

CDS 857 - 1276

```
/gene="1"  
/product="gp1"  
/function="terminase, small subunit"  
/locus tag="TinyPebbles_1"  
/note=Original Glimmer call @bp 857 has strength 5.45; Genemark calls  
start at 920  
/note=SSC: 857-1276 CP: yes SCS: both-g1 ST: SS BLAST-Start:  
[terminase small subunit [Mycobacterium phage SoilDragon] ],,NCBI, q1:s1  
100.0% 1.42676E-95 GAP: 0 bp gap LO: no RBS: Kibler 6, Karlin Medium,  
2.891, -2.6013996449736907, yes F: terminase, small subunit SIF-BLAST:  
,,[terminase small subunit [Mycobacterium phage SoilDragon]  
],,YP_010060046,100.0,1.42676E-95 SIF-HHPRED: Terminase_4 ; Phage  
terminase, small subunit,,,PF05119.17,48.2014,98.6 SIF-Syn:  
/note=1:1 Blast match with soildragon. Went with Glimmer call.  
Function supported by HHPRED and phagesdb  
CDS 1362 - 1682
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```
/gene="2"  
/product="gp2"  
/function="hypothetical protein"  
/locus tag="TinyPebbles_2"  
/note=Original Glimmer call @bp 1362 has strength 12.72; Genemark  
calls start at 1362  
/note=SSC: 1362-1682 CP: yes SCS: both ST: SS BLAST-Start:  
[hypothetical protein PBI_BXZ2_3 [Mycobacterium phage Bxz2] ],,NCBI,  
q1:s1 100.0% 6.97329E-69 GAP: 85 bp gap LO: yes RBS: Kibler 6, Karlin  
Medium, 3.1, -2.2364030944336752, yes F: hypothetical protein SIF-BLAST:  
,,[hypothetical protein PBI_BXZ2_3 [Mycobacterium phage Bxz2]  
],,NP_817594,100.0,6.97329E-69 SIF-HHPRED: L-shaped tail fiber protein  
p132; Bacteriophage, Siphophage, T5, baseplate, VIRAL PROTEIN; 3.45A  
{Escherichia phage T5},,,7QG9_0,92.4528,98.0 SIF-Syn:  
/note=Very solid HHPRED match for tail fiber proteins, but this is an  
uncommon function for this pham. stuck with NKF. 1:1 BLAST matches  
CDS 1682 - 2716
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```
/gene="3"  
/product="gp3"  
/function="minor tail protein"  
/locus tag="TinyPebbles_3"  
/note=Original Glimmer call @bp 1682 has strength 5.33; Genemark  
calls start at 1682  
/note=SSC: 1682-2716 CP: yes SCS: both ST: SS BLAST-Start: [tail  
fiber protein [Mycobacterium phage Bxz2] ],,NCBI, q1:s1 100.0% 0.0 GAP: -  
1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.541, -3.4283035164720754,  
yes F: minor tail protein SIF-BLAST: ,,[tail fiber protein [Mycobacterium  
phage Bxz2] ],,NP_817595,99.4186,0.0 SIF-HHPRED: SIF-Syn:  
/note=Called minor tail protein due strong phages db function  
frequency. Start site was supported by SS starterator, 1:1 BLAST matches  
with multiples phages and -4 gap, best SD score.  
CDS 2720 - 3352  
/gene="4"  
/product="gp4"  
/function="minor tail protein"  
/locus tag="TinyPebbles_4"
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/note=Original Glimmer call @bp 2720 has strength 8.07; Genemark calls start at 2720

/note=SSC: 2720-3352 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA_DAISHI_5 [Mycobacterium phage Daishi]],,NCBI, q1:s1 100.0% 3.90379E-142 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.994, -4.513079314654054, yes F: minor tail protein SIF-BLAST: ,, [hypothetical protein SEA_DAISHI_5 [Mycobacterium phage Daishi]],,QAY17443,100.0,3.90379E-142 SIF-HHPRED: Minor tail protein; Bacteriophage, tail tip, VIRAL PROTEIN;{Mycobacterium phage Bxb1}},,9D93_Pb,85.2381,99.7 SIF-Syn:

/note=Called minor tail protein. multiple 1:1 BLAST Matches. PhagesDB calls unknown function. HHPred has high match to minor tail protein, has been studied and created a full crystal structure of the protein and is awaiting publishing.

CDS 3361 - 3852

/gene="5"

/product="gp5"

/function="hypothetical protein"

/locus tag="TinyPebbles_5"

/note=Original Glimmer call @bp 3361 has strength 9.17; Genemark calls start at 3361

/note=SSC: 3361-3852 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_6 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 1.58451E-113 GAP: 8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.206, -2.45827804503836, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_6 [Mycobacterium phage Bxz2]],,NP_817597,100.0,1.58451E-113 SIF-HHPRED: SIF-Syn:

/note=Genemark and glimmer match (3361). Catches all coding potential. gap=8. SD=-2.458, yes its the best SD. 1:1. Suggested Start. Very low evidence of a solid function.

tRNA 3921 - 3996

/gene="6"

/product="tRNA-Asn(gtt) "

/locus tag="TINYPEBBLES_6"

/note=tRNA-Asn(gtt)

tRNA 4037 - 4113

/gene="7"

/product="tRNA-Trp(cca) "

/locus tag="TINYPEBBLES_7"

/note=tRNA-Trp(cca)

tRNA 4146 - 4220

/gene="8"

/product="tRNA-Leu(cag) "

/locus tag="TINYPEBBLES_8"

/note=tRNA-Leu(cag)

CDS 4250 - 4504

/gene="9"

/product="gp9"

/function="hypothetical protein"

/locus tag="TinyPebbles_9"

/note=Original Glimmer call @bp 4250 has strength 15.35; Genemark calls start at 4250

/note=SSC: 4250-4504 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_10 [Mycobacterium phage Bxz2]],,NCBI,

ql:s1 100.0% 1.76502E-50 GAP: 397 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.195, -2.033982896655645, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI_BXZ2_10 [Mycobacterium phage Bxz2]],,,NP_817598,100.0,1.76502E-50 SIF-HHPRED: SIF-Syn:

/note=Hypothetical protein, but no known function. NCBI Blast 1:1 for BXZ2. Longest ORF. Best SD start. Starterator suggested start. 4,250 start. Covers all coding potential.

CDS 4501 - 6045

/gene="10"

/product="gp10"

/function="lysin A"

/locus tag="TinyPebbles_10"

/note=Original Glimmer call @bp 4501 has strength 13.16; Genemark calls start at 4501

/note=SSC: 4501-6045 CP: yes SCS: both ST: SS BLAST-Start: [lysin A [Mycobacterium phage Spike509]],,,NCBI, ql:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.184, -4.4583299492266635, no F: lysin A SIF-BLAST: ,,[lysin A [Mycobacterium phage Spike509]],,,AJA41794,100.0,0.0 SIF-HHPRED: Peptidase_C47 ; Staphopain peptidase C47,,,PF05543.18,31.7121,99.3 SIF-Syn:

/note=Glimmer/GeneMark have the same start, -4 overlap, longest ORF (all coding potential covered), SS starterator (track 12), Spike509 1:1, Phages DB and HHpred suggest function: lysin A. It is not the best SD score, but the 218 base pair gap and glimmer start to discredit that gene with the better SD score.

CDS 6045 - 7010

/gene="11"

/product="gp11"

/function="lysin B"

/locus tag="TinyPebbles_11"

/note=Original Glimmer call @bp 6045 has strength 13.82; Genemark calls start at 6045

/note=SSC: 6045-7010 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI_BXZ2_12 [Mycobacterium phage Bxz2]],,,NCBI, ql:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.259, -4.011096051960258, no F: lysin B SIF-BLAST: ,,[hypothetical protein PBI_BXZ2_12 [Mycobacterium phage Bxz2]],,,NP_817600,100.0,0.0 SIF-HHPRED: c.69.1.30 (A:) Acetylxylin esterase {Penicillium purpurogenum [TaxId: 28575]} | CLASS: Alpha and beta proteins (a/b), FOLD: alpha/beta-Hydrolases, SUPFAM: alpha/beta-Hydrolases, FAM: Cutinase-like,,,SCOP_dlg66a_,52.0249,99.9 SIF-Syn:

/note=called Lysin B due to strong phagesdb function frequency. Start site was not supported by SS starterator, 1:1 BLAST matches with multiples phages and -1 gap, best SD score.

CDS 7040 - 8740

/gene="12"

/product="gp12"

/function="terminase, large subunit"

/locus tag="TinyPebbles_12"

/note=Original Glimmer call @bp 7040 has strength 15.75; Genemark calls start at 7088

/note=SSC: 7040-8740 CP: yes SCS: both-gl ST: NI BLAST-Start: [terminase large subunit [Mycobacterium phage Bxz2]],,,NCBI, ql:s1 100.0% 0.0 GAP: 29 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.044, -

2.338663114094478, yes F: terminase, large subunit SIF-BLAST:
 ,, [terminase large subunit [Mycobacterium phage Bxz2]
],,, NP_817601,100.0,0.0 SIF-HHPRED: Terminase large subunit; genome
 packaging, bacteriophage, ATPase, nuclease, VIRAL PROTEIN; HET: BR; 2.2A
 {Enterobacteria phage HK97},,, 6Z6D_A,91.6961,100.0 SIF-Syn:
 /note=Glimmer and gene start do not agree, they both capture all
 coding potential but glimmer has the longest orf and best SD score
 therefore Im gonna call glimmer as the correct start. Have multiple 1:1
 BLAST matches. Starterator shows the start site is not the suggested
 start site. Calling Terminase, Large subunit because we already have a
 called terminase small subunit. HHPred matches with multiple terminase
 units. Has conserved domains but does not have great matches.
 CDS 8737 - 10191
 /gene="13"
 /product="gp13"
 /function="portal protein"
 /locus tag="TinyPebbles_13"
 /note=Original Glimmer call @bp 8737 has strength 16.06; Genemark
 calls start at 8737
 /note=SSC: 8737-10191 CP: yes SCS: both ST: SS BLAST-Start: [portal
 protein [Mycobacterium phage Bxz2]],,,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp
 gap LO: yes RBS: Kibler 6, Karlin Medium, 1.847, -4.966271270034708, no
 F: portal protein SIF-BLAST: ,, [portal protein [Mycobacterium phage Bxz2]
],,, NP_817602,100.0,0.0 SIF-HHPRED: Portal protein; Bacteriophage, portal,
 VIRAL PROTEIN; {Mycobacterium phage Bxb1},,, 9D94_Fd,90.9091,100.0 SIF-Syn:
 /note=Glimmer and Genemark agree. Has the longest orf captures all
 coding potential but does not have the best SD score but the rest suggest
 this is the proper start. Calling portal protein. Everything suggest
 portal protein with multiple 1:1 BLAST and high HHPred hits along with
 the synteny as it follows a terminase gene.
 CDS 10188 - 11027
 /gene="14"
 /product="gp14"
 /function="capsid maturation protease"
 /locus tag="TinyPebbles_14"
 /note=Original Glimmer call @bp 10188 has strength 6.92; Genemark
 calls start at 10188
 /note=SSC: 10188-11027 CP: yes SCS: both ST: SS BLAST-Start: [head
 maturation protease [Mycobacterium phage PurpleHaze]],,,NCBI, q1:s1
 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.055, -
 2.394485424036831, yes F: capsid maturation protease SIF-BLAST: ,, [head
 maturation protease [Mycobacterium phage PurpleHaze]
],,, YP_010059973,100.0,0.0 SIF-HHPRED: Phage_min_cap2 ; Phage minor capsid
 protein 2,, , PF06152.16,55.1971,97.3 SIF-Syn:
 /note=Calling capsid maturation protease. Everything suggest this is
 the correct start site. Multiple 1:1 Blast matches. High call of this
 function in other matches. PhagesDB call this function 79% of the time.
 Also calling this function as it follows a portal protein.
 CDS 11086 - 11589
 /gene="15"
 /product="gp15"
 /function="scaffolding protein"
 /locus tag="TinyPebbles_15"

/note=Original Glimmer call @bp 11086 has strength 15.47; Genemark calls start at 11086

/note=SSC: 11086-11589 CP: yes SCS: both ST: SS BLAST-Start: [head scaffolding protein [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 2.28823E-114 GAP: 58 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.891, - 3.2535385006449706, yes F: scaffolding protein SIF-BLAST: ,, [head scaffolding protein [Mycobacterium phage Bxz2]],,NP_817604,100.0,2.28823E-114 SIF-HHPRED: Scaffold protein; major capsid protein, HK97-like fold, scaffolding protein, procapsid, VIRUS; 3.8A {Staphylococcus phage 80alpha},,,6BOX_g,67.0659,98.5 SIF-Syn:

