Basic Phage Information	
Phage Name	Losacky
Gene #	1
Stop Coordinate	513
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	1
Selected Function	NFK

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Glimmercall @bp 1 has strength 14.61.
program (Glimmer,	Both programs agree
GeneMark)?	
Is there evidence for	yes
coding potential?	
Is this gene present in	Ves the gene is conserved in MenE
other annotated	MenE gene $(1-522)$ pham 87060
genomes?	
Does the gene violate	20
any major guiding	
principles?	
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not supported):: 1
Glimmer and GeneMark	GeneMark Start Coordinate (type NA if not supported):: 1
suggest?	
Does the start site have	Considering start site 1
an associated Ribosome	Z score 2.816 the rest was the best rbs
Binding Site with a high	
score?	
Is the predicted start	Indicate the length of the ORF is with the predicted start
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the
If not, does the longest	upstream ORF. Does the proposed start site have a
ORF result in excessive	gap/overlap with the nearest upstream gene that does not
gene overlap (>30bp)?	violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.
Is this start site	Start site 1
conserved in other	Start 1: * found in 17 of 17 (100%) of genes in pham*
phage genomes as	Manual annotations of this start: 9 of 9
indicated by Starterator?	
Is this start site	Conserved with smal terminase sububit in phages Blett,
conserved in other	Antuna, and Bush
phage genomes as	
indicated by BlastP?	
	@Bp 1 because glimmer, genemark, starterator,
DECISION.	phamerator, and blastP agree.

Gathering Evidence	Explain Your Rationale
Does this protein align	DNA Master: Terminase small subunit
with a protein having a	E- value: 0.0E0
functional assignment in	
BlastP (phagesDB	
and/or GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align	Yes it does with DUF2774 unknown protein with a
with a protein having a	probablility score of 98.06
functional assignment in	
the PDB or other	
database in HHPred with	
a probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes, terminase small subunit with MenE Gene 1
adjacent to genes of	
known function and in a	
region of the genome	
that shows high	
conservation of gene	
order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at
transmembrane protein?	least 2 different transmembrane prediction programs.
Is the proposed function	Yes as hypothetical protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	2
Stop Coordinate	647
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	Yes – 3 Gene 1 – End site 513 Gene 2 – Start Site - 510
Selected Start Coordinate	510
Selected Function	NFK

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Yes - Original Glimmer call @bp 510 has strength 18.83
(Glimmer, GeneMark)?	
Is there evidence for	Yes
coding potential?	
Is this gene present in other annotated genomes?	Yes – Antuna gene 2 (501 - 638) pham 8570, MenE gene 2 (519 - 656) pham 8570, Pickles13 gene 2 (510 - 647) pham 8570, Warren gene 2 (519 - 656) pham 8570
Does the gene violate any major guiding principles?	No
DECISION:	Indicated by the evidence above, Losacky Gene 2 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: bp 510
	Genemark Start Coordinate. bp 510
Does the start site have an	2 nd Highest Z-Score: 1.573 3 rd Lowest Final Score: -6.770
Binding Site with a high score?	S * Lowest 1 mar Score0.110
Is the predicted start codon the longest ORF? If not.	No, the predicted start codon is the 2 nd longest ORF, with a length of 138
does the longest ORF	
result in excessive gene overlap (>30bp)?	The longest ORF, with a length of 222, does not have any excessive gene overlap.
Is this start site conserved	
in other phage genomes as indicated by Starterator?	Yes - The start number called the most often in the published annotations is 2, it was called in 9 of the 9 non-draft genes in the pham.
Is this start site conserved	Yes – Hypothetical Protein Antuna_2 and Hypothetical Protein
as indicated by BlastP?	warren_2
DECISION:	As indicated by Glimmer/GeneMark, Starterator, Phamerator, and all other evidence, the gene's start site is bp 510.

Gathering Evidence	Explain Your Rationale
Does this protein align with	
a protein having a	DNA Master: hypothetical protein
functional assignment in	E- value: 3.6E -20
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, it does with DUF3789 with a probability score of 95.24 which is an
a protein having a	unknown protein.
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes, as hypothetical protein
tound on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	3
Stop Coordinate	871
Direction (For/Rev)	for
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	644
Selected Function	NFK

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Yes both Original Glimmer call @bp 644 has strength 23.26
(Glimmer, GeneMark)?	
Is there evidence for	Yes there is coding potential
coding potential?	
Is this gene present in other annotated genomes?	Yes Antuna, MenE, and Pickles13 Antuna gene 3 (635 - 862)
	MenE gene 3 (653 - 880) Pickles13 gene 3 (644 - 868)pham 8381
Does the gene violate any major guiding principles?	по
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	They both suggest bp644
Does the start site have an associated Ribosome Binding Site with a high score?	Its z score was 1.695 and final score -5.621 this is pretty good as the other one only had an orf of 27
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Yes it is the longest with an orf length of 228 ORF
Is this start site conserved	Yes as The start number called the most often in the published
as indicated by Starterator?	pham. And the start site was called as to be bp664
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes it is most likely a hypothetical protein for appa, warren, and blett
DECISION:	Yes as glimmer/genemark, starterator, pharmarator, and coding potential agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Hypothetical Protein
a protein having a	2.83E-45
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Heterocyst differentiation control protein
a protein having a	Probability Score :61.35
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation	
of gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes Hypothetical Protein
found on the SEA-	
PHAGES approved	
DECISION:	NFK

Basic Phage Information	
Phage Name	Losacky
Gene #	4
Stop Coordinate	1050
Direction (For/Rev)	FWD
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	874
Selected Function	NKF

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 874 has strength 16.57. Both agree.
Is there evidence for coding potential?	Yes, both agree.
Is this gene present in other annotated genomes?	Yes, the genome is present in Men E. MenE gene 4 (883 - 1059) pham 213128
Does the gene violate any major guiding principles?	Discuss if there are any significant violations of the <u>Guiding</u> <u>Principles of Genome Annotation</u> with the gene call. Do you see significant overlap with other genes? Is it long enough? Are the genes before and after this gene in the same direction?
DECISION:	Respond here with YES or NO after reviewing the evidence gathered above.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate bp 874
and GeneMark suggest?	Genemark Start coordinate bp 874
Does the start site have an associated Ribosome Binding Site with a high score?	Final RBS score= -5.923 This was the lowest RBS score z- score= 1.469 This is the medium value
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes the start site is found in 12 of 13 genes (92.3%) of genes in pham
Is this start site conserved in other phage genomes as indicated by BlastP?	Provide the best BlastP match from NCBI, PhagesDB, and DNA Master with alignment in the format of (Q#:S#), where Q (query) is the sequence you are analyzing and S (subject) is the database match. List the e-value and alignment of the best match for all three BlastP sources.
	Note: If you are considering more than 1 start site, provide the same information for each proposed start site. Conserved with hypothetical protein Bush, Warren, and Blett (DNA Master)
DECISION:	Yes the start site should be bp 874 as shown above. Suppoting data; glimmer, phamerator, startator, blast.

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: hypothetical protein Bush
a protein having a	E value : 1.3E -32
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, this aligns with DUF2774 with the probability score of
a protein having a	98.06 but is a hypothetical protein.
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Hypothetical protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	5
Stop Coordinate	1163
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	1050
Selected Function	NFK

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 1050 has strength 8.98 Yes genemark and glimmer agree
Is there evidence for coding potential?	Yes, both genemark programs show coding potential
Is this gene present in other annotated genomes?	Yes, it is present in MenE MenE gene 5 (1059-1172) pham 216577
Does the gene violate any major guiding principles?	no
DECISION:	Yes. Glimmer, Genemark, and phamerator agree

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	<i>Glimmer Start Coordinate ::1050 GeneMark Start Coordinate ::1050</i>
Does the start site have an associated Ribosome Binding Site with a high score?	Considering start site bp: 1050 Z score: 2.760 which is the highest Z score Final score: -3.474 which is the highest Best RBS
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Indicate the length of the ORF is with the predicted start and the gap/overlap to the nearest stop codon of the upstream ORF. Does the proposed start site have a gap/overlap with the nearest upstream gene that does not violate the Guiding Principles? Note: if you are considering more than 1 start site, provide the
Is this start site conserved in other phage genomes as indicated by	Same Information for each proposed start site. Start 13: • Found in 15 of 20 (75.0%) of genes in pham • Manual Annotations of this start: 5 of 12
Starterator?	
Is this start site conserved in other phage genomes as indicated by BlastP?	Conserved with hypothetical protein in phages MenE, Blett, Antuna, Dropshot, Hot26
DECISION:	Yes it is a gene because Genemark/Glimmer, Phamerater, Starterator, and BlastP all agree that the start site is @bp 1050

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Hypothetical Protein
a protein having a	E value: 1.6E-18
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes as a Hypothetical protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NFK

Basic Phage Information	
Phage Name	Losacky
Gene #	6
Stop Coordinate	1396
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	1163
Selected Function	NKF

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Yes Original Glimmer call @bp 1163 has strength 5.69
(Glimmer, GeneMark)?	
Is there evidence for	Yes
coding potential?	
Is this gene present in other annotated genomes?	Yes it is present in MenE MenE gene 6 (1172 - 1405) pham 8812
Does the gene violate any major guiding principles?	no
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	@bp1163
and GeneMark suggest?	
Does the start site have an	Has a high z value 2.777 and a low final score -4.189 and since
associated Ribosome	there is only one other this is the best choice
Binding Site with a high	
score?	
Is the predicted start codon	Its not the longest ORF but it doesn't violate the guidelines
the longest ORF? If not,	
does the longest ORF	
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	
in other phage genomes	
as indicated by	Yes as most of them called it other than one The start number
Starterator?	called the most often in the published annotations is 8. it was called
	in 8 of the 9 non-draft genes in the nham so the start site is 1163
Is this start site conserved	Yes It is a hypothetical protein for warren, blett, and pickles13
in other phage genomes	
as indicated by BlastP?	
DECISION	Yes glimmer/genemark, starterator, pharmarator, blastp, coding
	potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Hypothetical protein Warren
a protein having a	E- value: 2.3E-40
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	No Quality Match, best match was DUF3622 of unknown function with
a protein having a	a probability of 24.84.
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation	
of gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes, hypothetical protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	10
Stop Coordinate	2846
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	Yes – 49 bp (Does not violate guiding principals) Gene 6 Stop Site – bp 1396 Gene 7 Start Site – bp 1347
Selected Start Coordinate	1347
Selected Function	Terminase, large subunit

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes - Original Glimmer call @bp 1347 has strength 17.64; GeneMark calls start at 1509
Is there evidence for coding potential?	Yes, there is evidence for coding potential.
Is this gene present in other annotated genomes?	Yes - MenE gene 7 (1518 - 2855) pham 1724, Warren gene 7 (1536 - 2879) pham 1724
Does the gene violate any major guiding principles?	No, the gene does not violate any major guiding principles.
DECISION:	Yes, as indicated by the evidence above, Losacky Gene 7 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: bp 1347
and GeneMark suggest?	GeneMark Start Coordinate: bp 1509
Does the start site have an	1 st Highest Z-Score: 2.825
Associated Ribosome	4" Lowest Final Score: -4.572
score?	
300161	
Is the predicted start codon	The predicted start codon (bp 1347) has the longest ORF length
the longest ORF? If not,	of 1500
does the longest ORF	
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	No - The start number called the most often in the published
In other phage genomes	annotations is 34, it was called in 17 of the 59 non-draft genes
as indicated by Starterator?	In the pham, but has no annotations for Losacky_7.
Starteratory	Alternatively, start number 26 was found in 16 of the 59 non-
	draft genes and has six manual annotations at bp 1509
Is this start site conserved	Yes – Phages MenE (Terminase Large Subunit). Blett
in other phage genomes	(Terminase Large Subunit), Warren (Terminase), Antuna
as indicated by BlastP?	(Terminase Large Subunit), and Phonegingi (Terminase Large
-	Subunit)
DECISION	As indicated by Glimmer, the RBS, and the coding potential, the
DEGIGIOIT	best possible start site for this gene is bp 1347.

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Terminase Large Subunit
a protein having a	0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Terminase Large subunit
a protein having a	Probability: 100
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Terminase Large Subunit
adjacent to genes of	MenE
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Terminase, Large Subunit
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Terminase, Large subunit

Basic Phage Information	
Phage Name	Losacky
Gene #	8
Stop Coordinate	2955
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	25
Selected Start Coordinate	2821
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 2821 has strength 2.48 ** not called by GeneMark
Is there evidence for coding potential?	No it overlaps with the gene before and after and there is no coding potential
Is this gene present in other annotated genomes?	No but there might be only one that is only slightly similar in Pickles13 gene 6 (2557 - 2832) pham 23316
Does the gene violate any major guiding principles?	It's a pretty small gene being less than 200bp it also overlaps with a previous gene
DECISION:	No gene mark didn't call it it also overlaps with other genes with not a lot of coding potential. It is not found in other genomes in pharmarator or starterator and is less than 200 bp. It needs to be deleted

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate (type NA if not supported)::
and Genemark suggest?	Genemark Start Coordinate (type NA If not supported)::
Does the start site have an associated Ribosome	List the final RBS score and Z-score of the currently predicted
Binding Site with a high	in your response if this is the best score or not.
score?	Note: if you are considering more than 1 start site, provide the
	same information for each proposed start site.
Is the predicted start codon	Indicate the length of the ORF is with the predicted start and the
does the longest ORF	Does the proposed start site have a gap/overlap with the
result in excessive gene overlap (>30bp)?	nearest upstream gene that does not violate the Guiding Principles?
	Notes if you are considering more then 4 start site, more ide the
	same information for each proposed start site.
Is this start site conserved	
as indicated by Starterator?	You will also need to provide the following information from Starterator: does the start match the consensus start site predicted from Starterator? If no, is the consensus start site not found in this ORF? If no, is there a better option for the consensus start site instead of the one predicted by Starterator? If Starterator doesn't reveal a consensus start site, you can record that Starterator was not informative.
	Note: if you are considering more than 1 start site, provide the same information for each proposed start site.
Is this start site conserved in other phage genomes as indicated by BlastP?	Provide the best BlastP match from NCBI, PhagesDB, and DNA Master with alignment in the format of (Q#:S#), where Q (query) is the sequence you are analyzing and S (subject) is the database match. List the e-value and alignment of the best match for all three BlastP sources.
	Note: if you are considering more than 1 start site, provide the same information for each proposed start site.
DECISION:	Record where you think the gene should start here and briefly explain your rationale.

