1 st Annotator: 2 nd Annot	tator: Function:	Annotation		
5' end: 3' end: Le	ngth:	Start position?		
 Is there coding potential based on Genemarks? (Y/N and description). Are there homologous genes based on a Blast search? (Answer) Is it longer than 120 bp (Y/N) Do other related phages agree (Phamerator) (Y/N) Direction: (Fwd/Rev) 	Function? Likely function from Phamerator (Answer) Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Blast: Phages DB: Likely Function from HHpred? (conserved domains and functional regions) NKF Membrane binding domain?	 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:				

INUICS.



<mark>1st Annotato</mark> Gisselle Treje		2 nd Annotator:		Function: Not a Gene]	Feature X Annotation		
5' end:	3' end:	Lei	ngth:			Start position?		
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	 Alignment agreem Source) Does it include all 	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>1st Annotator:</mark> Daniel	2 nd Anno Nir		Function: Hypothetical protein	Feature 1 Annotation	1
	nd: L	ength: 369		Start position?	
 Is there coding potential Genemarks? (Y/N and do Yes, bumpy but potential goe sequence Are there homologous g Blast search? (Answer) Yes Are there homologous g Blast search? (Answer) Yes Is it longer than 120 bp (Yes) Do other related phages (Phamerator) (Y/N) Yes Direction: (Fwd/Rev) Reverse Notes: 	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	 Glimmer: 1079 Glimmer Score: 10.51 GeneMark 1019 Starterator MAs for selected and for alt options (number, number alt MAs) 1040 14 MA'S, 1079 1 MA Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, N Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Y, 98% Does it include all of the functional region (HHpred)? No SD Score? Is there one higher? (number, Y/N) Y, -1.907 Gap, overlap, and spacing? (description) 	



1 st Annotator: 2 nd Annot Trenton Shappee			ator:	Function: hypothetical protein	Feature 2 Annotation				
5' end: 1225	3' end: 1037		ngth: ¹⁸⁹		Start position? Glimmer: 1225				
 Is there cod Genemarks Y Are there ho a Blast searce Is it longer t 	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)		 (Ansy both) Likel (Ansy both) Blast Phag prote Likel (cons regio) NKF 	: Function unknown 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?	 Glimmer Score: 5.91 GeneMark1225 Starterator MAs for selected and for alt options (number, number alt MAs) (Start: 13 @1225 has 6 MA's) Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) N,Y Is it the longest ORF? (Y/N) N it is the second longest Alignment agreement from Blast? (Y/N, Source) Y YDoes it include all of the functional region (HHpred)? No SD Score? Is there one higher? (number, Y/N)-2.845N Gap, overlap, and spacing? (description) 				
Notes:									

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



1 st Annotator: Phoenix		Annot sley Al		Function: PnuC-like]	Feature 4 Annotation
5' end: 2408 3' en 170			<mark>gth</mark> : ⁰⁸	Nicotinamide riboside transporter		Start position?
 Is there coding potentia Genemarks? (Y/N and de Are there homologous g a Blast search? (Answer) Yes Is it longer than 120 bp (yes Do other related phages (Phamerator) (Y/N) yes Direction: (Fwd/Rev) - Reverse 	l based on escription enes based) (Y/N)	d on	 Likel (Ansy or bo Blast Phag Likel (cons funct NKF 	: 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>1st Annota</mark> Nina	1 st Annotator: Nina Madal				Function : Membrane Protein]	Feature 5 Annotation
5' end: 2647	3' er 240		Leng 242			0	Start position? 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 st Annotator: 2 nd Anno Madison Renn		otator:Function:Unknown]	Feature 6 Annotation			
	5' end: 2832	3' end: 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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		^t Annotator: 2 nd Anno Madalyne		Madalyne DprA-like DNA]	Feature 7 Annotation
	5' end: 3344	3' end: 2829		<mark>ngth</mark> : ⁵¹⁶	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		options (number, number alt MAs) 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			MemtRNA	brane binding domain? ? No		-4 gap, 13 space
Ň	otes:						

1 st Annot Alex	74		otator: son	Function: Hypothetical Protein	Featu	re 8 Annotation
5' end: 3583	3' en 3341		ength: 243		Start position?	
 Is there cod Genemarks Yes Are there he a Blast sear Yes Is it longer t Yes 	than 120 bp (lated phages r) (Y/N) Fwd/Rev)	l based on escription). enes based on Y/N)	 Likel (Ans both Blast Phag Likel (cons regit Fiel NKF 	ix-turn-helix Domain Yes Ibrane binding domain? No	 GeneMar Starterate options (n 24 MA² Does it in and do Ga (Y/N, Y/N) Is it the log Alignmer Source) Y SD Score Y/N) -3.76 	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 st Annotator: 2 nd An Daniel	iel helix-turn-helix DNA		Feature 9 Annotation			
5' end: 3' end: 3936 3580	Length: 357	binding domain	Start position?			
 Is there coding potential based on Genemarks? (Y/N and description). Are there homologous genes based of a Blast search? (Answer) Are thore than 120 bp (Y/N) Do other related phages agree (Phamerator) (Y/N) Direction: (Fwd/Rev) Reverse 	(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	 Glimmer: 3936 Glimmer Score: 6.23 GeneMark: 3936 Starterator MAs for selected and for alt options (number, number alt MAs) 36 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y Is it the longest ORF? (Y/N) Y Alignment agreement from Blast? (Y/N, Source) Yes Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Y, -3.105 Gap, overlap, and spacing? (description) -8, 			
Notes:						

