks? No Are there hon a Blast search Yes Is it longer th Yes Do other rela (Phamerator) Yes Direction: (F - Revers	mologous g h? (Answer nan 120 bp ( nted phages ) (Y/N) wd/Rev)	e? I based o escriptio enes bas Y/N)	on on).	(Ans unl Likel (Ans both Blast Blast I Phag Phag Like (com regic Salar VKF Yes	known function y function from Blastp? wer using phagesDB, NCBI, or known function transform transform black wown function y Function from HHpred? served domains and functional ons) known function		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
N	otes:							

	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Alex		notator: Function:		] ]	Feature 62 Annotation			
	5' end: 44046 Is there codin Genemarks? Yes Are there hom a Blast search		e? l based of escription	n n).	(Ansv Unk □ Likel (Ansv both)	Hypothetical protein <b>Function?</b> y function from Phamerator wer) mown function y function from Blastp? y function from Blastp? wer using phagesDB, NCBI, or hypothetical protein : hypothetical protein		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 OPE? (Y/N) No	
	Yes Is it longer th Yes Do other rela (Phamerator) Yes Direction: (Fy - Revers	an 120 bp ( ted phages ) (Y/N) wd/Rev)	(Y/N)		Likel (cons regio Tra	nscription regulator Yes brane binding domain?	<ul> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes 100%</li> <li>SD Score? Is there one higher? (number, Y/N) -3.072 and no</li> <li>Gap, overlap, and spacing? (description) Gap of -4 and spacing of 16, no overlap</li> </ul>		
Ň	otes:								

1 <sup>st</sup> Annotator: 2 <sup>nd</sup> A Nina		2 <sup>nd</sup> Anno	notator:		<b>Function:</b> Hypothetical	] ]	Feature 62 Annotation	
<b>5' end:</b> 44135	<b>3' end</b> 44043		<mark>engt</mark> 92	<mark>h</mark> :	Protein	Start position?		
□ Is there codi Genemarks?	mologous ge h? (Answer) han 120 bp (Y ated phages : ) (Y/N)	based on scription). enes based on K/N)		or bo Fur Blast Fur Phag Fur Like (cons func NKF Yes Mem	action Unknown t: nction Unknown ges DB: action Unknown ly Function from HHpred? served domains and tional regions)	8	Glimmer Score: N/A GeneMark: 44135 Starterator MAs for selected and for alt options (number, number alt MAs) 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) 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:							F-5	



			Annot Gigi	Hypothetical			Feature 63 Annotation		
<b>5' end:</b> 44419	3' en 4413 t a gen	5 e?	Le	ngth: 285 Likel (Ansv	Function? y function from Phamerator ver): Function Unknown y function from Blastp? ver using phagesDB, NCBI, or : Function Unknown		<ul> <li>Glimmer Score: 10.77</li> <li>GeneMark: 44419</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs): 26 MA<sup>3</sup></li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes</li> </ul>		
<ul> <li>Are there here on a Blast single on a Blast sindle on a Blast single on a Blast single on a Blast single on</li></ul>	<sup>7</sup> K than 120 b <u>r</u> lated phago or) (Y/N)	) (Y/N)		<ul> <li>Phage</li> <li>Likely (consiregio Funct)</li> <li>NKF:</li> </ul>	Yes brane binding domain?: own	<ul> <li>Is it the longest ORF? (Y/N): No</li> <li>Alignment agreement from Blast? (Y/N, Source): Yes</li> <li>Does it include all of the functional region (HHpred)? 34% Coverage</li> <li>SD Score? Is there one higher? (number, Y/N): DNA Master</li> <li>Gap, overlap, and spacing? (description): Gap: -4, Overlap: None, Spacing: 10</li> </ul>			
Notes: Start (	Codon GT	'G	I	1					

<mark>1<sup>st</sup> Annotator:</mark> Aisley Allen	2 <sup>nd</sup> Anne Phoe	otator: nix	Function:	Feature 64 Annotation		
5' end:     3' en       44865     4441		ength: 450	Hypothetical Protein	Start position?		
<ul> <li>Is there coding potentia Genemarks? (Y/N and d Yes, it is a little suspicious the Are there homologous g a Blast search? (Answer Yes</li> <li>Is it longer than 120 bp ( Yes</li> <li>Do other related phages (Phamerator) (Y/N) No</li> <li>Direction: (Fwd/Rev) Reverse</li> </ul>	l based on escription). hough renes based on ) (Y/N)	<ul> <li>(Ansy both)</li> <li>Likel (Ansy both)</li> <li>Blast</li> <li>Phag</li> <li>Likel (consy central dehycons)</li> <li>NKF</li> <li>Mem</li> </ul>	Function? y function from Phamerator wer) N/A, no synteny y function from Blastp? wer using phagesDB, NCBI, or hypothetical protein :: function unknown y Function from HHpred? served domains and functional ms) Quinohemoprotein amine lrogenase YES brane binding domain? NO A? NO	<ul> <li>Glimmer: N/A</li> <li>Glimmer Score: N/A</li> <li>GeneMark 44865</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 1 MA</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes</li> <li>Is it the longest ORF? (Y/N) Yes</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) gap: -4 spacer: 11</li> </ul>		



	<mark>1<sup>st</sup> Annota</mark> Madison R		Anno	tator:	<b>Function</b> : Membrane Protein		Feature 65 Annotation		
	5' end: 44975 Is it Is there cod Genemarks	3' end: 44862 t a gene? ing potential base ? (Y/N and descrip	d on	Likely using Func	Function? y function from Phamerator ver): Function Unknown y function from Blastp? (Answer phagesDB, NCBI, or both): tion Unknown	0000	<b>Start position?</b> 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		
	on a Blast se Zagie and M Is it longer t Do other rel (Phamerato	omologous genes l earch? (Answer): Y like han 120 bp (Y/N): lated phages agree r) (Y/N): Yes Fwd/Rev): Reverse	ves, No	<ul> <li>Phage</li> <li>Likeh (consiregion mem</li> <li>NKF:</li> <li>Mem</li> </ul>	brane binding domain?: Yes rding to DEEP search		<ul> <li>Is it the longest ORF? (Y/N): No</li> <li>Alignment agreement from Blast? (Y/N, Source): Yes</li> <li>Does it include all of the functional region (HHpred)?: No</li> <li>SD Score? Is there one higher? (number, Y/N): -2.071, No</li> </ul>		
N	otes: Start (	Codon ATG							

	1st Annotator: Madalyne2nd Anno Nina			Function: Hypothetical Protein	]	Feature 66 Annotation	
<b>5' end:</b> 45079	<b>3' en</b> 4497	_		<mark>ngth</mark> : 108			Start position?
<ul> <li>Is there codi Genemarks?</li> <li>Are there hot a Blast searc Yes</li> <li>Is it longer the no</li> <li>Do other relation Yes</li> </ul>	mologous g h? (Answer han 120 bp ( ated phages ?) (Y/N) Fwd/Rev)	l based o escriptio renes bas ) (Y/N)		<ul> <li>Likel (Ansy both)</li> <li>Blast</li> <li>Phag</li> <li>Likel (cons regio</li> <li>NKF</li> </ul>	: Hypothetical Protein es DB: Hypothetical Protein y Function from HHpred? erved domains and functional ns) Hypothetical Protein Yes brane binding domain?		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)
Notes:							