/note=Catches all coding potential. Gap=58. Is not the LORF, SD score is -3.254, indicating the best SD score. Has 1:1 match. Suggested start. NCBI BLAST has 100% scaffolding protein identity, HHPRED has 98.5 probability of scaffolding protein.

CDS 11622 - 12614

/gene="16"

/product="gp16"

/function="major capsid protein"

/locus tag="TinyPebbles_16"

/note=Original Glimmer call @bp 11622 has strength 15.81; Genemark calls start at 11622

/note=SSC: 11622-12614 CP: yes SCS: both ST: NI BLAST-Start: [major capsid protein [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 0.0 GAP: 32 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.206, - 2.838489286749966, yes F: major capsid protein SIF-BLAST: ,, [major capsid protein [Mycobacterium phage Bxz2]],,NP_817605,100.0,0.0 SIF-HHPRED: Major capsid protein; HK97-fold, T=7, tailed bacteriophage, VIRUS; 2.6A {Gordonia phage Cozz},,,8ECK_C,96.0606,100.0 SIF-Syn:

/note=Captures all coding potential. Gap is 32, and is LORF. SD is -2.838 which is the best score. 1:1 BLAST match. Non informative. HHPRED has 100 probability of major capsid protein, NCBI BLAST also has 100 chance its major capsid protein.

CDS 12685 - 12870

/gene="17"

/product="gp17"

/function="head-to-tail adaptor"

/locus tag="TinyPebbles_17"

/note=Original Glimmer call @bp 12685 has strength 4.93; Genemark calls start at 12685

/note=SSC: 12685-12870 CP: no SCS: both ST: SS BLAST-Start: [head-tail connector protein [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 8.20634E-35 GAP: 70 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.082, - 4.85287563363746, no F: head-to-tail adaptor SIF-BLAST: ,, [head-tail connector protein [Mycobacterium phage Bxz2]],,NP_817606,100.0,8.20634E-35 SIF-HHPRED: Hypothetical protein yqbF; two-domain, Bsu26130, YqbF, NESG, Structural Genomics, PSI-2, Protein Structure Initiative, Northeast Structural Genomics Consortium; NMR {Bacillus subtilis} SCOP: a.140.3.2, d.344.1.1, 1.1.1.1,,,2HJQ_A,40.9836,76.2 SIF-Syn:

/note=Glimmer and GeneMark start = 12685 and 12870 stop, all coding potential is not covered, Large 70 base pair gap, not the best SD score, longest ORF, 1:1 BLAST match, starterator results: SS, PhagesDB suggested function: head to tail connector protein. HHpred: suggests bacillus crystal structure must have an alignment to determine the head-to-tail

adapter function and states the head to tail connector protein is the former name of the head-to-tail adapter function.

CDS 12879 - 13250

/gene="18"

/product="gp18"

/function="head-to-tail adaptor"

/locus tag="TinyPebbles_18"

/note=Original Glimmer call @bp 12879 has strength 11.41; Genemark calls start at 12879

/note=SSC: 12879-13250 CP: yes SCS: both ST: SS BLAST-Start: [head-tail adaptor Ad1 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 1.1567E-82 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.63, - 3.6859871712346846, yes F: head-to-tail adaptor SIF-BLAST: ,, [head-tail adaptor Ad1 [Mycobacterium phage Bxz2]],,NP_817607,100.0,1.1567E-82 SIF-HHPRED: Head-to-tail adaptor; Bacteriophage, portal, VIRAL PROTEIN;{Mycobacterium phage Bxb1},,,9D94_Ga,98.374,99.9 SIF-Syn:

/note=Captures all coding potential. Gap is 8. LORF, with best SD score of -3.686. BLAST shows multiple 1:1 ratios. Suggested start. HHPRED probability of 99.9 for head to tail adaptor. BLAST had 100% probability of head to tail adaptor.

CDS 13247 - 13381

/gene="19"

/product="gp19"

/function="hypothetical protein"

/locus tag="TinyPebbles_19"

/note=Original Glimmer call @bp 13247 has strength 11.56; Genemark calls start at 13247

/note=SSC: 13247-13381 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_191 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 2.19972E-22 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.165, -4.290417282676006, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_191 [Mycobacterium phage Bxz2]],,NP_817608,100.0,2.19972E-22 SIF-HHPRED: SIF-Syn:

/note=-4 bp gap between genes, not all coding potential covered from genemark. 1:1 comparison with Bxz2 - hypothetical protein. Other phages BLAST matches specify function unknown. Suggested start in starterator

CDS 13378 - 13746

/gene="20"

/product="gp20"

/function="head-to-tail stopper"

/locus tag="TinyPebbles_20"

/note=Original Glimmer call @bp 13378 has strength 11.81; Genemark calls start at 13378

/note=SSC: 13378-13746 CP: yes SCS: both ST: SS BLAST-Start: [head closure Hc1 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 3.57153E-84 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.722, - 5.172539920119419, no F: head-to-tail stopper SIF-BLAST: ,, [head closure Hc1 [Mycobacterium phage Bxz2]],,NP_817609,100.0,3.57153E-84 SIF-HHPRED: Head-to-tail stopper; Bacteriophage, portal, VIRAL PROTEIN;{Mycobacterium phage Bxb1},,,9D94_Hc,98.3607,99.8 SIF-Syn:

/note=Glimmer and Gene Mark Agree 13378 for start. Stop site is 13756. Not the longest ORF. All coding potential. Suggested start was 24. Not the best SD score. 1:1 with phage Bxz2. 4 base pair overlap.

CDS 13748 - 14107

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/gene="21"
/product="gp21"
/function="hypothetical protein"
/locus tag="TinyPebbles_21"
/note=Original Glimmer call @bp 13748 has strength 9.61; Genemark
calls start at 13748
/note=SSC: 13748-14107 CP: yes SCS: both ST: SS BLAST-Start: [tail
completion or Neck1 protein [Mycobacterium phage Bxz2] ],,NCBI, q1:s1
100.0% 8.14969E-82 GAP: 1 bp gap LO: yes RBS: Kibler 6, Karlin Medium,
1.982, -4.618714563851943, no F: hypothetical protein SIF-BLAST: ,, [tail
completion or Neck1 protein [Mycobacterium phage Bxz2]
],,NP_817610,100.0,8.14969E-82 SIF-HHPRED: DUF5403 ; Family of unknown
function (DUF5403),,,PF17395.7,94.958,99.6 SIF-Syn:
/note=NKF, other possible proteins. 1:1 with Bxz2. Glimmer and
GeneMark agree at 13748. All coding potential. Longest ORF and best SD
score. only 1 BP gap.
CDS 14118 - 14525
/gene="22"
/product="gp22"
/function="tail terminator"
/locus tag="TinyPebbles_22"
/note=Original Glimmer call @bp 14118 has strength 12.88; Genemark
calls start at 14118
/note=SSC: 14118-14525 CP: no SCS: both ST: NI BLAST-Start: [tail
terminator [Mycobacterium phage Bxz2] ],,NCBI, q1:s1 100.0% 5.8681E-94
GAP: 10 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.311, -
3.898968357315439, no F: tail terminator SIF-BLAST: ,, [tail terminator
[Mycobacterium phage Bxz2] ],,NP_817611,100.0,5.8681E-94 SIF-HHPRED: Tail
terminator; Bacteriophage, portal, VIRAL PROTEIN;{Mycobacterium phage
Bxb1},,,9D94_Ic,99.2593,99.9 SIF-Syn:
/note=Glimmer and GeneMark agree for start: 14118 and stop 14525, not
all coding potential is covered, gap is 10 base pairs, not the longest
ORF, best SD score, starterator results are NI, BLAST match 1:1, BLAST
and HHpred function state tail terminator.
CDS 14556 - 15152
/gene="23"
/product="gp23"
/function="major tail protein"
/locus tag="TinyPebbles_23"
/note=Original Glimmer call @bp 14556 has strength 17.49; Genemark
calls start at 14580
/note=SSC: 14556-15152 CP: yes SCS: both-gl ST: SS BLAST-Start:
[major tail protein [Mycobacterium phage PurpleHaze] ],,NCBI, q1:s1
100.0% 1.25148E-141 GAP: 30 bp gap LO: yes RBS: Kibler 6, Karlin Medium,
2.966, -2.794070146961553, yes F: major tail protein SIF-BLAST: ,, [major
tail protein [Mycobacterium phage PurpleHaze]
],,YP_010059982,100.0,1.25148E-141 SIF-HHPRED: Major tail protein;
Bacteriophage, tail tube, VIRUS, VIRAL PROTEIN;{Mycobacterium phage
Bxb1},,,9D9L_J,96.4646,99.9 SIF-Syn:
/note=captures all coding potential, longest orf, suggested start on
starterator, HHPRED and BLAST call major tail protein. Gap is 30 and the
sd score is -2.794. Agrees with Glimmer, not Genemark
CDS 15266 - 15664
/gene="24"

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/product="gp24"
/function="tail assembly chaperone"
/locus tag="TinyPebbles_24"
  /note=Original Glimmer call @bp 15266 has strength 13.48; Genemark
calls start at 15266
  /note=SSC: 15266-15664 CP: yes SCS: both ST: SS BLAST-Start: [tail
assembly chaperone [Mycobacterium phage Bxz2] ],,NCBI, q1:s1 100.0%
3.21992E-86 GAP: 113 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.297, -
4.395041241556842, no F: tail assembly chaperone SIF-BLAST: ,, [tail
assembly chaperone [Mycobacterium phage Bxz2]
],,NP_817613,100.0,3.21992E-86 SIF-HHPRED: GP24_25 ; Mycobacteriophage
tail assembly protein,,,PF17388.7,95.4545,100.0 SIF-Syn:
  /note=Glimmer and GeneMark agree of a 13748 start. 14107 stop.
Longest ORF. 1 base pair gap. Best SD score. All coding potential.. 1:1
match for Bxz2. Suggested start was 65. I double checked and it is a tail
assembly chaperone with multiple PhageDB blasts with good HHPred hits
CDS join(15266..15640,15640..16062)
  /gene="25"
  /product="gp25"
  /function="tail assembly chaperone"
  /locus tag="TinyPebbles_25"
  /note=
  /note=SSC: 15266-16062 CP: yes SCS: neither ST: NI BLAST-Start: [tail
assembly chaperone [Mycobacterium phage JHC117] ],,NCBI, q1:s1 100.0% 0.0
GAP: -399 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.297, -
4.395041241556842, no F: tail assembly chaperone SIF-BLAST: ,, [tail
assembly chaperone [Mycobacterium phage JHC117] ],,YP_009635615,100.0,0.0
SIF-HHPRED: GP24_25 ; Mycobacteriophage tail assembly
protein,,,PF17388.7,47.5472,100.0 SIF-Syn:
  /note=Gap is -399, SD score is -4.395 (not the LORF). BLAST has a 1:1
match. Catches all coding capacity. Pham is not informative.
CDS 16062 - 19088
  /gene="26"
  /product="gp26"
  /function="tape measure protein"
  /locus tag="TinyPebbles_26"
  /note=Original Glimmer call @bp 16062 has strength 11.66; Genemark
calls start at 16062
  /note=SSC: 16062-19088 CP: yes SCS: both ST: NI BLAST-Start: [tail
length tape measure protein [Mycobacterium phage Bxz2] ],,NCBI, q1:s1
100.0% 0.0 GAP: -2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.949, -
3.5800013779028776, no F: tape measure protein SIF-BLAST: ,, [tail length
tape measure protein [Mycobacterium phage Bxz2] ],,NP_817615,100.0,0.0
SIF-HHPRED: Tapemeasure protein; Bacteriophage, tail tip, VIRAL
PROTEIN; {Mycobacterium phage Bxb1},,,9D93_Nb,74.3056,100.0 SIF-Syn:
  /note=Glimmer and GeneMark agree start site of 16062, -1 overlap.
HHPRED and BLAST call tape measure protein with 1:1 correlation.
Starterator NI multiple different start sites found, Best SD score
CDS 19095 - 20468
  /gene="27"
  /product="gp27"
  /function="minor tail protein"
  /locus tag="TinyPebbles_27"