	1 st Annotator: 2 nd Anno Trenton		Annot	ator:	Function: helix-turn-helix DNA binding domain	Feature 10 Annotation		
	5' end: 4144	3' end: 3929		<mark>ngth</mark> : 216	protein		Start position?	
	 Is there coding (Y/N and descrives) YES on DNA master in potential Are there homonon search? (Answer Yes) Is it longer than Yes 	d phages agree (Phamerat	Blast	 (Ansy helix) Likel using Blast protei Phag doma Likel (consy region protei NKF No 	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>1st Annota</mark> Aisley All		Anno	tator:	Function : Ribbon helix-helix	Feature 11 Annotation		
	5' end: 4248 3' end: 4361			Length: ¹¹³ DNA binding domain protein			Start position?	
	Is it	t a gene?		Function? Likely function from Phamerator (Answer)ribbon-helix-helix DNA binding domain protein 			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	 Likely function from Blastp? (Answer using phagesDB, NCBI, or both) ribbon-helix-helix DNA binding domain protein Blast: ribbon-helix-helix DNA binding domain protein 			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		 domain protein Phages DB: ribbon-helix-helix DNA binding domain protein 			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	;	NKFMembrane binding domain? NO			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>1st Annotato</mark> Phoenix	Dr: 2 nd	2 nd Annotator:		Function: helix-turn-helix DNA binding domain		Feature 12 Annotation	
5' end: 4358	3' end: 5116		ngth: ⁶⁵¹			Start position?	
 Is there coding Genemarks? (Y yes Are there hom a Blast search? yes Is it longer that yes 	ed phages agree Y/N)		 Likel (Ansy both) doma Blast Phag term Likel (cons regio NKF 	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: ¹⁷⁴			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)		 (Answing Hyp) Likely using Hyp) Blast: Hyp) Phage Unic Likely (conserve) Likely (conserve) NKF Yes 	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 st Annota Nina		Anno Madiso		Function: Ribbon Helix-Helix DNA		Feature 15 Annotation
5' end: 5449	3' end: 5823		ength: 375 Binding Domair			Start position? Glimmer: 5449
 Is there codi Genemarks? Yes Are there hor a Blast searc Yes Is it longer the Yes 	t a gene? 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)		 (Anservice) (Anservice) Like (Anservice) Blass Bind Pha DNA Like (con reginged) NKH 	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>1st Annota</mark> Madison F		Annot Nina	notator: ina		Function : Terminase]	Feature 16 Annotation
5798 7309			ength: 1512		Start position? Glimmer: 5798 		
 Is there codi Genemarks? Yes Are there ho a Blast searc Is it longer the Do other relation 	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
	5' end: 7306 3' end: 7644				ength: 339			Start position?
	 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 				(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	Start position? 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 st Annotator: Alex		2 nd Annotator: Madalyne			Function: Major capsid and	F	eature 19 Annotation
5' end: 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	 (Ansv Ca Likel using Cap Blast Phag Prot Likel (cons regio cove NKF No 	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>1st Annota</mark> Phoenix		2 nd	2 nd Annotator: Trenton		Function: Hypothetical Protein		Feature 20 Annotation				
	5' end: 12930							Start position? Glimmer: 12930				
0 0 0	 Is there codin Genemarks? Are there hon a Blast search - yes Is it longer th - yes Do other rela (Phamerator) - yes 	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		
5' en 13250						D	Start position? 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)		 mpi Likely using p mpi Blast: mpi Phage: Phage: pi Likely domai NKF 	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>1st Annota</mark> Josh	tor:	2 nd	Annot	ator:	Function: Hypothetical Protein]]	Feature 22 Annotation
5' end: 15147	3' en 1588	_		ength: 735		8	Start position? 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 st Annotator: Sara	2 nd Annotator: Josh		Function:	Feature 23 Annotation
5' end: 15891 1639	d: Length:		Hypothetical Protein	Start position?
 Is there coding potentia Genemarks? (Y/N and d Y Are there homologous g a Blast search? (Answer Y Is it longer than 120 bp d Do other related phages (Phamerator) (Y/N) Y Direction: (Fwd/Rev) Fwd Notes: 	ll based on lescription). genes based on (Y/N)	 (Ansy Hype) Likel (Ansy both) Blast Phag Likel (consy region Non NKF 	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	 Glimmer: 15891 Glimmer Score: 17.64 GeneMark 15891 Starterator MAs for selected and for alt options (number, number alt MAs) 4 @15891 has 36 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y.Y Is it the longest ORF? (Y/N) Y Alignment agreement from Blast? (Y/N, Source) Y, Hyperion 26 Does it include all of the functional region (HHpred)? N SD Score? Is there one higher? (number, Y/N) -1.290 N Gap, overlap, and spacing? (description) 9



ı st Annota Group]]	Feature 24 Annotation
5' end: 16422	3' en 1736	9	ngth: 948	Function?	0000	Start position? Glimmer: 16422 Glimmer Score: 13.07 GeneMark: 16446 Starterator MAs for selected and for alt	
 Is there codi Genemarks? Yes Are there ho a Blast searc Yes Is it longer the Yes Do other relation (Phamerator Yes Direction: (Fer the search of th	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)	 Blas Phag Like HHI and Men 	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		 Starterator MAS for selected and for all options (number, number alt MAS) 221 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes- Includes all coding potential. No- genemark and glimmer do not agree Is it the longest ORF? (Y/N) Alignment agreement from Blast? (Y/N, Source) Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) There is a gap of 30 and a space of 10 	
Notos:						10-5	



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



1 st Annotator Phoenix			tator:	Function:]	Feature 26 Annotation	
5' end: 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		 Blast Phag Likel (cons regio NKF 	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>1st Annotator:</mark> Daniel	2 nd 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?
 Is there coding potential Genemarks? (Y/N and de Yes) Are there homologous ge a Blast search? (Answer) Yes Is it longer than 120 bp (Yes) Do other related phages (Phamerator) (Y/N) Yes Direction: (Fwd/Rev) Forward 	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	 Glimmer: 20430 Glimmer Score: 9 GeneMark 20430 Starterator MAs for selected and for alt options (number, number alt MAs) No MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Yes, 99% Does it include all of the functional region (HHpred)? Yes SD Score? Is there one higher? (number, Y/N) No, -2.071 Gap, overlap, and spacing? (description)





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	 Glimmer: 21278 Glimmer Score: 8.83 GeneMark21278 Starterator MAs for selected and for alt options (number, number alt MAs) (Start: 20 @21278 has 36 MA's), Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) N,Y Is it the longest ORF? (Y/N) N second longest Alignment agreement from Blast? (Y/N, Source) Y Does it include all of the functional region (HHpred)? No SD Score? Is there one higher? (number, Y/N)-5.541 N Gap, overlap, and spacing? (description) No 		



	st Annotator: 2 nd Anno Madalyne Madis				Function :]	Feature 29 Annotation
 5' end: 21810 Is there codin Genemarks? Are there hor Blast search? Is it longer the Do other rela (Phamerator) Direction: (Further of the search) - 	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	 Likely (Ansv both) Blast: Phage chape Likely (cons regio NKF 	: 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 st 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			
 Is there cod Genemarks Yes Are there ho a Blast searcy Yes Is it longer ty Yes 			(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 st Annotator: 2 nd Anno Trenton Shappee			Tail Chaperone		Feature 31 Annotation		
5' end: 22265	3' end: 22917		ngth: 854	Protein	Start position?		
 Is there codin Genemarks? Are there hon a Blast search Yes Is it longer the Yes Do other rela (Phamerator) Yes Direction: (F Fwd 		ed on	Tail Likely using Tail Blast: Phage Likely domai Tail NKF n Memh No U tRNA?	orane binding domain? [•] no	 Glimmer Score: None GeneMark None Starterator MAs for selected and for alt options (number, number alt MAs) There is none Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)NN Is it the longest ORF? (Y/N) Yes Alignment agreement from Blast? (Y/N, Source) There is none Does it include all of the functional region (HHpred)?Yes SD Score? Is there one higher? (number, Y/N) -2.224 N Gap, overlap, and spacing? (description) It overlaps with 31 		
Notes There	was a nrogram	med ti	anglatio	nal frameshift	And the second s		