	<mark>1<sup>st</sup> Annota</mark> Phoeni		2 <sup>nd</sup> Annot	ator:	helix-turn-helix DNA		Feature 67 Annotation
	<b>5' end:</b> 45300	<b>3' end:</b> 45076		ngth: 225	<b>r unction</b> y function from Phamerator wer) urn-helix DNA binding domain protein y function from Blastp? (Answer chagesDB, NCBI, or both) urn-helix DNA binding domain protein : urn-helix DNA binding domain protein y Function from HHpred? kerved domains and functional ns) urn-helix DNA binding domain protein brane binding domain?	0000	Start position? Glimmer: None Glimmer Score: None
	Is there codi Genemarks? Yes Are there ho a Blast search Yes Is it longer th Yes	nan 120 bp (Y/N nted phages ag ) (Y/N) 'wd/Rev)	ased on cription). es based on N)	(Answ helix-tu Likely using helix-tu Blast: helix-tu Phage helix-tu Likely (conso region helix-tu			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:
N	otes:						

1 <sup>st</sup> Annotator: Gigi Trejo	tator:	<b>Function:</b> helix-turn-helix DNA binding domain	Feature 68 Annotation		
5' end:       3' end:       Le         45,300       45,076       45	ength: 225	omunig uomani	Start position?		
<ul> <li>Is there coding potential based on Genemarks? (Y/N and description).</li> <li>Are there homologous genes based on a Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp (Y/N) Yes</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> <li>Directions (Ibrd (Dec))</li> </ul>	(Ansv heli Likel using Blast heli Phag heli Likel (cons regio heli	x-turn-helix DNA binding domain y function from Blastp? (Answer ; phagesDB, NCBI, or both) : x-turn-helix DNA binding domain es DB: x-turn-helix DNA binding domain y Function from HHpred? erved domains and functional	<ul> <li>Glimmer: 47691</li> <li>Glimmer Score: 9.16</li> <li>GeneMark: 47691</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 47691 36 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y</li> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes 100%</li> <li>Does it include all of the functional region (HHpred)? Yes</li> <li>SD Score? Is there one higher? (number, Y/N) Y, -2.377</li> </ul>		
<ul> <li>Direction: (Fwd/Rev)</li> <li>Reverse</li> <li>Notes:</li> </ul>	No Mem No L tRNA	brane binding domain? ? No	Gap, overlap, and spacing? (description) Gap: 522 Overlap: 10		



• • • • • • • • • • • • • • • • • • •	<mark>ngth</mark> :		
	869		Start position?
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	<ul> <li>Likel (Ans: or bc DN</li> <li>Blasti</li> <li>Blasti</li> <li>DN</li> <li>Phag</li> <li>DN</li> <li>Phag</li> <li>DN</li> <li>Likel</li> <li>(construct</li> <li>DN</li> <li>NKF</li> <li>NKF</li> <li>Mem</li> </ul>	A primase/helicase	<ul> <li>Glimmer: 47691</li> <li>Glimmer Score: 9.16</li> <li>GeneMark: 47691</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>47691 has 36 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes, Yes</li> <li>Is it the longest ORF? (Y/N) Yes</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes,</li> <li>Does it include all of the functional region (HHpred)? Yes</li> <li>SD Score? Is there one higher? (number, Y/N) -5.414, Yes, -2.377</li> <li>Gap, overlap, and spacing? (description) 178 gap (lowest)</li> </ul>



			Annot Madiso			]	Feature 70 Annotation	
	<b>5' end:</b> 49363	<b>3' er</b> 4787	_		ngth: 493			Start position?
	Is there coding Genemarks? (Y/ Yes Are there homol search? (Answer Yes Is it longer than Yes Do other related (Y/N) Yes Direction: (Fwd Reverse	logous genes r) 1 120 bp (Y/N) d phages agr	sed on iption). s based on )		(Ar F Lik (Ar bot F Bla Ph: C C C C C C C C C C C C C C C C C C C	niction unknown st: Function unknown ages DB: Function unknown ely Function from HHpred? nserved domains and functional ions) ell Wall Surface Anchor Protein, out 14% coverage F 0 mbrane binding domain?		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
NL	otoge							10-5



5' end:       3' end:       Length:       DNA Binding Protein Domain         49755       3' end:       258         Is it a gene?       Function?       Glimmer: 49724 Glimmer Score: 15.08 GeneMark: 49775         Is there coding potential based on Genemarks? (Y/N and description).       Likely function from Phanerator (Hanswer)       Start position?         Are there homologous genes based on a Blast search? (Answer) yes       Likely function from Planser20 M. ONA Binding Domain       Jages DB:         Blast (Phanerator) (Y/N) yes       Likely function from Hlipred? (couserved domains and functional Domain       Blast: Note (Couserved domains and functional Domain a binding domain? yes       Alignment agreement from Blast? (Y/N, Source)         Do other related phages agree (Phanerator) (Y/N) yes       Likely function from Hlipred? (couserved domains and functional Domain       Blast: Note (Couserved domains and functional Domain       Alignment agreement from Blast? (Y/N, Source)         Do other related phages agree (Phanerator) (Y/N) yes       Likely Function from Hlipred? (couserved domains and functional Domain       Start position?         NKF (Source)       NKF (Source)       Blast       Couser in include all of the functional region (Mimore)         NKF (Source)       NKF (Source)       Source)       Source)         Direction: (Fwd/Rev) Reverse       Bushas       Blast source)       Source)       Source)         NKF       NKF <th>ı<sup>st</sup> Annota Nina</th> <th colspan="2">1<sup>st</sup> Annotator: 2<sup>nd</sup> Anno Nina</th> <th>tator:</th> <th colspan="2"><b>Function</b>: Ribbon-Helix-Helix</th> <th>Feature 71 Annotation</th>	ı <sup>st</sup> Annota Nina	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Nina		tator:	<b>Function</b> : Ribbon-Helix-Helix		Feature 71 Annotation
<ul> <li>Is there coding potential based on Genemarks? (Y/N and description).</li> <li>Are there homologous genes based on a Blast search? (Answer)</li> <li>Yes</li> <li>Is it longer than 120 bp (Y/N)</li> <li>Yes</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> <li>Yes</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> <li>Yes</li> <li>Direction: (Fwd/Rev)</li> <li>Birst: (Fwd/Rev)</li> <li>Direction: (Fwd/Rev)</li> <li>Birst: (Fwd/R</li></ul>				U	U		-
Notes	<ul> <li>Is there codi Genemarks?</li> <li>Are there ho a Blast searcy yes</li> <li>Is it longer thy yes</li> <li>Do other relation (Phameratory yes</li> <li>Direction: (Figure 1)</li> </ul>	ng potential based (Y/N and descript mologous genes ba h? (Answer) han 120 bp (Y/N) ated phages agree (Y/N)		(Ansv Rib Doi U Likely using Rib Doi Blast: Rib Doi O Phage Likely (cons regio) Rib Doi NKF No	y function from Phamerator ver) bon-Helix-Helix Binding main y function from Blastp? (Answer phagesDB, NCBL, or both) bon-Helix-Helix DNA Binding main bon-Helix-Helix DNA Binding main es DB: y Function from HHpred? erved domains and functional ns) bon-Helix-Helix DNA Binding main		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