```


/note=Original Glimmer call @bp 19095 has strength 11.97; Genemark calls start at 19191

/note=SSC: 19095-20468 CP: yes SCS: both-gl ST: NI BLAST-Start: [minor tail protein [Mycobacterium phage Grum1]],,NCBI, q1:s1 100.0% 0.0 GAP: 6 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.121, - 2.7645180226256008, yes F: minor tail protein SIF-BLAST: ,, [minor tail protein [Mycobacterium phage Grum1]],,AXC37651,100.0,0.0 SIF-HHPRED: Minor tail protein; Bacteriophage, tail tip, VIRAL PROTEIN;{Mycobacterium phage Bxb1},,,9D93_Mf,99.7812,100.0 SIF-Syn:

/note=Glimmer and GeneStart do not agree but going with the glimmer start due to the SD score and gaps. Start is 19095 and stop is 20468, All coding capacity is covered, best SD, longest ORF, 6 base pair gap, BLAST 1:1 ratio, HHpred function suggests minor tail protein

CDS 20465 - 22261

/gene="28"

/product="gp28"

/function="minor tail protein"

/locus tag="TinyPebbles_28"

/note=Original Glimmer call @bp 20465 has strength 17.16; Genemark calls start at 20465

/note=SSC: 20465-22261 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage HashRod]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.071, - 4.349108688274226, no F: minor tail protein SIF-BLAST: ,, [minor tail protein [Mycobacterium phage HashRod]],,WNN93890,100.0,0.0 SIF-HHPRED: Minor tail protein; Bacteriophage, tail tip, VIRAL PROTEIN;{Mycobacterium phage Bxb1},,,9D93_Oa,99.3311,100.0 SIF-Syn:

/note=Called Minor tail protein due to strong phagesdb function frequency. Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and -4 gap, not best final score however.

CDS 22284 - 22727

/gene="29"

/product="gp29"

/function="minor tail protein"

/locus tag="TinyPebbles_29"

/note=Original Glimmer call @bp 22284 has strength 7.7; Genemark calls start at 22284

/note=SSC: 22284-22727 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 3.68661E-106 GAP: 22 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.106, - 4.274735973818826, no F: minor tail protein SIF-BLAST: ,, [minor tail protein [Mycobacterium phage Bxz2]],,NP_817618,100.0,3.68661E-106 SIF-HHPRED: DUF2744 ; Protein of unknown function (DUF2744),,,PF10910.13,89.7959,100.0 SIF-Syn:

/note=Called minor tail protein due to phagesdb function frequency. Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and 22 gap, not best final score however (SD). We are calling it a minor tail protein due to synteny.

CDS 22738 - 23052

/gene="30"

/product="gp30"

/function="minor tail protein"

/locus tag="TinyPebbles_30"

/note=Original Glimmer call @bp 22738 has strength 11.64; Genemark calls start at 22738

/note=SSC: 22738-23052 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 2.06502E-67 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.965, - 4.574282075258586, no F: minor tail protein SIF-BLAST: ,, [minor tail protein [Mycobacterium phage Bxz2]],,NP_817619,100.0,2.06502E-67 SIF-HHPRED: SIF-Syn:

/note=Called minor tail protein due to phagesdb function frequency. Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and 10 gap, not best final score however (SD), is the longest ORF. We are calling it a minor tail protein due to synteny. CDS 23049 - 23354

/gene="31"
/product="gp31"
/function="minor tail protein"
/locus tag="TinyPebbles_31"

/note=Original Glimmer call @bp 23049 has strength 10.84; Genemark calls start at 23049

/note=SSC: 23049-23354 CP: yes SCS: both ST: NI BLAST-Start: [minor tail protein [Mycobacterium phage BuzzBuzz]],,NCBI, q1:s1 100.0% 1.52224E-66 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.598, - 5.496236447618654, no F: minor tail protein SIF-BLAST: ,, [minor tail protein [Mycobacterium phage BuzzBuzz]],,ANU79366,100.0,1.52224E-66 SIF-HHPRED: DUF2746 ; Protein of unknown function (DUF2746),,,PF10874.13,94.0594,99.9 SIF-Syn:

/note=Called minor tail protein due to phagesdb function frequency. Start site was not supported by SS starterator, 1:1 BLAST matches with multiples phages and -4 gap (strong), not best final score however (SD). We are calling it a minor tail protein due to synteny. CDS 23366 - 25117

/gene="32"
/product="gp32"
/function="minor tail protein"
/locus tag="TinyPebbles_32"

/note=Original Glimmer call @bp 23366 has strength 12.96; Genemark calls start at 23366

/note=SSC: 23366-25117 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage BuzzBuzz]],,NCBI, q1:s1 100.0% 0.0 GAP: 11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.206, - 1.993391246735709, yes F: minor tail protein SIF-BLAST: ,, [minor tail protein [Mycobacterium phage BuzzBuzz]],,ANU79367,100.0,0.0 SIF-HHPRED: Minor tail protein; Bacteriophage, tail tip, VIRAL PROTEIN;{Mycobacterium phage Bxb1},,,9D93_Pb,39.4511,99.9 SIF-Syn:

/note=Called minor tail protein due to phagesdb function frequency. Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and 11 gap, best final score (SD). We are calling it a minor tail protein due sytenty and within stretch of minor tail proteins after tape measure. CDS 25117 - 25398

/gene="33"
/product="gp33"
/function="minor tail protein"
/locus tag="TinyPebbles_33"

/note=Original Glimmer call @bp 25117 has strength 12.22; Genemark calls start at 25117

/note=SSC: 25117-25398 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_METHUSELAH_33 [Mycobacterium phage Methuselah]],,NCBI, q1:s1 100.0% 1.06608E-60 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.121, -2.4634880269616195, yes F: minor tail protein SIF-BLAST: ,, [hypothetical protein PBI_METHUSELAH_33 [Mycobacterium phage Methuselah]],,AGK87234,100.0,1.06608E-60 SIF-HHPRED: UPF0154 ; Uncharacterised protein family (UPF0154),,,PF03672.18,31.1828,62.6 SIF-Syn:

/note=Calling minor tail protein. Captures all coding potential and uses the suggested start site. have multiple 1:1 BLAST matches. Split between minor tail protein and NKF calls but we are calling Minor tail protein due to the syntenicity as it typically follow a tape measure protein CDS complement (25459 - 25725)

/gene="34"

/product="gp34"

/function="hypothetical protein"

/locus tag="TinyPebbles_34"

/note=Original Glimmer call @bp 25725 has strength 9.15; Genemark calls start at 25725

/note=SSC: 25725-25459 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_33 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 3.76503E-57 GAP: 17 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.966, -2.5052746077145835, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_33 [Mycobacterium phage Bxz2]],,NP_817622,100.0,3.76503E-57 SIF-HHPRED: SIF-Syn:

/note=Multiple 1:1 Blast Matches. Calling NKF, got good HHPred matches but those relate to eukaryotic cells therefore I am calling NKF. Everything suggest we use the suggested start site.