Notes: There was a programmed translational frameshift



1 st Annotator: Trenton		tator: Tape measure Protein		Feature 32 Annotation	
5' end: 22926	3' end: 26219	Lengt 3294			Start position?
 Is there coding podescription). Yes Are there homolog (Answer) Is it longer than 12 Yes 	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	 Glimmer Score: 9.17 GeneMark22926 Starterator MAs for selected and for alt options (number, number alt MAs) (Start: 2 @22926 has 28 MA's), Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YY Is it the longest ORF? (Y/N)Y Alignment agreement from Blast? (Y/N, Source) V Does it include all of the functional region (HHpred)?
Notes:					1-1



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



1st Annotator:2nd AnnoMadison RennTrento			Function : Minor Tail Protein	Feature 34 Annotation		
5' end: 27588	3' e 1 305			ngth: 2922		Start position?
 Is there codi Genemarks: Yes Are there ho on a Blast set Is it longer t Do other rel (Phamerato) Direction: (I 	? (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	 (Ansv (Ansv both) Blast Phag Likel (cons regio Filam NKF: 	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		Function : 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	 Start position? Glimmer: 30509 Glimmer Score: 8.57 GeneMark 30509 Starterator MAs for selected and for alt options (number, number alt MAs) 81 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes and Yes Is it the longest ORF? (Y/N) Yes Alignment agreement from Blast? (Y/N, Source) Yes 100% SD Score? Is there one higher? (number, Y/N) -3.394, Yes -3.262 Gap, overlap, and spacing? (description) 		
D	 Direction: (Fwd/Rev) Forward 				 Memi No tRNA 	brane binding domain? ? No	4		
N	otes:				1				

<mark>1st Annotator:</mark> Aisley Allen	2 nd Anno	otator:	Function:	Feature 36 Annotation
5' end: 3' en 31660 3242		ength: 762	Hypothetical protein	Start position?
 Is there coding potential Genemarks? (Y/N and de YES Are there homologous g a Blast search? (Answer) Is it longer than 120 bp (YES Do other related phages (Phamerator) (Y/N) YES Direction: (Fwd/Rev) FORWARD Notes: 	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	 Glimmer: 31660 Glimmer Score: 6.35 GeneMark 31660 Starterator MAs for selected and for alt options (number, number alt MAs) 33 Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES YES Is it the longest ORF? (Y/N) YES Alignment agreement from Blast? (Y/N, Source) Does it include all of the functional region (HHpred)? 5.93% SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) Gap: -1 space: 12



1 st Annotator: Phoenix		2 nd Annotator: Nina			Function : Hypothetical Protein	Feature 37 Annotation	
5' end: 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?	 Glimmer: 32433 Glimmer Score: 11.05 GeneMark: 32433 Starterator MAs for selected and for alt options (number, number alt MAs) Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes Is it the longest ORF? (Y/N) yes Alignment agreement from Blast? (Y/N, Source)yes Does it include all of the functional regio (HHpred)?yes SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) -52, 10 	Dn
Noto:							Ants



	1st Annotator:2nd AnDanielAisley		<mark>Annot</mark> sley Al		Function: Hypothetical protein	F	eature 38 Annotation	
	32698 33081 Is it a gene? 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 st Annotator: Trenton		2 nd A	nnot	ator:	Function: Hypothetical Protien]	Feature 39 Annotation
5' end: 33081	3' en 3327			<mark>1gth</mark> : 92			Start position?
 Is there codim Genemarks? (Kinda Theres just) Are there hom search? (Answ Is it longer that Yes Do other relat (Y/N) Y 	 search? (Answer) No Is it longer than 120 bp (Y/N) Yes Do other related phages agree (Phamerator) (Y/N) Y 			(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 st Annotator: Nina		2 nd Annotator: Phoenix		or:	Function : Membrane Protein]	Feature 40 Annotation	
5' end: 33275			U	ength: 689		Start position? Glimmer: 33275 Glimmer Score: 10.75 GeneMark: 33275 		
 Is there codir Genemarks? Are there hor a Blast search yes Is it longer th yes Do other rela (Phamerator) yes Direction: (Further the search searc	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 st Annotator: Aisley Allen		Annot	tator:	Function: endolysin		Feature 41 Annotation
5' end: 34067	3' en 3485			<mark>ngth</mark> : ⁷⁸⁹			Start position?
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			 Glimmer Score: 10.47 GeneMark34034 Starterator MAs for selected and for alt options (number, number alt MAs) 32 Does it include all of the coding potential 	
Are there hon a Blast search YES	 Is there coding potential based on Genemarks? (Y/N and description). YES Are there homologous genes based on a Blast search? (Answer) YES 					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	
 Is it longer than 120 bp (Y/N) YES Do other related phages agree (Phamerator) (Y/N) NO, there is a dip (?) Direction: (Fwd/Rev) Forward 			 Like (con func Struc NKF 	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)	
			 Membrane binding domain? NO tRNA? NO 		Gap: 102 spacer: 7		



	notator: 2 nd 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	Is it a gene? 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	 Glimmer: 35287 Glimmer Score: 7.59 GeneMark: 35332 Starterator MAs for selected and for alt options (number, number alt MAs) 33 MA'8 Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y (moderate), No Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Yes Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Y, -1.907 Gap, overlap, and spacing? (description) -32. 		