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	PHAGES Official Function List to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully velled for
	approval.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	9
Stop Coordinate	4525
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	43
Selected Start Coordinate	2912
Selected Function	Portal PRotein

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Yes, however they are called at different points
(Glimmer, GeneMark)?	
Is there evidence for	Ves there is evidence for coding notential
coding potential?	res, there is evidence for county potential
Is this gene present in	It is present in other genes
other annotated genomes?	it is present in other genes
Does the gene violate any	
major guiding principles?	NO
DECISION	
DECISION.	It is a gene

What start site do Glimmer and GeneMark suggest?Original Glimmer call 2912, Original GeneMark call 2975Does the start site have an associated Ribosome Binding Site with a high score?2912 is best option has high z value 2.249 and low final scor 4.4752975 is second choice a Provide the best BlastP match from NCBI, PhagesDB, and DNA Master with alignment in the for of (Q#:S#), where Q (query) is the sequence, you are analyz and S (subject) is the database match. List the e-value and alignment of the best match for all three BlastP sources.Note: if you are considering more than 1 start site, provide th same information for each proposed start site. and has a z value of 1.941 and a final score of -4.475Is the predicted start codon the longest ORFF result in excessive gene overlap (>30bp)?The first option 2912 has an overlap which is 43 The second oneIs this start site conserved in other phage genomes as indicated by Starterator?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2657 portal protein [Microbacterium phage Bush]	Gathering Evidence	Explain Your Rationale
and GeneMark suggest?Does the start site have an associated Ribosome Binding Site with a high score?2912 is best option has high z value 2.249 and low final scor 4.4752975 is second choice a Provide the best BlastP match from NCBI, PhagesDB, and DNA Master with alignment in the for of (Q#:S#), where Q (query) is the sequence, you are analyz and S (subject) is the database match. List the e-value and alignment of the best match for all three BlastP sources.Note: if you are considering more than 1 start site, provide the same information for each proposed start site. and has a z value of 1.941 and a final score of -4.475Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?The first option 2912 has an overlap which is 43 The second oneThe start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in other phage genomes as indicated by BlastP?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2657 portal protein [Microbacterium phage Bush]	What start site do Glimmer	Original Glimmer call 2912 Original GeneMark call 2975
Does the start site have an associated Ribosome Binding Site with a high score?2912 is best option has high z value 2.249 and low final scor 4.475Binding Site with a high score?2975 is second choice a Provide the best BlastP match from NCBI, PhagesDB, and DNA Master with alignment in the for of (Q#:S#), where Q (query) is the sequence, you are analyz and S (subject) is the database match. List the e-value and alignment of the best match for all three BlastP sources.Note: if you are considering more than 1 start site, provide th same information for each proposed start site. and has a z value of 1.941 and a final score of -4.475Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?Is this start site conserved in other phage genomes as indicated by Starterator?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2663 portal protein [Microbacterium phage Bush]	and GeneMark suggest?	
associated Ribosome Binding Site with a high score?4.4752975 is second choice a Provide the best BlastP match from NCBI, PhagesDB, and DNA Master with alignment in the form of (Q#:S#), where Q (query) is the sequence, you are analyz and S (subject) is the database match. List the e-value and alignment of the best match for all three BlastP sources.Note: if you are considering more than 1 start site, provide th same information for each proposed start site. and has a z value of 1.941 and a final score of -4.475Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?The first option 2912 has an overlap which is 43 The second oneIs this start site conserved in other phage genomes as indicated by Starterator?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2663 portal protein [Microbacterium phage Bush]	Does the start site have an	2912 is best option has high z value 2.249 and low final score -
Binding Site with a high score?2975 is second choice a Provide the best BlastP match from NCBI, PhagesDB, and DNA Master with alignment in the form of (Q#:S#), where Q (query) is the sequence, you are analyz and S (subject) is the database match. List the e-value and alignment of the best match for all three BlastP sources.Note: if you are considering more than 1 start site, provide th same information for each proposed start site. and has a z value of 1.941 and a final score of -4.475Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?Is this start site conserved in other phage genomes as indicated by Starterator?Is this start site conserved in other phage genomes as indicated by BlastP?Is this start site conserved in other phage genomes as indicated by BlastP?	associated Ribosome	4.475
score?2975 is second choice a Provide the best BlastP match from NCBI, PhagesDB, and DNA Master with alignment in the form of (Q#:S#), where Q (query) is the sequence, you are analyz and S (subject) is the database match. List the e-value and alignment of the best match for all three BlastP sources.Note: if you are considering more than 1 start site, provide th same information for each proposed start site. and has a z value of 1.941 and a final score of -4.475Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?The first option 2912 has an overlap which is 43 The second oneIs this start site conserved in other phage genomes as indicated by Starterator?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2663 portal protein [Microbacterium phage Bush]	Binding Site with a high	
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does the longest ORF result in excessive gene overlap (>30bp)?Is this start site conserved in other phage genomes as indicated by Starterator?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2657 portal protein [Microbacterium phage Bush]	the longest ORF? If not,	The second one
result in excessive gene overlap (>30bp)?Is this start site conserved in other phage genomes as indicated by Starterator?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2657 portal protein [Microbacterium phage Bush]	does the longest ORF	
Overlap (>30bp)?Is this start site conserved in other phage genomes as indicated by Starterator?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2657 portal protein [Microbacterium phage Bush]	result in excessive gene	
Is this start site conserved in other phage genomes as indicated by Starterator?The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft gene in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15 MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2657 portal protein [Microbacterium phage Bush]	Overlap (>30bp)?	
MA's at bp 2912Is this start site conserved in other phage genomes as indicated by BlastP?2678 portal protein [Microbacterium phage Blett] 2657 portal protein [Microbacterium phage MenE] 2657 portal protein [Microbacterium phage Bush]	in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 30, it was called in 22 of the 60 non-draft genes in the pham. (Start: 14 @2912 has 15 MA's) Although the best start site seems to be site 14, as it has 15
in other phage genomes as indicated by BlastP? 2678 portal protein [Microbacterium phage Biett] 2663 portal protein [Microbacterium phage MenE] 2657 portal protein [Microbacterium phage Bush]		MA'S AT DP 2912
as indicated by BlastP? 2657 portal protein [Microbacterium phage Bush]	is this start site conserved	2678 portal protein [Microbacterium phage Biett]
	in other phage genomes	2003 portal protein [Microbacterium phage MenE]
2653 portal protein [Microbacterium phage Antuna]	as indicated by Diastr?	2653 portal protein [Microbacterium phage Bush]
DECISION: Based on the evidence above the best start site is 2912	DECISION:	Based on the evidence above the best start site is 2912
2653 portal protein [Microbacterium phage Antuna]	in other phage genomes as indicated by BlastP?	2663 portal protein [Microbacterium phage MenE] 2657 portal protein [Microbacterium phage Bush] 2653 portal protein [Microbacterium phage Antuna]

Gathering Evidence	Explain Your Rationale
Does this protein align with	Portal Protein
a protein having a	E-value: 0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Portal protein with 100 probabbility
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	MenE
adjacent to genes of	Portal Protein
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	
transmembrane protein?	
Is the proposed function	Portal Protein
tound on the SEA-	
PHAGES approved	
function list?	
DECISION:	Portal Protein

Basic Phage Information	
Phage Name	Losacky
Gene #	10
Stop Coordinate	4694
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	4512
Selected Function	NKF

Gathering Evidence	Explain Your Rationale
Was the gene called by an	Called by Glimmer but not by Genemark
auto-annotation program	Original Glimmer call @bp 4512 has strength 12.23**not called
(Glimmer, GeneMark)?	by Genemark
Is there evidence for	Ves Both genemarks agree for coding potential
coding potential?	res. Dein genemarks agree for coaing potential
Is this gene present in	Yes. The genome is present in Antuna
other annotated genomes?	Antuna gene 8 (4348-4539) pham 34084
Does the gene violate any	No.
major guiding principles?	
DECISION	
DECISION.	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate (type NA if not supported):: 4512
and GeneMark suggest?	GeneMark Start Coordinate (type NA if not supported):: NA
Does the start site have an associated Ribosome Binding Site with a high score?	For bp::4512 Final RBS score: -3.329 Z value: 2.825 All RBS values were the greatest.
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	
Is this start site conserved in other phage genomes as indicated by Starterator?	Start 1: • Found in 2 of 2 (100.0%) of genes in pham
Is this start site conserved in other phage genomes as indicated by BlastP?	Conserved with hypothetical protein in Warren
DECISION:	Yes the start site should be 4512. Although it was not called by genemark, Glimmer, Phamerator, Starterator, and Blast have called them.

Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10 ⁻⁴ or smaller with appropriate coverage? List the most informative BlastP match from each source PhagesDB: NCBI: DNA Master: Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage? Hint: you may have already found this information from annotation decision #2. Provide the alignment (q#:s#) and e- value. It is only necessary to provide one match from each database. Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage? No Quality match. The closest match was MBD_C; with a probability of 52.25. Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order? No Synteny Observed. Is this gene a possible transmembrane protein? If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs. Is the proposed function found on the SEA- PHAGES approved function list? YEF	Gathering Evidence	Explain Your Rationale
a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10-4 or smaller with appropriate coverage? NCBI: DNA Master: Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage? No Quality match. The closest match was MBD_C; with a probability of 90% or greater with appropriate coverage? Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order? No Synteny Observed. Is the proposed function found on the SEA-PHAGES approved function list? If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs. Is the proposed function found on the SEA-PHAGES approved function list? VKF	Does this protein align with	List the most informative BlastP match from each source
functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10 ⁻⁴ or smaller with appropriate coverage? NCBI: DNA Master: DNA Master: DNA Master: Hint: you may have already found this information from annotation decision #2. Provide the alignment (q#:s#) and e- value. It is only necessary to provide one match from each database. Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage? No Quality match. The closest match was MBD_C ; with a probability of 52.25. Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order? No Synteny Observed. Is this gene a possible transmembrane protein? If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs. Is the proposed function found on the SEA- PHAGES approved function list? Yes, as a hypothetical protein.	a protein having a	PhagesDB:
BlastP (phagesDB and/or GenBank) with an alignment of 10 ⁴ or smaller with appropriate coverage? DNA Master: Hint: you may have already found this information from annotation decision #2. Provide the alignment (q#:s#) and e- value. It is only necessary to provide one match from each database. Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage? No Quality match. The closest match was MBD_C ; with a probability of 52.25. Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order? No Synteny Observed. Is this gene a possible transmembrane protein? If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs. Is the proposed function found on the SEA- PHAGES approved function list? Yes, as a hypothetical protein.	functional assignment in	NCBI:
GenBank) with an alignment of 10-4 or smaller with appropriate coverage?Hint: you may have already found this information from annotation decision #2. Provide the alignment (q#:s#) and e- value. It is only necessary to provide one match from each database.Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?No Quality match. The closest match was MBD_C ; with a probability of 52.25.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?NKF	BlastP (phagesDB and/or	DNA Master:
alignment of 10 ⁻⁴ or smaller with appropriate coverage?Hint: you may have already found this information from annotation decision #2. Provide the alignment (q#:s#) and e- value. It is only necessary to provide one match from each database.Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?No Quality match. The closest match was MBD_C ; with a probability of 52.25.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?YKEDECISION:NKE	GenBank) with an	
smaller with appropriate coverage?annotation decision #2. Provide the alignment (q#:s#) and e- value. It is only necessary to provide one match from each database.Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?No Quality match. The closest match was MBD_C ; with a probability of 52.25.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?NKE	alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
coverage?value. It is only necessary to provide one match from each database.Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?No Quality match. The closest match was MBD_C; with a probability of 52.25.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?Yes, as a hypothetical protein.DECISION:NKF	smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
database.Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?No Quality match. The closest match was MBD_C ; with a probability of 52.25.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?Yes, as a hypothetical protein.DECISION:N/KF	coverage?	value. It is only necessary to provide one match from each
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?No Quality match. The closest match was MBD_C; with a probability of 52.25.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?IKEDECISION:NKE		database.
a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?probability of 90% or greater with appropriate coverage?Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?YES, indicate supporting data from at least 2 different transmembrane protein.DECISION:NKE	Does this protein align with	No Quality match. The closest match was MBD_C ; with a
functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?No Synteny Observed.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?Yes, as a hypothetical protein.DECISION:NKF	a protein having a	probability of 52.25.
the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?No Synteny Observed.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?Yes, as a hypothetical protein.DECISION:NKF	functional assignment in	
in HHPred with a probability of 90% or greater with appropriate coverage? Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order? Is this gene a possible transmembrane protein? Is the proposed function found on the SEA- PHAGES approved function list? DECISION: NKE	the PDB or other database	
probability of 90% or greater with appropriate coverage?No Synteny Observed.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?Yes, as a hypothetical protein.DECISION:NKE	in HHPred with a	
greater with appropriate coverage?No Synteny Observed.Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?Yes, as a hypothetical protein.DECISION:NKE	probability of 90% or	
coverage? No Synteny Observed. Is this gene located No Synteny Observed. adjacent to genes of region of the genome that known function and in a region of the genome that region of the genome that shows high conservation of gene order? If the answer is YES, indicate supporting data from at least 2 Is this gene a possible If the answer is YES, indicate supporting data from at least 2 transmembrane protein? different transmembrane prediction programs. Is the proposed function Yes, as a hypothetical protein. found on the SEA- PHAGES approved pHAGES approved NKF	greater with appropriate	
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?No Synteny Observed.Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane protein.Is the proposed function found on the SEA- PHAGES approved function list?Yes, as a hypothetical protein.DECISION:NKE	coverage?	
adjacent to genes of known function and in a region of the genome that shows high conservation of gene order? If the answer is YES, indicate supporting data from at least 2 different transmembrane protein? Is this gene a possible transmembrane protein? If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs. Is the proposed function found on the SEA- PHAGES approved function list? Yes, as a hypothetical protein. DECISION: NKF	Is this gene located	No Synteny Observed.
known function and in a region of the genome that shows high conservation of gene order?If the answer is YES, indicate supporting data from at least 2 different transmembrane protein?Is this gene a possible transmembrane protein?If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.Is the proposed function found on the SEA- PHAGES approved function list?Yes, as a hypothetical protein.DECISION:NKE	adjacent to genes of	
region of the genome that shows high conservation of gene order? If the answer is YES, indicate supporting data from at least 2 different transmembrane protein different transmembrane prediction programs. Is the proposed function found on the SEA- PHAGES approved function list? Yes, as a hypothetical protein. DECISION: NKE	Known function and in a	
shows high conservation of gene order? Is this gene a possible transmembrane protein? If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs. Is the proposed function found on the SEA-PHAGES approved function list? Yes, as a hypothetical protein. DECISION: NKE	region of the genome that	
Is this gene a possible If the answer is YES, indicate supporting data from at least 2 transmembrane protein? different transmembrane prediction programs. Is the proposed function Yes, as a hypothetical protein. found on the SEA- Yes, as a hypothetical protein. PHAGES approved NKE	shows high conservation of	
Is this gene a possible If the answer is YES, indicate supporting data from at least 2 transmembrane protein? different transmembrane prediction programs. Is the proposed function found on the SEA-PHAGES approved function list? Yes, as a hypothetical protein. DECISION: NKE	gene order?	If the answer is VES, indicate supporting data from at least 2
Is the proposed function found on the SEA- Yes, as a hypothetical protein. PHAGES approved function list? NKE	transmembrane protein?	different transmembrane prediction programs
found on the SEA- PHAGES approved function list? DECISION: NKF	Is the proposed function	Ves as a hypothetical protein
PHAGES approved function list?	found on the SEA	res, as a hypothetical protein.
function list? DECISION: NKF	PHAGES approved	
DECISION: NKF	function list?	
	DECISION:	NKE

Basic Phage Information	
Phage Name	Losacky
Gene #	11
Stop Coordinate	5796
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	4681
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Yes Both.
program (Glimmer,	Original Glimmer call @bp 4681 has strength 20.44
GeneMark)?	
Is there evidence for	Yes
coding potential?	
Is this gene present in	Yes. The gene is present in MenE
other annotated	MenE gene 9 (4648-5763) pham 187115
genomes?	
Does the gene violate	The gene is one of the longer ones but does not violate
any major guiding	the principles.
principles?	
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not supported)::4681
Glimmer and GeneMark	GeneMark Start Coordinate (type NA if not
suggest?	supported)::4681
Does the start site have	The final RBS score is -4.654
an associated Ribosome	The Z value is 2.189
Binding Site with a high	Both values are amongst the higher values, but are not the
score?	highest.
Is the predicted start	
codon the longest ORF?	
If not, does the longest	
ORF result in excessive	
gene overlap (>30bp)?	
Is this start site	Start 8:
conserved in other	Found in 2 of 40 (5.0%) of genes in pham
phage genomes as	No manual annotations of this start
indicated by Starterator?	
Is this start site	The gene is conserved with hypothetical protein in phages
conserved in other	Bush, Antuna, and MenE
phage genomes as	
indicated by BlastP?	
	I think the Gene should start @bp::4681 because the gene
DECISION:	is present as shown in glimmer, genemark, phamerator,
	starterator, and blastP.