1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Trenton	otator:	Function:	Feature 72 Annotation
<b>5' end:</b> 49942 <b>3' end:</b> 49772	ength: 171	Hypothetical Protein	<b>Start position?</b> Glimmer: 49942
<ul> <li>Is it a gene?</li> <li>Is there coding potential based on Genemarks? (Y/N and description).</li> <li>Are there homologous genes based on a Blast search? (Answer)</li> <li>Are there homologous genes based on a Blast search? (Answer)</li> <li>Is it longer than 120 bp (Y/N)</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> <li>Direction: (Fwd/Rev)</li> <li>Reverse</li> </ul>	(Ans No Likel (Ans both Blast Den Blast Phag Likel (com regio	y function from Blastp? wer using phagesDB, NCBI, or ) <b>: Hypothetical protein</b> ges DB: Hypothetical protein by Function from HHpred? served domains and functional ons) Yes brane binding domain?	<ul> <li>Glimmer Score: 15.59</li> <li>GeneMark49942</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>(Start: 10 @50044 has 15 MA's),</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY</li> <li>Is it the longest ORF? (Y/N)Y</li> <li>Alignment agreement from Blast? (Y/N, Source)Y</li> <li>Does it include all of the functional region (HHpred)? Yes</li> <li>SD Score? Is there one higher? (number, Y/N)Y-7.830</li> <li>Gap, overlap, and spacing? (description) No</li> </ul>
Notes:			

1st Annotator:2nd AnnoGisselle TrejoJosh					<b>Function</b> : Membrane Protein	Feature 73 Annotation				
5' end:       3' end:       La         50,207       50,028       La				ength: 180			<b>Start position?</b> Glimmer: 50,207 Glimmer Score: 4.78 GeneMark: 50,207 Starterator MAs for selected and for alt options (number, number alt MAs)			
<ul> <li>Is there cod Genemarks Yes</li> <li>Are there ho on a Blast so - Yes</li> <li>Is it longer t - Yes</li> <li>Do other rel (Phamerato Yes</li> </ul>	omologous earch? (An than 120 bj lated phag r) (Y/N)	ial based on description genes based swer) o (Y/N)		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			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:				1						

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<mark>1<sup>st</sup> Annot</mark> Madison		Anno	tator:	Function:	Feature 74 Annotation	
<b>5' end:</b> 50532	<b>3' end:</b> 50191		<mark>ngth</mark> : <sup>516</sup>	Hypothetical Protein	<b>Start position?</b>	
<ul> <li>Is there conditions of the second seco</li></ul>	it a gene? oding potential base ts? (Y/N and descrip homologous genes f search? (Answer): Y iminumJesus, Baby r than 120 bp (Y/N): related phages agree tor) (Y/N): Yes	oased es, Dotz Yes	<ul> <li>(Ansv funct</li> <li>Likely (Ansv both)</li> <li>Blast</li> <li>Phag</li> <li>Likely (cons regio</li> <li>NKF:</li> </ul>	brane binding domain?: own	<ul> <li>Glimmer Score: 17.06</li> <li>GeneMark: 50532</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs): 36</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes</li> <li>Is it the longest ORF? (Y/N): No</li> <li>Alignment agreement from Blast? (Y/N, Source): Yes</li> <li>Does it include all of the functional region (HHpred)?: 27% coverage</li> <li>SD Score? Is there one higher? (number, Y/N): DNA Master</li> </ul>	
Notes: Start	Codon ATG		1			

				Anno Nina		<b>Function</b> : Hypothetical	Feature 75 Annotation		
	5' end:     3' end:     I       50836     50525     I			ngth: 312	Protein		Start position?		
	Is i	t a gen	e?		Function?			Glimmer: 50836 Glimmer Score: 12.61 GeneMark: 50836 Starterator MAs for selected and for alt	
D	Is there coding potential based on Genemarks? (Y/N and description).: Yes			n n).:	<ul> <li>Likely function from Phamerator (Answer): Function Unknown</li> <li>Likely function from Blastp? (Answer using phagesDB, NCBI, or both): Function Unknown</li> </ul>			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?	
D	Are there ho a Blast searc	mologous g h? (Answer	<b>genes bas</b> ): Yes, Sal	ed on lyK	<ul> <li>Blast: Hypothetical Protein</li> <li>Phages DB: Function Unknown</li> </ul>			(Y/N, Y/N): Yes Is it the longest ORF? (Y/N): No Alignment agreement from Blast? (Y/N,	
D	□ Is it longer than 120 bp (Y/N): Yes					ely Function from HHpred? Iserved domains and functional ons): No data for HHPRED	D	Source): No BLAST report available Does it include all of the functional region (HHpred)?: No – 28% coverage	
۵	Do other rela (Phamerator	ther related phages agree merator) (Y/N): Yes, SallyK			🗅 Mer	?: Yes nbrane binding domain?: nown	•	phospholipase SD Score? Is there one higher? (number,	
	Direction: (Fwd/Rev): Reverse					<b>A?:</b> No	•	Y/N): DNA Master Gap, overlap, and spacing? (description): Gap: -8, Overlap: , Spacer: 11	
N	otes: Start (	rodon AT	<b>T</b> C					forte	

## Notes: Start Codon ATG



<mark>1<sup>st</sup> Annota</mark> Nina				<b>motator:</b> ey Allen		<b>Function</b> : Hypothetical	] ]	Feature 76 Annotation
I Is there codi Genemarks? Are there hor a Blast search Yes I Is it longer th Yes	mologous g h? (Answer 1an 120 bp (	29 e? l based o escriptio enes bas ) Y/N)	on on).		Like Phar Fur Like (Ans or bo Fur Blas Fur Phag Fur Like (conc	nction Unknown		Start position? Glimmer: 51092 Glimmer Score: 11.68 GeneMark: 51092 Starterator MAs for selected and for alt options (number, number alt MAs) MAS Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) 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 (HIpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description)
Direction: (F	wd/Rev)				Yes	brane binding domain? \?		Gap= -4, Space= 15
Notes:								

1 <sup>st</sup> Annotator: Alex	2 <sup>nd</sup> Anno	otator:	Function:	Feature 77 Annotation		
			Hypothetical protein	Start position	?	
<ul> <li>Is there coding potent Genemarks? (Y/N and Yes</li> <li>Are there homologous a Blast search? (Answ No</li> <li>Is it longer than 120 b Yes</li> <li>Do other related phag (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev) Reverse</li> <li>Notes:</li> </ul>	ial based on description). genes based on er) o (Y/N)	<ul> <li>(Ansyleta)</li> <li>Likel (Ansyleta)</li> <li>Blast</li> <li>Phag</li> <li>Likel (construction)</li> <li>NKF</li> <li>Mem Unkr</li> </ul>	Yes brane binding domain?	<ul> <li>Glimmer: 51553</li> <li>Glimmer Score: 14.41</li> <li>GeneMark: 51544</li> <li>Starterator MAs for selected an options (number, number alt M 1 MA's</li> <li>Does it include all of the coding and do Genemark and Glimme (Y/N, Y/N) Yes and No</li> <li>Is it the longest ORF? (Y/N) Yes</li> <li>Alignment agreement from Bla Source) Yes 97%</li> <li>Does it include all of the functi (HHpred)? 49%</li> <li>SD Score? Is there one higher? Y/N) -1.748</li> <li>Gap, overlap, and spacing? (des Gap: -1, Overlap: None Spaci</li> </ul>	1As) g potential r agree? ast? (Y/N, onal region (number, scription)	