				^d Annotator: Aisley Allen		Function: Hypothetical Protein	Feature 43 Annotation
	5' end: 3' end: Le 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		 Likely (Ansy both) Blast Phagy Likely (cons regio NKF 	: 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>1st Annota</mark> Madison R		Anno Danio	el DNAJ Like		Feature 44 Annotation		
	5' end: 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	 (Ansyleta) Likel (Ansyleta) both check Blast Phag Likel (consyleta) NKF: Mem 	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	*					

Ð

<mark>1st Annota</mark> Phoenix		Annotat	tor:	Function: hypothetical protein	Feature 4	5 Annotation	
5' end: 36548	3' end: 36360 t a gene?	Leng 306	6 I Likely (Answ	Function?	 Glimmer: 36548 Glimmer Score: 1 GeneMark 36548 Starterator MAs 	2	
 yes Are there hom Blast search? (Is it longer that yes 	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	 Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes Is it the longest ORF? (Y/N) yes Alignment agreement from Blast? (Y/N, Source)yes Does it include all of the functional region (HHpred)?yes SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description)125, 17 		
Notes:							

	1st Annotator: Gigi Trejo2nd Anno Danie				Feature 46 Annotation		
	5' end: 3' end: Le 36750 36,541		ngth: 210		Start position?		
	 Is there codi Genemarks? Yes Are there ho a Blast searc No Is it longer the Yes Do other relation No 			(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 st Annotator: Alex	2 nd	Annot	tator:	Function :	ł	Feature 47 Annotation
	5' end: 3	ential based o nd descriptio ous genes base swer) bp (Y/N) ages agree	n n).	 (Ansv Cas Likel (Ansv both) Blast Blast Phage Cas Cas Likel (cons regio Cas NKF1 Mem no 	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	. ² No		

	Annotator: sley Allen	Function: Hypothetical protein	Feature 48 Annotation
5' end: 39958 38966	Length: 993		Start position? Glimmer: 30958
 Is there coding potential based of Genemarks? (Y/N and description Yes) Are there homologous genes base a Blast search? (Answer) Yes Are there homologous genes base 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 	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	 Glimmer Score: 7.95 GeneMark: 39958 Starterator MAs for selected and for alt options (number, number alt MAs) 25 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Yes Does it include all of the functional region (HHpred)? Yes SD Score? Is there one higher? (number, Y/N) Yes, -1.907 Gap, overlap, and spacing? (description)
Notes:			

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





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

	1 st Annotator: 2 nd Anno Madison Renn Phoer		Annot Phoen		Function : Hypothetical		Feature 51 Annotation
5' end: 41239	3' en 4105	_		ngth: 186	Protein		Start position? Glimmer: 41239 Glimmer Score: 41054
 Is there codi Genemarks: - Yes Are there ho on a Blast se - Yes Is it longer t - Yes Is it longer t - Yes Do other rel (Phamerato - Yes Direction: (I - Reverse 	omologous earch? (An han 120 bj ated phag r) (Y/N)	ial base descrip genes l swer) o (Y/N)	based	 (Ansv - Ft Likely (Ansv both) Blast: Phage Likely (constregio funct NKF: 	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		
 Is there coding potential based on Genemarks? (Y/N and description). Y 	 Likely function from Phamerator (Answer) None Likely function from Blastp? (Answer using phagesDB, NCBI, or both) No Blast: hypothetical protein Phages DB: Function unknown 		a	@41508 has 13 MA's)		
 Are there homologous genes based on a Blast search? (Answer) No 				(Y/N, Y/N)YY Is it the longest ORF? (Y/N)N it is the second longest		
 Is it longer than 120 bp (Y/N) Yes Do other related phages agree (Phamerator) (Y/N) 	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	 Mem tRNA No 	brane binding domain? .?		Little overlap on both ends		



	1 st Annotator: 2 nd Anno Madalyne		2 nd Annotator: Function: MazG-like nucleotide]	Feature 53 Annotation
	5' end: 41900	3' end: 41508		<mark>ngth</mark> : ³⁹³	pyrophosphohydrolas e		Start position?
	Is it a gene?			Function? 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	wer) MazG-like nucleotide phosphohydrolase		options (number, number alt MAs) 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>			Blast: MazG-like nucleotide pyrophosphohydrolase Phages DB: 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 st Annotator: Gisselle Trejo Phoen					Function: Single-stranded		Feature 54 Annotation
	5' end: 42,772	3' en 42,0			ngth: 714	DNA-binding protein		Start position? 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 st Annota Alex	1 st Annotator: Alex 2 nd 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).	 (Ansv unk Likel (Ansv both) unk Blast: Phage Likel (cons regio NKF No 	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 st Annotator Aisley Allen		Anno	tator:	Function:		Feature 56 Annotation
	5' end: 43093	3' end: 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	 (Ansv (Ansv both) prote Blast: Phage Likely (cons regio 89.19 NKF V 	: 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:						

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1 st Annotator: Madalyne	2 nd Annotato Madison	r: Function: Hypothetical Protein	Feature 57 Annotation
5' end: 3' end 43338 43102	: Lengtl 237	1:	Start position?
 Is there coding potential bas Genemarks? (Y/N and described of the second of	sed on iption). yes based on a) Yes ee	Function? Likely function from Phamerator (Answer) Hypothetical Protein Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Blast: Hypothetical Protein Phages DB: Hypothetical Protein Likely Function from HHpred? (conserved domains and functional regions) NKF Membrane binding domain? tRNA?	 Glimmer: 43338 Glimmer Score: 12.42 GeneMark 43338 Starterator MAs for selected and for alt options (number, number alt MAs) 43338 has 24 MAs Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) yes and yes Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Yes Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description)



<mark>1st Annotator:</mark> Aisley Allen			Function: Unknown function	Feature 58 Annotation		
5' end: 3' en 43416 4354		e <mark>ngth</mark> : 132		Start position?		
 Is there coding potentia Genemarks? (Y/N and d YES Are there homologous g a Blast search? (Answer Is it longer than 120 bp (YES Do other related phages (Phamerator) (Y/N) NO Direction: (Fwd/Rev) Forward 	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	 Glimmer: 43416 Glimmer Score: 3.57 GeneMark N/A Starterator MAs for selected and for alt options (number, number alt MAs) N/A Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) no genemark available. Is it the longest ORF? (Y/N) NO Alignment agreement from Blast? (Y/N, Source) YES Does it include all of the functional region (HHpred)? 41.86% SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) gap: 77 space: 18 		