Gathering Evidence	Explain Your Rationale
Does this protein align	DNA Master: head morphogenesis
with a protein having a	E value: 0.0E0
functional assignment	
in BlastP (phagesDB	
and/or GenBank) with	
an alignment of 10 ⁻⁴ or	
smaller with	
appropriate coverage?	
Does this protein align	Yes, it does with 8QQN_PH a probability score of 99.24
with a protein having a	
functional assignment	
in the PDB or other	
database in HHPred	
with a probability of	
90% or greater with	
appropriate coverage?	
Is this gene located	muF-like minor capsule protein
adjacent to genes of	
known function and in	
a region of the genome	
that shows high	
conservation of gene	
order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least
transmembrane	2 different transmembrane prediction programs.
protein?	
Is the proposed	Hypothetical Protein
function found on the	
SEA-PHAGES	
approved function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	12
Stop Coordinate	6101
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	5793
Selected Function	Immunity Protein

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	They disagree they gave two start points Original Glimmer call @bp 5793 has strength 15.07; GeneMark calls start at 5826
coding potential?	Yes
Is this gene present in other annotated genomes?	Yes MenE gene 10 (5760 - 6080) pham 212415, Bush gene 10 (5649 - 5960) pham 212415, Blett gene 10 (5646 - 5966) pham 212415, Antuna gene 10 (5629 - 5952) pham 212415
Does the gene violate any major guiding principles?	No not really they are both long enough to be considered a gene
DECISION:	Yes it is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Original Glimmer call @bp 5793 has strength 15.07; GeneMark calls start at 5826
Does the start site have an associated Ribosome Binding Site with a high score?	5793 is promising as 2.599 z value and a final score –3.789 5826 has a 1.234 z value and a final score of –6.464 The first one is more promosing as it has the highest z value and lowest final score
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The start site at 5793 is the longest open reading frame and the second one is the second largest one
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes starterator has the 5793 as its bp
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes its conserved to be a hypothetical protien for menE, Antuna, Bush, Pickles13
DECISION:	The Start site is 5793 in glimmer starterator phamerator blastp and coding potential agree
Gathering Evidence	Explain Your Rationale
----------------------------------	---
Does this protein align with	DNA Master: Hypothetical Protein Bush
a protein having a	
functional assignment in	E Value: 1.0E - 38
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, this is a quality match. This aligns with Imm35 with a
a protein having a	probability score of 99.48.
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
Known function and in a	
region of the genome that	
shows high conservation of	
gene order ?	N1/A
transmombrano protoin?	N/A
Is the proposed function	Vec
found on the SEA	100
PHACES approved	
function list?	
DECISION	Immunity protein

Basic Phage Information	
Phage Name	Losacky
Gene #	13
Stop Coordinate	6302
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	N/A
Selected Start Coordinate	6111
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 6111 has strength 21.65; GeneMark calls start at 6153
Is there evidence for coding potential?	Yes
Is this gene present in other annotated genomes?	<i>Yes</i> - Antuna gene 11 (5949 - 6149) pham 8957, MenE gene 11 (6086 - 6277) pham 8957, and Warren gene 11 (6000 - 6191) pham 8957
Does the gene violate any major guiding principles?	No
DECISION:	Based on the evidence above, Losacky gene 13 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 6111
and GeneMark suggest?	GeneMark Start Coordinate: 6153
	Die 0444
Does the start site have an	
associated Ribosome	5 th Highest Z-Score: 1.798
Binding Site with a high score?	6 th Lowest Final Score: -6.585
	Bp 6153
	4 th Highest Z-Score: 1.896
	3 rd Lowest Final Score: -5.994
Is the predicted start codon	Yes, the predicted start codons have the two longest ORFs.
the longest ORF? If not,	
does the longest ORF	Bp 6111 has an ORF length of 192
result in excessive gene	Bp 6153 has an ORF length of 150
overlap (>30bp)?	
Is this start site conserved	
in other phage genomes	
as indicated by	Yes - The start number called the most often in the published
Starterator?	annotations is 4, it was called in 7 of the 9 non-draft genes in
	the pham
	This is the best start number, as it is the anhy with 7 menual
	This is the best start number, as it is the only with 7 manual
le this start site conserved	Annolations at up 0111. Vos Antuna 11 (Hypothotical Protoin) MonE 11
in other phage genemos	(Hypothetical Protein) Plott 11 (Hypothetical Protein)
as indicated by BlastP2	Phonogingi 11 (Hypothetical Protoin) Warran 11 (Hypothetical
as mulcaled by blastr ?	Protein)
DECISION	Based off Glimmer, the ORF length, and Starterator, the best
DECISION:	start site for gene 13 is bp 6111

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master:hypothetical protien antuna
a protein having a	E value 4.7E-38
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	NO QUALITY MATCH it is a hypothetical protien
a protein having a	To prove no quality Adeno_100 ; Late 100kD protein, 42.69%
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes, It is a hypothetical protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	14
Stop Coordinate	7204
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	6401
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Glimmer call @bp 6401 has strength 17.00;
program (Glimmer,	GeneMark call start at 6428
GeneMark)?	
Is there evidence for	Yes, both agree there is evidence for coding potential
coding potential?	
Is this gene present in	Yes, the gene is conserved in
other annotated	MenE gene 12 (6376-7182) pham 216344
genomes?	
Does the gene violate	No
any major guiding	
principles?	
DECISION:	Yes.

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not supported)::
Glimmer and GeneMark	6401
suggest?	GeneMark Start Coordinate (type NA if not supported)::
	6428
Does the start site have	Final RBS score: -8.041
an associated Ribosome	Z score: 0.388
Binding Site with a high	Both are the lowest values
score?	Start position @bp 6401
Is the predicted start	NA
codon the longest ORF?	
If not, does the longest	
ORF result in excessive	
gene overlap (>30bp)?	
Is this start site	Yes the start site is found in 17 of 38 (44.7%) of genes in
conserved in other	pham
phage genomes as	
indicated by Starterator?	
Is this start site	Yes it is conserved with a hypothetical protein with Hot26
conserved in other	and Warren
phage genomes as	
indicated by BlastP?	
DECISION	Yes, the start site should be @bp 6401 because Glimmer,
	Phamerator, and Starterator agree.

Gathering Evidence	Explain Your Rationale
Does this protein align	DNA Master:Scaffolding protien dropshot
with a protein having a	
functional assignment in	E-value:0.0e0
BlastP (phagesDB	
and/or GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align	Scaffold protein 97.2%
with a protein having a	
functional assignment in	
the PDB or other	
database in HHPred with	
a probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes it is scaffolding protein
adjacent to genes of	
known function and in a	
region of the genome	
that shows high	
conservation of gene	
order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at
transmembrane protein?	least 2 different transmembrane prediction programs.
Is the proposed function	Yes it is scaffolding protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Scaffolding protein

Basic Phage Information	
Phage Name	Losacky
Gene #	15
Stop Coordinate	8093
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	7221
Selected Function	Major Capsid Protein

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes, Original Glimmer call @bp 7221 has strength 17.09
Is there evidence for coding potential?	yes
Is this gene present in other annotated genomes?	Yes it is present in other genomes Dropshot gene 12 (6931 - 7809) pham 2582 MenE gene 13 (7199 - 8077) pham 2582 Warren gene 13 (7110 - 8006) pham 2582
Does the gene violate any major guiding principles?	No
DECISION:	It is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	bp7221
Does the start site have an associated Ribosome Binding Site with a high score?	<i>It is pretty well as its got a z value of 2.311 and a final score of – 4.626</i>
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	It is the longest ORF
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes 42 of 42 of the non drafted genes all agree on start site 2 Losacky also all agree on start site 2
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes it is conserved as a major capsid protien in blett, bush, and warren, and a major head protien in Appa
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Major Capsid Protein
a protein having a	
functional assignment in	E-Value: 0.0E0
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, this is a quality match. This aligns with Major Capsid
a protein having a	Protein with a probability change of 99.96.
functional assignment in	
ine PDB or other database	
IN HHPTed with a	
greater with appropriate	
greater with appropriate	
Is this gene located	Ves – Maior Cansid Protein
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation	
of gene order?	
Is this gene a possible	N/A
transmembrane protein?	
Is the proposed function	Yes
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Major Capsid Protein

Basic Phage Information	
Phage Name	Losacky
Gene #	16
Stop Coordinate	8563
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	N/A
Selected Start Coordinate	8147
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 8147 has strength 15.77; GeneMark calls start at 8093
Is there evidence for coding potential?	Yes, there is evidence of coding potential.
Is this gene present in other annotated genomes?	<i>Yes,</i> Antuna gene 14 (7951 - 8421) pham 8234, MenE gene 14 (8081 - 8551) pham 8234, and Phonegingi gene 13 (7807 - 8277) pham 8234
Does the gene violate any major guiding principles?	No
DECISION:	Based on the evidence above, Losacky Gene 16 is a

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 8147
and GeneMark suggest?	GeneMark Start Coordinate: 8093
and Genemark Suggest!	Genewark Start Coordinate. 0095
Does the start site have an	Bp 8147
associated Ribosome	4 th Highest Z-Score: 2.320
Binding Site with a high	3 rd Lowest Final Score: -4.909
score?	
	Bp 8093
	1 st Highest Z-Score: 3.081
	1 st Lowest Final Score: -2.845
Is the predicted start codon	The two predicted start codons are not the longest ORFs, as bp
the longest ORF? If not,	8093 has an ORF length of 471, and bp 8147 has an ORF
does the longest ORF	length of 417.
result in excessive gene	
overlap (>30bp)?	The start codon with the longest ORF length of 882, bp 7682,
	does result in excessive gene overlap.
Is this start site conserved	
in other phage genomes	Yes, the start number called the most often in the published
as indicated by	annotations is 4, it was called in 7 of the 9 non-draft genes in
Starterator?	the pham.
	This scome to be the best start site for the gone as start site 4
	has 7 manual annotations at bn 8003
Is this start site conserved	Yes – Blett_14 (Hypothetical Protein), Phonegingi_13
in other phage genomes	(Hypothetical Protein), Antuna_14 (Hypothetical Protein),
as indicated by BlastP?	Dropshot_13 (Hypothetical Protein)
DECISION	Based off of Genemark, Starterator, and the RBS, the best start
	site is 8093.

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: hypothetical protein
a protein having a	E value 0.0e0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	NO QUALITY MATCH hypothetical protien
a protein having a	<i>Proof</i> putative pyruvate dehydrogenase 53%
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes it is a hypothetical protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Yes it is a hypothetical protein

Basic Phage Information	
Phage Name	Losacky
Gene #	17
Stop Coordinate	9128
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	8634
Selected Function	Head-to-Tail Adaptor

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 8634 has strength 15.93
(Glimmer, GeneMark)?	
Is there evidence for	Yes, both agree
coding potential?	
Is this gene present in other annotated genomes?	Yes, the genome is present in MenE gene 15 (8622 - 9116) pham 223159
Does the gene violate any	No
major guiding principles?	
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer and GeneMark both suggest start site @bp8634
Does the start site have an associated Ribosome Binding Site with a high score?	<i>List Final RBS score was= -4.001 which makes it the highest Z- score= 2.63 which is the second highest</i>
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Indicate the length of the ORF is with the predicted start and the gap/overlap to the nearest stop codon of the upstream ORF. Does the proposed start site have a gap/overlap with the nearest upstream gene that does not violate the Guiding Principles? Note: if you are considering more than 1 start site, provide the same information for each proposed start site
Is this start site conserved in other phage genomes as indicated by Starterator?	Start 18: • Found in 34 of 58 (58.6%) of genes in pham
Is this start site conserved in other phage genomes as indicated by BlastP?	Head to tail adapter in phages Warren, Tuna, Blett
DECISION:	Yes @bp 8634 is found to be the start site as agree by glimmer, DNA master, phamerator.

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Head-to-Tail Adaptor phage Appa
a protein having a	
functional assignment in	E-Value: 0.0E0
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, this is a quality match. This aligns with Head-Tail
a protein having a	Connector Protein with a probability chance of 99.74
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes – Head-to-Tall Adaptor
adjacent to genes of	
Known function and in a	
region of the genome that	
shows high conservation of	
gene order?	N1/A
transmombrano protoin?	N/A
le the proposed function	Voc
found on the SEA	100
DHACES approved	
function list?	
	Head-to-Tail Adaptor

Basic Phage Information	
Phage Name	Losacky
Gene #	18
Stop Coordinate	9448
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3 bp overlap
Selected Start Coordinate	9125
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 9125 has strength 18.97
(Glimmer, GeneMark)?	
Is there evidence for	VAS
coding potential?	
Is this gene present in other annotated genomes?	Yes the gene is present MenE gene 16 (9113 - 9436) pham 222932
Does the gene violate any	No
major guiding principles?	
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Both Glimmer and GeneMark suggest start site at @bp 9125
Does the start site have an associated Ribosome Binding Site with a high score?	Final RBS score is = -5.206 which is the second highest Z score is = 2.104 which is the highest
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Indicate the length of the ORF is with the predicted start and the gap/overlap to the nearest stop codon of the upstream ORF. Does the proposed start site have a gap/overlap with the nearest upstream gene that does not violate the Guiding Principles? Note: if you are considering more than 1 start site, provide the same information for each proposed start site
Is this start site conserved in other phage genomes as indicated by Starterator?	Start 40: • Found in 19 of 160 (11.9%) of genes in pham • Manual Annotations of this start: 10 of 136
Is this start site conserved in other phage genomes as indicated by BlastP?	Head to tail stopper found in phages Warren and Blett
DECISION:	Yes, evidence suggest start site is at @bp 9125 as agreed by glimmer, DnaMaster, and phamerator.

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Head-to-tail stopper Warren
a protein having a	E value 0.0e0
functional assignment in	
BlastP (phagesDB and/or	Head-to-tail connector protein Appa
GenBank) with an	E value 0.0e0
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes Head-to-tail stopper 99.57%
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes sytenty observed head to tail stopper
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes Head-to-tail stopper
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Yes Head-to-tail stopper

Basic Phage Information	
Phage Name	Losacky
Gene #	19
Stop Coordinate	9804
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	9499
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Glimmer call @bp 9499 has strength 18.76;
program (Glimmer,	GeneMark calls start at 9445
GeneMark)?	
Is there evidence for	Yes there is evidence for coding potential
coding potential?	
Is this gene present in	Yes, the gene is present in
other annotated	MenE gene 17 (9433 - 9792) pham 764
genomes?	
Does the gene violate	
any major guiding	по
principles?	
DECISION:	Yes it is a gene.

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not supported)::
Glimmer and GeneMark	9499
suggest?	GeneMark Start Coordinate (type NA if not supported)::
	9445
Does the start site have	For bp 9445:
an associated Ribosome	The z score is 2.784 and the final score is -4.256 (the
Binding Site with a high	highest on all value)
score?	For bp 9499
	The z value is 1.606 and the final score is -5.717
Is the predicted start	Indicate the length of the ORF is with the predicted start
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the
If not, does the longest	upstream ORF. Does the proposed start site have a
ORF result in excessive	gap/overlap with the nearest upstream gene that does not
gene overlap (>30bp)?	violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.
Is this start site	
conserved in other	
phage genomes as	Start 31: • Found in 56 of 162 (34.6%) of genes in pham
indicated by Starterator?	
	Gene: Losacky_19 Start: 9499, Stop: 9804, Start Num: 46
	Candidate Starts for Losacky_19: (Start: 31 @9445 has 45
	MA's)
Is this start site	The start site is conserved with a hypothetical protein in
conserved in other	warren, ph\onegini, pickles13, and firecastle
phage genomes as	
indicated by BlastP?	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.

DECISION:

I think the gene should start @bp 9499 because glimmer, phamerator, starterator, and blastP agree.

Gathering Evidence	Explain Your Rationale
Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10 ⁻⁴ or smaller with appropriate coverage?	DNA Master: Hypothetical Protein Appa E- value: 0.0E0
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	Yes, it does with PF21822.2 with a probability score of 60.62
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	No Synteny Observed.
Is this gene a possible transmembrane protein?	<i>If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.</i>
Is the proposed function found on the SEA- PHAGES approved function list?	Yes, as hypothetical protein
DECISION:	

Basic Phage Information	
Phage Name	Losacky
Gene #	20
Stop Coordinate	10244
Direction (For/Rev)	Foward
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	9801
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original glimmer call @bp 9801 has strength 12.24
(Glimmer, GeneMark)?	
Is there evidence for	Yes
coding potential?	
Is this gene present in	Vac ManE (CA) 18 210/61 (125) Dicklos12 (CA) 210/61(125)
other annotated genomes?	Tes, Merie (GA) 18 219401 (155), Pickles 15 (GA) 219401 (155)
Does the gene violate any	No it does not violate any
major guiding principles?	
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	They suggest start site 9801
Does the start site have an associated Ribosome Binding Site with a high score?	It has a high z value of 2.805 and a low final score of -3.447
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon with an length of 444, is the longest ORF
Is this start site conserved in other phage genomes as indicated by Starterator?	(Start: 14 @9801 has 9 MA's) The start number called the most often in the published annotation is 14, and was called in 71 of the 138 non-draft genes in the pham.
Is this start site conserved in other phage genomes as indicated by BlastP?	Tail terminator [Microbacterium phage Appa] Tail terminator [Microbacterium phage Blett] Tail terminator [Microbacterium phage Warren] Tail terminator [Microbacterium phage Antuna] Tail terminator [Microbacterium phage Phonegigi]
DECISION:	Based on the evidence, the best start site is 9801

Gathering Evidence	Explain Your Rationale
Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10 ⁻⁴ or smaller with appropriate coverage?	List the most informative BlastP match from each source PhagesDB: NCBI: DNA Master: Tail terminator Appa E value 0.0e0 Hint: you may have already found this information from annotation decision #2. Provide the alignment (q#:s#) and e- value. It is only necessary to provide one match from each database.
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	Tail terminator protein 99.36%
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	Yes synteny observed it is a tail terminator protien
Is this gene a possible transmembrane protein?	If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.
Is the proposed function found on the SEA- PHAGES approved function list?	Yes.
DECISION:	Yes It is a tail terminator protien

Basic Phage Information	
Phage Name	Losacky
Gene #	21
Stop Coordinate	10772
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	N/A
Selected Start Coordinate	10260
Selected Function	Tail assembly chaperone

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 10260 has strength 12.39
(Glimmer, GeneMark)?	
Is there evidence for	Yes, there is evidence for coding potential.
coding potential?	
Is this gene present in other annotated genomes?	Yes, Antuna gene 19 (10118 - 10630) pham 85343, MenE gene 19 (10248 - 10760) pham 85343, and Phonegingi gene 18 (9980 - 10492) pham 85343
Does the gene violate any major guiding principles?	No
DECISION:	Based on the evidence above, gene 21 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 10260
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an associated Ribosome Binding Site with a high score?	1 st Highest Z-Score: 3.142 1 st Lowest Final Score: -2.786
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon is the longest ORF, with an ORF length of 513.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 16, it was called in 49 of the 92 non-draft genes in the pham.
	Although, the best start number for this gene is 22, as it has 24 manual annotations for bp 10260.
Is this start site conserved	Yes – Appa (Major tail protein), Pickles13 (Major tail protein),
in other phage genomes	Warren (Major tail protein), Phonegingi (Major tail protein), and
as indicated by BlastP?	Blett (Major tail protein).
DECISION:	Based off Starterator, Genemark, and the RBS, bp 10260 is the best start codon.