CDS complement (25743 - 27311)

/gene="35"

/product="gp35"

/function="serine integrase"

/locus tag="TinyPebbles_35"

/note=Original Glimmer call @bp 27311 has strength 9.51; Genemark calls start at 27311

/note=SSC: 27311-25743 CP: yes SCS: both ST: NI BLAST-Start: [integrase [Mycobacterium phage Spike509]],,NCBI, q1:s1 100.0% 0.0 GAP: 92 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.666, -6.817610668516407, no F: serine integrase SIF-BLAST: ,, [integrase [Mycobacterium phage Spike509]],,AJA41819,100.0,0.0 SIF-HHPRED: INTEGRASE; HYDROLASE, SERINE RECOMBINASE, UNIDIRECTIONAL, SITE-SPECIFIC RECOMBINATION; 2.15A {STREPTOMYCES PHAGE PHIC31},,,4BQQ_B,63.6015,100.0 SIF-Syn:

/note=Captures all coding potential. Gap is 92, and the SD score is -6.818 (but not the best SD score). HHPRED and NCBI BLAST have 100 probability of it being an integrase. 1:1 BLAST matches

CDS 27404 - 27835

/gene="36"

/product="gp36"

/function="hypothetical protein"

/locus tag="TinyPebbles_36"

/note=Original Glimmer call @bp 27404 has strength 4.57; Genemark calls start at 27398

/note=SSC: 27404-27835 CP: yes SCS: both-gl ST: SS BLAST-Start:
[excisionase [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 1.4138E-91
GAP: 92 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.206, -
2.58321678164666, yes F: hypothetical protein SIF-BLAST: ,, [excisionase
[Mycobacterium phage Bxz2]],,NP_817624,100.0,1.4138E-91 SIF-HHPRED:
DUF2637 ; Protein of unknown function (DUF2637),,,PF10935.13,77.6224,99.7
SIF-Syn:

/note=Gap is 92 and it is not the LORF. Suggested start. It catches
all coding capacity. Has 1:1 BLAST ratio and a SD score of -2.583 (the
second best SD score). HHPRED has 99.7 probability that it is a protein
of unknown, and most other findings show unknown function.

CDS complement (27917 - 28048)

/gene="37"

/product="gp37"

/function="Hypothetical Protein"

/locus tag="TinyPebbles_37"

/note=Original Glimmer call @bp 28048 has strength 15.83; Genemark
calls start at 28048

/note=SSC: 28048-27917 CP: yes SCS: both ST: SS BLAST-Start:
[hypothetical protein PBI_SPIKE509_38 [Mycobacterium phage Spike509]
],,NCBI, q1:s1 100.0% 6.98278E-20 GAP: 0 bp gap LO: yes RBS: Kibler 6,
Karlin Medium, 2.966, -2.794070146961553, yes F: Hypothetical Protein
SIF-BLAST: ,, [hypothetical protein PBI_SPIKE509_38 [Mycobacterium phage
Spike509]],,AJA41821,100.0,6.98278E-20 SIF-HHPRED: SIF-Syn:

/note=Gap is 0 and the SD score is -2.794 (best SD score). The blast
ratio is 1:1, and catches all the coding capacity. It is the LORF and is
suggested start. NCBI BLAST shows that it is a hypothetical protein,
HHPRED showing poor probabilities.

CDS complement (28049 - 28192)

/gene="38"

/product="gp38"

/function="hypothetical protein"

/locus tag="TinyPebbles_38"

/note=Original Glimmer call @bp 28192 has strength 13.4; Genemark
calls start at 28192

/note=SSC: 28192-28049 CP: yes SCS: both ST: SS BLAST-Start:
[hypothetical protein PBI_METHUSELAH_38 [Mycobacterium phage Methuselah]
],,NCBI, q1:s1 100.0% 1.65864E-23 GAP: 0 bp gap LO: yes RBS: Kibler 6,
Karlin Medium, 2.891, -2.6013996449736907, yes F: hypothetical protein
SIF-BLAST: ,, [hypothetical protein PBI_METHUSELAH_38 [Mycobacterium phage
Methuselah]],,AGK87239,100.0,1.65864E-23 SIF-HHPRED: SIF-Syn:

/note=Called NKF due to phagesdb function frequency. Start site was
supported by SS starterator, 1:1 BLAST matches with multiples phages and
0 gap, best final score (SD).

CDS complement (28193 - 28576)

/gene="39"

/product="gp39"

/function="deoxycytidylate deaminase"

/locus tag="TinyPebbles_39"

/note=Original Glimmer call @bp 28348 has strength 5.53; Genemark
calls start at 28348

/note=SSC: 28576-28193 CP: yes SCS: both-cs ST: NI BLAST-Start: [dCMP
deaminase [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 2.36761E-86
GAP: 122 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.1, -

3.0637723674875006, yes F: deoxycytidylate deaminase SIF-BLAST: ,, [dCMP deaminase [Mycobacterium phage Bxz2]],, NP_817627, 100.0, 2.36761E-86 SIF-HHPRED: DEOXYCYTIDYLATE DEAMINASE; PYRIMIDINE METABOLISM, NUCLEOTIDE BIOSYNTHESIS, ZINC, HEXAMER, HYDROLASE, METAL-BINDING, PHOSPHOPROTEIN, ALLOSTERIC ENZYME; 2.1A {HOMO SAPIENS} SCOP:

c.97.1.0,,, 2W4L_D, 97.6378, 99.9 SIF-Syn:

/note=The starterator is not informative, we went against the start site due to not reaching full coding potential. There is a 62 count with a 65 percent frequency for deoxycytidylate deaminase.

CDS complement (28699 - 28866)

/gene="40"

/product="gp40"

/function="hypothetical protein"

/locus tag="TinyPebbles_40"

/note=Original Glimmer call @bp 28866 has strength 12.66; Genemark calls start at 28866

/note=SSC: 28866-28699 CP: yes SCS: both ST: SS BLAST-Start:

[hypothetical protein PBI_METHUSELAH_40 [Mycobacterium phage Methuselah]],, NCBI, q1:s1 100.0% 1.72101E-30 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.1, -2.2364030944336752, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_METHUSELAH_40 [Mycobacterium phage Methuselah]],, AGK87241, 100.0, 1.72101E-30 SIF-HHPRED: Uncharacterized lipoprotein YifL; Lipopolysaccharide, Lipoprotein, LptDE, MEMBRANE PROTEIN; HET: PCJ; 2.98A {Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)},, 8H1R_F, 41.8182, 98.2 SIF-Syn:

/note=Called unknown function due to phages db function frequency not calling anything, phages db blast was all unknown. Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and -4 gap, best final score (SD).

CDS complement (28863 - 29102)

/gene="41"

/product="gp41"

/function="hypothetical protein"

/locus tag="TinyPebbles_41"

/note=Original Glimmer call @bp 29102 has strength 6.23; Genemark calls start at 29102

/note=SSC: 29102-28863 CP: yes SCS: both ST: SS BLAST-Start:

[hypothetical protein PBI_BXZ2_39 [Mycobacterium phage Bxz2]],, NCBI, q1:s1 100.0% 1.97025E-51 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.418, -3.6723131374959377, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_39 [Mycobacterium phage Bxz2]],, NP_817628, 100.0, 1.97025E-51 SIF-HHPRED: SIF-Syn:

/note=The gap is -8 and it. Suggested start. It catches all coding capacity. no known function

CDS complement (29095 - 29493)

/gene="42"

/product="gp42"

/function="hypothetical protein"

/locus tag="TinyPebbles_42"

/note=Original Glimmer call @bp 29493 has strength 11.64; Genemark calls start at 29493

/note=SSC: 29493-29095 CP: yes SCS: both ST: SS BLAST-Start:

[hypothetical protein PBI_BXZ2_40 [Mycobacterium phage Bxz2]],, NCBI,

q1:s1 100.0% 5.52004E-90 GAP: -14 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.195, -2.0162541296952132, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_40 [Mycobacterium phage Bxz2]],,,NP_817629,100.0,5.52004E-90 SIF-HHPRED: Cep57_CLD_2 ; Centrosome localisation domain of PPC89,,,PF14197.11,43.9394,96.1 SIF-Syn:

/note=Called NKF due to phagesdb function frequency not suggesting anything and Phages db blast was unknown for all suggested. Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and -14 gap, best final score (SD).

CDS complement (29480 - 29665)

/gene="43"

/product="gp43"

/function="hypothetical protein"

/locus tag="TinyPebbles_43"

/note=Original Glimmer call @bp 29665 has strength 13.97; Genemark calls start at 29665

/note=SSC: 29665-29480 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA_BUZZBUZZ_43 [Mycobacterium phage BuzzBuzz]],,,NCBI, q1:s1 100.0% 1.28171E-35 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.013, -4.553144366458975, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein SEA_BUZZBUZZ_43 [Mycobacterium phage BuzzBuzz]],,,ANU79378,100.0,1.28171E-35 SIF-HHPRED: SIF-Syn:

/note=All coding capacity captured, starterator suggested start, -1 gap, 1:1 NCBI match for hypothetical protein, BLAST matches for unknown function

CDS complement (29665 - 29859)

/gene="44"

/product="gp44"

/function="hypothetical protein"

/locus tag="TinyPebbles_44"

/note=Original Glimmer call @bp 29859 has strength 17.1; Genemark calls start at 29859

/note=SSC: 29859-29665 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_42 [Mycobacterium phage Bxz2]],,,NCBI, q1:s1 100.0% 3.90772E-36 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.966, -2.523003374675015, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_42 [Mycobacterium phage Bxz2]],,,NP_817631,100.0,3.90772E-36 SIF-HHPRED: CELL DIVISION PROTEIN ZAPB; FTSZ, SEPTUM, COILED-COIL, CELL DIVISION, CELL CYCLE, HYPOTHETICAL PROTEIN; 2.8A {ESCHERICHIA COLI},,,2JEE_B,96.875,96.2 SIF-Syn:

/note=GeneMark and Glimmer agree. Best SD Score and longest ORF. SS was 7. Function unknown, cell division protein? 1:1 match with Bxz2. All coding potential.

CDS complement (29859 - 30041)

/gene="45"

/product="gp45"

/function="hypothetical protein"

/locus tag="TinyPebbles_45"

/note=Original Glimmer call @bp 30041 has strength 7.65; Genemark calls start at 30041

/note=SSC: 30041-29859 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_43 [Mycobacterium phage Bxz2]],,,NCBI, q1:s1 100.0% 3.28742E-35 GAP: 30 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.949, -3.5288488554554966, yes F: hypothetical protein SIF-

