CDS 418 - 1176

/gene="1"

/product="gp1"

/function="Hypothetical Protein"

/locus tag="Tucker\_1"

/note=Genemark calls start at 487

/note=SSC: 418-1176 CP: yes SCS: genemark-cs ST: SS BLAST-Start: [hypothetical protein X820\_gp001 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 0.0 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.812, -3.4463192436492656, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp001 [Mycobacterium phage CloudWang3] ],,YP\_008856774,100.0,0.0 SIF-HHPRED: DUF4417 ; Domain of unknown function (DUF4417),,,PF14386.9,68.254,100.0 SIF-Syn:

CDS 1089 - 1925

/gene="2"

/product="gp2"

/function="metalloprotease"

/locus tag="Tucker\_2"

/note=Original Glimmer call @bp 1089 has strength 8.16; Genemark calls start at 1089

/note=SSC: 1089-1925 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp002 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 0.0 GAP: -88 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.187, -4.27608723048325, no F: metalloprotease SIF-BLAST: ,,[hypothetical protein X820\_gp002 [Mycobacterium phage CloudWang3] ],,YP\_008856775,100.0,0.0 SIF-HHPRED: M34\_PPEP; Pro-Pro endopeptidase (PPEP) and similar proteins; belongs to peptidase family M34.,,,cd20183,67.9856,99.8 SIF-Syn:

CDS 1925 - 2146

/gene="3"

/product="gp3"

/function="Hypothetical Protein"

/locus tag="Tucker\_3"

/note=Original Glimmer call @bp 1925 has strength 8.77; Genemark calls start at 1925

/note=SSC: 1925-2146 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp003 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.4283E-45 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.676, -3.147993589957652, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp003 [Mycobacterium phage CloudWang3] ],,YP\_008856776,100.0,1.4283E-45 SIF-HHPRED: SIF-Syn:

CDS 2143 - 2439

/gene="4"

/product="gp4"

/function="HNH endonuclease"

/locus tag="Tucker\_4"

/note=

/note=SSC: 2143-2439 CP: yes SCS: neither ST: SS BLAST-Start: [HNH endonuclease [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.25169E-64 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.527, -5.631526093152131, no F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Mycobacterium phage CloudWang3] ],,YP\_008856777,100.0,1.25169E-64 SIF-HHPRED: SIF-Syn:

/note=Added this gene.

CDS 2482 - 2952

/gene="5"

/product="gp5"

/function="terminase, small subunit"

/locus tag="Tucker\_5"

/note=Original Glimmer call @bp 2482 has strength 9.51; Genemark calls start at 2482

/note=SSC: 2482-2952 CP: yes SCS: both ST: SS BLAST-Start: [terminase small subunit [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.01905E-109 GAP: 42 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.902, -2.66371296573402, no F: terminase, small subunit SIF-BLAST: ,,[terminase small subunit [Mycobacterium phage CloudWang3] ],,YP\_008856778,100.0,1.01905E-109 SIF-HHPRED: Terminase\_4 ; Phage terminase, small subunit,,,PF05119.15,45.5128,98.5 SIF-Syn:

CDS 3037 - 3999

/gene="6"

/product="gp6"

/function="minor tail protein"

/locus tag="Tucker\_6"

/note=Original Glimmer call @bp 3037 has strength 12.35; Genemark calls start at 3037

/note=SSC: 3037-3999 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 0.0 GAP: 84 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.11, -2.6835611257758942, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Zaka] ],,YP\_008859116,100.0,0.0 SIF-HHPRED: SIF-Syn:

/note=NCBI provided evidence for this function.