Gathering Evidence	Explain Your Rationale
Does this protein align with	E-Value: 0.0E0
a protein having a	
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, this protein aligns with DUF2774 with the probability score of
a protein having a	98.06.
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes, tail assembly chaperone.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes, tail assembly chaperone.
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Tail assembly chaperone.

Basic Phage Information	
Phage Name	Losacky
Gene #	22
Stop Coordinate	11335
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	10847
Selected Function	Hypothetical protein

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program (Glimmer, GeneMark)?	Yes, Original Glimmer call @bp 10847 has strength 16.43
Is there evidence for	Yes
coding potential?	
	Yes it is
Is this gene present in other annotated genomes?	Dropshot gene 19 (10567 - 11055) pham 21809
	MenE gene 20 (10835 - 11323) pham 218091
Does the gene violate any major guiding principles?	No
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	10847bp
Does the start site have an associated Ribosome Binding Site with a high score?	Its got an alright score with a z value of 1.443 and a final score -6.054
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Its the longest ORF and captures all the coding potential
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes Start 3: • Found in 16 of 40 (40.0%) of genes in pham this is the start site which it is found in
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes, it is a Tail assembly chaperone for blett, bush, appa, and dropshot
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: tail assembly chaperone [Blett]
a protein having a	E-value: 0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	According to HHPred, there is no quality match, however the
a protein having a	best match is phage tail protein with a probability of 57.35 and a
functional assignment in	database score of 25.89
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed, appears as hypothetical protein.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is the proposed function	Yes, the proposed hypothetical protein is present on the SEA-
found on the SEA-	PHAGES approved function list.
PHAGES approved	
function list?	
DECISION:	Hypothetical protein

Basic Phage Information	
Phage Name	Losacky
Gene #	23
Stop Coordinate	11622
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3 bp overlap
Selected Start Coordinate	11332
Selected Function	NKF

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 11332 has strength 11.35
(Glimmer, GeneMark)?	
Is there evidence for	Yes
coding potential?	
Is this gene present in	No the gene is not present in other genomes as stated by
other annotated genomes?	phamerator
Does the gene violate any	No
major guiding principles?	
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer and GeneMark suggest start site at @bp 11332
Does the start site have an associated Ribosome Binding Site with a high score?	Final RBS score= -5.070 which makes it the highest Z- score= 2.024 which is the third lowest score
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Indicate the length of the ORF is with the predicted start and the gap/overlap to the nearest stop codon of the upstream ORF. Does the proposed start site have a gap/overlap with the nearest upstream gene that does not violate the Guiding Principles? Note: if you are considering more than 1 start site, provide the same information for each proposed start site.
Is this start site conserved in other phage genomes as indicated by Starterator?	Start 3: • Found in 5 of 8 (62.5%) of genes in pham • No Manual Annotations of this start. • Called 100.0% of time when present
Is this start site conserved in other phage genomes as indicated by BlastP?	Tail assembly chaperone by phages bush,Drops, Blett, Warren, and Appa
DECISION:	Yes, the start is @bp 11332 as suggested by glimmer, DNAmaster, and phamerator

Gathering Evidence	Explain Your Rationale
Does this protein align with	E-Value: 0.0E0
a protein having a	
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, this protein aligns with Phage_Gp15 with a probabilty score
a protein having a	of 96.96.
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes, there is Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	No
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF.

Basic Phage Information	
Phage Name	Losacky
Gene #	24
Stop Coordinate	13845
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	11647
Selected Function	Tape measure protein

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Glimmer call @bp 11647 has strength 20.72
program (Glimmer,	Both Glimmer and Genemark agree
GeneMark)?	
Is there evidence for	Yes there is evidence for coding potential
coding potential?	
Is this gene present in	Yes, the gene is present in
other annotated	MenE gene 22 (11635 - 13833) pham 223170
genomes?	
Does the gene violate	
any major guiding	по
principles?	
DECISION:	Yes it is a gene.

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not supported)::
Glimmer and GeneMark	11647
suggest?	GeneMark Start Coordinate (type NA if not supported)::
	11647
Does the start site have	@bp 11647
an associated Ribosome	The z value is 2.298 and the final score is –4.299
Binding Site with a high	The values are amongst the greater but are not the
score?	greatest.
Is the predicted start	Indicate the length of the ORF is with the predicted start
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the
If not, does the longest	upstream ORF. Does the proposed start site have a
ORF result in excessive	gap/overlap with the nearest upstream gene that does not
gene overlap (>30bp)?	violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.
Is this start site	
conserved in other	Start 12: • Found in 23 of 55 (41.8%) of genes in pham •
phage genomes as	Manual Annotations of this start: 12 of 41
indicated by Starterator?	
Is this start site	The start site is conserved with a tape measure protein
conserved in other	with phages antunna, blett, warren, and bush
phage genomes as	
indicated by BlastP?	
	I think the gene should start @bp 11647 because
	glimmmer, genemark, phamerator, starterator, and BlastP
Gathering Evidence	Explain Your Rationale
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Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10 ⁻⁴ or smaller with appropriate coverage?	DNA Master: tape measure protein [Antuna] E-value: 0.0E0
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	According to HHPred, the best match is tape measure protein with a probability of 99.87 and database score of 175.07.
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	Yes, the proposed function, tape measure protein, appears in the order after the tail assembly chaperone, and is followed by a minor tail protein. Synteny is observed in Appa and Blett.
Is the proposed function found on the SEA- PHAGES approved function list?	Yes, the proposed tape measure protein is present on the SEA-PHAGES approved function list.
DECISION:	tape measure protein

Basic Phage Information	
Phage Name	Losacky
Gene #	25
Stop Coordinate	14705
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	13845
Selected Function	Tape measure protein

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Yes Original Glimmer call @bp 13845 has strength 18.23
(Glimmer, GeneMark)?	
Is there evidence for	Yes
coding potential?	
	Yes MenE gene 23 (13833 - 14693) pham 222795
Is this gene present in	Warren gene 23 (13763 - 14623) pham 222795
other annotated genomes?	
	Dropshot gene 22 (13565 - 14425) pham 222795
Deep the game violate any	No
Does the gene violate any	NO
major guiding principles?	
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	13845 bp
and Genemark suggest?	
Does the start site have an associated Ribosome Binding Site with a high score?	Yes its got a z value of 2.734 and a final score of –3.586
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Yes does not have gene overlap
Is this start site conserved	Yes our gene is Start 45: • Found in 89 of 379 (23.5%) of
in other phage genomes	genes in pham
as indicated by	
Starterator?	
Is this start site conserved	Yes, it is conserved as minor tail protien in Antuna, Warren,
in other phage genomes	Appa, blett, and bush
as indicated by BlastP?	
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: minor tail protein [Antuna]
a protein having a	E-value: 0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	According to HHPred, the best match is hypothetical protein
a protein having a	with a probability of 99.96 and a database score of 183.82.
functional assignment in	Another plausible protein is the minor tail protein with a
the PDB or other database	probability of 99.84 and a database score of 161.13.
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes, the proposed function, tape measure protein, appears in
adjacent to genes of	the order after the tail assembly chaperone, and is followed by a
known function and in a	minor tail protein. Synteny is observed in Phonegingi and
region of the genome that	Warren.
shows high conservation of	
gene order?	
Is the proposed function	Yes, the proposed tape measure protein is an approved function
found on the SEA-	in the SEA PHAGES approved functions list.
PHAGES approved	
function list?	
DECISION:	Tape measure protein

Basic Phage Information	
Phage Name	Losacky
Gene #	26
Stop Coordinate	16573
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	14705
Selected Function	Minor tail protein

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program	Yes, Original Glimmer call @bp 14705 has strength 17.37
(Glimmer, GeneMark)?	
Is there evidence for coding potential?	yes
Is this gene present in other annotated genomes?	Yes Dropshot gene 23 (14425 - 16293) pham 223253
	MenE gene 24 (14693 - 16561) pham 223253
	Warren gene 24 (14623 - 16491) pham 223253
Does the gene violate any	по
major guiding principles?	
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	14705bp
Does the start site have an associated Ribosome Binding Site with a high score?	Yes its got a z value of 2.332 and a final score of –4.374
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	No but it doesn't have an excessive gene overlap like the start site with the biggest ORF
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes The start number called the most often in the published annotations is 45, it was called in 23 of the 31 non-draft genes in the pham. Genes that call this "Most Annotated" start: • Antuna_24, Appa_23, Blett_24, Bush_24, Carrillo_25, Cicada_23, CookieDog_24, Dropshot_23, FireCastle_21, Goodman_22, Guzman_25, Htur_21, IndiRoo_21, Jakelyne_26, Jera_22, Johann_22, Linayshia_21, Losacky_26, MenE_24, Milani_22, Olympi_22, PermaG_22, PhillyJawn_24, Phingu_26, Phonegingi_23, Pickles13_23, Rasovi_21, SBlackberry_21, TurboVicky_21, Typher_23, Violeta_25, Warren_24, Zanella_21,
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes it is conserved as a Minor tail protein for Antuna, dropshot Blett, and Appa
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: minor tail protein Antuna
a protein having a	e- value: 0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, it aligns with minor tail protein with the probability of 99.97.
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes, minor tail protein
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Yes this gene should be assigned with function minor tail
	protein.

Basic Phage Information		
Phage Name	Losacky	
Gene #	27	
Stop Coordinate	16888	
Direction (For/Rev)	For	
Gap (Overlap) with Previous Gene	7	
Selected Start Coordinate	16580	
Selected Function	NKF	

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program	Yes Original Glimmer call @bp 16580 has strength 12.85
Is there evidence for coding potential?	yes
Is this gene present in other annotated genomes?	Yes its present in Dropshot gene 24 (16300 - 16608) pham 3528 MenE gene 25 (16568 - 16876) pham 3528
Does the gene violate any major guiding principles?	No
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	16580 bp
Does the start site have an	Yes it has a z value 3.044 and a final score –3.190 which is the
associated Ribosome Binding Site with a high	best one
score?	
Is the predicted start codon	Yes does not have an excessive gene overlap
does the longest ORF	
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	Yes Start 8: • Found in 38 of 38 (100.0%) of genes in pham •
as indicated by	time when present • Phage (with cluster) where this start called:
Starterator?	Antuna_25 (GA), Appa_24 (GA), Ariadne_49 (EC), Blett_25
	(GA), Bush_25 (GA), Carrillo_26 (GA), Cicada_24 (EJ), CookieDog_25 (GA), Dropsbot_24 (GA), Gipa_42 (EC)
	Gingerbug 21 (GF), Goodman 23 (EJ), Guzman 26 (GA),
	Htur_22 (EJ), Jakelyne_27 (GA), Jera_23 (EJ), Johann_23 (EJ),
	Linayshia_22 (EJ), Losacky_27
Is this start site conserved	Yes it is conserved as a hypothetical protien in blett, bush,
as indicated by BlastP?	Pickles13, and Warren
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: hypothetical protein
a protein having a	E- value: 0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	No quality align. The closest was a.43.1.4 (A:) Omega transcriptional
a protein having a	repressor with a probability of 60.9.
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed. The closest was
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
is the proposed function	Yes
found on the SEA-	
PHAGES approved	
DECISION:	INKE

Basic Phage Information	
Phage Name	Losacky
Gene #	28
Stop Coordinate	17633
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	N/A
Selected Start Coordinate	16899
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 16899 has strength 19.35
(Glimmer, GeneMark)?	
Is there evidence for	Yes, there is evidence for coding potential.
coding potential?	
Is this gene present in other annotated genomes?	<i>Yes</i> - Antuna gene 26 (16757 - 17491) pham 221169, MenE gene 26 (16887 - 17621) pham 221169, and Phonegingi gene 25 (16664 - 17398) pham 221169
Does the gene violate any major guiding principles?	No
DECISION:	Based on the evidence above, gene 28 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: bp 16899
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an	Ath Highest 7-Score: 1.800
associated Ribosome	5 th Lowest Final Score: -6 580
Binding Site with a high	
score?	
Is the predicted start codon	The predicted start codon is the longest ORF, with an ORF
the longest ORF? If not,	length of 735.
does the longest ORF	
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	
in other phage genomes	The start number called the most often in the published
as indicated by	annotations is 12, it was called in 142 of the 145 non-draft
Starterator?	genes in the pham.
	Start number 12 is the best start site, as this gene has 142
	manual annotations for bp 16899 at start number 12.
Is this start site conserved	Yes – Antuna (Minor tail protein), Appa (Head protein), Bush
in other phage genomes	(Minor tail protein), Blett (Minor tail protein), and Warren (Minor
as indicated by BlastP?	tail protein).
DECISION:	Based off Starterator, Glimmer, and the ORF length, the best
BEGIGIGI	start site is bp 16899.

O o the option of Excision of a	Evelain Vaue Dationale
Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master:
a protein having a	E value 0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	PHAGES Official Function List to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	29
Stop Coordinate	18471
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	N/A
Selected Start Coordinate	17650
Selected Function	N/A

Commented [MM1]: for function DNA master said minor tail protein and HHpred said closet with tyrosine- protein with 99% and phamerator said nothing

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 17650 has strength 11.67
Is there evidence for coding potential?	Yes, there is evidence for coding potential.
Is this gene present in other annotated genomes?	Yes - Antuna gene 27 (17508 - 18329) pham 219400, MenE gene 27 (17638 - 18459) pham 219400, and Phonegingi gene 26 (17413 - 18234) pham 219400
Does the gene violate any major guiding principles?	No
DECISION:	Based on the evidence above, gene 29 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 17650
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Dese the start site house an	Ath Lliphoot 7 Occurs 4 700
Does the start site have an	4" Hignest Z-Score: 1.730
Rinding Site with a high	5.492
Binding Site with a high	
SCOLE :	
Is the predicted start codon	The predicted start codon is the longest ORF, with an ORF
the longest ORF? If not,	length of 822.
does the longest ORF	
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	
in other phage genomes	The start number called the most often in the published
as indicated by	annotations is 10, it was called in 91 of the 175 non-draft genes
Starterator?	in the pham.
	Start number 10 is the best start number, as there are 01
	manual appointations at bn 17650
Is this start site conserved	Yes – Delagarza (Minor tail protein) Lesiram (Minor tail protein)
in other phage genomes	FireCastle (Minor tail protein), Milani (Minor tail protein), Sucha
as indicated by BlastP?	(Minor tail protein).
DECISION:	Based off Starterator, Glimmer, and the ORF length, the start codon is 17650.