BLAST: ,, [hypothetical protein PBI_BXZ2_43 [Mycobacterium phage Bxz2]],, NP_817632, 100.0, 3.28742E-35 SIF-HHPRED: SIF-Syn:
 /note=SS was 2. Longest ORF and best SD Score. Glimmer and GeneMark agree. Reverse Gene. NKF. 1:1 match with Bxz2
 CDS complement (30072 - 31886)
 /gene="46"
 /product="gp46"
 /function="DNA polymerase I"
 /locus tag="TinyPebbles_46"
 /note=Original Glimmer call @bp 31886 has strength 13.56; Genemark calls start at 31886
 /note=SSC: 31886-30072 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_44 [Mycobacterium phage Bxz2]],, NCBI, q1:s1 100.0% 0.0 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.082, -4.325675514574479, no F: DNA polymerase I SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_44 [Mycobacterium phage Bxz2]],, NP_817633, 100.0, 0.0 SIF-HHPRED: Apicoplast DNA polymerase; DNA polymerase, exonuclease, apicoplast, Plasmodium falciparum, REPLICATION, TRANSFERASE; HET: EDO, PEG; 2.5A {Plasmodium falciparum (isolate 3D7)},,, 7SXQ_A, 97.6821, 100.0 SIF-Syn:
 /note=Longest ORF but not longest SD score. Glimmer and GeneMark agree on 31,886 start. This is a reverse gene. Stop is 30,072. Suggested start is 248. All coding potential encoded. 1:1 match with Methuselah, DNA polymerase I.
 CDS complement (31896 - 32084)
 /gene="47"
 /product="gp47"
 /function="hypothetical protein"
 /locus tag="TinyPebbles_47"
 /note=Original Glimmer call @bp 32084 has strength 12.07; Genemark calls start at 32084
 /note=SSC: 32084-31896 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_45 [Mycobacterium phage Bxz2]],, NCBI, q1:s1 100.0% 2.0081E-36 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.311, -3.9166971242758706, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_45 [Mycobacterium phage Bxz2]],, NP_817634, 100.0, 2.0081E-36 SIF-HHPRED: SIF-Syn:
 /note=Longest ORF, covers all coding potential. 1:1 NCBI Blast - hypothetical proteins - Bxz2. Starterator suggested start site. NKF
 CDS complement (32093 - 32341)
 /gene="48"
 /product="gp48"
 /function="helix-turn-helix DNA binding domain"
 /locus tag="TinyPebbles_48"
 /note=Original Glimmer call @bp 32341 has strength 11.35; Genemark calls start at 32341
 /note=SSC: 32341-32093 CP: yes SCS: both ST: NI BLAST-Start: [HTH DNA binding protein [Mycobacterium phage Bxz2]],, NCBI, q1:s1 100.0% 4.60199E-52 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.814, -3.4175091270247986, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,, [HTH DNA binding protein [Mycobacterium phage Bxz2]],, NP_817635, 100.0, 4.60199E-52 SIF-HHPRED: SIF-Syn:

/note=not suggested start site in starterator - not informative, best SD score, 1:1 NCBI matches for HTH binding domain protein, BLAST matches for HTH binding domain

CDS complement (32334 - 32522)

/gene="49"

/product="gp49"

/function="hypothetical protein"

/locus tag="TinyPebbles_49"

/note=Original Glimmer call @bp 32522 has strength 15.75; Genemark calls start at 32522

/note=SSC: 32522-32334 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_47 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 8.24723E-37 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.949, -3.30700010583914, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_47 [Mycobacterium phage Bxz2]],,NP_817636,100.0,8.24723E-37 SIF-HHPRED: SIF-Syn:

/note=starterator suggested start, longest ORF, NCBI 1:1 matches for hypothetical protein, BLAST matches for function unknown. Some call lipoprotein but only called in 5 phages. Best SD score

CDS complement (32532 - 33239)

/gene="50"

/product="gp50"

/function="ThyX-like thymidylate synthase"

/locus tag="TinyPebbles_50"

/note=Original Glimmer call @bp 33239 has strength 11.16; Genemark calls start at 33239

/note=SSC: 33239-32532 CP: yes SCS: both ST: SS BLAST-Start: [thymidylate synthase [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 4.66576E-172 GAP: 59 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.544, -3.8690725721777643, yes F: ThyX-like thymidylate synthase SIF-BLAST: ,, [thymidylate synthase [Mycobacterium phage Bxz2]],,NP_817637,100.0,4.66576E-172 SIF-HHPRED: Thymidylate synthase thyX; ThyX, thymidylate synthase, FAD, Flavoprotein, Methyltransferase, Nucleotide biosynthesis, Transferase; HET: FAD; 2.3A {Corynebacterium glutamicum},,,3FNN_A,97.4468,100.0 SIF-Syn:

/note=Glimmer and GeneMark agreed start: 33,239 and stop 32,532, all coding potential is covered, longest ORF, best SD score, 59 base pair gap, starterator results are the suggested start, NCBI 1:1 blast match, HHpred evidence collected for Thymidylate synthase.

CDS complement (33299 - 33886)

/gene="51"

/product="gp51"

/function="hypothetical protein"

/locus tag="TinyPebbles_51"

/note=Original Glimmer call @bp 33886 has strength 10.97; Genemark calls start at 33886

/note=SSC: 33886-33299 CP: no SCS: both ST: NI BLAST-Start: [hypothetical protein PBI_METHUSELAH_49 [Mycobacterium phage Methuselah]],,NCBI, q1:s1 100.0% 1.22922E-139 GAP: 31 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.695, -3.6716023243868, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_METHUSELAH_49 [Mycobacterium phage Methuselah]],,AGK87250,100.0,1.22922E-139 SIF-HHPRED: SIF-Syn:

/note=Glimmer and GeneMark agreed start 33886 and 33299 stop, 31 base pair gap, longest ORF, not the best SD score, not all coding potential

was covered, starterator results are non-informative, NCBI blast match 1:1 for a hypothetical protein, HHpred results show a less than 90% probability therefore no evidence was collected.

CDS complement (33918 - 35936)

/gene="52"

/product="gp52"

/function="ribonucleotide reductase"

/locus tag="TinyPebbles_52"

/note=Original Glimmer call @bp 35936 has strength 10.99; Genemark calls start at 35936

/note=SSC: 35936-33918 CP: yes SCS: both ST: NI BLAST-Start: [ribonucleotide reductase [Mycobacterium phage Methuselah]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.044, -2.8035499123971284, yes F: ribonucleotide reductase SIF-BLAST: ,, [ribonucleotide reductase [Mycobacterium phage Methuselah]],,AGK87251,100.0,0.0 SIF-HHPRED: RIBONUCLEOSIDE TRIPHOSPHATE REDUCTASE; 10-stranded alpha-beta barrel, central finger loop, OXIDOREDUCTASE; 1.75A {Lactobacillus leichmannii} SCOP: c.7.1.4,,,1L1L_B,99.8512,100.0 SIF-Syn:

/note=Glimmer and GeneMark start agree: 35,936 and 33918 stop, reverse gene, longest ORF, 4 base pair overlap, best SD, starterator results are non-informative, NCBI blast 1:1, HHpred suggests ribonucleoside triphosphate reductase.

CDS complement (35933 - 36139)

/gene="53"

/product="gp53"

/function="hypothetical protein"

/locus tag="TinyPebbles_53"

/note=Original Glimmer call @bp 36139 has strength 17.44; Genemark calls start at 36139

/note=SSC: 36139-35933 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI_BXZ2_51 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 5.23528E-43 GAP: -11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.814, -2.827683592113848, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_51 [Mycobacterium phage Bxz2]],,NP_817640,100.0,5.23528E-43 SIF-HHPRED: GP52 ; Phage gene product 52,,,PF17468.7,88.2353,100.0 SIF-Syn:

/note=Multiple 1:1 BLAST matches. Start site has a -11 overlap but has great SD score has ATG start codon, and has longest ORF therefore I called this the correct start site. Calling NKF because nothing has been called, has a 100% phage gene product hit from HHpred but clicking the link, it states its a family of NKF of genes found in mycobacterium.

CDS complement (36129 - 36242)

/gene="54"

/product="gp54"

/function="hypothetical protein"

/locus tag="TinyPebbles_54"

/note=Original Glimmer call @bp 36242 has strength 13.04; Genemark calls start at 36242

/note=SSC: 36242-36129 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein AVV34_gp44 [Mycobacterium phage MarQuardt]],,NCBI, q1:s1 100.0% 3.85742E-17 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.966, -2.583959800616441, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein AVV34_gp44 [Mycobacterium phage MarQuardt]

] , , YP_009198481, 100.0, 3.85742E-17 SIF-HHPRED: YL1_C ; YL1 nuclear protein C-terminal domain, , , PF08265.16, 37.8378, 74.2 SIF-Syn:

/note=Multiple 1:1 BLAST matches. Calling NKF because there is not any leads on any function. Low HHPred matches. Start site is perfect as it has -4 overlap with great SD score though it is not the longest ORF, it still captures all coding potential.

CDS complement (36239 - 36961)

/gene="55"

/product="gp55"

/function="DNA binding protein"

/locus tag="TinyPebbles_55"

/note=Original Glimmer call @bp 36961 has strength 12.86; Genemark calls start at 36961

/note=SSC: 36961-36239 CP: yes SCS: both ST: SS BLAST-Start: [DNA binding protein [Mycobacterium phage Rummer]] , , NCBI, q1:s1 100.0% 4.65919E-167 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.916, - 4.679270584912496, no F: DNA binding protein SIF-BLAST: , , [DNA binding protein [Mycobacterium phage Rummer]] , , WPH58629, 98.3333, 4.65919E-167 SIF-HHPRED: RNA polymerase sigma factor; sigma factor, Streptomyces, transcription, ECF56; HET: GOL; 2.2A {Streptomyces tsukubensis NRRL18488} , , , 7QH5_B, 75.0, 99.5 SIF-Syn:

/note=Gap is 3 and it is the LORF. Has the best SD score of -4.679, and catches all the coding potential . Suggested start and has a NCBI BLAST ratio of 1:1. HHPRED and NCBI BLAST have high probability of it being a RNA polymerase sigma factor (99.5). There is not enough information to call it RNA polymerase sigma factor, so it is concluded that this is a DNA binding protein.

CDS complement (36965 - 37732)

/gene="56"

/product="gp56"

/function="metallophosphatase"

/locus tag="TinyPebbles_56"

/note=Original Glimmer call @bp 37732 has strength 14.43; Genemark calls start at 37732

/note=SSC: 37732-36965 CP: yes SCS: both ST: NI BLAST-Start: [metallo-phosphoesterase [Mycobacterium phage Bxz2]] , , NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.907, - 4.7784408226142965, no F: metallophosphatase SIF-BLAST: , , [metallo-phosphoesterase [Mycobacterium phage Bxz2]] , , NP_817643, 100.0, 0.0 SIF-HHPRED: SIF-Syn:

/note=Gap is -4 and it is the LORF. The SD score is the second best at -4.778. Captures all the coding potential and is not informative. The NCBI BLAST match is 1:1 and NCBI BLAST also shows that is most likely metallophosphoesterase at a 100% identity probability.