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				Anno Trento		<b>Function</b> : Hypothetical		Feature 78 Annotation	
	<b>5' end:</b> 51825	3' en 5155	3		ength: 273 Function?			<b>Start position?</b> Glimmer: 51825 Glimmer Score: 10.62	
	<ul> <li>Genemarks? (Y/N and description).: Yes</li> <li>Are there homologous genes based on a Blast search? (Answer): Yes, AluminumJesus</li> <li>Is it longer than 120 bp (Y/N): Yes</li> <li>Do other related phages agree (Phamerator) (Y/N): Yes</li> </ul>				<ul> <li>Likel (Ansy both)</li> <li>Blast</li> <li>Phag</li> <li>Likel (cons regio</li> <li>NKF:</li> </ul>	y function from Phamerator wer): Hypothetical Protein y function from Blastp? wer using phagesDB, NCBI, or : Unknown Function : Function Unknown es DB: Function Unknown y Function from HHpred? served domains and functional ns): Hypothetical Protein Yes brane binding domain?:	<ul> <li>GeneMark: 51825</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs): 3 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes</li> <li>Is it the longest ORF? (Y/N): No</li> <li>Alignment agreement from Blast? (Y/N, Source): Yes</li> <li>Does it include all of the functional region (HHpred)?: No</li> <li>SD Score? Is there one higher? (number, Y/N): DNA Master</li> <li>Gap, overlap, and spacing? (description) : Gap: -4, Overlap: No overlap Spacing: 9</li> </ul>		
N	otes: Start C	odon Gl	ſG						

	1st Annotator:2nd AnnoMadalyne SiskPhoen		tator: ix	Function: Hypothetical Protein	]	Feature 79 Annotation
<b>5' end:</b> 52154	<b>3' end:</b> L 51825		Length: 330			Start position?
<ul> <li>Is there codi Genemarks? Yes</li> <li>Are there ho a Blast searc Yes</li> <li>Is it longer the Yes</li> <li>Do other relation (Phamerator Yes</li> <li>Direction: (F Reverse</li> </ul>	mologous g h? (Answer) 1an 120 bp ( ated phages ) (Y/N)	l based on escription). enes based ) Y/N)	<ul> <li>Likely (Ansy both)</li> <li>Blast:</li> <li>Phage</li> <li>Likely (cons regio</li> <li>NKF y</li> </ul>	: Hypothetical Protein es DB: Hypothetical Protein y Function from HHpred? erved domains and functional ns) Hypothetical Protein yes brane binding domain? no		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:						And



	1 <sup>st</sup> Annota Gigi Tre			2 <sup>nd</sup> Annotat Madalyne		Function: hypothetical	Feature 80 Annotation
	5' end: 52,433 Is there codin Genemarks? Ves Are there hor a Blast search Yes Is it longer th Yes Do other rela (Phamerator Yes Direction: (F	mologous g h? (Answer) 1an 120 bp ( ated phages ) (Y/N)	9 e? I based o escriptio enes bas ) Y/N)	on on).	(Ans h Like (Ans both Blas h Phas h Like (con regid NKF Yes	ypothetical protein y function from Blastp? wer using phagesDB, NCBI, or ypothetical protein es DB: ypothetical protein ypothetical protein ypothetical protein ypothetical protein ypothetical protein served domains and functional ons)	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? Yes. Yes To so genemark and Glimmer agree? 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 (Hpred)? Yes So Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) Gap: -4 Spacing: 12
Ň	- Revers	se			D tRNA NO	N?	

	<mark>1<sup>st</sup> Annota</mark> Daniel		2 <sup>nd</sup> Anno Madaly			<b>Function</b> : hypothetical	Feature 81 Annotation
	5' end: 52930 Is there coding Genemarks? Yes Are there how a Blast search Yes Is it longer th Yes Do other rela (Phamerator Yes Direction: (F	524 t a gel ng potenti (Y/N and mologous h? (Answe nan 120 bp nan 120 bp ated phage ) (Y/N)	ial based o descriptio genes bas er) o (Y/N)	n m).	(Ans Like (Ans bot) Blas Blas Pha Pha Like (con regi NC NKH Ye	iypothetical protein t: hypothetical protein ges DB: hypothetical protein by Function from HHpred? served domains and functional ons) s	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 To be it include all of the coding potential and do Genemark and Glimmer agree? (Y.N, Y/N) Yes, Yes No Alignment agreement from Blast? (Y/N, No Alignment agreement from Blast? (Y/N, No Mos it include all of the functional region (HIPred)? No So Score? Is there one higher? (number, No So Score? Is there one higher? (number, (N) -1.784, N0 Gap, overlap, and spacing? (description) (Jap 2)
N	- Revers	se				A?	

1 <sup>st</sup> Annotator: Madalyne		2 <sup>nd</sup> Annotator:		tator:	Function: Hypothetical Protein	Feature 82 Annotation				
<b>5' end:</b> 53466				ength: 534		<b>Start position?</b>				
<ul> <li>Is there codin Genemarks?</li> <li>Are there hon Blast search?</li> <li>Is it longer th</li> <li>Do other rela (Phamerator)</li> <li>Direction: (Fy)</li> </ul>	nologous ger (Answer) Yes an 120 bp (Y/ ted phages a (Y/N) Yes	oased on cription). Y nes based o S 'N) Yes gree		<ul> <li>Likeh (Ansv both)</li> <li>Blast:</li> <li>Phage</li> <li>Likeh (cons regio</li> <li>NKF</li> </ul>	: Hypothetical protein es DB: Major capsid hexamer y Function from HHpred? erved domains and functional ns) Hypothetical Protein brane binding domain?	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:										





	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> A Phoenix	nnot	ator:	Function: Hypothetical protein	Feature 83 Annotation	n	
	5' end:     3' end:       53765     53463		<mark>ngth</mark> : 303		<b>Start position?</b>		
	<b>Is there coding potential based on</b> Genemarks? (Y/N and description). Are there homologous genes based on Blast search? (Answer) Is it longer than 120 bp (Y/N) yes Do other related phages agree (Phamerator) (Y/N) - n0 Direction: (Fwd/Rev)	ıa	(Ansv – hy Likely (Ansv both) – Hy Blast: D Blast: D Phage Likely (cons regio – Ti D NKF	Tpothetical Tpothetica	<ul> <li>Glimmer: 53651</li> <li>Glimmer Score: 8.26</li> <li>GeneMark 53651</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) no</li> <li>Is it the longest ORF? (Y/N) yes</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description)118, 9</li> </ul>		
N	- Reverse		<b>t</b> RNA	? no	110, y		