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Gathering Evidence	Explain Your Rationale
Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10 ⁻⁴ or smaller with appropriate coverage?	DNA Master: minor tail protein E score: 0.0E0
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	Yes, this aligns with receptor type tyrosine- protein phosphate with a probability of 96.99.
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	NO, enter No Synteny Observed.
Is this gene a possible transmembrane protein?	If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs.
Is the proposed function found on the SEA- PHAGES approved function list?	Indicate a response with a Yes or No response. Once you have arrived at a functional decision, check the <u>SEA-PHAGES Official Function List</u> to ensure that you are following the guidelines for function naming. Functions that are not present on the approved list must be carefully vetted for approval.
DECISION:	If you believe this gene should be assigned, please write the name of the function here. If the evidence does not support a functional call, record "NKF" for no known function. 50-70% of phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	30
Stop Coordinate	18770
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	N/A
Selected Start Coordinate	18510
Selected Function	NKF

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 18510 has strength 21.44
Is there evidence for coding potential?	Yes, there is evidence for coding potential.
Is this gene present in other annotated genomes?	<i>Yes</i> - Antuna gene 28 (18326 - 18628) pham 219586, MenE gene 28 (18498 - 18758) pham 219586, and Phonegingi gene 27 (18231 - 18533) pham 219586
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 30 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate: 18510 GeneMark Start Coordinate: N/A
Does the start site have an associated Ribosome Binding Site with a high score?	5 th Highest Z-Score: 0.977 4 th Lowest Final Score: -7.028
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon is not the longest ORF, as it has an ORF length of 261. The longest ORF, with an ORF length of 402, results in excessive gene overlap of 102 base pairs.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 23, it was called in 41 of the 82 non-draft genes in the pham. This is the best start number for this gene, as it has 41 manual annotations at bp 18510.
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes – MenE (Hypothetical Protein), Blett (Hypothetical Protein), and Antuna (Hypothetical Protein).
DECISION:	Based off Starterator and Glimmer, the best start codon is bp 18510

Gathering Evidence	Explain Your Rationale
Does this protein align with a protein having a	PhagesDB: hypothetical protein (MenE) E-value: 4.2E-37
functional assignment in BlastP (phagesDB and/or	
GenBank) with an	
smaller with appropriate	
Does this protein align with a protein having a functional assignment in	The most informative HHPred match is DUF6802, a family of unknown function, with a score of 86.91, meaning that it is a hypothetical protein.
the PDB or other database in HHPred with a	
greater with appropriate coverage?	
Is this gene located	No synteny observed; hypothetical protein.
adjacent to genes of known function and in a	
region of the genome that	
shows high conservation of gene order?	
Is the proposed function	Yes.
found on the SEA-	
FINCES approved	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	31
Stop Coordinate	19656
Direction (For/Rev)	Foward
Gap (Overlap) with Previous Gene	7
Selected Start Coordinate	18763
Selected Function	Endolysin

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 18763 has strength 13.96
(Glimmer, GeneMark)?	
Is there evidence for	Vaa
coding potential?	765
Is this gene present in	Yes, MenE (GA) 18 212354 (164), Pickles13 (GA)121354 (164)
other annotated genomes?	
Does the gene violate any	NO
major guiding principles?	
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate (18763)
and GeneMark suggest?	
Does the start site have an	Yes because it has the highest z value of 2.641 and a final
associated Ribosome	score –3.691
Binding Site with a high	
score?	
Is the predicted start codon	
the longest ORF? If not,	
does the longest ORF	Yes, it holds as the longest ORF with a length of 894
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	
in other phage genomes	The start number called the most often in the published
as indicated by	annotations is 40, it was called in 46 of the 135 non-draft genes
Starterator?	in the pham.
Is this start site conserved	1450 lysin A [Microbacterium phage Appa]
in other phage genomes	1448 endolysin [Microbacterium phage Dropshot]
as indicated by BlastP?	1426 endolysin [Microbacterium phage Blett]
	1309 Iysin A [Microbacterium phage Warren]
	1268 Iysin A [Microbacterium phage Pickles13
DECISION:	Yes, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Lysin A (Phage Appa) and Endolysin (Phage Blett)
a protein having a	
functional assignment in	Lvsin A E-Value: 0.0E0
BlastP (phagesDB and/or	
GenBank) with an	Endolysin E-Value: 0.0E0
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, this is a quality match. This aligns with Endolysin with a
a protein having a	probability chance of 99.12
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes – Endolysin and Lysin A
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	N/A
transmembrane protein?	
Is the proposed function	Yes – Endolysin is found on the approved functions list
found on the SEA-	
PHAGES approved	
	<u>Finale brain</u>
DECISION:	Enaoiysin

Basic Phage Information	
Phage Name	Losacky
Gene #	32
Stop Coordinate	20029
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	19715
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes Original Glimmer call @bp 19715 has strength 15.34
Is there evidence for coding potential?	yes
Is this gene present in other annotated genomes?	Yes it is found in Appa gene 29 (19438 - 19752) pham 8687 MenE gene 30 (19703 - 20017) pham 8687 Pickles13 gene 29 (19856 - 20170) pham 8687
Does the gene violate any major guiding principles?	No
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Bp 19715
Does the start site have an associated Ribosome Binding Site with a high score?	Yes its got the highest z value 2.691 and a final score –3.671
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	It is the longest open reading frame
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes Start 4: • Found in 17 of 19 (89.5%) of genes in pham • Manual Annotations of this start: 9 of 10 • Called 100.0% of time when present • Phage (with cluster) where this start called: Antuna_30 (GA), Appa_29 (GA), Blett_30 (GA), Bush_30 (GA), Carrillo_31 (GA), CookieDog_30 (GA), Dropshot_29 (GA), Guzman_31 (GA), Jakelyne_32 (GA), Losacky_32 (GA),
Is this start site conserved in other phage genomes as indicated by BlastP?	It is conserved as a hypothetical protein in Pickles13, warren, Blett
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: hypothetical protein appa
a protein having a	E value0.0e0
functional assignment in	Membrane protein blett
BlastP (phagesDB and/or	E value 0.0e0
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Family of unknown function 97.26% this is a hypothetical protein
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes, it is a hypothetical protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	33
Stop Coordinate	20691
Direction (For/Rev)	Foward
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	20026
Selected Function	Hypothetical Protein

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 18763 has strength 18.16 Genemark called 20110
Is there evidence for coding potential?	Yes
Is this gene present in other annotated genomes?	Yes, MenE 14633 (12)
Does the gene violate any major guiding principles?	NO
DECISION:	Yes

Cathoring Evidence	Explain Your Pationalo
what start site do Gilmmer	Glimmer Start Coordinate (20026)
and GeneMark suggest?	GeneMark Start Coordinate (20110)
Does the start site have an	Glimmer start site marks a z value of 2.621 and a final score of
associated Ribosome	-4.574
Binding Site with a high	Genemark start site marks a z value of 1.228 and a final score
score?	of -7.049
Is the predicted start codon	Neither start codon have the longest ORF
the longest ORE? If not	
does the longest OPE	Instead start 100/15 has the langest being 7/17
	Instead Start 19940 has the longest, being 147
overiap (>30bp)?	
Is this start site conserved	
in other phage genomes	The start number called the most often in the published
as indicated by	annotations is 2, it was called in 7 of the 9 non-draft genes in
Starterator?	the pham.
Is this start site conserved	971 membrane protein [Microbacterium phage Bush]
in other phage genomes	943 hypothetical protein SEA DROPSHOT 30 [MIcrobacterium
as indicated by BlastP?	phage Dropshot
,	937 minor tail Microbacterium phage Appal
	914 membrane protein [Microbacterium phage Blett]
	906 membrane protein [Microbacterium phage Antuna]
DECISION	The alimmer start site agrees
	The ginniner start site agrees

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Membrane Protein (Phage Bush), Hypothetical
a protein having a	Protein (Phage Dropshot), and Minor Tail (Phage Appa)
functional assignment in	
BlastP (phagesDB and/or	Membrane Protein E-Value: 0.0E0
GenBank) with an	
alignment of 10 ⁻⁴ or	Hypothetical Protein E-Value: 0.0E0
smaller with appropriate	
coverage?	Minor Tail E-Value: 0.0E0
Does this protein align with	No quality matches
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	N/A
transmembrane protein?	
Is the proposed function	NO
found on the SEA-	
PHAGES approved	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	34
Stop Coordinate	21269
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3 bp overlap
Selected Start Coordinate	20688
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program	Original Glimmer call @bp 20688 has strength 20.63; GeneMark calls start at 20706
(Glimmer, GeneMark)?	
Is there evidence for	Yes
coding potential?	
Is this gene present in other annotated genomes?	Yes found in Bush gene 32 (20536 - 21117) pham 5847
Does the gene violate any major guiding principles?	No it does not violate any
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate @bp 20688
and GeneMark suggest?	GeneMark Start Coordinate @bp 20706
Does the start site have an associated Ribosome Binding Site with a high score?	Final RBS score= -8.059 making it the second lowest Z score = 0.411 making it the second smallest @bp 20688
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Indicate the length of the ORF is with the predicted start and the gap/overlap to the nearest stop codon of the upstream ORF. Does the proposed start site have a gap/overlap with the nearest upstream gene that does not violate the Guiding Principles?
	Note: If you are considering more than 1 start site, provide the same information for each proposed start site.
Is this start site conserved	
in other phage genomes	Start 6:
as indicated by	• Found in 17 of 22 (77.3%) of genes in pham
Starterator?	Manual Annotations of this start: 9 of 13
	Start: 6 @20688
Is this start site conserved in other phage genomes as indicated by BlastP?	Membrane protein in phage Appa
DECISION:	Yes, Start site should be @bp 20688 as indicted by phamerator and Glimmer

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Membrane protein Appa
a protein having a	E value 0.0e0
functional assignment in	
BlastP (phagesDB and/or	Holin Antuna
GenBank) with an	E value 0.0e0
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Phage_holin_7_1 97.61%
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes syteny observed holin
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes it is holin
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Yes it is holin

Basic Phage Information	
Phage Name	Losacky
Gene #	35
Stop Coordinate	21453
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	NA
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Glimmer call @bp 21328 has strength 0.78 ** not
program (Glimmer,	called by GeneMark
GeneMark)?	
Is there evidence for	No there is no evidence
coding potential?	
Is this gene present in other annotated genomes?	Yes, the gene is present in MenE gene 33 (21310 - 21441) pham 14633
Does the gene violate any major guiding principles?	The gene has an overlap of 59 bp and although it reaches the requirement lengthwise, it is still small (125)
DECISION:	No it is not a gene

Basic Phage Information	
Phage Name	Losacky
Gene #	36
Stop Coordinate	21906
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	N/A
Selected Start Coordinate	21478
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 21478 has strength 16.71
(Glimmer, GeneMark)?	
Is there evidence for	Yes, there is evidence for coding potential.
coding potential?	
Is this gene present in other annotated genomes?	Yes - Antuna gene 34 (21327 - 21767) pham 88838 and Phonegingi gene 33 (21220 - 21648) pham 88838.
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 36 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: bp 21478
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an	1 st Highest Z-Score: 2.906
associated Ribosome	1 st Lowest Final Score: -3.761
Binding Site with a high	
Score?	
Is the predicted start codon	The predicted start codon is not the longest ORF, as it has an
the longest ORF? If not,	ORF length of 429.
does the longest ORF	
result in excessive gene	The longest start codon is bp 21454, with an ORF length of 453.
overlap (>30bp)?	There is no excessive gene overlap.
Is this start site conserved	The start number called the most often in the published
in other phage genomes	annotations is 2, it was called in 2 of the 4 non-draft genes in
as indicated by	the pham.
Starterator	This is the best start number, as it has 2 manual annotations at
	bp 21478.
Is this start site conserved	Yes – Phonegingi (Hypothetical Protein), Pickles13
in other phage genomes	(Hypothetical Protein), Blett (Hypothetical Protein), and Antuna
as indicated by BlastP?	(Hypothetical Protein).
DECISION:	Based off Starterator, Glimmer, and the RBS, the best start
	codon is bp 21478.

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Hypothetical Protein Appa
a protein having a	E Value: 0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	Yes, it does with PF16081.10 with a probability score of 97.52
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	
found on the SEA-	
PHAGES approved	
	If you believe this gene should be assigned, please write the
DECISION:	functional call record "NKE" for no known function 50,70% of
	nunctional call, record INKE for no known lunction. 50-70% of
	phage genes fail into the NKF category.
Basic Phage Information	
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Phage Name	Losacky
Gene #	37
Stop Coordinate	22226
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	21903
Selected Function	Hypothetical Protein

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Climmer call @bp 21003 bas strength 20.12
program (Glimmer,	Onginal Gilminer can wop 21903 has strength 20.12
GeneMark)?	
Is there evidence for	Yes there is evidence for coding potential
coding potential?	
Is this gene present in	Yes, the gene is present in
other annotated	MenE gene 35 (21762 - 22106) pham 8172
genomes?	
Does the gene violate	
any major guiding	no
principles?	
DECISION:	Yes it is a gene.

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not supported)::
Glimmer and GeneMark	21903
suggest?	GeneMark Start Coordinate (type NA if not supported)::
	21903
Does the start site have	For bp 21903
an associated Ribosome	The z value is 1.515 and the final score is –5.914
Binding Site with a high	It is around the medium value based on the data
score?	
Is the predicted start	Indicate the length of the ORF is with the predicted start
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the
If not, does the longest	upstream ORF. Does the proposed start site have a
ORF result in excessive	gap/overlap with the nearest upstream gene that does not
gene overlap (>30bp)?	violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.
Is this start site	
conserved in other	
phage genomes as	Start 15: • Found in 14 of 14 (100.0%) of genes in pham •
indicated by Starterator?	Manual Annotations of this start: 8 of 8
Is this start site	The start site is conserved with a hypothetical protein with
conserved in other	phages hot26, warren, dropshot, blett, and pickles13
phage genomes as	
indicated by BlastP?	
	The gene should start at 21903 because glimmer,
DECISION.	genemark, phamerator, starterator, and blast p agree.

Gathering Evidence	Explain Your Rationale
Does this protein align	DNA Master: hypothetical protein
with a protein having a	E value 0.0e0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align	NO QUALITY MATCH it is a hypothetical protein
with a protein having a	<i>Proof</i> Cyc-maltodext_N 73.39%
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation	
of gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes it is a hypothetical protein
found on the SEA-PHAGES	
approved function list?	
	Yes it is a hypothetical protein
DECISION:	

Basic Phage Information	
Phage Name	Losacky
Gene #	38
Stop Coordinate	22672
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	22223
Selected Function	Hypothetical Protein

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Yes, Original Glimmer call @bp 22223 has strength 25.01
(Glimmer, GeneMark)?	
Is there evidence for	yes
coding potential?	
Is this gene present in other annotated genomes?	Y <i>es it is present in</i> Appa gene 35 (21958 - 22407) pham 8611, MenE gene 36 (22106 - 22552) pham 8611
Does the gene violate any major guiding principles?	по
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Bp 22223
Does the start site have an associated Ribosome Binding Site with a high score?	Yes its got a high z value 3.246 and a final score of –2.584
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Not the longest ORF but does not result in excessive gene overlap while the longest ORF does
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes Start 10: • Found in 17 of 17 (100.0%) of genes in pham • Manual Annotations of this start: 9 of 9 • Called 94.1% of time when present • Phage (with cluster) where this start called: Antuna_36 (GA), Appa_35 (GA), Blett_35 (GA), Bush_36 (GA), Carrillo_37 (GA), CookieDog_35 (GA), Dropshot_35 (GA), Guzman_35 (GA), Losacky_38
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes it is conserved as a hypothetical protien in Warren, MenE, and Blett
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Hypothetical Protein (Phage Appa)
a protein having a	
functional assignment in	E-Value: 0.0E0
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	No quality matches
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	N/A
transmembrane protein?	
Is the proposed function	Yes – Hypothetical Protein
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	39
Stop Coordinate	22836
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes – 3 bp
Selected Start Coordinate	22669
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program	Original Glimmer call @bp 22669 has strength 26 24
(Glimmer, GeneMark)?	
Is there evidence for coding potential?	Yes, there is evidence for coding potential
Is this gene present in other annotated genomes?	<i>Yes</i> - MenE gene 37 (22549 - 22716) pham 8178, Phonegingi gene 36 (22441 - 22599) pham 8178, Warren gene 36 (22457 - 22615) pham 8178
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 39 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 22669
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an associated Ribosome Binding Site with a high score?	1 st Highest Z-Score: 1.730 1 st Lowest Final Score: -5.492
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon is the longest ORF, with an ORF length of 168.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 3, it was called in 9 of the 9 non-draft genes in the pham. This is the best start site, as bp 22669 has 9 manual annotations at start site 3
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes – Appa (Hypothetical protein) and Pickles13 (Membrane Protein)
DECISION:	Based on all the evidence above, the start codon for gene 39 is bp 22669

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: hypothetical protien Appa
a protein having a	E value 3.7e -25
functional assignment in	
BlastP (phagesDB and/or	Membrane protien Pickles13
GenBank) with an	E value 4.5e-18
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	No Quality Match is considered for this as in phages db and
a protein having a	phamerator dont agree with it and it is low
functional assignment in	SPC12 90.47%
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes believed hypothetical protien
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	40
Stop Coordinate	23396
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	22833
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Climmer call @bn 22833 bas strength 20.58
program (Glimmer,	Chymar Chinnier Can Wop 22003 has strength 20.00
GeneMark)?	
Is there evidence for	Yes this is coding potential as shown in genemark
coding potential?	
Is this gene present in	Yes, the geneome is present in
other annotated	MenE gene 38 (22713 - 23276) pham 224130
genomes?	
Does the gene violate	20
any major guiding	
principles?	
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark	Glimmer and GeneMark suggest start site @bp22833
suggest?	
Does the start site have an associated Ribosome Binding Site with a high score?	z-score = 1.504 final RBS score= -5.854
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Indicate the length of the ORF is with the predicted start and the gap/overlap to the nearest stop codon of the upstream ORF. Does the proposed start site have a gap/overlap with the nearest upstream gene that does not violate the Guiding Principles?
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes Start 159: • Found in 171 of 694 (24.6%) of genes in pham • Manual Annotations of this start: 14 of 581 • Called 14.6% of time when present
Is this start site conserved in other phage genomes as indicated by BlastP?	The start site is conserved with holin in phages antuna, dropshot, blett, and phonegini
DECISION:	Yes I think the start site should start at bp 22833, because genemark, glimmer, phamerator, starterator, and blastp, all agree on the same.