1 st Annotator: Phoenix	tator: Function: Hypothetical protein	Feature 59 Annotation
5' end: 3' end: L 43520 43410 43410	ngth: 111	Start position?
 Is there coding potential based on Genemarks? (Y/N and description). Are there homologous genes based on a Blast search? (Answer) Is it longer than 120 bp (Y/N) no Do other related phages agree (Phamerator) (Y/N) yes Direction: (Fwd/Rev) Reverse 	Function? Likely function from Phamerator (Answer) Hypothetical protein Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Hypothetical protein Blast: function unknown Phages DB: no data Likely Function from HHpred? (conserved domains and functional regions) unknown function NKF Membrane binding domain? tRNA? no	 Glimmer: Glimmer Score: GeneMark 43520 Starterator MAs for selected and for alt options (number, number alt MAs) Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Is it the longest ORF? (Y/N) Alignment agreement from Blast? (Y/N, Source) Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description)4, 18



	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 st Annotator: 2 nd 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 Function? 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?	 Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Yes 100% SD Score? Is there one higher? (number, Y/N) -3.072 and no Gap, overlap, and spacing? (description) Gap of -4 and spacing of 16, no overlap 		
Ň	otes:								

1 st Annotator: 2 nd A Nina		2 nd Anno	notator:		Function: Hypothetical]]	Feature 62 Annotation	
5' end: 44135	3' end 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		
5' end: 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		 Glimmer Score: 10.77 GeneMark: 44419 Starterator MAs for selected and for alt options (number, number alt MAs): 26 MA³ Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes 		
 Are there here on a Blast single on a Blast sindle on a Blast single on a Blast single on a Blast single on	⁷ K than 120 b <u>r</u> lated phago or) (Y/N)) (Y/N)		 Phage Likely (consiregio Funct) NKF: 	Yes brane binding domain?: own	 Is it the longest ORF? (Y/N): No Alignment agreement from Blast? (Y/N, Source): Yes Does it include all of the functional region (HHpred)? 34% Coverage SD Score? Is there one higher? (number, Y/N): DNA Master Gap, overlap, and spacing? (description): Gap: -4, Overlap: None, Spacing: 10 			
Notes: Start (Codon GT	'G	I	1					

<mark>1st Annotator:</mark> Aisley Allen	2 nd Anne Phoe	otator: nix	Function:	Feature 64 Annotation		
5' end: 3' en 44865 4441		ength: 450	Hypothetical Protein	Start position?		
 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 Is it longer than 120 bp (Yes Do other related phages (Phamerator) (Y/N) No Direction: (Fwd/Rev) Reverse 	l based on escription). hough renes based on) (Y/N)	 (Ansy both) Likel (Ansy both) Blast Phag Likel (consy central dehycons) NKF Mem 	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	 Glimmer: N/A Glimmer Score: N/A GeneMark 44865 Starterator MAs for selected and for alt options (number, number alt MAs) 1 MA Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes Is it the longest ORF? (Y/N) Yes Alignment agreement from Blast? (Y/N, Source) Yes Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) gap: -4 spacer: 11 		



	<mark>1st Annota</mark> Madison R		Anno	tator:	Function : 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	Start position? Glimmer: None Glimmer Score: None GeneMark: 44975 Starterator MAs for selected and for alt options (number, number alt MAs): 5 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): No		
	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	 Phage Likeh (consiregion mem NKF: Mem 	brane binding domain?: Yes rding to DEEP search		 Is it the longest ORF? (Y/N): No Alignment agreement from Blast? (Y/N, Source): Yes Does it include all of the functional region (HHpred)?: No SD Score? Is there one higher? (number, Y/N): -2.071, No 		
N	otes: Start (Codon ATG							

	1st Annotator: Madalyne2nd Anno Nina			Function: Hypothetical Protein]	Feature 66 Annotation	
5' end: 45079	3' en 4497	_		<mark>ngth</mark> : 108			Start position?
 Is there codi Genemarks? Are there hot a Blast searc Yes Is it longer the no Do other relation Yes 	mologous g h? (Answer han 120 bp (ated phages ?) (Y/N) Fwd/Rev)	l based o escriptio renes bas) (Y/N)		 Likel (Ansy both) Blast Phag Likel (cons regio NKF 	: 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>1st Annota</mark> Phoeni		2 nd Annot	ator:	helix-turn-helix DNA		Feature 67 Annotation
	5' end: 45300	3' end: 45076		ngth: 225	r unction 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 st Annotator: Gigi Trejo	tator:	Function: 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?		
 Is there coding potential based on Genemarks? (Y/N and description). Are there homologous genes based on a Blast search? (Answer) Yes Is it longer than 120 bp (Y/N) Yes Do other related phages agree (Phamerator) (Y/N) Directions (Ibrd (Dec)) 	(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	 Glimmer: 47691 Glimmer Score: 9.16 GeneMark: 47691 Starterator MAs for selected and for alt options (number, number alt MAs) 47691 36 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Y, Y Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Yes 100% Does it include all of the functional region (HHpred)? Yes SD Score? Is there one higher? (number, Y/N) Y, -2.377 		
 Direction: (Fwd/Rev) Reverse Notes: 	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	 Likel (Ans: or bc DN Blasti Blasti DN Phag DN Phag DN Likel (construct DN NKF NKF Mem 	A primase/helicase	 Glimmer: 47691 Glimmer Score: 9.16 GeneMark: 47691 Starterator MAs for selected and for alt options (number, number alt MAs) 47691 has 36 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes, Yes Is it the longest ORF? (Y/N) Yes Alignment agreement from Blast? (Y/N, Source) Yes, Does it include all of the functional region (HHpred)? Yes SD Score? Is there one higher? (number, Y/N) -5.414, Yes, -2.377 Gap, overlap, and spacing? (description) 178 gap (lowest)