ı <sup>st</sup> Annotato Trenton	or:	2 <sup>nd</sup>	Annot Nina		Function: Hypothetical protein	Feature 84 Annota	tion
<b>5' end:</b> 53971	3' en 5364			ngth: 324		Start position?	
<ul> <li>Is there coding Genemarks? (Yes there is coding)</li> <li>Are there hom a Blast search? Yes</li> <li>Is it longer that Yes</li> <li>Do other relate (Phamerator) (Yes</li> <li>Direction: (Fw - Reverse)</li> </ul>	ologous g ? (Answer an 120 bp ( ed phages (Y/N) vd/Rev)	ll based o escriptio I genes bas ) (Y/N)		(Ansv Non Likely (Ansv both) Blast Blast Phag Likely (cons regio No	y function from Blastp? ver using phagesDB, NCBI, or Nd : unknown Function es DB: hypothetical protein y Function from HHpred? erved domains and functional ns) there is no known function brane binding domain? No	<ul> <li>Glimmer: 53971</li> <li>Glimmer Score: 13.23</li> <li>GeneMark53980</li> <li>Starterator MAs for selected and for options (number, number alt MAs)</li> <li>(Start: 3 @53971 has 18 MA's</li> <li>Does it include all of the coding pote and do Genemark and Glimmer agree (Y/N, Y/N)YN</li> <li>Is it the longest ORF? (Y/N) <ul> <li>It has the Second longest ORF</li> <li>Alignment agreement from Blast? (Y Source) Y</li> <li>Does it include all of the functional in (HHpred)? yes</li> <li>SD Score? Is there one higher? (num Y/N)-4.062</li> <li>Gap, overlap, and spacing? (description No significant gaps or overlaps</li> </ul> </li> </ul>	ential ee? Y/N, region nber,
Notes:							Ż

		otator: Function: ison Unknown function		Feature 85 Annotation
5' end:       3' en         54288       5396		ength: 321		Start position?
<ul> <li>Is there coding potentia Genemarks? (Y/N and d yes</li> <li>Are there homologous g a Blast search? (Answer yes</li> <li>Is it longer than 120 bp ( yes</li> <li>Do other related phages (Phamerator) (Y/N) yes</li> <li>Direction: (Fwd/Rev) Reverse</li> </ul>	l based on escription). renes based on ) (Y/N)	(Ansv No know) Likel (Ansv both, Function Blast Function Phag Function Likel (cons regio Ribosom NKF no	n function y function from Blastp? wer using phagesDB, NCBI, or unknown : unknown y BB: unknown y Function from HHpred? served domains and functional ons) al protein brane binding domain?	<ul> <li>Glimmer: 54288</li> <li>Glimmer Score: 11.04</li> <li>GeneMark 54288</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>3587</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)</li> <li>Yes, yes</li> <li>Is it the longest ORF? (Y/N) yes</li> <li>Alignment agreement from Blast? (Y/N, Source) yes</li> <li>Does it include all of the functional region (HHpred)? yes</li> <li>SD Score? Is there one higher? (number, Y/N) no</li> <li>Gap, overlap, and spacing? (description)</li> <li>Gap: 8, spacer: 8</li> </ul>



1 <sup>st</sup> Annotator: Madalyne Sisk	2 <sup>nd</sup> .	Annot	lator:	Function: Hypothetical Protein	Feature 86 Annotation
	end: 297		<mark>ngth</mark> : <sup>573</sup>		Start position?
<ul> <li>Is there coding potent Genemarks? (Y/N and Yes</li> <li>Are there homologous a Blast search? (Answayes</li> <li>Is it longer than 120 by Yes</li> <li>Do other related phag (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev) Reverse</li> </ul>	tial based or description s genes base er) p (Y/N)		<ul> <li>Likely (Answ both)</li> <li>Blast:</li> <li>Phage</li> <li>Likely (consv region</li> <li>NKF</li> </ul>	Function? by function from Phamerator wer) Hypothetical Protein by function from Blastp? wer using phagesDB, NCBI, or t: Hypothetical Protein ges DB: Hypothetical Protein by Function from HHpred? served domains and functional brane binding domain?	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)
- Notos:					Les .



	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Annot Nina				or:	<b>Function</b> : Hypothetical	Feature 87 Annotation		
	<b>5' end:</b> 55483	<b>3' end:</b> 54866		<mark>ngt</mark> l 617	<mark>h</mark> :	Protein		Start position?	
	Is there codi Genemarks?	t a gene? Ing potential based of (Y/N and description mologous genes based of the second		•	Hy Like (Ans or be	Function? ly function from nerator (Answer) pothetical Protein ly function from Blastp? wer using phagesDB, NCBI, oth)		Glimmer Score: 9.95 GeneMark: 55444 Starterator MAs for selected and for alt options (number, number alt MAs) 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	
□ Ye Ye	a Blast search? (Answer) Ves Is it longer than 120 bp (Y/N) O other related phages agree (Phamerator) (Y/N) Direction: (Fwd/Rev) Reverse				<ul> <li>Hypothetical Protein</li> <li>Blast: Hypothetical Protein</li> <li>Phages DB: Hypothetical Protein</li> <li>Likely Function from HHpred? (conserved domains and functional regions) Hypothetical Protein</li> <li>NKF Yes</li> <li>Membrane binding domain? NO</li> </ul>			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	
	atac				tRNA	<b>A</b> ?		ħ≁-€	



	<mark>1<sup>st</sup> Annotat</mark> Alex	or:	2 <sup>nd</sup>	Anno <sup>®</sup> Phoen			] ]	Feature 88 Annotation
	<b>5' end:</b> 55728	<b>3' en</b> 5546	_		<mark>ngth</mark> : 249	Hypothetical protein		<b>Start position?</b>
	Is it	t a gen	e?		D j	<b>Function?</b> Likely function from Phamerator Answer) unknown function		Glimmer: 55728 Glimmer Score: 10.22 GeneMark: 55728 Starterator MAs for selected and for alt options (number, number alt MAs)
Ç	Is there coding potential based on Genemarks? (Y/N and description). Yes			on on).	<ul> <li>(Answer) unknown function</li> <li>Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Hypothetical protein</li> </ul>			25 MA's Does it include all of the coding potential and do Genemark and Glimmer agree?
ç	Are there hon a Blast search No	nologous g 1? (Answer)	enes bas )	sed on	<ul> <li>Blast: unknown function</li> <li>Phages DB: Unknown function</li> </ul>		8	(Y/N, Y/N) Yes and Yes Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N,
ç	■ Is it longer the Yes	-				Likely Function from HHpred? (conserved domains and functional regions) Structural and		Source) Yes Does it include all of the functional region
ſ	Do other related phages agree (Phamerator) (Y/N) Yes			ŀ	Functional Protein NKF Yes	D	(HHpred)? Yes SD Score? Is there one higher? (number, Y/N) -4.705, yes -3.072	
ç	Direction: (Fv	wd/Rev)				Membrane binding domain? No	D	<b>Gap. overlap. and spacing? (description)</b> Gap: -1 Overlap: None Spacing: 9
	- Revers	e			• t	tRNA? No		



	<mark>1<sup>st</sup> Annota</mark> Gigi Tre			<b>Anno</b> Aadaly		Function: Hypothetical	]_]	Feature 89 Annotation
	<b>5' end:</b> 56,210	<b>3' en</b>			ngth: 483	Protein		Start position?
		t a gen ng potentia (Y/N and do mologous g h? (Answer) nan 120 bp ( nan 120 bp ( nan 120 bp ( uted phages ) (Y/N) wd/Rev)	e? l based o escriptio enes base Y/N)	n n).	<ul> <li>Like (Ans Hy</li> <li>Like (Ans both</li> <li>Blas</li> <li>Hy</li> <li>Blas</li> <li>Hy</li> <li>Pha</li> <li>Hy</li> <li>Like (con regi</li> <li>NKH</li> <li>Ye</li> </ul>	pothetical protein t: pothetical protein ges DB: pothetical protein ty Function from HHpred? served domains and functional ons) s hbrane binding domain? A?		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
N	otes:							