Gathering Evidence	Explain Your Rationale
Does this protein align	DNA Master: endonuclease Appa
with a protein having a	E value: 0.0E0
functional assignment in	
BlastP (phagesDB	RuvC-Like Resolvase Pickles13
and/or GenBank) with an	E value 0.0E0
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align	Yes RuvC resolvase 99.93%
with a protein having a	
functional assignment in	
the PDB or other	
database in HHPred with	
a probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes RuvC-Like Resolvase
adjacent to genes of	
known function and in a	
region of the genome	
that shows high	
conservation of gene	
order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least
transmembrane protein?	2 different transmembrane prediction programs.
Is the proposed function	Yes it is RuvC-Like Resolvase
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	RuvC-Like Resolvase

Basic Phage Information	
Phage Name	Losacky
Gene #	41
Stop Coordinate	24484
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes – 3 bp
Selected Start Coordinate	23393
Selected Function	Exonuclease

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 23393 has strength 23.90
Is there evidence for coding potential?	Yes, there is evidence for coding potential
Is this gene present in other annotated genomes?	<i>Yes</i> - MenE gene 39 (23273 - 24364) pham 45958, Phonegingi gene 38 (23165 - 24256) pham 45958, Warren gene 38 (23181 - 24272) pham 45958
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 41 is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 23393
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an associated Ribosome Binding Site with a high score?	1 st Highest Z-Score: 3.246 1 st Lowest Final Score: -2.584
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon is the longest ORF, with an ORF length of 1092
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 8, it was called in 42 of the 60 non-draft genes in the pham <i>This is not the best start site for gene 41. The best start site is</i>
	start site 9, which has 9 manual annotations at bp 23393
Is this start site conserved	Yes – Blett (Exonuclease), Dropshot (RecE-Like Exonuclease),
in other phage genomes as indicated by BlastP?	and MenE (RecE-Like Exonuclease)
DECISION:	Based off Glimmer, the RBS, and the ORF length, the best start codon for gene 41 is bp 23393

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: RecE-like Recombination Nuclease (phage Appa),
a protein having a	Exonuclease (phage Blett), RecE-like Exonuclease (phage
functional assignment in	MenE)
BlastP (phagesDB and/or	
GenBank) with an	RecE-like Recombination E-Value: 0.0E0
alignment of 10 ⁻⁴ or	Exonuclease E-Value: 0.0E0
smaller with appropriate	RecE-like Exonuclease: 0.0E0
coverage?	
Does this protein align with	Yes, this is a quality match. This aligns with lambda
a protein having a	exonuclease with a probability chance of 99.9
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes - Exonuclease
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	N/A
transmembrane protein?	
Is the proposed function	Yes
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Exonuclease

Basic Phage Information	
Phage Name	Losacky
Gene #	42
Stop Coordinate	25485
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes – 3 bp
Selected Start Coordinate	24481
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
(Glimmer, GeneMark)?	Original Glimmer call @bp 24481 has strength 22.10
Is there evidence for coding potential?	Yes, there is evidence for coding potential
Is this gene present in other annotated genomes?	<i>Yes</i> - MenE gene 40 (24361 - 25365) pham 87972, Phonegingi gene 39 (24253 - 25311) pham 87972, Warren gene 39 (24269 - 25318) pham 87972
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 42 is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 24481
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an associated Ribosome Binding Site with a high score?	1 st Highest Z-Score: 3.246 1 st Lowest Final Score: -2.584
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon is the longest ORF, with an ORF length of 1005
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 1, it was called in 9 of the 9 non-draft genes in the pham. <i>This is the best start site for gene 42, as it has 9 manual</i>
	annotations at bp 24481
Is this start site conserved	Yes – Antuna (Rec I-like ssDNA binding protein), Warren
In other phage genomes	(Rec I -IIKe ssDINA binding protein), and Blett (Rec I -IIKe ssDNA binding protein)
as indicated by BlastP?	Dinuing protein)
DECISION:	42 is bp 24481

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Rec T –like ssDNA binding protein [Antuna]
a protein having a	
functional assignment in	E-value: 0.0E0
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	According to HHPred, the best match is the Recombination
a protein having a	protein bet with a probability of 99.79 and a database score of
functional assignment in	149.86, however the better match is the RecT DNA binding
the PDB or other database	protein with a probability of 99.07 and database score of 100.74.
IN HHPred with a	
probability of 90% or	
greater with appropriate	
	Van the proposed function. Reat like coDNA hinding protain
adjacent to genes of	res, the proposed function, Rect-like ssDNA binding protein,
known function and in a	appears in the order alter the exonuclease, and is followed by a
region of the genome that	nypolitelical protein. Synteny is observed in warren.
shows high conservation of	
aene order?	
Is the proposed function	No, the proposed Rec T-like ssDNA Binding protein is not a part
found on the SEA-	of the approved SEA PHAGES function list. Blast Phamerator
PHAGES approved	and HHPred call Rec T-like ssDNA Binding protein while on the
function list?	list there is only Rec T-like DNA pairing protein.*
DECISION:	Rec T like ssDNA binding protein*

Basic Phage Information	
Phage Name	Losacky
Gene #	43
Stop Coordinate	25847
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	N/A
Selected Start Coordinate	25485
Selected Function	Hypothetical Protein

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program	Original Glimmer call @bp 25485 has strength 16.60
(Glimmer, GeneMark)?	Ves there is evidence for coding potential
coding potential?	res, more is evidence for couring potential
Is this gene present in other annotated genomes?	Yes - MenE gene 41 (25365 - 25727) pham 180, Phonegingi gene 40 (25311 - 25673) pham 180, and Warren gene 40 (25318 - 25680) pham 180
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 43 is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 25485
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an	4 th Highest Z-Score: 1.701
associated Ribosome Binding Site with a high score?	4 th Lowest Final Score: -6.377
Is the predicted start codon	The predicted start codon is the longest ORF, with an ORF
the longest ORF? If not,	length of 363
result in excessive dene	
overlap (>30bp)?	
Is this start site conserved	The start number called the most often in the published
in other phage genomes	annotations is 17, it was called in 103 of the 303 non-draft
as indicated by Starterator?	genes in the pham.
	This is not the best start site for gene 43. The best start site for
	gene 43 is start site 26, as it has 10 manual annotations at bp 25485
Is this start site conserved	Yes – Antuna (Hypothetical Protein), StrawberryJamm
in other phage genomes as indicated by BlastP?	(Hypothetical Protein), GrassBoy (Hypothetical Protein)
DECISION:	Based off Glimmer and the ORF, the best start codon for gene 43 is bp 25485

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: Hypothetical Protein (phage Warren)
a protein having a	
functional assignment in	E-Value: 0.0E0
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	No
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	No Synteny Observed.
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	N/A
transmembrane protein?	
Is the proposed function	Yes
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Hypothetical Protein

Basic Phage Information	
Phage Name	Losacky
Gene #	44
Stop Coordinate	26217
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	7
Selected Start Coordinate	25840
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	Vac Original Climmer cell @bp 25840 bac strength 0.76
(Glimmer, GeneMark)?	Yes, Original Gimmer call @bp 25840 has strength 9.76
Is there evidence for	yes
coding potential?	
Is this gene present in other annotated genomes?	Yes Appa gene 41 (25620 - 25997) pham 224141, Pickles13 gene 40 (25930 - 26307) pham 224141, and Antuna gene 42 (25698 - 26075) pham 224141
Does the gene violate any major guiding principles?	по
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Bp 25840
and GeneMark suggest?	
Does the start site have an	
associated Ribosome	Yes its got a z value of 2.051 and a final score of -5.435
Binding Site with a high	
score?	
Is the predicted start codon	Yes
the longest ORF? If not,	
does the longest ORF	
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	
In other phage genomes	Vee Deere (with eluster) where this start called, Anture 40
as indicated by	Yes, • Phage (with cluster) where this start called: Antuna_42
Starterator?	(GA) , Appa_41 (GA), Biett_41 (GA), Busn_42 (GA), Carrillo_43
	(GA), CookieDog_41 (GA), Dropsnot_41 (GA), Guzman_41
	(GA) , Jakelyne_44 (GA), Losacky_44 (GA), MenE_42 (GA),
	PhiliyJawn_42 (GA), Phingu_44 (GA), Phonegingi_41 (GA),
	Pickles13_40 (GA), Violeta_43 (GA), Warren_41 (GA),
Is this start site conserved	Yes it is conserved as a HNH endonuclease in warren, blett,
in other phage genomes	And bush
as indicated by BlastP?	
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master: HNH endonuclease blett
a protein having a	E Value: 0.0E0
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	HNH ENDONUCLEASE 94.45%
a protein having a	
functional assignment in	
the PDB or other database	
in HHPred with a	
probability of 90% or	
greater with appropriate	
coverage?	
Is this gene located	Yes syntenty observed HNH ENDONUCLEASE
adjacent to genes of	
known function and in a	
region of the genome that	
shows high conservation of	
gene order?	
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Yes HNH endonuclease
found on the SEA-	
PHAGES approved	
function list?	
DECISION:	Yes HNH endonuclease

Basic Phage Information	
Phage Name	Losacky
Gene #	45
Stop Coordinate	27055
Direction (For/Rev)	for
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	26243
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program	Yes, Original Glimmer call @bp 26243 has strength 15.06
(Glimmer, GeneMark)?	
Is there evidence for coding potential?	yes
Is this gene present in other annotated genomes?	Yes it is present in Appa gene 42 (26023 - 26835) pham 221605, MenE gene 43 (26123 - 26959) pham 221605, and Pickles13 gene 41 (26333 - 27145) pham 221605
Does the gene violate any major guiding principles?	no
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	bp 26243
and GeneMark suggest?	
Does the start site have an associated Ribosome Binding Site with a high score?	Yes has a high z value of 2.794 and a final score of –3.469
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	yes
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes, Start 6: • Found in 31 of 36 (86.1%) of genes in pham • Manual Annotations of this start: 13 of 24 • Called 77.4% of time when present • Phage (with cluster) where this start called: Antuna_43 (GA), Appa_42 (GA), Blett_42 (GA), Bush_43 (GA), Cardigan_119 (DD), Carrillo_44 (GA), CookieDog_42 (GA), Daredevil_78 (DL), Dropshot_42 (GA), Guzman_42 (GA), Jakelyne_45 (GA), Jinkies_48 (FL), Losacky_45 (GA)
Is this start site conserved	It is conserved as an replication initiation protein in Appa, RepA-
in other phage genomes	like replication initiator in blett, and a hypothetical protien in
as indicated by BlastP?	Antuna, Pickles13, and Bush
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	DNA Master:
a protein having a	
functional assignment in	
BlastP (phagesDB and/or	
GenBank) with an	
alignment of 10 ⁻⁴ or	
smaller with appropriate	
coverage?	
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
snows nigh conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	Indiaste e recepcione prediction programs.
is the proposed function	Once you have arrived at a functional decision, check the SEA
DUACES approved	Once you have arrived at a functional decision, check the <u>SEA-</u>
function list2	the guidelines for function List to ensure that you are following
	present on the approved list must be carefully vetted for
	approval
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	losacky
Gene #	46
Stop Coordinate	27396
Direction (For/Rev)	27052
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	27052
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes Original Glimmer call @bp 27052 has strength 22.83
Is there evidence for coding potential?	yes
Is this gene present in other annotated genomes?	Yes it is present in Appa gene 43 (26832 - 27176) pham 219897, Antuna gene 44 (26934 - 27266) pham 219897, and Pickles13 gene 42 (27142 - 27486) pham 219897
Does the gene violate any major guiding principles?	по
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	bp 27052
Does the start site have an associated Ribosome Binding Site with a high score?	Yes it has a z value of 2.906 and a final score of –3.171
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Yes it is the longest
Is this start site conserved in other phage genomes as indicated by Starterator?	Yes Start 10: • Found in 40 of 40 (100.0%) of genes in pham • Manual Annotations of this start: 27 of 28 • Called 97.5% of time when present • Phage (with cluster) where this start called: Antuna_44 (GA), Appa_43 (GA), BENtherdunthat_89 (DN1), BearBQ_89 (DN), Blett_43 (GA), BotCity_92 (DN), Bunnybear_67 (CZ), Bush_44 (GA), Carrillo_45 (GA), CookieDog_43 (GA), DelaGarza_44 (GF), Dropshot_43 (GA), Getalong_92 (DN1), Gingerbug_43 (GF), Guzman_43 (GA), Jace_39 (singleton), Jakelyne_46 (GA), Kenna_84 (DN1), Lesiram_45 (GF), Losacky_46 (GA),
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes it is conserved as hypothetical protien in appa, and warren. DNAc-like helicase loader in pickles13. Helicase loader in phonegingi and antuna
DECISION:	Yes glimmer/genemark, starterator, pharmarator, blastp, coding potential all agree

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
snows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
DUACES approved	Once you have arrived at a functional decision, check the <u>SEA-</u>
function list2	the guidelines for function List to ensure that you are following
	the guidelines for function naming. Functions that are not
	approval
	approval.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	47
Stop Coordinate	28697
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes – 3 bp
Selected Start Coordinate	27393
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program	Original Glimmer call @bp 27393 has strength 22.39
(Glimmer, GeneMark)?	
Is there evidence for coding potential?	Yes, there is evidence for coding potential
Is this gene present in other annotated genomes?	Yes - MenE gene 45 (27285 - 28589) pham 192284, Phonegingi gene 44 (27219 - 28523) pham 192284, and Warren gene 44 (27229 - 28533) pham 192284
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 47 is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 27393
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an associated Ribosome Binding Site with a high score?	Z-Score: 1.825 Final Score: -5.289
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon is the 2 nd longest ORF, with an ORF length of 1305. The start codon that is the longest ORF, with an ORF length of 1563, has excessive gene overlap of 161 base pairs.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 23, it was called in 128 of the 250 non-draft genes in the pham. This is not the best start site for gene 47. The best start site for gene 47 is start site 27, as it has 7 manual annotations at bp 27393.
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes – Phonegingi (DnaB-like dsDNA helicase), Antuna (DnaB- like dsDNA helicase), and MenE (DnaB-like dsDNA helicase)
DECISION:	Based off Glimmer, Starterator, and the ORF, the best start codon for gene 47 is 27393

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION:	name of the function here. If the evidence does not support a
	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	48
Stop Coordinate	28908
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes – 19 bp
Selected Start Coordinate	28678
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 28678 has strength 19.50; GeneMark calls start at 28699
Is there evidence for coding potential?	Yes, there is evidence for coding potential
Is this gene present in other annotated genomes?	Yes - MenE gene 46 (28591 - 28800) pham 34042
Does the gene violate any	No
major guiding principles?	
DECISION:	Based off the evidence above, gene 48 is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 28678
and GeneMark suggest?	GeneMark Start Coordinate: 28699
Does the start site have an	Bp 28678
associated Ribosome	3 rd Highest Z-Score: 1.632
Binding Site with a high score?	2 nd Lowest Final Score: -5.684
	Bp 28699
	4 th Highest Z-Score: 1.233
	6 th Lowest Final Score: -7.487
Is the predicted start codon	The predicted start codon (bp 28678) is the longest ORF, with
the longest ORF? If not,	an ORF length of 231
does the longest ORF	
result in excessive gene	
overlap (>30bp)?	
is this start site conserved	I ne start number called the most often in the published
In other phage genomes	the pham
Starterator?	
	This is the best start number for gene 48, as it has 2 manual
	annotations at bp 28699
Is this start site conserved	Yes – Antuna (Hypothetical Protein)
in other phage genomes	
as indicated by BlastP?	
DECISION:	Based off Glimmer, the RBS, and the ORF, the best start codon is bp 28678