			Annot Madiso]	Feature 70 Annotation	
	5' end: 49363	3' er 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>ıst Annota Nina</th> <th colspan="2">1st Annotator: 2nd Anno Nina</th> <th>tator:</th> <th colspan="2">Function: Ribbon-Helix-Helix</th> <th>Feature 71 Annotation</th>	ı st Annota Nina	1 st Annotator: 2 nd Anno Nina		tator:	Function : Ribbon-Helix-Helix		Feature 71 Annotation
 Is there coding potential based on Genemarks? (Y/N and description). Are there homologous genes based on a Blast search? (Answer) Yes Is it longer than 120 bp (Y/N) Yes Do other related phages agree (Phamerator) (Y/N) Yes Do other related phages agree (Phamerator) (Y/N) Yes Direction: (Fwd/Rev) Birst: (Fwd/Rev) Direction: (Fwd/Rev) Birst: (Fwd/R				U	U		-
Notes	 Is there codi Genemarks? Are there ho a Blast searcy yes Is it longer thy yes Do other relation (Phameratory yes Direction: (Figure 1) 	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 st Annotator: 2 nd Anno Trenton	otator:	Function:	Feature 72 Annotation
5' end: 49942 3' end: 49772	ength: 171	Hypothetical Protein	Start position? Glimmer: 49942
 Is it a gene? Is there coding potential based on Genemarks? (Y/N and description). Are there homologous genes based on a Blast search? (Answer) Are there homologous genes based on a Blast search? (Answer) Is it longer than 120 bp (Y/N) Do other related phages agree (Phamerator) (Y/N) Direction: (Fwd/Rev) Reverse 	(Ans No Likel (Ans both Blast Den Blast Phag Likel (com regio	y function from Blastp? wer using phagesDB, NCBI, or) : Hypothetical protein ges DB: Hypothetical protein by Function from HHpred? served domains and functional ons) Yes brane binding domain?	 Glimmer Score: 15.59 GeneMark49942 Starterator MAs for selected and for alt options (number, number alt MAs) (Start: 10 @50044 has 15 MA's), Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY Is it the longest ORF? (Y/N)Y Alignment agreement from Blast? (Y/N, Source)Y Does it include all of the functional region (HHpred)? Yes SD Score? Is there one higher? (number, Y/N)Y-7.830 Gap, overlap, and spacing? (description) No
Notes:			

1st Annotator:2nd AnnoGisselle TrejoJosh					Function : Membrane Protein	Feature 73 Annotation				
5' end: 3' end: La 50,207 50,028 La				ength: 180			Start position? Glimmer: 50,207 Glimmer Score: 4.78 GeneMark: 50,207 Starterator MAs for selected and for alt options (number, number alt MAs)			
 Is there cod Genemarks Yes Are there ho on a Blast so - Yes Is it longer t - Yes Do other rel (Phamerato Yes 	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>1st Annot</mark> Madison		Anno	tator:	Function:	Feature 74 Annotation	
5' end: 50532	3' end: 50191		<mark>ngth</mark> : ⁵¹⁶	Hypothetical Protein	Start position?	
 Is there conditions of the second seco	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	 (Ansv funct Likely (Ansv both) Blast Phag Likely (cons regio NKF: 	brane binding domain?: own	 Glimmer Score: 17.06 GeneMark: 50532 Starterator MAs for selected and for alt options (number, number alt MAs): 36 Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes Is it the longest ORF? (Y/N): No Alignment agreement from Blast? (Y/N, Source): Yes Does it include all of the functional region (HHpred)?: 27% coverage SD Score? Is there one higher? (number, Y/N): DNA Master 	
Notes: Start	Codon ATG		1			

				Anno Nina		Function : 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).:	 Likely function from Phamerator (Answer): Function Unknown Likely function from Blastp? (Answer using phagesDB, NCBI, or both): Function Unknown 			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	genes bas): Yes, Sal	ed on lyK	 Blast: Hypothetical Protein Phages DB: Function Unknown 			(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					A?: No	•	Y/N): DNA Master Gap, overlap, and spacing? (description): Gap: -8, Overlap: , Spacer: 11	
N	otes: Start (rodon AT	T C					forte	

Notes: Start Codon ATG



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

P

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

	1st Annotator:2nd AnnoMadalyne SiskPhoen		tator: ix	Function: Hypothetical Protein]	Feature 79 Annotation
5' end: 52154	3' end: L 51825		Length: 330			Start position?
 Is there codi Genemarks? Yes Are there ho a Blast searc Yes Is it longer the Yes Do other relation (Phamerator Yes Direction: (F Reverse 	mologous g h? (Answer) 1an 120 bp (ated phages) (Y/N)	l based on escription). enes based) Y/N)	 Likely (Ansy both) Blast: Phage Likely (cons regio NKF y 	: 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 st Annota Gigi Tre			2 nd 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>1st Annota</mark> Daniel		2 nd Anno Madaly			Function : 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 st Annotator: Madalyne		2 nd Annotator:		tator:	Function: Hypothetical Protein	Feature 82 Annotation				
5' end: 53466				ength: 534		Start position?				
 Is there codin Genemarks? Are there hon Blast search? Is it longer th Do other rela (Phamerator) Direction: (Fy) 	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		 Likeh (Ansv both) Blast: Phage Likeh (cons regio NKF 	: 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 st Annotator: 2 nd A Phoenix	nnot	ator:	Function: Hypothetical protein	Feature 83 Annotation	n	
	5' end: 3' end: 53765 53463		<mark>ngth</mark> : 303		Start position?		
	Is there coding potential based on 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	 Glimmer: 53651 Glimmer Score: 8.26 GeneMark 53651 Starterator MAs for selected and for alt options (number, number alt MAs) Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) no Is it the longest ORF? (Y/N) yes Alignment agreement from Blast? (Y/N, Source) Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description)118, 9 		
N	- Reverse		t RNA	? no	110, y		



ı st Annotato Trenton	or:	2 nd	Annot Nina		Function: Hypothetical protein	Feature 84 Annota	tion
5' end: 53971	3' en 5364			ngth: 324		Start position?	
 Is there coding Genemarks? (Yes there is coding) Are there hom a Blast search? Yes Is it longer that Yes Do other relate (Phamerator) (Yes Direction: (Fw - Reverse) 	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	 Glimmer: 53971 Glimmer Score: 13.23 GeneMark53980 Starterator MAs for selected and for options (number, number alt MAs) (Start: 3 @53971 has 18 MA's Does it include all of the coding pote and do Genemark and Glimmer agree (Y/N, Y/N)YN Is it the longest ORF? (Y/N) It has the Second longest ORF Alignment agreement from Blast? (Y Source) Y Does it include all of the functional in (HHpred)? yes SD Score? Is there one higher? (num Y/N)-4.062 Gap, overlap, and spacing? (description No significant gaps or overlaps 	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?
 Is there coding potentia Genemarks? (Y/N and d yes Are there homologous g a Blast search? (Answer yes Is it longer than 120 bp (yes Do other related phages (Phamerator) (Y/N) yes Direction: (Fwd/Rev) Reverse 	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?	 Glimmer: 54288 Glimmer Score: 11.04 GeneMark 54288 Starterator MAs for selected and for alt options (number, number alt MAs) 3587 Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes, yes Is it the longest ORF? (Y/N) yes Alignment agreement from Blast? (Y/N, Source) yes Does it include all of the functional region (HHpred)? yes SD Score? Is there one higher? (number, Y/N) no Gap, overlap, and spacing? (description) Gap: 8, spacer: 8