	ı <sup>st</sup> Annotator: Daniel		2 <sup>nd</sup> Annotator:		tator:	<b>Function</b> : Hypothetical		Feature 90 Annotation
	<b>5' end:</b> 56773				ength: <sup>567</sup>			<b>Start position?</b>
	<ul> <li>Is there coding potential based on Genemarks? (Y/N and description). Yes</li> <li>Are there homologous genes based on a Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp (Y/N) Yes</li> <li>Do other related phages agree (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev)</li> <li>Men No</li> </ul>				(Ansy Hyr Likel (Ansy both) Blast Hyr Phag Hyr Likel (cons regio No NKF Yes	bothetical protein y function from Blastp? wer using phagesDB, NCBI, or obthetical protein es DB: othetical protein y Function from HHpred? served domains and functional ms) brane binding domain?		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
N	otes:				1			

<mark>1<sup>st</sup> Annotator</mark> Madalyne	: 2 <sup>nd</sup>	Annot	tator:	<b>Function</b> : Hypothetical Protein	Feature 91 Annotation
<b>5' end:</b> 57059	<b>3' end:</b> 56886		ngth: 174		Start position?
Is it a Is there coding p Genemarks? (Y/N Are there homolo a Blast search? (A Sea Is it longer than n Yes Do other related (Phamerator) (Y/N Direction: (Fwd/N Reverse	ogous genes bas Answer) 120 bp (Y/N) phages agree ⁄N)		(Ansv Likeh (Ansv both) Blast: Phage Likeh (cons regio	: Hypothetical Protein es DB: Hypothetical Protein y Function from HHpred? erved domains and functional ns) brane binding domain?	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:			1		

	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Phoenix		Annotator: Nina		Function: Hypothetical protein	Fe	eature 92 Annotation				
	<b>5' end:</b> 57383	5' end: 3' end: Lo					<b>Start position?</b> <ul> <li>Glimmer: 57283</li> <li>Glimmer Score: 12.08</li> </ul>				
	Is there codin Genemarks? - yes Are there hon a Blast search - no Is it longer th yes Do other rela (Phamerator - yes Direction: (F - Rever	mologous g h? (Answer nan 120 bp nted phages ) (Y/N) wd/Rev)	ll based o escriptio genes bas ) (Y/N)		(Ansv - Likel (Ansv both) - H Blast D Phag Likel (cons regio - h NKF	y function from Blastp? ver using phagesDB, NCBI, or ypothetical protein : function unknown es DB: tape measure protein y Function from HHpred? erved domains and functional ns) ypothetical brane binding domain?	<ul> <li>GeneMark: 57283</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes</li> <li>Is it the longest ORF? (Y/N) yes</li> <li>Alignment agreement from Blast? (Y/N, Source) yes</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description)8, 11</li> </ul>				
N	lotes:										

			<sup>1</sup> Annotator: Madalyne		<b>Function</b> :		Feature 93 Annotation	
	<b>5' end:</b> 57440 <b>3' end:</b> 57276				ength: 165 Function?			<b>Start position?</b> Glimmer: 57440 Glimmer Score: 13.28
	Is there codi Genemarks? No Are there ho a Blast searc Ye Is it longer th Ye Do other rela (Phamerator Ye	<ul> <li>It is not a genre.</li> <li>Likely is (Answer Function). No</li> <li>Likely is (Answer Function). No</li> <li>Likely is (Answer Function).</li> <li>Likely is (Answer Function).</li> <li>Likely is (Answer Function).</li> <li>Likely is (Answer Function).</li> <li>Blast: Particular is the second sec</li></ul>			y function from Phamerator ver) iction unknown y function from Blastp? ver using phagesDB, NCBI, or hypothetical protein : hypothetical protein es DB: unknown function y Function from HHpred? erved domains and functional ns) posomal protein		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	
ľ	Notes:							

1st Annotator:2nd AnnoAlsley AllenPhoen		tator: nix	Function: Hypothetical protein	Feature 94 Annotation
5' end:     3' en       57851     5749		ngth: 360		Start position?
<ul> <li>Is there coding potentia Genemarks? (Y/N and d Yes</li> <li>Are there homologous g a Blast search? (Answer Yes</li> <li>Is it longer than 120 bp ( yes</li> <li>Do other related phages (Phamerator) (Y/N) Yes sallyK 97</li> <li>Direction: (Fwd/Rev) reverse</li> </ul>	l based on escription). renes based on ) (Y/N)	Unknow Like (Ans or bo Hypothe Blas Unknow Phag Function Like (con func Hypothe NKF no Mem no	ly function from Blastp? wer using phagesDB, NCBI, oth) tical protein	<ul> <li>Glimmer: 57852</li> <li>Glimmer Score: 10.02</li> <li>GeneMark 57836</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)</li> <li>No</li> <li>Is it the longest ORF? (Y/N) yes</li> <li>Alignment agreement from Blast? (Y/N, Source) yes</li> <li>Does it include all of the functional region (HHpred)? Yes</li> <li>SD Score? Is there one higher? (number, Y/N) No</li> <li>Gap, overlap, and spacing? (description) \ Gap: -19, Spacer: 15</li> </ul>



	<mark>1<sup>st</sup> Annota</mark> Madison R		Anno	tator:	<b>Function</b> :	Feature 95 Annotation			
	<b>5' end:</b> 58090	<b>3' end:</b> 57833		ength: 258		Start position?			
	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):				Function? by function from nerator (Answer) by function from Blastp? wer using phagesDB, NCBI, oth) t: ges DB: by Function from HHpred? served domains and tional regions) brane binding domain? A?	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)			
ľ	Notes:								

<mark>1<sup>st</sup> Annota</mark> Nina	1st Annotator: Nina2nd Anno Aisley A				<b>Function</b> : Hypothetical	Feature 96 Annotation			
<b>5' end:</b> 58224		e <b>nd:</b> 087	Length: 137		Protein		Start position?		
Is there cod Genemarks	omologous ch? (Answo han 120 bj ated phag r) (Y/N)	ial based on description) genes based er) o (Y/N)		(Ansy Likel (Ansy both) Blast Phag Likel (cons regio	brane binding domain?	34 0 0 0	Glimmer: 58224 Glimmer Score: 15.06 GeneMark: 58224 Starterator MAs for selected and for alt options (number, number alt MAs) 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:							ES		





	1 <sup>st</sup> Annota Alex	i <mark>tor:</mark>	2 <sup>nd</sup> Annot Gigi				Function:		Feature 97 Annotation
	<b>5' end:</b> 58550	<b>3' en</b> 5822	21	Lengt 330				<b>Start position?</b> Glimmer: 58490 Glimmer Score: 10.6 GeneMark: 58550	
	Is there codi Genemarks? No, no ma Are there ho a Blast searc no Is it longer th Ye Do other rela (Phameraton No Direction: (F	ng potentia (Y/N and d atches found mologous g h? (Answer han 120 bp ( s ted phages (Y/N)	l based o escriptio l enes bas ) (Y/N)		<ul> <li>Likel (Ansy both)</li> <li>Blast</li> <li>Phag</li> <li>Likel (cons regio Ribo</li> <li>NKF</li> </ul>	y function from Phamerator ver) unknown function y function from Blastp? ver using phagesDB, NCBI, or unknown function : hypothetical protein es DB: unknown function y Function from HHpred? erved domains and functional ns) osome hibernator Yes brane binding domain? No		<ul> <li>Starterator MAs for selected and for alt options (number, number alt MAs) No MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) No and No</li> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) Not really 64%</li> <li>SD Score? Is there one higher? (number, Y/N) -4.910, yes -2.934</li> </ul>	
Ň	lotes:								