CDS 3999 - 4664

/gene="7"

/product="gp7"

/function="minor tail protein"

/locus tag="Tucker\_7"

/note=Original Glimmer call @bp 3999 has strength 5.4; Genemark calls start at 3999

/note=SSC: 3999-4664 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp007 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.99356E-145 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.554, -3.4283035164720754, yes F: minor tail protein SIF-BLAST: ,,[hypothetical protein X820\_gp007 [Mycobacterium phage CloudWang3] ],,YP\_008856780,100.0,1.99356E-145 SIF-HHPRED: SIF-Syn:

CDS 4661 - 5359

/gene="8"

/product="gp8"

/function="minor tail protein"

/locus tag="Tucker\_8"

/note=Original Glimmer call @bp 4661 has strength 9.09; Genemark calls start at 4661

/note=SSC: 4661-5359 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp008 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.93056E-153 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.991, -4.6353190821692705, no F: minor tail protein SIF-BLAST: ,,[hypothetical protein X820\_gp008 [Mycobacterium phage CloudWang3] ],,YP\_008856781,100.0,1.93056E-153 SIF-HHPRED: SIF-Syn:

tRNA 5402 - 5474

/gene="9"

/product="tRNA-Asn(gtt)"

/locus tag="TUCKER\_9"

/note=tRNA-Asn(gtt)

tRNA 5479 - 5552

/gene="10"

/product="tRNA-Trp(cca)"

/locus tag="TUCKER\_10"

/note=tRNA-Trp(cca)

CDS complement (5435 - 5554)

/gene="11"

/product="gp11"

/function="Hypothetical Protein"

/locus tag="Tucker\_11"

/note=Original Glimmer call @bp 5554 has strength 1.78

/note=SSC: 5554-5435 CP: yes SCS: glimmer ST: SS BLAST-Start: GAP: 141 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.72, -5.487588532164551, no F: Hypothetical Protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

/note=Only comparison to be made is w/ BABullseye\_10.

tRNA 5594 - 5666

/gene="12"

/product="tRNA-Gln(ctg)"

/locus tag="TUCKER\_12"

/note=tRNA-Gln(ctg)

CDS 5696 - 5854

/gene="13"

/product="gp13"

/function="Hypothetical Protein"

/locus tag="Tucker\_13"

/note=Original Glimmer call @bp 5696 has strength 14.99; Genemark calls start at 5696

/note=SSC: 5696-5854 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X828\_gp102 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 3.3992E-28 GAP: 141 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.11, -2.6835611257758942, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp102 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858436,100.0,3.3992E-28 SIF-HHPRED: Rap1a ; Rap1a immunity proteins,,,PF18602.4,73.0769,92.5 SIF-Syn:

CDS 5854 - 7065

/gene="14"

/product="gp14"

/function="lysin A"

/locus tag="Tucker\_14"

/note=Original Glimmer call @bp 5854 has strength 8.39; Genemark calls start at 5854

/note=SSC: 5854-7065 CP: yes SCS: both ST: SS BLAST-Start: [LysA [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.087, -4.429150775994987, no F: lysin A SIF-BLAST: ,,[LysA [Mycobacterium phage Artemis2UCLA] ],,YP\_008858437,100.0,0.0 SIF-HHPRED: Peptidase\_M15\_4 ; D-alanyl-D-alanine carboxypeptidase,,,PF13539.9,17.866,99.1 SIF-Syn:

CDS 7065 - 7496

/gene="15"

/product="gp15"

/function="holin"

/locus tag="Tucker\_15"

/note=Original Glimmer call @bp 7065 has strength 9.22; Genemark calls start at 7065

/note=SSC: 7065-7496 CP: yes SCS: both ST: SS BLAST-Start: [holin [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 1.41381E-93 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.122, -4.801936092881806, no F: holin SIF-BLAST: ,,[holin [Mycobacterium phage Artemis2UCLA] ],,YP\_008858438,100.0,1.41381E-93 SIF-HHPRED: Phage\_holin\_7\_1 ; Mycobacterial 2 TMS Phage Holin (M2 Hol) Family,,,PF16081.8,83.2168,100.0 SIF-Syn:

CDS 7533 - 9287

/gene="16"

/product="gp16"

/function="terminase, large subunit"

/locus tag="Tucker\_16"

/note=Original Glimmer call @bp 7533 has strength 10.17; Genemark calls start at 7533