CDS complement (37729 - 38022)

/gene="57"

/product="gp57"

/function="hypothetical protein"

/locus tag="TinyPebbles_57"

/note=Original Glimmer call @bp 38022 has strength 12.03; Genemark calls start at 38022

/note=SSC: 38022-37729 CP: yes SCS: both ST: SS BLAST-Start: [phosphofructokinase [Mycobacterium phage Bxz2]] , , NCBI, q1:s1 100.0% 7.78285E-65 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.371, -

4.236320103611762, yes F: hypothetical protein SIF-BLAST:
 ,, [phosphofructokinase [Mycobacterium phage Bxz2]
],,, NP_817644,100.0,7.78285E-65 SIF-HHPRED: SIF-Syn:
 /note=Calling NKF. Have good HHPred hits but coverages are low so NKF
 seems appropriate. Start site is good and has multiple 1:1 BLAST matches.
 Nothing truly indicating its proper function.
 CDS complement (38019 - 38183)
 /gene="58"
 /product="gp58"
 /function="hypothetical protein"
 /locus tag="TinyPebbles_58"
 /note=Original Glimmer call @bp 38183 has strength 16.58; Genemark
 calls start at 38183
 /note=SSC: 38183-38019 CP: yes SCS: both ST: SS BLAST-Start:
 [hypothetical protein AVV34_gp40 [Mycobacterium phage MarQuardt]],,,NCBI,
 q1:s1 100.0% 3.96028E-30 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin
 Medium, 2.486, -3.5445441946970573, yes F: hypothetical protein SIF-
 BLAST: ,, [hypothetical protein AVV34_gp40 [Mycobacterium phage MarQuardt]
],,, YP_009198485,100.0,3.96028E-30 SIF-HHPRED: SIF-Syn:
 /note=Called unknown function due to phages db function frequency
 having no call, phages db blast was all unknown. Start site was supported
 by SS starterator, 1:1 BLAST matches with multiples phages and -4 gap,
 best final score (SD). HHPred had no notable evidence.
 CDS complement (38180 - 38272)
 /gene="59"
 /product="gp59"
 /function="hypothetical protein"
 /locus tag="TinyPebbles_59"
 /note=Genemark calls start at 38272
 /note=SSC: 38272-38180 CP: yes SCS: genemark ST: SS BLAST-Start:
 [hypothetical protein AVV34_gp39 [Mycobacterium phage MarQuardt]],,,NCBI,
 q1:s1 100.0% 2.49173E-12 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin
 Medium, 2.9, -3.4105598537121566, yes F: hypothetical protein SIF-BLAST:
 ,, [hypothetical protein AVV34_gp39 [Mycobacterium phage MarQuardt]
],,, YP_009198486,100.0,2.49173E-12 SIF-HHPRED: SIF-Syn:
 /note=Glimmer did not call this gene. Length of 94 with an overlap of
 -4. Covers coding potential. Has 1:1 match
 CDS complement (38269 - 38928)
 /gene="60"
 /product="gp60"
 /function="DNA primase"
 /locus tag="TinyPebbles_60"
 /note=Original Glimmer call @bp 38928 has strength 11.62; Genemark
 calls start at 38835
 /note=SSC: 38928-38269 CP: yes SCS: both-gl ST: NI BLAST-Start: [DNA
 primase [Mycobacterium phage Jobu08]],,,NCBI, q1:s1 100.0% 1.18645E-160
 GAP: -185 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.121, -
 2.7645180226256008, yes F: DNA primase SIF-BLAST: ,, [DNA primase
 [Mycobacterium phage Jobu08]],,, YP_008126298,100.0,1.18645E-160 SIF-
 HHPRED: DNA primase; structural genomics, DNA-binding, primase,
 truncation, Seattle Structural Genomics Center for Infectious Disease,
 SSGCID, TRANSFERASE; HET: SO4; 2.4A {Pseudomonas aeruginosa (strain ATCC
 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 /
 PAO1)} SCOP: e.13.1.0,,,5VAZ_B,97.2603,99.8 SIF-Syn:

/note=Called DNA Primase due to phages db function frequency having multiple count of DNA Primase, phages db blast was also calling similar. Start site was glimmer supported best, 1:1 BLAST matches with multiples phages and very large overlap, after added second DNA primase based on other A3 phages, best final score (SD).
CDS complement (38744 - 39151)
/gene="61"
/product="gp61"
/function="DNA primase"
/locus tag="TinyPebbles_61"
/note=
/note=SSC: 39151-38744 CP: yes SCS: neither ST: NI BLAST-Start: [DNA primase [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 2.10934E-94 GAP: 23 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.653, - 3.635743271219807, no F: DNA primase SIF-BLAST: ,, [DNA primase [Mycobacterium phage Bxz2]],,NP_817647,100.0,2.10934E-94 SIF-HHPRED: DNA primase; Zinc Ribbon, TOPRIM, RNA POLYMERASE, DNA REPLICATION, TRANSFERASE; 2.0A {Aquifex aeolicus},,,2AU3_A,63.7037,98.9 SIF-Syn:
/note=Gene not called by Glimmer or Genemark. Added due to large gap, presence of coding potential in the gap, and presence in closely related A3 phages. 1:1 BLAST match with multiple phages. DNA primase function called based on HHPRED and presence in most A3 phages.
CDS complement (39175 - 39651)
/gene="62"
/product="gp62"
/function="endonuclease VII"
/locus tag="TinyPebbles_62"
/note=Original Glimmer call @bp 39651 has strength 6.28; Genemark calls start at 39651
/note=SSC: 39651-39175 CP: yes SCS: both ST: SS BLAST-Start: [endonuclease VII [Mycobacterium phage BuzzBuzz]],,NCBI, q1:s1 100.0% 1.75651E-113 GAP: -20 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.476, -3.5660483139923818, yes F: endonuclease VII SIF-BLAST: ,, [endonuclease VII [Mycobacterium phage BuzzBuzz]],,ANU79395,100.0,1.75651E-113 SIF-HHPRED: Restriction endonuclease Hpy99I; ENDONUCLEASE-DNA COMPLEX, RESTRICTION ENZYME, HPY99I, PSEUDOPALINDROME, HYDROLASE-DNA COMPLEX; HET: 1PE; 1.5A {Helicobacter pylori},,,3GOX_B,82.2785,99.8 SIF-Syn:
/note=Covers coding potential. 477 length with a large overlap of 20 bp. Smaller SD score. 1:1 BLAST match
CDS complement (39632 - 39736)
/gene="63"
/product="gp63"
/function="hypothetical protein"
/locus tag="TinyPebbles_63"
/note=Genemark calls start at 39736
/note=SSC: 39736-39632 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA_LOUIE6_64 [Mycobacterium phage Louie6]],,NCBI, q1:s1 100.0% 1.09354E-15 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.071, -4.429150775994987, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein SEA_LOUIE6_64 [Mycobacterium phage Louie6]],,AOZ64834,100.0,1.09354E-15 SIF-HHPRED: SIF-Syn:
/note=Called unknown function due to phages db function frequency having 0 count of a call on protein, phages db blast was all unknown.

Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and 1 gap, best final score (SD).

CDS complement (39733 - 40557)

/gene="64"

/product="gp64"

/function="hydrolase"

/locus tag="TinyPebbles_64"

/note=Original Glimmer call @bp 40557 has strength 11.34; Genemark calls start at 40557

/note=SSC: 40557-39733 CP: yes SCS: both ST: SS BLAST-Start: [esterase [Mycobacterium phage Louie6]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.272, -4.060971128237648, no F: hydrolase SIF-BLAST: ,, [esterase [Mycobacterium phage Louie6]],,AOZ64835,100.0,0.0 SIF-HHPRED: ESTERASE; HYDROLASE, ALPHA BETA HYDROLASE; 1.03A {PLANCTOMYCETES BACTERIUM R1} SCOP: 1.1.1.1, c.69.1.0,,,4UHC_A,93.4307,100.0 SIF-Syn:

/note=Glimmer and GeneMark agree on 40,557 start. Reverse gene. Not the longest ORF but the best SD score. Suggested start is 35. -4 gap! hydrolase or esterlase. 1:1 match with KADY.

CDS complement (40554 - 40973)

/gene="65"

/product="gp65"

/function="hypothetical protein"

/locus tag="TinyPebbles_65"

/note=Original Glimmer call @bp 40973 has strength 9.8; Genemark calls start at 40964

/note=SSC: 40973-40554 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA_KADY_66 [Mycobacterium phage KADY]],,NCBI, q1:s1 100.0% 3.85456E-97 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.077, -4.336252278353151, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein SEA_KADY_66 [Mycobacterium phage KADY]],,ASM62483,100.0,3.85456E-97 SIF-HHPRED: mSLOG ; Minimal SLOG domain,,,PF22565.1,89.2086,99.8 SIF-Syn:

/note=Glimmer and GeneMark do not have an agreed start site (40973 and 40964), but going with the glimmer start due to the base pair overlap of 4, all coding potential is covered, not the longest ORF, NCBI 1:1 blast match, HHpred results show a hypothetical protein, calling no known function due to the low probability of DNA processing chain A

CDS complement (40970 - 41227)

/gene="66"

/product="gp66"

/function="hypothetical protein"

/locus tag="TinyPebbles_66"

/note=Original Glimmer call @bp 41200 has strength 13.28; Genemark calls start at 41200

/note=SSC: 41227-40970 CP: yes SCS: both-cs ST: NI BLAST-Start: [hypothetical protein AVV42_gp34 [Mycobacterium phage Anubis]],,NCBI, q1:s1 100.0% 1.55735E-54 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.535, -5.841922269023699, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein AVV42_gp34 [Mycobacterium phage Anubis]],,YP_009219130,100.0,1.55735E-54 SIF-HHPRED: GP63 ; Gene product 63,,,PF17471.7,83.5294,100.0 SIF-Syn:

/note=Changed the start site. Suggested start not matched. All coding potential. NKF, gene product. -4 BP overlap (perfect). LORF, but not the best SD Score. 1:1 BLAST match with multiple phages
CDS complement (41224 - 42033)

/gene="67"

/product="gp67"

/function="DnaB-like dsDNA helicase"

/locus tag="TinyPebbles_67"

/note=Original Glimmer call @bp 42033 has strength 15.49; Genemark calls start at 42012

/note=SSC: 42033-41224 CP: yes SCS: both-gl ST: NI BLAST-Start: [DnaB-like dsDNA helicase [Mycobacterium phage BuzzBuzz]],,NCBI, ql:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.107, -4.351233803319953, no F: DnaB-like dsDNA helicase SIF-BLAST: ,, [DnaB-like dsDNA helicase [Mycobacterium phage BuzzBuzz]],,ANU79399,100.0,0.0 SIF-HHPRED: Replicative DNA helicase; Helicase, DnaB, Helicase loader protein, DnaC, Structural Genomics, REPLICATION, HYDROLASE; 3.1A {Escherichia coli},,,6KZA_B,94.4238,100.0 SIF-Syn:

/note=Not suggested start in starterator, 1:1 matches in NCBI, 100% HHPRED match for replicative DNA helicase, other phages listed as DnaB-like dsDNA helicase

CDS complement (42033 - 42107)

/gene="68"

/product="gp68"

/function="hypothetical protein"

/locus tag="TinyPebbles_68"

/note=

/note=SSC: 42107-42033 CP: no SCS: neither ST: NI BLAST-Start: [hypothetical protein SEA_LOUIE6_69 [Mycobacterium phage Louie6]],,NCBI, ql:s1 100.0% 2.36226E-5 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.399, -3.790975366313636, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein SEA_LOUIE6_69 [Mycobacterium phage Louie6]],,AOZ64838,100.0,2.36226E-5 SIF-HHPRED: SIF-Syn:

/note=Gene not called by Glimmer or Genemark. Added due to gap, small amount of coding potential, 4 BP overlap and presence in other A3 phages. 1:1 BLAST matches