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION:	name of the function here. If the evidence does not support a
	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.
Basic Phage Information	
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Phage Name	Losacky
Gene #	49
Stop Coordinate	29402
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes – 3 bp
Selected Start Coordinate	28911
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 28911 has strength 17.38
Is there evidence for coding potential?	Yes, there is evidence for coding potential
Is this gene present in other annotated genomes?	Yes - MenE gene 47 (28803 - 29294) pham 219249, Phonegingi gene 45 (28583 - 29074) pham 219249, and Warren gene 45 (28593 - 29075) pham 219249
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 49 is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 28911
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an associated Ribosome Binding Site with a high score?	1 st Highest Z-Score: 2.784 1 st Lowest Final Score: -4.256
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon is the longest ORF, with an ORF length of 492
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 97, it was called in 208 of the 519 non-draft genes in the pham.
	This is not the best start number. The best start number for gene 49 is start number 96, as it has 100 manual annotations at bp 28911
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes – Phonegingi (SSB protein), MenE (SSB protein), and Bush (SSB protein)
DECISION:	Based off the evidence above, the best start codon for gene 49 is bp 28911

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION:	name of the function here. If the evidence does not support a
	TUNCTIONAL CALL, RECORD TINK F" FOR NO KNOWN TUNCTION. 50-70% Of
	pnage genes tall into the INKIF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	50
Stop Coordinate	30034
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	29501
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Yes Original Glimmer call @bp 29360 has strength 19.18; GeneMark calls start at 29501
Is there evidence for coding potential?	yes
Is this gene present in other annotated genomes?	Yes but not in our cluster it appears in Beans_66, Abba_66, and King2_64
Does the gene violate any major guiding principles?	no
DECISION:	yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (bp 29360):: GeneMark Start Coordinate (29501)::
Does the start site have an associated Ribosome Binding Site with a high score?	Bp29360 has a z value of 1.410 and a final score of –6.690 Bp29501 has a z value of 0.977 and a final score of –7.028
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	No they aren't the longest bp29360 has a 42 bp overlap And bp29501 has no overlap
Is this start site conserved in other phage genomes as indicated by Starterator?	Starterator calls for start site 13 which is bp29360 Starterator hasn't called for start 29 which is is bp29501
Is this start site conserved in other phage genomes as indicated by BlastP?	It is conserved as a Parb-like nuclease domain protien in blett, Warren, and Phonegingi. It is a ParB-like parition protien
DECISION:	The best start site that glimmer, starterator, coding potential and phamerator is bp29360

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
Tound on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	PHAGES Official Function List to ensure that you are following
function list?	the guidelines for function harming. Functions that are not
	present on the approved list must be carefully velled for
	αρριοναι.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	51
Stop Coordinate	30653
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	Yes – 7 bp
Selected Start Coordinate	30027
Selected Function	N/A

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)? Is there evidence for coding potential?	Original Glimmer call @bp 30027 has strength 18.30 Yes, there is evidence for coding potential
Is this gene present in other annotated genomes?	Yes - Antuna gene 49 (29896 - 30522) pham 227566, MenE gene 49 (29918 - 30544) pham 227566, Warren gene 47 (29704 - 30330) pham 227566
Does the gene violate any major guiding principles?	No
DECISION:	Based on the evidence above, gene 51 is a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: bp 30027
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an associated Ribosome Binding Site with a high score?	1 st Lowest Final Score: -4.323 3 rd Highest Z-Value: 2.465
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon is the longest ORF, with an ORF length of 627.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 3, it was called in 27 of the 28 non-draft genes in the pham.
	This is the best start number, as bp 30027 has 27 manual annotations at start number 3.
Is this start site conserved	Yes – Bush (Acetyltransferase), Dropshot (Acetyltransferase),
in other phage genomes as indicated by BlastP?	and Warren (Acetyltransferase)
DECISION:	Based off all the evidence above, the best start codon for gene 51 is bp 30027.

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
Tound on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	PHAGES Official Function List to ensure that you are following
function list?	the guidelines for function harming. Functions that are not
	present on the approved list must be carefully velled for
	αρριοναι.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	52
Stop Coordinate	31137
Direction (For/Rev)	For
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	30811
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program	Original Glimmer call @bp 30811 has strength 20.97
Is there evidence for coding potential?	Yes
Is this gene present in other annotated genomes?	Yes - Antuna gene 51 (30680 - 31006) pham 8860, MenE gene 51 (30702 - 31028) pham 8860, and Warren gene 49 (30488 - 30826) pham 8860
Does the gene violate any major guiding principles?	No
DECISION:	Based off the evidence above, gene 52 is a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: 30811
and GeneMark suggest?	GeneMark Start Coordinate: N/A
Does the start site have an	1 st Lowest Final Score: -2.584
associated Ribosome	1 st Highest Z-Score: 3.246
Binding Sile with a high score?	
300101	
Is the predicted start codon	The predicted start codon is not the longest ORF.
the longest ORF? If not,	
does the longest ORF	The longest ORF is the start codon 30685, which does not
overlap (>30bp)?	result in excessive gene overlap.
Is this start site conserved	The start number called the most often in the published
in other phage genomes	annotations is 2, it was called in 9 of the 9 non-draft genes in
as indicated by	the pham.
Starterator?	This is the best start number for gone 52, as by 20811 bas 0
	manual annotations at this start number
Is this start site conserved	Yes – MenE (Hypothetical Protein), Blett (Hypothetical Protein),
in other phage genomes	and Phonegingi (Hypothetical Protein)
as indicated by BlastP?	
DECISION:	Based off all the evidence above, the best start codon for gene
	52 is bp 30811.

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION:	name of the function here. If the evidence does not support a
	TUNCTIONAL CALL, RECORD TINK F" FOR NO KNOWN TUNCTION. 50-70% Of
	pnage genes tall into the INKIF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	53
Stop Coordinate	32239
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	31187
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Both GeneMark and Glimmer called this gene
(Glimmer, GeneMark)?	
Is there evidence for	There is evidence for coding potential
coding potential?	
Is this gene present in other annotated genomes?	This gene is conserved in MenE (gene 52), Pickles13 (gene 49), and Dropshot (gene 50).
Does the gene violate any major guiding principles?	There are no significant violations of the guiding principles.
DECISION:	Yes, this is likely a gene.

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Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate: bp 31187
and GeneMark suggest?	GeneMark Start Coordinate: bp 31187
Does the start site have an	The RBS score of the predicted start site is –7.323 and the Z
associated Ribosome	value is 1.088, which is not very high.
Binding Site with a high	
score?	
Is the predicted start codon	The ORF length is 1053, which is the longest, with no overlap to
the longest ORF? If not,	the nearest upstream ORF.
does the longest ORF	
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	The start number called the most often in the published
in other phage genomes	annotations is 82, it was called in 126 of the 391 non-draft
as indicated by	genes in the pham. This is not the predicted start for Losacky.
Starterator?	
	Start number 64 is 31187 in Losacky.
Is this start site conserved	Hypothetical protein Warren, Blett, and Appa.
in other phage genomes	
as indicated by BlastP?	
DECISION	Bp 31187, based on Genemark/Glimmer, Phamerator,
DECISION.	Starterator, and coding potential.

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION:	name of the function here. If the evidence does not support a
	TUNCTIONAL CALL, RECORD TINK F" FOR NO KNOWN TUNCTION. 50-70% Of
	pnage genes tall into the INKIF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	54
Stop Coordinate	
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 32385.
(Glimmer, GeneMark)?	
Is there evidence for	There is coding potential.
coding potential?	
Is this gene present in	Yes, it is present in Appa, Blett, and Warren.
other annotated genomes?	
Does the gene violate any	This gene does not violate the major quiding principles
major guiding principles?	This gene does not violate the major guiding principles.
DECISION:	This is likely a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate :: bp 32385 GeneMark Start Coordinate :: bp 32385
Does the start site have an associated Ribosome Binding Site with a high score?	The Z-score of gene 54 is 3.010 and the RBS score is –3.432.
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon has an ORF of 378 and is the most desirable.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 1 @bp 32385, it was called in 8 of the 9 non-draft genes in the pham. Start 1 is @bp 32385 in Zahlia.
Is this start site conserved in other phage genomes as indicated by BlastP?	Hypothetical protein Blett, Warren, Bush, Pickles13, and Phonegingi.
DECISION:	<i>Bp</i> @32385 based on Glimmer/Genemark, Phamerator, coding potential, and Starterator.

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION:	name of the function here. If the evidence does not support a
	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	losacky
Gene #	55
Stop Coordinate	33049
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	@bp 32783
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 32783 has strength 7.08 ** not called by GeneMark
Is there evidence for coding potential?	Yes there is coding potential
Is this gene present in other annotated genomes?	Yes, MenE gene 54 (32665 - 32940) pham 224255
Does the gene violate any major guiding principles?	No violation
DECISION:	Yes

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (type NA if not supported):: GeneMark Start Coordinate (type NA if not supported)::
Does the start site have an	Final RBS score = -5.689
Binding Site with a high score?	
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Indicate the length of the ORF is with the predicted start and the gap/overlap to the nearest stop codon of the upstream ORF. Does the proposed start site have a gap/overlap with the nearest upstream gene that does not violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide the same information for each proposed start site.
Is this start site conserved	
as indicated by	• Manual Annotations of this start: 1 of 214 • Called 11 8% of time
Starterator?	when present
Is this start site conserved	
as indicated by BlastP?	
DECISION:	Start site should be @bp 32783 as agreed by Glimmer, starterator, and phamarator

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION:	name of the function here. If the evidence does not support a
	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information		
Phage Name	Losacky	
Gene #	56	
Stop Coordinate	33189	
Direction (For/Rev)	Forward	
Gap (Overlap) with Previous Gene	none	
Selected Start Coordinate	33046	
Selected Function		

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 33046.
(Glimmer, GeneMark)?	
Is there evidence for	There is coding potential.
coding potential?	
Is this gene present in	Yes, it is present in Blett, MenE, and Warren.
other annotated genomes?	
Does the gene violate any	This gene does not violate the major quiding principles
major guiding principles?	This gene does not violate the major guiding principles.
DECISION:	This is likely a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate :: bp 33046 GeneMark Start Coordinate :: bp 33046
Does the start site have an associated Ribosome Binding Site with a high score?	The Z-score of gene 62 is 1.472 and the RBS score is –6.747.
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon has an ORF of 144 and is the most desirable.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 1 @bp 33046, it was called in 8 of the 8 non-draft genes in the pham. Start 1 is @bp 33046 in Zahlia.
Is this start site conserved in other phage genomes as indicated by BlastP?	Membrane protein Appa.
DECISION:	<i>Bp</i> @33046 based on Glimmer/Genemark, Phamerator, coding potential, and Starterator.

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
snows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
is the proposed function	Indicate a response with a Yes or No response.
DUACES approved	Once you have arrived at a functional decision, check the <u>SEA-</u>
function list2	the guidelines for function List to ensure that you are following
	present on the approved list must be carefully vetted for
	approval
	approval.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	57
Stop Coordinate	33536
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	33186
Selected Function	

Gathering Evidence	Explain Your Rationale	
Was the gene called by		
an auto-annotation	Original Climmer call @bn 23186 bas strength 18 61	
program (Glimmer,	Onginal Gilminer can wop 55100 has strength 10.01	
GeneMark)?		
Is there evidence for	Yes there is coding potential	
coding potential?		
Is this gene present in	Ves the gene is present in	
other annotated	MonE gono 56 (22077 22427) pham 8461	
genomes?	Mene gene 30 (33077 - 33427) phan 6407	
Does the gene violate	20	
any major guiding	110	
principles?		
DECISION:	Yes, it is a gene	

Gathering Evidence	Explain Your Rationale	
What start site do	Glimmer Start Coordinate (type NA if not	
Glimmer and GeneMark	supported)::33186	
suggest?	GeneMark Start Coordinate (type NA if not	
	supported)::33186	
Does the start site have	The final RBS score is -7.152 and the z score Is 0.883	
an associated Ribosome	The final score is the second smallest, and the z score is	
Binding Site with a high	the second smallest	
score?		
Is the predicted start	Indicate the length of the ORF is with the predicted start	
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the	
If not, does the longest	upstream ORF. Does the proposed start site have a	
ORF result in excessive	gap/overlap with the nearest upstream gene that does not	
gene overlap (>30bp)?	violate the Guiding Principles?	
	Note: if you are considering more than 1 start site, provide	
	the same information for each proposed start site.	
Is this start site	The start site is conserved	
conserved in other	Start 6:	
phage genomes as	 Found in 17 of 18 (94.4%) of genes in pham 	
indicated by Starterator?	 Manual Annotations of this start: 9 of 9 	
Is this start site	This start site is hypothetical protein in Bush, Blett, Hot26,	
conserved in other	Pickles13, Warren	
phage genomes as		
indicated by BlastP?		
DECISION	Yes the start site should start @bp 33186 because	
	glimmer, genemark, phamerator, starterator, and blastP	

Basic Phage Information		
Phage Name	Losacky	
Gene #	58	
Stop Coordinate	33859	
Direction (For/Rev)	FOR	
Gap (Overlap) with Previous Gene	3	
Selected Start Coordinate	33533	
Selected Function		

Gathering Evidence	Explain Your Rationale
Was the gene called by an auto-annotation program (Glimmer, GeneMark)?	Original Glimmer call @bp 33509 GeneMark calls start at @bp 33533
Is there evidence for coding potential?	Yes there is evidence for coding potential
Is this gene present in other annotated genomes?	Yes, MenE gene 57 (33424 - 33750) pham 88022
Does the gene violate any major guiding principles?	No violation for principles
DECISION:	Yes it can be a gene

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate : @bp 33509
and GeneMark suggest?	GeneMark Start Coordinate : @bp 33533
Does the start site have an	<i>Z-</i> score @bp 33533 = 2.703 which is the 3 rd highest score
associated Ribosome	RBS score @bp 33533 = -3.569 which is the second highest
Binding Site with a high	
score?	z- score @bp 33509 = -7.993 making it the lowest
	RBS score @bp 33509 = 1.005 making it the second lowest
Is the predicted start codon	Indicate the length of the ORF is with the predicted start and the
the longest ORF? If not,	gap/overlap to the nearest stop codon of the upstream ORF.
does the longest ORF	Does the proposed start site have a gap/overlap with the
result in excessive gene	nearest upstream gene that does not violate the Guiding
overlap (>30bp)?	Principles?
	Note: if you are considering more than 1 start site, provide the
	Note. If you are considering more than 1 start site, provide the
Le this start site concentred	Ves. Start 7 @hr 22522; a Found in 17 of 17 / 100 0%) of some in
in other phage generation	res, start / @bp 33533: • Found in 17 of 17 (100.0%) of genes in
as indicated by	pham • Manual Annotations of this start: 9 of 9 • Called 52.9% of
Starterator?	time when present
Otarterator	Start, @bp 33509 Start 6: • Found in 15 of 17 (88.2%) of genes in
	pham • No Manual Annotations of this start. • Called 53.3% of time
	when present
Is this start site conserved	DNA binding protein with Atuna and Blett
In other phage genomes	
as indicated by BlastP?	Otartaita abauld ha @hn 22522 ao anno al hu ata da sta ha ing
DECISION:	Start site should be (000 33533 as agreed by starterator having
	y manual annotation as well as Genewark agreeing .