	<mark>1<sup>st</sup> Annota</mark> Danie		<b>2</b> <sup>nd</sup>	2 <sup>nd</sup> Annotat		<b>Function</b> : Hypothetical	] ]	Feature 98 Annotation
	5' end: 59011 IS i Is there codi Genemarks? Yes Are there ho a Blast searc Yes Is it longer th Yes Do other rela (Phamerator Yes Direction: (F	mologous g h? (Answer) han 120 bp ( ated phages ) (Y/N)	7 E ? I based o escriptio enes bas	n m).	(Ansv Hyp Likel (Ansv both) Hyp Blast Hyp Phag Hyp Likel (cons regio No NKF Yes	bothetical protein y function from Blastp? wer using phagesDB, NCBI, or oothetical protein es DB: oothetical protein y Function from HHpred? erved domains and functional ns) brane binding domain?		Start position? Simmer: 50011 Minmer Score: 14.87 GeneMark: 50011 Starterator MAs for selected and for alt outputs (number, number alt MAs) 5001 23 MA'S Does it include all of the coding potential and do Genemark and Glimmer agree? (YN, Y/N) Yes Yes To set the longest ORF? (Y/N) Yes Magnment agreement from Blast? (Y/N, Source) Yes 90.7% Does it include all of the functional region (Hpred)? No SD Score? Is there one higher? (number, M.) -3.580, N0 Gap, overlap, and spacing? (description) 3 gap
N	- Rever	se			No			

1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Phoenix	tator:	Function: Hypothetical protein	Feature 99 Annotation	
	ngth: 309		<b>Start position?</b>	
<ul> <li>Is it a gene?</li> <li>Is there coding potential based on Genemarks? (Y/N and description). Yes</li> <li>Are there homologous genes based on a Blast search? (Answer) Yes</li> <li>Is it longer than 120 bp (Y/N) - yes</li> <li>Do other related phages agree (Phamerator) (Y/N) yes</li> <li>Direction: (Fwd/Rev) - Reverse</li> </ul>	(Answ - H Likel (Ansy both) - H Blast D Blast D Phag Likel (cons regio - h	ypóthetical protein y function from Blastp? ver using phagesDB, NCBI, or ypothetical protein : hypothetical es DB: Major tail protein y Function from HHpred? erved domains and functional ns) ypothetical brane binding domain? no	<ul> <li>Glimmer Score: 13.77</li> <li>GeneMark 59326</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>59326 23 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES</li> <li>Is it the longest ORF? (Y/N) YES</li> <li>Alignment agreement from Blast? (Y/N, Source) YES</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) - 10, 10</li> </ul>	
Notes:				

1 <sup>st</sup> Annotator:2 <sup>nd</sup> AnnoAisley AllenMadalyne			Function: hypothetical protein	Annotation	
<b>5' end: 3' en</b> 59714 5936		ength: 351		Start position?	
<ul> <li>Is there coding potentia Genemarks? (Y/N and d yes</li> <li>Are there homologous g a Blast search? (Answer yes</li> <li>Is it longer than 120 bp ( yes</li> <li>Do other related phages (Phamerator) (Y/N) no</li> <li>Direction: (Fwd/Rev) Reverse</li> </ul>	l based on escription). enes based on ) (Y/N)	(Ans none Likel (Ans both Hypothet Blast Function Phag Function Likel (cons regit NICOTINA PHOSPHO TRANSFEF NKF none Mem none	ly function from Blastp? wer using phagesDB, NCBI, or lical protein t: unknown ges DB: unknown ly Function from HHpred? served domains and functional ns) TE RiBOSYLTRANSFERASE;	<ul> <li>Glimmer: 59714</li> <li>Glimmer Score: 13.37</li> <li>GeneMark 59714</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) yes!</li> <li>Is it the longest ORF? (Y/N) yes</li> <li>Alignment agreement from Blast? (Y/N, Source) yes</li> <li>Does it include all of the functional region (HHpred)? no</li> <li>SD Score? Is there one higher? (number, Y/N) no</li> <li>Gap, overlap, and spacing? (description) Gap: -4, spacer: 11</li> </ul>	n



	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Madison Renn <b>Trent</b>			<b>Function</b> : Hypothetical		Feature 101 Annotation		
	<b>5' end:</b> 60142	<b>3' en</b> 5971 <b>t a gen</b> ng potentia (Y/N and d mologous g h? (Answer sus and Bab	Id: II I I I I I I I I I I I I	Dn Dn).: Sed on HyK,	ngth: 432	<ul> <li>32</li> <li>Function?</li> <li>Likely function from Phamerator (Answer): Hypothetical Protein</li> <li>Likely function from Blastp? (Answer using phagesDB, NCBI, or both): Function Unknown</li> <li>Blast: Function Unknown</li> <li>Phages DB: No data available</li> </ul>		<b>Start position?</b> 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
	Do other rela (Phamerator) Direction: (F	wd/Rev): R	everse		<ul> <li>NKF:</li> <li>Mem</li> <li>tRNA</li> </ul>	brane binding domain?: No		SD Score? Is there one higher? (number, Y/N): DNA Master Gap, overlap, and spacing? (description): Gap: 45, Spacer: 8
N	otes: ATG St	tart Codo	n					

ı <sup>st</sup> Annota Nina		<sup>d</sup> Annotator:		<b>Function:</b> Hypothetical		Feature 102 Annotation
<ul> <li>Is there cod Genemarks</li> <li>Are there he a Blast search</li> <li>Is it longer to No</li> <li>Do other reformed (Phameratory</li> </ul>	60277 60188 <b>Is it a gene?</b> 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)		<ul> <li>Protein</li> <li>Protein</li> <li>B9</li> <li>Function?</li> <li>Likely function from Phamerator (Answer) Hypothetical protein</li> <li>Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Hypothetical Protein</li> <li>Blast: Function Unknown</li> <li>Phages DB: Unknown Function</li> <li>Likely Function from HHpred? (conserved domains and functional regions) function unknown</li> <li>NKF ves</li> </ul>		23 0 0 0 0 0 0 0	Start position? Glimmer: N/A Glimmer Score: N/A GeneMark: 60277 Starterator MAs for selected and for alt options (number, number alt MAs) 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 (Hpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) Gap=-104, Space=10
<ul> <li>Direction: ( Reverse</li> <li>Notes:</li> </ul>	Fwd/Rev)		u tRNA	?		