CDS complement (42104 - 42166)

/gene="69"

/product="gp69"

/function="hypothetical protein"

/locus tag="TinyPebbles_69"

/note=

/note=SSC: 42166-42104 CP: yes SCS: neither ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_66 [Mycobacterium phage Bxz2]],,NCBI, ql:s1 100.0% 1.11696E-4 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.409, -3.628472733356124, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_66 [Mycobacterium phage Bxz2]],,NP_817655,100.0,1.11696E-4 SIF-HHPRED: SIF-Syn:

/note=Gene not called by Glimmer or Genemark. Added due to gap, small amount of coding potential, 4 BP overlap and presence in other A3 phages. 1:1 BLAST matches

CDS complement (42163 - 42471)

/gene="70"

/product="gp70"

```

/function="helix-turn-helix DNA binding domain"
/locus tag="TinyPebbles_70"
/note=Original Glimmer call @bp 42417 has strength 15.46; Genemark
calls start at 42417
/note=SSC: 42471-42163 CP: yes SCS: both-cs ST: NI BLAST-Start:
[hypothetical protein SEA_LOUIE6_71 [Mycobacterium phage Louie6] ],,NCBI,
q1:s1 100.0% 1.09665E-68 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin
Medium, 2.814, -2.9063687850157054, yes F: helix-turn-helix DNA binding
domain SIF-BLAST: ,, [hypothetical protein SEA_LOUIE6_71 [Mycobacterium
phage Louie6] ],,AOZ64840,100.0,1.09665E-68 SIF-HHPRED: SIF-Syn:
/note=Best SD but not longest ORF. Glimmer and GeneMark agree. -4 BP
overlap. Not the Original selected gene because this one was better. 1:1
match with Louie6.
CDS complement (42468 - 42662)
/gene="71"
/product="gp71"
/function="hypothetical protein"
/locus tag="TinyPebbles_71"
/note=Original Glimmer call @bp 42662 has strength 11.72; Genemark
calls start at 42662
/note=SSC: 42662-42468 CP: yes SCS: both ST: SS BLAST-Start:
[hypothetical protein KIJ58_gp28 [Mycobacterium phage SoilDragon]
],,NCBI, q1:s1 100.0% 6.39167E-39 GAP: -4 bp gap LO: no RBS: Kibler 6,
Karlin Medium, 2.966, -2.523003374675015, yes F: hypothetical protein
SIF-BLAST: ,, [hypothetical protein KIJ58_gp28 [Mycobacterium phage
SoilDragon] ],,YP_010060113,100.0,6.39167E-39 SIF-HHPRED: SIF-Syn:
/note=-4 gap, best SD score, all coding potential covered,
starterator suggested start, 1:1 NCBI matches for hypothetical protein,
phagesdb blast all call no known function
CDS complement (42659 - 42874)
/gene="72"
/product="gp72"
/function="hypothetical protein"
/locus tag="TinyPebbles_72"
/note=Original Glimmer call @bp 42871 has strength 12.59; Genemark
calls start at 42871
/note=SSC: 42874-42659 CP: yes SCS: both-cs ST: NI BLAST-Start:
[hypothetical protein SEA_BUZZBUZZ_68 [Mycobacterium phage BuzzBuzz]
],,NCBI, q1:s1 100.0% 2.36052E-45 GAP: -4 bp gap LO: yes RBS: Kibler 6,
Karlin Medium, 1.936, -5.738304291908741, no F: hypothetical protein SIF-
BLAST: ,, [hypothetical protein SEA_BUZZBUZZ_68 [Mycobacterium phage
BuzzBuzz] ],,ANU79402,100.0,2.36052E-45 SIF-HHPRED: DUF2188 ;
Uncharacterized protein conserved in bacteria
(DUF2188),,,PF09954.14,45.0704,95.5 SIF-Syn:
/note=Change start site to 42874, best SD score, -4 bp overlap, not
suggested start in starterator. 1:1 NCBI matches for hypothetical
proteins, phages db blast all match for unknown function, 95% HHPRED
probability for uncharacterized protein
CDS complement (42871 - 43098)
/gene="73"
/product="gp73"
/function="hypothetical protein"
/locus tag="TinyPebbles_73"

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/note=Original Glimmer call @bp 43098 has strength 11.63; Genemark calls start at 43098

/note=SSC: 43098-42871 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI_BXZ2_70 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 7.90373E-47 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.206, -2.0111200136961407, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_70 [Mycobacterium phage Bxz2]],,NP_817659,100.0,7.90373E-47 SIF-HHPRED: SIF-Syn:

/note=Glimmer and GeneMark start site 43,098 and stop 42,871, covers all coding potential, longest ORF, best SD score, 4 base pair overlap, no blast match, NI starterator, NKF

CDS complement (43095 - 43235)

/gene="74"

/product="gp74"

/function="hypothetical protein"

/locus tag="TinyPebbles_74"

/note=Original Glimmer call @bp 43235 has strength 10.38; Genemark calls start at 43235

/note=SSC: 43235-43095 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein KIJ58_gp25 [Mycobacterium phage SoilDragon]],,NCBI, q1:s9 100.0% 4.07662E-23 GAP: 28 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.966, -2.442961286954254, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein KIJ58_gp25 [Mycobacterium phage SoilDragon]],,YP_010060116,85.1852,4.07662E-23 SIF-HHPRED: SIF-Syn:

/note=Glimmer and GeneMark start site 43235 and stop 43095, all coding potential is covered, best SD score, 28 base pair gap, longest ORF, starterator results are suggested start, NCBI no blast match, HHpred does not have data with a high probability to call a function, thus NKF is called.

CDS complement (43264 - 44079)

/gene="75"

/product="gp75"

/function="Cas4 exonuclease"

/locus tag="TinyPebbles_75"

/note=Original Glimmer call @bp 44079 has strength 10.87; Genemark calls start at 44079

/note=SSC: 44079-43264 CP: yes SCS: both ST: NI BLAST-Start: [Cas4 exonuclease [Mycobacterium phage BuzzBuzz]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.966, -2.583959800616441, yes F: Cas4 exonuclease SIF-BLAST: ,, [Cas4 exonuclease [Mycobacterium phage BuzzBuzz]],,ANU79405,100.0,0.0 SIF-HHPRED: Cas4_I-A; CRISPR/Cas system-associated protein Cas4. CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) and associated Cas proteins comprise a system for heritable host defense by prokaryotic cells against phage and other foreign DNA.,,cd09659,96.679,99.9 SIF-Syn:

/note=Glimmer and GeneMark start site 44079 and stop 43264, all coding potential is covered, best SD score, 4 base pair overlap, not the longest ORF, starterator results are not informative, NCBI 1:1 blast match, HHpred Cas system-associated protein Cas4.

CDS complement (44076 - 44510)

/gene="76"

/product="gp76"

/function="hypothetical protein"

/locus tag="TinyPebbles_76"

/note=Original Glimmer call @bp 44510 has strength 7.35; Genemark calls start at 44378

/note=SSC: 44510-44076 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA_BUZZBUZZ_72 [Mycobacterium phage BuzzBuzz]],,NCBI, q1:s1 100.0% 1.78094E-100 GAP: 15 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.465, -3.50848394673489, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein SEA_BUZZBUZZ_72 [Mycobacterium phage BuzzBuzz]],,ANU79406,100.0,1.78094E-100 SIF-HHPRED: GP70 ; Gene product 70,,,PF17429.7,35.4167,99.8 SIF-Syn:

/note=Calling NKF, Glimmer and genestart do not agree but Glimmer is correct. Glimmer start site uses the suggested start site, has a smaller gap, uses the longest ORF and captures all the coding potential.

/note=Multiple 1:1 BLAST matches. HHPred has 99% with a hypothetical protein and every other call has been NFK therefore I am calling NKF. CDS complement (44526 - 45035)

/gene="77"

/product="gp77"

/function="immunity repressor"

/locus tag="TinyPebbles_77"

/note=Original Glimmer call @bp 45035 has strength 6.97; Genemark calls start at 45071

/note=SSC: 45035-44526 CP: yes SCS: both-gl ST: NI BLAST-Start: [immunity repressor [Mycobacterium phage KADY]],,NCBI, q1:s1 100.0% 1.59166E-119 GAP: 360 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.629, -4.068367735406665, no F: immunity repressor SIF-BLAST: ,, [immunity repressor [Mycobacterium phage KADY]],,ASM62493,100.0,1.59166E-119 SIF-HHPRED: Immunity repressor; Immunity repressor, helix-turn-helix motif, DNA binding protein, GENE REGULATION, GENE REGULATION-DNA complex; HET: MSE; 2.79A {Mycobacterium phage TopsytheTRex},,,7TZ1_A,94.0828,100.0 SIF-Syn:

/note=Calling immunity repressor. Inclined to stick with glimmer start thought it does not appear in the starterator report. There is a big gap. Inclined to use glimmer start because of the common ATG start codon. Multiple 1:1 BLAST matches. HHPred has 100% match with an immunity repressor. Many PhagesDB matches have called for Immunity Repressor. CDS complement (45396 - 45659)

/gene="78"

/product="gp78"

/function="hypothetical protein"

/locus tag="TinyPebbles_78"

/note=Original Glimmer call @bp 45659 has strength 3.8; Genemark calls start at 45659

/note=SSC: 45659-45396 CP: yes SCS: both ST: NI BLAST-Start: [site-specific recombination directionality factor RDF [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 3.57982E-57 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.349, -4.66341334897022, no F: hypothetical protein SIF-BLAST: ,, [site-specific recombination directionality factor RDF [Mycobacterium phage Bxz2]],,NP_817664,100.0,3.57982E-57 SIF-HHPRED: SIF-Syn:

/note=Has a gap of -4, and it is not the LORF. HAS a SD score of -4.663 which is the second best SD score. It captures all the coding potential and is non informative. BLAST match has a 1:1 ratio. There are several calls for site-specific recombination directionality factor RDF, but there is not any evidence that supports that call.

CDS complement (45656 - 45835)
 /gene="79"
 /product="gp79"
 /function="hypothetical protein"
 /locus tag="TinyPebbles_79"
 /note=Original Glimmer call @bp 45835 has strength 11.1; Genemark calls start at 45835
 /note=SSC: 45835-45656 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein M611_gp18 [Mycobacterium phage Jobu08]],,NCBI, q1:s1 100.0% 2.61504E-34 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.814, -2.9063687850157054, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein M611_gp18 [Mycobacterium phage Jobu08]],,YP_008126315,100.0,2.61504E-34 SIF-HHPRED: SIF-Syn:
 /note=Gap is 2 and it is the LORF. The SD score is -2.906. BLAST match is a 1:1 ratio. It captures all the coding potential. Pham starterator is suggested start. NCBI BLAST calls for a hypothetical protein, but there is no evidence from Phagesdb BLAST that call for this.
 CDS complement (45838 - 46071)
 /gene="80"
 /product="gp80"
 /function="hypothetical protein"
 /locus tag="TinyPebbles_80"
 /note=Original Glimmer call @bp 46071 has strength 18.08; Genemark calls start at 46071