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
snows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
DUACES approved	Once you have arrived at a functional decision, check the <u>SEA-</u>
function list2	the guidelines for function List to ensure that you are following
	the guidelines for function naming. Functions that are not
	approval
	approval.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Zahlia
Gene #	59
Stop Coordinate	34317
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	33922
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Both GeneMark and Glimmer called this gene
(Glimmer, GeneMark)?	
Is there evidence for	There is evidence for coding potential
coding potential?	
Is this gene present in other annotated genomes?	This gene is conserved in MenE (gene 57), Pickles13 (gene 54), and Dropshot (gene 55).
Does the gene violate any major guiding principles?	There are no significant violations of the guiding principles.
DECISION:	Yes, this is likely a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	<i>Glimmer Start Coordinate: bp 33922</i> <i>GeneMark Start Coordinate: bp 33922</i>
Does the start site have an associated Ribosome Binding Site with a high score?	The RBS score of the predicted start site is –4.133 and the Z value is 2.415, which is nearly the highest.
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The ORF length is 396, which is not the longest, with no overlap to the nearest upstream ORF.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 9, it was called in 9 of the 9 non-draft genes in the pham. Start number 9 is 33922 in Losacky.
Is this start site conserved in other phage genomes as indicated by BlastP?	Hypothetical protein n Warren, Blett, and Appa.
DECISION:	<i>Bp 33922, based on Genemark/Glimmer, Phamerator, Starterator, and coding potential.</i>

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
Tound on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	PHAGES Official Function List to ensure that you are following
function list?	the guidelines for function harming. Functions that are not
	present on the approved list must be carefully velled for
	αρριοναι.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
DECISION:	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	60
Stop Coordinate	34751
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	34314
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Climmer call @bn 24214 bas strangth 19 16
program (Glimmer,	Onginal Gillinner can wop 34314 has strength 10.10
GeneMark)?	
Is there evidence for	Yes there is coding potential
coding potential?	
Is this gene present in	Ves the gene is present in
other annotated	MenE gene 50 $(3/205 - 3/6/2)$ pham 22/058
genomes?	Mene gene 59 (54205 - 54042) pham 224956
Does the gene violate	20
any major guiding	110
principles?	
DECISION:	Yes, it is a gene

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not
Glimmer and GeneMark	supported)::34314
suggest?	GeneMark Start Coordinate (type NA if not
	supported)::3314
Does the start site have	The final RBS score is -5.164 and the z score Is 2.419
an associated Ribosome	These scores are the largest of the rest, the z score is the
Binding Site with a high	second largest
score?	
Is the predicted start	Indicate the length of the ORF is with the predicted start
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the
If not, does the longest	upstream ORF. Does the proposed start site have a
ORF result in excessive	gap/overlap with the nearest upstream gene that does not
gene overlap (>30bp)?	violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.
Is this start site	The start site is conserved
conserved in other	Start 8:
phage genomes as	 Found in 17 of 17 (100.0%) of genes in pham
indicated by Starterator?	 Manual Annotations of this start: 9 of 9
Is this start site	This start site is conserved with a helix-turn-helix DNA-
conserved in other	binding protein in Antunna, Bush, Blett, Warren, and MenE
phage genomes as	
indicated by BlastP?	
	Yes the start site should start @ bp 34314 because
	glimmer, genemark, phamerator, starterator, and blastP

Basic Phage Information	
Phage Name	Losacky
Gene #	61
Stop Coordinate	35244
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	25
Selected Start Coordinate	34726
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Climmer call @hp 24726 hea strangth 20.11
program (Glimmer,	Onginal Gilminer can wop 54720 has strength 20.11
GeneMark)?	
Is there evidence for	Yes there is coding potential
coding potential?	
Is this gene present in	Ves the gene is present in
other annotated	MenE gene 60 $(3/617 - 35135)$ pham 85852
genomes?	Menie gene 60 (34017 - 33133) phan 63632
Does the gene violate	20
any major guiding	110
principles?	
DECISION:	Yes, it is a gene

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not
Glimmer and GeneMark	supported)::34726
suggest?	GeneMark Start Coordinate (type NA if not
	supported)::34726
Does the start site have	The final RBS score is -2.112 and the z score Is 3.414
an associated Ribosome	These scores are the largest of the rest, the z score is the
Binding Site with a high	second largest
score?	
Is the predicted start	Indicate the length of the ORF is with the predicted start
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the
If not, does the longest	upstream ORF. Does the proposed start site have a
ORF result in excessive	gap/overlap with the nearest upstream gene that does not
gene overlap (>30bp)?	violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.
Is this start site	The start site is conserved
conserved in other	Start 6:
phage genomes as	 Found in 17 of 62 (27.4%) of genes in pham
indicated by Starterator?	 Manual Annotations of this start: 9 of 49
Is this start site	This start site is conserved with a DNA binding protein in
conserved in other	Antunna, Blett
phage genomes as	
indicated by BlastP?	
DECISION:	Yes the start site should start @ bp 34726 because
	glimmer, genemark, phamerator, starterator, and blastP
Basic Phage Information	
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Phage Name	Losacky
Gene #	62
Stop Coordinate	35717
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	35241
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 35241 has strength 17.52
(Glimmer, GeneMark)?	
Is there evidence for	Ves GeneMark indicates coding potential
coding potential?	Tes, Genemark indicates county potential
Is this gene present in other annotated genomes?	Yes, MenE gene 61 (35132 - 35608) pham 8740
Does the gene violate any	No
major guiding principles?	
DECISION:	Yes, evidences indicates gene is present

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer and GeneMark both suggest start site @bp 35241
Does the start site have an associated Ribosome Binding Site with a high score?	RBS score = -5.360 Z- score = 1.798
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	Indicate the length of the ORF is with the predicted start and the gap/overlap to the nearest stop codon of the upstream ORF. Does the proposed start site have a gap/overlap with the nearest upstream gene that does not violate the Guiding Principles? Note: if you are considering more than 1 start site, provide the same information for each proposed start site.
Is this start site conserved in other phage genomes as indicated by Starterator?	Start 1: • Found in 16 of 17 (94.1%) of genes in pham • Manual Annotations of this start: 8 of 9 • Called 100.0% of time when present
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes hypothetical protein phage Antuna, Bush, Warren, PhoneGingi, and HOT 26
DECISION:	The gene should start @bp 35241 as inticated by phamarator, DNA master, and startarator.

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION:	functional call report "NKE" for no known function 50,70% of
	nunctional call, record INKE for no known function. 50-70% of
	priage genes fail into the NNF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	63
Stop Coordinate	36546
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	1
Selected Start Coordinate	35734
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 35734.
(Glimmer, GeneMark)?	
Is there evidence for	There is coding potential.
coding potential?	
Is this gene present in	Yes, it is present in Warren, MenE, and Blett.
other annotated genomes?	
Does the gene violate any	This gene has 1 hase pair overlap with the previous gene
major guiding principles?	This gene has T base pair overlap with the previous gene.
DECISION:	This is likely a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer	Glimmer Start Coordinate :: bp 35734
and GeneMark suggest?	GeneMark Start Coordinate :: bp 35734
Does the start site have an associated Ribosome Binding Site with a high score?	The Z-score of gene 63 is 3.246 and the RBS score is –2.584.
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The predicted start codon has the longest ORF of 813 and is the most desirable.
Is this start site conserved	The start number called the most often in the published
In other phage genomes	annotations is 1 @bp 35/34, it was called in 8 of the 8 non-draft
Starterator?	Start 1 is bp @35734 in Zahlia.
Is this start site conserved	Hypothetical protein Warren, Dropshot, Blett, and Antuna.
in other phage genomes as indicated by BlastP?	
DECISION:	<i>Bp</i> @35734 based on Glimmer/Genemark, Phamerator, coding potential, and Starterator.

Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	If the answer is YES, evaluate the proposed function in the gene
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	64
Stop Coordinate	37292
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	36546
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 36546
(Glimmer, GeneMark)?	
Is there evidence for	There is coding potential.
coding potential?	
Is this gene present in	Yes, it is present in Bush, Dropshot, and Phonegingi
other annotated genomes?	
Does the gene violate any	This gene has 1 hase pair overlap with the previous gene
major guiding principles?	This gene has T base pair overlap with the previous gene.
DECISION:	This is likely a gene.

Cothoring Evidence	Evalain Vaur Patianala
Gathering Evidence	
What start site do Glimmer	Glimmer Start Coordinate (type NA if not supported):: bp 36546
and GeneMark suggest?	GeneMark Start Coordinate (type NA if not supported):: bp
	36546
Does the start site have an	
associated Ribosome	The 7-score of gene 64 is 1 893 and the RBS score is -5092
Binding Site with a high	
score?	
30010 :	
	The predicted start adder has an ODE of 747 the largest ODE
Is the predicted start codon	The predicted start codon has an ORF of 747, the longest ORF
the longest ORF? If not,	is start codon 36543 with an ORF of 750. However, start 36546
does the longest ORF	is more desriable.
result in excessive gene	
overlap (>30bp)?	
Is this start site conserved	The start number called the most often in the published
in other phage genomes	annotations is 11 @bp 36546, it was called in 14 of the 17 non-
as indicated by	draft genes in the pham.
Starterator?	Start 2 is bp @36546 in Zahlia.
Is this start site conserved	Terminase small subunit Blett, Antuna, and Bush.
in other phage genomes	Hypothetical protein Warren.
as indicated by BlastP?	Rnase E Appa
,	Bp @36546 based on Glimmer/Genemark Phamerator coding
DECISION:	notential and Starterator

	Г
Gathering Evidence	Explain Your Rationale
Does this protein align with	List the most informative BlastP match from each source
a protein having a	PhagesDB:
functional assignment in	NCBI:
BlastP (phagesDB and/or	DNA Master:
GenBank) with an	
alignment of 10 ⁻⁴ or	Hint: you may have already found this information from
smaller with appropriate	annotation decision #2. Provide the alignment (q#:s#) and e-
coverage?	value. It is only necessary to provide one match from each
	database.
Does this protein align with	List the most informative HHPred match, including database
a protein having a	source and probability score. It is only necessary to provide the
functional assignment in	best match.
the PDB or other database	
in HHPred with a	Note: If you believe there is not a quality HHPred match, type
probability of 90% or	No Quality Match and list the data for the best match available
greater with appropriate	to affirm the poor quality of the result and to document that
coverage?	HHPred was considered.
Is this gene located	<i>If the answer is YES, evaluate the proposed function in the gene</i>
adjacent to genes of	order. Examine the adjacent genes found in the most closely
known function and in a	related annotated phage (hint: use Phamerator) and record the
region of the genome that	function of the genes found on each side of the gene in the
shows high conservation of	same pham in the most closely related phage. If the answer is
gene order?	NO, enter No Synteny Observed.
Is this gene a possible	If the answer is YES, indicate supporting data from at least 2
transmembrane protein?	different transmembrane prediction programs.
Is the proposed function	Indicate a response with a Yes or No response.
found on the SEA-	Once you have arrived at a functional decision, check the <u>SEA-</u>
PHAGES approved	<u>PHAGES Official Function List</u> to ensure that you are following
function list?	the guidelines for function naming. Functions that are not
	present on the approved list must be carefully vetted for
	approval.
	If you believe this gene should be assigned, please write the
DECISION	name of the function here. If the evidence does not support a
	functional call, record "NKF" for no known function. 50-70% of
	phage genes fall into the NKF category.

Basic Phage Information	
Phage Name	Losacky
Gene #	65
Stop Coordinate	351
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	none
Selected Start Coordinate	37277
Selected Function	

[Text Wrapping Break]

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation program (Glimmer	Original Glimmer call @bp 37277 has strength 15.47
GeneMark)?	
Is there evidence for	Yes, there is coding potential.
coding potential?	
Is this gene present in	
other annotated	Yes, it is conserved in Phonegingi.
genomes?	
Does the gene violate	The gene doesn't violate any major guiding principles
any major guiding	The gene doesn't violate any major guiding principles.
principles?	
DECISION:	Yes, this is most likely a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate (type NA if not supported):: @bp 37277 GeneMark Start Coordinate (type NA if not supported):: @bp 37277
Does the start site have an associated Ribosome Binding Site with a high score?	Considering bp 37277, final score is -6.070, and the Z- value is 1.435.
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The length of the ORF with the predicted start codon 37277 bp, which is the longest ORF, and doesn't result in overlap.
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number of Losacky is 7.
Is this start site conserved in other phage genomes as indicated by BlastP?	Yes, in hypothetical protein SEA_BLETT_62, SEA_BUSH_63, SEA_WARREN_62, SEA_PHONEGINGI_64.
DECISION:	<i>Bp 37277 based on glimmer/genemark, coding potential, starterator, and phamerator.</i>

Basic Phage Information	
Phage Name	Losacky
Gene #	66
Stop Coordinate	38100
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	0
Selected Start Coordinate	37627
Selected Function	

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Climmer call @bn 37627 bas strength 16.46
program (Glimmer,	Onginal Gilminer can wop 57627 has strength 10.40
GeneMark)?	
Is there evidence for	Yes there is coding potential
coding potential?	
Is this gene present in	Yes the gene is present in
other annotated	MenE gene 65 (37503 - 37973) pham 8415
genomes?	
Does the gene violate	20
any major guiding	110
principles?	
DECISION:	Yes, it is a gene

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not
Glimmer and GeneMark	supported)::37627
suggest?	GeneMark Start Coordinate (type NA if not
	supported)::37627
Does the start site have	The final RBS score is -4.699, and the z score Is 1.435
an associated Ribosome	These scores are the largest of the rest, the z score is the
Binding Site with a high	second largest
score?	
Is the predicted start	Indicate the length of the ORF is with the predicted start
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the
If not, does the longest	upstream ORF. Does the proposed start site have a
ORF result in excessive	gap/overlap with the nearest upstream gene that does not
gene overlap (>30bp)?	violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.
Is this start site	The start site is conserved
conserved in other	Start 6:
phage genomes as	 Found in 17 of 17 (100.0%) of genes in pham
indicated by Starterator?	 Manual Annotations of this start: 9 of 9
Is this start site	This start site is conserved with a hypothetical protein in
conserved in other	bush, hot26, menE, and warren
phage genomes as	
indicated by BlastP?	
DECISION	Yes the start site should start @ bp 37627 because
	glimmer, genemark, phamerator, starterator, and blastP

Basic Phage Information	
Phage Name	Losacky
Gene #	67
Stop Coordinate	38402
Direction (For/Rev)	Forward
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	38097
Selected Function	NKF

Gathering Evidence	Explain Your Rationale
Was the gene called by an	
auto-annotation program	Original Glimmer call @bp 38097 and has strength 16.20
(Glimmer, GeneMark)?	
Is there evidence for	Yes, because both GeneMark programs show coding potential.
coding potential?	
Is this gene present in	Yes, it is conserved in Bush and MenE.
other annotated genomes?	
Does the gene violate any	No, it does not violate any major guiding principles.
major guiding principles?	
DECISION:	This is most likely a gene.

Gathering Evidence	Explain Your Rationale
What start site do Glimmer and GeneMark suggest?	Glimmer Start Coordinate @bp 38097
Does the start site have an associated Ribosome Binding Site with a high score?	Considering bp @38097, The associated RBS score is -4.392 with a final score of -5.227 and the Z value is 1.896.
Is the predicted start codon the longest ORF? If not, does the longest ORF result in excessive gene overlap (>30bp)?	The length of the ORF with the predicted start codon is 306 (bp @38097).
Is this start site conserved in other phage genomes as indicated by Starterator?	The start number called the most often in the published annotations is 10, it was called in 6 of the 11 non-draft genes in the pham. Starterator says site 10 is bp @38097 in Losacky.
Is this start site conserved in other phage genomes as indicated by BlastP?	Hypothetical protein for MenE, Antuna, Blett, and Warren.
DECISION:	<i>Bp</i> @38097, based on GeneMark, coding potential, starterator, and phamerator.

Gathering Evidence	Explain Your Rationale
Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10 ⁻⁴ or smaller with appropriate coverage?	DNA Master: Hypothetical protein (MenE) E-value: 0
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	The most informative HHPred match is SDH_N_domain; Saccharopine dehydrogenase N-terminal domain. The probability is 70.42. This low probability shows that it is a hypothetical protein.
Is this gene located adjacent to genes of known function and in a region of the genome that shows high conservation of gene order?	No synteny observed; hypothetical protein.
Is the proposed function found on the SEA- PHAGES approved function list?	Yes
DECISION:	NKF

Basic Phage Information	
Phage Name	Losacky
Gene #	68
Stop Coordinate	38554
Direction (For/Rev)	FOR
Gap (Overlap) with Previous Gene	3
Selected Start Coordinate	38399
Selected Function	

Annotation Decision #1: Is this a Gene?

Gathering Evidence	Explain Your Rationale
Was the gene called by	
an auto-annotation	Original Climmer call @bn 38300 bas strength 14 73
program (Glimmer,	Onginal Gillinner can wop 50599 has strength 14.75
GeneMark)?	
Is there evidence for	Yes there is coding potential
coding potential?	
Is this gene present in	Yes the gene is present in
other annotated	MenE gene 67 (38272 - 38427) pham 8617
genomes?	
Does the gene violate	20
any major guiding	110
principles?	
DECISION:	Yes, it is a gene

Gathering Evidence	Explain Your Rationale
What start site do	Glimmer Start Coordinate (type NA if not
Glimmer and GeneMark	supported)::38399
suggest?	GeneMark Start Coordinate (type NA if not
	supported)::38399
Does the start site have	The final RBS score is -4.548, and the z score is 2.171
an associated Ribosome	These scores are the largest of the rest
Binding Site with a high	
score?	
Is the predicted start	Indicate the length of the ORF is with the predicted start
codon the longest ORF?	and the gap/overlap to the nearest stop codon of the
If not, does the longest	upstream ORF. Does the proposed start site have a
ORF result in excessive	gap/overlap with the nearest upstream gene that does not
gene overlap (>30bp)?	violate the Guiding Principles?
	Note: if you are considering more than 1 start site, provide
	the same information for each proposed start site.
Is this start site	The start site is conserved
conserved in other	Start 7:
phage genomes as	 Found in 10 of 10 (100.0%) of genes in pham
indicated by Starterator?	
Is this start site	This start site is conserved with a hypothetical protein in
conserved in other	antenna, strawberryjamm, grassboy, and teehee
phage genomes as	
indicated by BlastP?	
	Yes the start site should startc @ bp 38399 because
	glimmer, genemark, phamerator, starterator, and blastP