1 st Annotator: Madalyne Sisk	2 nd .	Annot	lator:	Function: Hypothetical Protein	Feature 86 Annotation
	end: 297		<mark>ngth</mark> : ⁵⁷³		Start position?
 Is there coding potent Genemarks? (Y/N and Yes Are there homologous a Blast search? (Answayes Is it longer than 120 by Yes Do other related phag (Phamerator) (Y/N) Yes Direction: (Fwd/Rev) Reverse 	tial based or description s genes base er) p (Y/N)		 Likely (Answ both) Blast: Phage Likely (consv region NKF 	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 st Annotator: 2 nd Annot Nina				or:	Function : Hypothetical	Feature 87 Annotation		
	5' end: 55483	3' end: 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				 Hypothetical Protein Blast: Hypothetical Protein Phages DB: Hypothetical Protein Likely Function from HHpred? (conserved domains and functional regions) Hypothetical Protein NKF Yes Membrane binding domain? NO 			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	A ?		ħ≁-€	



	<mark>1st Annotat</mark> Alex	or:	2 nd	Anno [®] Phoen]]	Feature 88 Annotation
	5' end: 55728	3' en 5546	_		<mark>ngth</mark> : 249	Hypothetical protein		Start position?
	Is it	t a gen	e?		D j	Function? 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).	 (Answer) unknown function Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Hypothetical protein 			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	 Blast: unknown function Phages DB: Unknown function 		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	Gap. overlap. and spacing? (description) Gap: -1 Overlap: None Spacing: 9
	- Revers	e			• t	tRNA? No		



	<mark>1st Annota</mark> Gigi Tre			Anno Aadaly		Function: Hypothetical]_]	Feature 89 Annotation
	5' end: 56,210	3' en			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).	 Like (Ans Hy Like (Ans both Blas Hy Blas Hy Pha Hy Like (con regi NKH Ye 	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 st Annotator: Daniel		2 nd Annotator:		tator:	Function : Hypothetical		Feature 90 Annotation
	5' end: 56773				ength: ⁵⁶⁷			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) Men No 				(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>1st Annotator</mark> Madalyne	: 2 nd	Annot	tator:	Function : Hypothetical Protein	Feature 91 Annotation
5' end: 57059	3' end: 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 st Annotator: 2 nd Phoenix		Annotator: Nina		Function: Hypothetical protein	Fe	eature 92 Annotation				
	5' end: 57383	5' end: 3' end: Lo					Start position? Glimmer: 57283 Glimmer Score: 12.08 				
	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?	 GeneMark: 57283 Starterator MAs for selected and for alt options (number, number alt MAs) Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)yes Is it the longest ORF? (Y/N) yes Alignment agreement from Blast? (Y/N, Source) yes Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description)8, 11 				
N	lotes:										

			¹ Annotator: Madalyne		Function :		Feature 93 Annotation	
	5' end: 57440 3' end: 57276				ength: 165 Function?			Start position? 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	 It is not a genre. Likely is (Answer Function). No Likely is (Answer Function). No Likely is (Answer Function). Likely is (Answer Function). Likely is (Answer Function). Likely is (Answer Function). Blast: Particular is the second sec			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?
 Is there coding potentia Genemarks? (Y/N and d Yes Are there homologous g a Blast search? (Answer Yes Is it longer than 120 bp (yes Do other related phages (Phamerator) (Y/N) Yes sallyK 97 Direction: (Fwd/Rev) reverse 	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	 Glimmer: 57852 Glimmer Score: 10.02 GeneMark 57836 Starterator MAs for selected and for alt options (number, number alt MAs) Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) No Is it the longest ORF? (Y/N) yes Alignment agreement from Blast? (Y/N, Source) yes Does it include all of the functional region (HHpred)? Yes SD Score? Is there one higher? (number, Y/N) No Gap, overlap, and spacing? (description) \ Gap: -19, Spacer: 15



	<mark>1st Annota</mark> Madison R		Anno	tator:	Function :	Feature 95 Annotation			
	5' end: 58090	3' end: 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>1st Annota</mark> Nina	1st Annotator: Nina2nd Anno Aisley A				Function : Hypothetical	Feature 96 Annotation			
5' end: 58224		e nd: 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 st Annota Alex	i <mark>tor:</mark>	2 nd Annot Gigi				Function:		Feature 97 Annotation
	5' end: 58550	3' en 5822	21	Lengt 330				Start position? 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)		 Likel (Ansy both) Blast Phag Likel (cons regio Ribo NKF 	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		 Starterator MAs for selected and for alt options (number, number alt MAs) No MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) No and No Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) Not really 64% SD Score? Is there one higher? (number, Y/N) -4.910, yes -2.934 	
Ň	lotes:								

	<mark>1st Annota</mark> Danie		2 nd	2 nd Annotat		Function : 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 st Annotator: 2 nd Anno Phoenix	tator:	Function: Hypothetical protein	Feature 99 Annotation	
	ngth: 309		Start position?	
 Is it a gene? Is there coding potential based on Genemarks? (Y/N and description). Yes Are there homologous genes based on a Blast search? (Answer) Yes Is it longer than 120 bp (Y/N) - yes Do other related phages agree (Phamerator) (Y/N) yes Direction: (Fwd/Rev) - Reverse 	(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	 Glimmer Score: 13.77 GeneMark 59326 Starterator MAs for selected and for alt options (number, number alt MAs) 59326 23 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) YES Is it the longest ORF? (Y/N) YES Alignment agreement from Blast? (Y/N, Source) YES Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) - 10, 10 	
Notes:				

1 st Annotator:2 nd AnnoAisley AllenMadalyne			Function: hypothetical protein	Annotation	
5' end: 3' en 59714 5936		ength: 351		Start position?	
 Is there coding potentia Genemarks? (Y/N and d yes Are there homologous g a Blast search? (Answer yes Is it longer than 120 bp (yes Do other related phages (Phamerator) (Y/N) no Direction: (Fwd/Rev) Reverse 	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;	 Glimmer: 59714 Glimmer Score: 13.37 GeneMark 59714 Starterator MAs for selected and for alt options (number, number alt MAs) Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) yes! Is it the longest ORF? (Y/N) yes Alignment agreement from Blast? (Y/N, Source) yes Does it include all of the functional region (HHpred)? no SD Score? Is there one higher? (number, Y/N) no Gap, overlap, and spacing? (description) Gap: -4, spacer: 11 	n