 /note=SSC: 46071-45838 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_77 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 1.3723E-48 GAP: 1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.544, -3.8690725721777643, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_77 [Mycobacterium phage Bxz2]],,NP_817666,100.0,1.3723E-48 SIF-HHPRED: SIF-Syn:
 /note=Gap is 1 and it is the LORF. Has a SD score of -3.869 (the best given SD score). The NCBI Blast ratio is 1:1. It captures all the coding potential, and the Pham starterator is suggested start. NCBI Blast calls for a hypothetical protein, but there is no found evidence of this call.
 CDS complement (46073 - 46303)
 /gene="81"
 /product="gp81"
 /function="hypothetical protein"
 /locus tag="TinyPebbles_81"
 /note=Original Glimmer call @bp 46303 has strength 10.07; Genemark calls start at 46303
 /note=SSC: 46303-46073 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_78 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 9.93535E-46 GAP: 1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.481, -5.666694514137862, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_78 [Mycobacterium phage Bxz2]],,NP_817667,100.0,9.93535E-46 SIF-HHPRED: TPR_4 ; Tetratricopeptide repeat,,,PF07721.19,25.0,88.2 SIF-Syn:
 /note=Called unknown function due to phages db function frequency having 0 count of a call on protein, phages db blast was all unknown. Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and 1 gap, best final score (SD).
 CDS complement (46305 - 47072)
 /gene="82"

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/product="gp82"
/function="hypothetical protein"
/locus tag="TinyPebbles_82"
  /note=Original Glimmer call @bp 47072 has strength 14.57; Genemark
calls start at 47072
  /note=SSC: 47072-46305 CP: yes SCS: both ST: SS BLAST-Start:
[hypothetical protein PBI_BXZ2_79 [Mycobacterium phage Bxz2] ],,NCBI,
ql:s1 100.0% 0.0 GAP: 96 bp gap LO: no RBS: Kibler 6, Karlin Medium,
2.465, -4.16062280240617, no F: hypothetical protein SIF-BLAST:
,,[hypothetical protein PBI_BXZ2_79 [Mycobacterium phage Bxz2]
],,NP_817668,100.0,0.0 SIF-HHPRED: SIF-Syn:
  /note=1:1 matches, 768 length with a gap of 96, Suggested start site,
Glimmer, and Genemark agree with start sit being 47072. This is a reverse
gene
CDS complement (47169 - 47414)
  /gene="83"
  /product="gp83"
  /function="hypothetical protein"
  /locus tag="TinyPebbles_83"
  /note=Original Glimmer call @bp 47414 has strength 14.0; Genemark
calls start at 47414
  /note=SSC: 47414-47169 CP: yes SCS: both ST: SS BLAST-Start:
[hypothetical protein PBI_BXZ2_80 [Mycobacterium phage Bxz2] ],,NCBI,
ql:s1 100.0% 2.16061E-50 GAP: 17 bp gap LO: yes RBS: Kibler 6, Karlin
Medium, 2.465, -3.649482460397077, no F: hypothetical protein SIF-BLAST:
,,[hypothetical protein PBI_BXZ2_80 [Mycobacterium phage Bxz2]
],,NP_817669,100.0,2.16061E-50 SIF-HHPRED: SIF-Syn:
  /note=Gene has 1:1 blast matches, It has a length of 246 with a gap
of 17. It has full coding potential. The start site is the suggested
start site, Glimmer and Genemark agree on 47414 as the start site.
CDS complement (47432 - 47815)
  /gene="84"
  /product="gp84"
  /function="hypothetical protein"
  /locus tag="TinyPebbles_84"
  /note=Original Glimmer call @bp 47815 has strength 12.57; Genemark
calls start at 47821
  /note=SSC: 47815-47432 CP: yes SCS: both-gl ST: SS BLAST-Start:
[hypothetical protein AVT20_gp14 [Mycobacterium phage Tiffany] ],,NCBI,
ql:s1 100.0% 3.39105E-87 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin
Medium, 2.465, -3.5707972674952195, yes F: hypothetical protein SIF-
BLAST: ,,[hypothetical protein AVT20_gp14 [Mycobacterium phage Tiffany]
],,YP_009195183,100.0,3.39105E-87 SIF-HHPRED: SIF-Syn:
  /note=Called unknown function due to phages db function frequency
having 0 count of a call on protein, phages db blast was all unknown.
Start site was supported by SS starterator, 1:1 BLAST matches with
multiples phages and -4 gap, best final score (SD). Glimmer and genemark
didn't agree but glimmer looked better overall.
CDS complement (47812 - 48027)
  /gene="85"
  /product="gp85"
  /function="hypothetical protein"
  /locus tag="TinyPebbles_85"

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/note=Original Glimmer call @bp 48027 has strength 10.36; Genemark calls start at 48027

/note=SSC: 48027-47812 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_82 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 2.76748E-41 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.465, -3.5707972674952195, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_82 [Mycobacterium phage Bxz2]],,NP_817671,100.0,2.76748E-41 SIF-HHPRED: SIF-Syn:

/note=Called unknown function due to phages phages db blast was all unknown. Start site was supported by SS starterator, 1:1 BLAST matches with multiples phages and 12 gap, best final score (SD). Glimmer and genemark did agree. Called UNknown due to HHpred did not support Phagesdb Function Frequency and Count on the Frequency was low.

CDS complement (48040 - 48198)

/gene="86"

/product="gp86"

/function="hypothetical protein"

/locus tag="TinyPebbles_86"

/note=Original Glimmer call @bp 48198 has strength 8.62; Genemark calls start at 48198

/note=SSC: 48198-48040 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI_BXZ2_83 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 7.75898E-29 GAP: 1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.071, -4.411422009034556, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_83 [Mycobacterium phage Bxz2]],,NP_817672,100.0,7.75898E-29 SIF-HHPRED: DUF5419 ; Family of unknown function (DUF5419),,,PF17441.7,96.1538,99.8 SIF-Syn:

/note=Multiple 1:1 BLAST MATCHES. Everyone calls NKF and I will too but we have an HHpred toxin/antitoxin hit with good coverage. Might have to comeback to review. Start site is agreed but is not informative on Starterator as it does not have the most common annotated start site.

CDS complement (48200 - 48508)

/gene="87"

/product="gp87"

/function="hypothetical protein"

/locus tag="TinyPebbles_87"

/note=Original Glimmer call @bp 48508 has strength 9.84; Genemark calls start at 48508

/note=SSC: 48508-48200 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_84 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 1.07087E-65 GAP: 30 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.265, -3.9967659997675007, no F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_84 [Mycobacterium phage Bxz2]],,NP_817673,100.0,1.07087E-65 SIF-HHPRED: DUF6520 ; Family of unknown function (DUF6520),,,PF20130.4,61.7647,74.5 SIF-Syn:

/note=Calling NKF. Multiple 1:1 BLAST matches but everything shows NKF. We got the correct start site but even HHpred doesn't hit a good hypothetical protein match. Not much information so I am calling NKF

CDS complement (48539 - 49258)

/gene="88"

/product="gp88"

/function="hypothetical protein"

/locus tag="TinyPebbles_88"

/note=Original Glimmer call @bp 49258 has strength 16.29; Genemark calls start at 49258

/note=SSC: 49258-48539 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein M611_gp09 [Mycobacterium phage Jobu08]],,NCBI, q1:s1 100.0% 9.65658E-178 GAP: 26 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.653, -3.170856472917156, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein M611_gp09 [Mycobacterium phage Jobu08]],,YP_008126324,100.0,9.65658E-178 SIF-HHPRED: SIF-Syn:

/note=Gap is 26 and it is the LORF. SD score is -3.171 (best SD score). BLAST ratio is 1:1 and it collects all the coding potential. The PHAM starterator is suggested start. NCBI BLAST is showing that is a hypothetical protein but there is not enough evidence to support their claim.

CDS complement (49285 - 49401)

/gene="89"

/product="gp89"

/function="hypothetical protein"

/locus tag="TinyPebbles_89"

/note=Original Glimmer call @bp 49401 has strength 17.12; Genemark calls start at 49401

/note=SSC: 49401-49285 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI_BXZ2_86 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 1.12212E-17 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.044, -2.2763497933341483, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_86 [Mycobacterium phage Bxz2]],,NP_817675,100.0,1.12212E-17 SIF-HHPRED: DUF5606 ; Domain of unknown function (DUF5606),,,PF18347.6,73.6842,92.1 SIF-Syn:

/note=Glimmer and GeneMark agree. Longest ORF and best SD score. All coding potential. Not suggested start. NKF. 1:1 ratio with Bxz2.

CDS complement (49414 - 49536)

/gene="90"

/product="gp90"

/function="hypothetical protein"

/locus tag="TinyPebbles_90"

/note=Original Glimmer call @bp 49536 has strength 10.56; Genemark calls start at 49536

/note=SSC: 49536-49414 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI_BXZ2_87 [Mycobacterium phage Bxz2]],,NCBI, q1:s1 100.0% 2.39369E-20 GAP: 13 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.949, -2.5410833118725082, yes F: hypothetical protein SIF-BLAST: ,, [hypothetical protein PBI_BXZ2_87 [Mycobacterium phage Bxz2]],,NP_817676,100.0,2.39369E-20 SIF-HHPRED: Miniprotein EEHEE_rd4_0871; miniprotein, EEHEE-type, DE NOVO PROTEIN; NMR {Escherichia coli},,,8SKD_A,42.5,93.3 SIF-Syn:

/note=starterator suggested start, best SD score, captures all coding potential, 1:1 NCBI Blast matches for hypothetical protein. Phagesdb matches all call NKF

CDS complement (49550 - 49708)

/gene="91"

/product="gp91"

/function="hypothetical protein"

/locus tag="TinyPebbles_91"

/note=Original Glimmer call @bp 49708 has strength 9.65; Genemark calls start at 49708

/note=SSC: 49708-49550 CP: yes SCS: both ST: SS BLAST-Start:
[hypothetical protein PBI_BXZ2_88 [Mycobacterium phage Bxz2]],,NCBI,
ql:s1 100.0% 1.71319E-30 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin
Medium, 2.9, -2.5823297389851954, yes F: hypothetical protein SIF-BLAST:
,,[hypothetical protein PBI_BXZ2_88 [Mycobacterium phage Bxz2]
],,NP_817677,100.0,1.71319E-30 SIF-HHPRED: SIF-Syn:

/note=Glimmer and GeneMark agreed start site 49,708 and stop site
49,550, longest ORF, best SD score, all coding potential is covered,
starterator results are the SS, 163 base pair gap, BLAST 1:1 match,
function is probably a protein of some sort but the HHpred data doesn't
suggest a high enough probability to collect evidence on it.