1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Annotato			tator:	Function:	F	eature 103 Annotation		
5' end:	5' end: 3' end: Lo		ength:			Start position?		
<ul> <li>Is there codi Genemarks?</li> <li>Are there ho a Blast searc</li> <li>Is it longer the Do other relation</li> </ul>	t a gene? ng potential based o (Y/N and description mologous genes bas h? (Answer) nan 120 bp (Y/N) ated phages agree ) (Y/N)		<ul> <li>Like (Ans or bo</li> <li>Blast</li> <li>Phag</li> <li>Like (cons func</li> <li>NKF</li> </ul>	t: ges DB: ly Function from HHpred? served domains and tional regions) abrane binding domain?		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:								

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1 <sup>st</sup> Annotator: Nina		Anno	tator:	<b>Function</b> : Hypothetical	Feature 104 Annotation	
<b>5' end:</b> 60423	<b>3' end:</b> 60277		<mark>ngth</mark> : 146	Protein		Start position?
<ul> <li>Is there codin Genemarks? (</li> <li>Are there hon a Blast search Yes</li> <li>Is it longer that Yes</li> <li>Do other relat (Phamerator) Yes</li> <li>Direction: (Fv)</li> </ul>			<ul> <li>Like (Ans or bo</li> <li>Blass</li> <li>Phag</li> <li>Like (construct</li> <li>NKF</li> </ul>	nction Unknown t: pothetical Protein ges DB: pothetical Protein ly Function from HHpred? served domains and tional regions)		Glimmer: 60423 Glimmer Score: 6.72 GeneMark: 6042 Starterator MAs for selected and for alt options (number, number alt MAs) IAs 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
- Revers	9e			-		Gap- 30, Space- 10



	1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Alex		2 <sup>nd</sup> A	<sup>nd</sup> Annotator:		Function:	] ]	Feature 105 Annotation	
	5' end:       3' end:       Let         60762       60460       Is it a gene?         Is there coding potential based on Genemarks? (Y/N and description).			Function?Likely function from Phamerator (Answer) unknown functionLikely function from Blastp? (Answer using phagesDB, NCBI, or both) unknown functionBlast: hypothetical proteinPhages DB: hypothetical functionLikely Function from HHpred? 		0000	<ul> <li>Glimmer Score: 9.68</li> <li>GeneMark: 60735</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)         <sup>25</sup> MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree?</li> </ul>		
	Yes Is it longer the Yes Do other relation (Phameraton Yes Direction: (F Reverse	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)				<ul> <li>and do Genemark and Glimmer agree? (Y/N, Y/N) no and no</li> <li>Is it the longest ORF? (Y/N) No</li> <li>Alignment agreement from Blast? (Y/N, Source) 93%</li> <li>SD Score? Is there one higher? (number, Y/N) -4.228, yes -3.440</li> <li>Gap, overlap, and spacing? (description) Gap of -4, no overlap. Spacing of 10</li> </ul>			
ľ	Notes:								

<mark>1<sup>st</sup> Annotator:</mark> Gigi	2 <sup>nd</sup> Annotator:		Function: Unknown function	Feature 107 Annotation
<b>5' end:</b> 60974 6075		ength: 216		Start position?
<ul> <li>Is there coding potentia Genemarks? (Y/N and d Yes</li> <li>Are there homologous g a Blast search? (Answer Yes</li> <li>Is it longer than 120 bp ( Yes</li> <li>Do other related phages (Phamerator) (Y/N) Yes</li> <li>Direction: (Fwd/Rev) - Reverse</li> </ul>	l based on escription). renes based on ) (Y/N)	(Ansy unk Likel (Ansy both) unk Blast unk Phag unk Likel (cons regio	trown function y function from Blastp? wer using phagesDB, NCBI, or trown function trown function es DB: trown function y Function from HHpred? werved domains and functional ns) brane binding domain?	<ul> <li>Glimmer Score: 9.94</li> <li>GeneMark:</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 33 MAs</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes</li> <li>Is it the longest ORF? (Y/N)</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description) Gap: 186 Overlap: Spacing: 9</li> </ul>



1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Annotator: 2 <sup>nd</sup> Annotator		2 <sup>nd</sup> Anno	tator:	<b>Function</b> : Hypothetical Protein	Annotation	
<b>5' end:</b> 60174	<b>3' end:</b> 60308		<mark>ngth</mark> : 135		Start position?	
<ul> <li>Is there codi Genemarks?</li> <li>Y</li> <li>Are there hon a Blast search No</li> <li>Is it longer th Yes</li> <li>Do other rela (Phamerator)</li> </ul>				Function? y function from Phamerator ver) y function from Blastp? wer using phagesDB, NCBI, or : None es DB: None y Function from HHpred? erved domains and functional ns) hing with enough coverage brane binding domain? ? No	<ul> <li>Glimmer: 60308</li> <li>Glimmer Score: 3.58</li> <li>GeneMark:None</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs)</li> <li>Not displayed</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY</li> <li>Is it the longest ORF? (Y/N) Y</li> <li>Alignment agreement from Blast? (Y/N, Source)No</li> <li>Does it include all of the functional region (HHpred)?Yes</li> <li>SD Score? Is there one higher? (number, Y/N)N</li> <li>Gap, overlap, and spacing? (description)</li> </ul>	1



1 <sup>st</sup> Annotator: Daniel	otator:	<b>Function</b> : Hypothetical protein	Feature 107 Annotation
<b>5' end:</b> 61856 <b>3' end:</b> 61161	ength: 696		<ul> <li>Start position?</li> <li>Glimmer: 61856</li> <li>Glimmer Score: 10.52</li> <li>GeneMark: 61775</li> <li>Starterator MAs for selected and for alt options (number, number alt MAs) 61856 30 MA's; 61775 1 MA's</li> <li>Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes, No</li> <li>Is it the longest ORF? (Y/N) Yes</li> <li>Alignment agreement from Blast? (Y/N, Source) Yes</li> <li>Does it include all of the functional region (HHpred)? No</li> <li>SD Score? Is there one higher? (number, Y/N) -4.177, Yes</li> <li>Gap, overlap, and spacing? (description) o</li> </ul>
<b>Is it a gene?</b>	Like	Function? by function from merator (Answer)	
<ul> <li>Is there coding potential based on Genemarks? (Y/N and description).</li> <li>Yes</li> <li>Are there homologous genes based on a Blast search? (Answer)</li> </ul>	<ul> <li>Likely f</li> <li>(Answe or both unknown</li> <li>Blast:</li> <li>Unknown</li> <li>Phages</li> <li>Likely f</li> <li>(conser</li> </ul>	known function ly function from Blastp? wer using phagesDB, NCBI, oth) known function t: known function ges DB: known function ly Function from HHpred? served domains and tional regions) known function	
<ul> <li>Is it longer than 120 bp (Y/N)</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> </ul>			
<ul> <li>Yes</li> <li>Direction: (Fwd/Rev)</li> <li>Reverse</li> </ul>	□ NKF Yes □ Men		
			hourse



1 <sup>st</sup> Annotator: 2 <sup>nd</sup> Anno Madison Renn	tator: Function:	Feature 108 Annotation		
<b>5' end: 3' end: Le</b> 61857	ngth:	<b>Start position?</b>		
Is it a gene?	<b>Function</b> ?	n Starterator MAs for selected and for alt options (number, number alt MAs)		Glimmer Score: GeneMark: Starterator MAs for selected and for alt
□ Is there coding potential based on Genemarks? (Y/N and description).	Likely function from Blastp? (Answer using phagesDB, NCBI, or both)	Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)		
<ul> <li>Are there homologous genes based on a Blast search? (Answer)</li> <li>Is it longer than 120 bp (Y/N)</li> <li>Do other related phages agree (Phamerator) (Y/N)</li> <li>Direction: (Fwd/Rev)</li> </ul>	<ul> <li>Blast:</li> <li>Phages DB:</li> <li>Likely Function from HHpred? (conserved domains and functional regions)</li> <li>NKF</li> <li>Membrane binding domain?</li> </ul>	<ul> <li>Is it the longest ORF? (Y/N)</li> <li>Alignment agreement from Blast? (Y/N, Source)</li> <li>Does it include all of the functional region (HHpred)?</li> <li>SD Score? Is there one higher? (number, Y/N)</li> <li>Gap, overlap, and spacing? (description)</li> </ul>		
Notes:	□ tRNA?			