	1 st Annotator: 2 nd Anno Madison Renn Trent			Function : Hypothetical		Feature 101 Annotation		
	5' end: 60142	3' en 5971 t a gen 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	 32 Function? Likely function from Phamerator (Answer): Hypothetical Protein Likely function from Blastp? (Answer using phagesDB, NCBI, or both): Function Unknown Blast: Function Unknown Phages DB: No data available 		Start position? Glimmer: 60142 Glimmer Score: 12.58 GeneMark: 60142 Starterator MAs for selected and for alt options (number, number alt MAs): 8 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N): Yes Is it the longest ORF? (Y/N): No Alignment agreement from Blast? (Y/N, Source): Yes Does it include all of the functional region (HHpred)?: No
	Do other rela (Phamerator) Direction: (F	wd/Rev): R	everse		 NKF: Mem tRNA 	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 st Annota Nina		^d Annotator:		Function: Hypothetical		Feature 102 Annotation
 Is there cod Genemarks Are there he a Blast search Is it longer to No Do other reformed (Phameratory 	60277 60188 Is it a gene? Is there coding potential based on Genemarks? (Y/N and description). Are there homologous genes based on a Blast search? (Answer) Is it longer than 120 bp (Y/N) Do other related phages agree (Phamerator) (Y/N)		 Protein Protein B9 Function? Likely function from Phamerator (Answer) Hypothetical protein Likely function from Blastp? (Answer using phagesDB, NCBI, or both) Hypothetical Protein Blast: Function Unknown Phages DB: Unknown Function Likely Function from HHpred? (conserved domains and functional regions) function unknown NKF ves 		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
 Direction: (Reverse Notes: 	Fwd/Rev)		u tRNA	?		

1 st Annotator: 2 nd Annotato			tator:	Function:	F	eature 103 Annotation		
5' end:	5' end: 3' end: Lo		ength:			Start position?		
 Is there codi Genemarks? Are there ho a Blast searc Is it longer the Do other relation 	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)		 Like (Ans or bo Blast Phag Like (cons func NKF 	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:								

R

1 st Annotator: Nina		Anno	tator:	Function : Hypothetical	Feature 104 Annotation	
5' end: 60423	3' end: 60277		<mark>ngth</mark> : 146	Protein		Start position?
 Is there codin Genemarks? (Are there hon a Blast search Yes Is it longer that Yes Do other relat (Phamerator) Yes Direction: (Fv) 			 Like (Ans or bo Blass Phag Like (construct NKF 	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 st Annotator: 2 nd Alex		2 nd A	nd 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	 Glimmer Score: 9.68 GeneMark: 60735 Starterator MAs for selected and for alt options (number, number alt MAs) ²⁵ MA's Does it include all of the coding potential and do Genemark and Glimmer agree? 		
	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)				 and do Genemark and Glimmer agree? (Y/N, Y/N) no and no Is it the longest ORF? (Y/N) No Alignment agreement from Blast? (Y/N, Source) 93% SD Score? Is there one higher? (number, Y/N) -4.228, yes -3.440 Gap, overlap, and spacing? (description) Gap of -4, no overlap. Spacing of 10 			
ľ	Notes:								

<mark>1st Annotator:</mark> Gigi	2 nd Annotator:		Function: Unknown function	Feature 107 Annotation
5' end: 60974 6075		ength: 216		Start position?
 Is there coding potentia Genemarks? (Y/N and d Yes Are there homologous g a Blast search? (Answer Yes Is it longer than 120 bp (Yes Do other related phages (Phamerator) (Y/N) Yes Direction: (Fwd/Rev) - Reverse 	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?	 Glimmer Score: 9.94 GeneMark: Starterator MAs for selected and for alt options (number, number alt MAs) 33 MAs Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes Is it the longest ORF? (Y/N) Alignment agreement from Blast? (Y/N, Source) Yes Does it include all of the functional region (HHpred)? SD Score? Is there one higher? (number, Y/N) Gap, overlap, and spacing? (description) Gap: 186 Overlap: Spacing: 9



1 st Annotator: 2 nd Annotator: 2 nd Annotator		2 nd Anno	tator:	Function : Hypothetical Protein	Annotation	
5' end: 60174	3' end: 60308		<mark>ngth</mark> : 135		Start position?	
 Is there codi Genemarks? Y Are there hon a Blast search No Is it longer th Yes Do other rela (Phamerator) 				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	 Glimmer: 60308 Glimmer Score: 3.58 GeneMark:None Starterator MAs for selected and for alt options (number, number alt MAs) Not displayed Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N)YY Is it the longest ORF? (Y/N) Y Alignment agreement from Blast? (Y/N, Source)No Does it include all of the functional region (HHpred)?Yes SD Score? Is there one higher? (number, Y/N)N Gap, overlap, and spacing? (description) 	1



1 st Annotator: Daniel	otator:	Function : Hypothetical protein	Feature 107 Annotation
5' end: 61856 3' end: 61161	ength: 696		 Start position? Glimmer: 61856 Glimmer Score: 10.52 GeneMark: 61775 Starterator MAs for selected and for alt options (number, number alt MAs) 61856 30 MA's; 61775 1 MA's Does it include all of the coding potential and do Genemark and Glimmer agree? (Y/N, Y/N) Yes, No Is it the longest ORF? (Y/N) Yes Alignment agreement from Blast? (Y/N, Source) Yes Does it include all of the functional region (HHpred)? No SD Score? Is there one higher? (number, Y/N) -4.177, Yes Gap, overlap, and spacing? (description) o
Is it a gene?	Like	Function? by function from merator (Answer)	
 Is there coding potential based on Genemarks? (Y/N and description). Yes Are there homologous genes based on a Blast search? (Answer) 	 Likely f (Answe or both unknown Blast: Unknown Phages Likely f (conser 	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	
 Is it longer than 120 bp (Y/N) Do other related phages agree (Phamerator) (Y/N) 			
 Yes Direction: (Fwd/Rev) Reverse 	□ NKF Yes □ Men		
			hourse



1 st Annotator: 2 nd Anno Madison Renn	tator: Function:	Feature 108 Annotation		
5' end: 3' end: Le 61857	ngth:	Start position?		
Is it a gene?	Function ?	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)		
 Are there homologous genes based on a Blast search? (Answer) Is it longer than 120 bp (Y/N) Do other related phages agree (Phamerator) (Y/N) Direction: (Fwd/Rev) 	 Blast: Phages DB: Likely Function from HHpred? (conserved domains and functional regions) NKF Membrane binding domain? 	 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:	□ tRNA?			