/note=SSC: 7533-9287 CP: yes SCS: both ST: SS BLAST-Start: [terminase large subunit [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 0.0 GAP: 36 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.976, -2.523003374675015, yes F: terminase, large subunit SIF-BLAST: ,,[terminase large subunit [Mycobacterium phage Artemis2UCLA] ],,YP\_008858439,100.0,0.0 SIF-HHPRED: DNA packaging protein Gp17; large terminase, Alternative initiation, ATP-binding, DNA-binding, Hydrolase, Nuclease, Nucleotide-binding; HET: PO4; 2.8A {Bacteriophage T4},,,3CPE\_A,90.9247,100.0 SIF-Syn:

CDS 9284 - 10750

/gene="17"

/product="gp17"

/function="portal protein"

/locus tag="Tucker\_17"

/note=Original Glimmer call @bp 9284 has strength 9.83; Genemark calls start at 9284

/note=SSC: 9284-10750 CP: yes SCS: both ST: SS BLAST-Start: [portal protein [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.991, -4.696275508110696, no F: portal protein SIF-BLAST: ,,[portal protein [Mycobacterium phage Artemis2UCLA] ],,YP\_008858440,100.0,0.0 SIF-HHPRED: PORTAL PROTEIN; BACTERIOPHAGE SPP1, DNA TRANSLOCATION, MOLECULAR MOTOR, VIRAL PORTAL PROTEIN, VIRAL PROTEIN; HET: CA, HG; 3.4A {BACTERIOPHAGE SPP1},,,2JES\_Q,88.1148,100.0 SIF-Syn:

CDS 10747 - 11631

/gene="18"

/product="gp18"

/function="capsid maturation protease"

/locus tag="Tucker\_18"

/note=Original Glimmer call @bp 10747 has strength 7.3; Genemark calls start at 10747

/note=SSC: 10747-11631 CP: yes SCS: both ST: SS BLAST-Start: [capsid maturation protease [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.97, -2.5359491958734357, yes F: capsid maturation protease SIF-BLAST: ,,[capsid maturation protease [Mycobacterium phage Artemis2UCLA] ],,YP\_008858441,100.0,0.0 SIF-HHPRED: Phage\_min\_cap2 ; Phage minor capsid protein 2,,,PF06152.14,57.8231,95.1 SIF-Syn:

CDS 11681 - 12202

/gene="19"

/product="gp19"

/function="scaffolding protein"

/locus tag="Tucker\_19"

/note=Original Glimmer call @bp 11681 has strength 10.31; Genemark calls start at 11681

/note=SSC: 11681-12202 CP: no SCS: both ST: SS BLAST-Start: [scaffolding protein [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 1.2771E-120 GAP: 49 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.902, -3.2535385006449706, yes F: scaffolding protein SIF-BLAST: ,,[scaffolding protein [Mycobacterium phage Artemis2UCLA] ],,YP\_008858442,100.0,1.2771E-120 SIF-HHPRED: Scaffold protein; major capsid protein, HK97-like fold, scaffolding protein, procapsid, VIRUS; 3.72A {Staphylococcus phage 80alpha},,,6B0X\_a,39.8844,98.3 SIF-Syn:

CDS 12235 - 13206

/gene="20"

/product="gp20"

/function="major capsid protein"

/locus tag="Tucker\_20"

/note=Original Glimmer call @bp 12235 has strength 15.65; Genemark calls start at 12235

/note=SSC: 12235-13206 CP: yes SCS: both ST: SS BLAST-Start: [major capsid protein [Mycobacterium phage Koko] ],,NCBI, q1:s1 100.0% 0.0 GAP: 32 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.976, -2.794070146961553, yes F: major capsid protein SIF-BLAST: ,,[major capsid protein [Mycobacterium phage Koko] ],,YP\_010061341,99.6904,0.0 SIF-HHPRED: major capsid protein; acne, bacteriophage, HK97-like, VIRUS; 3.7A {Propionibacterium phage PA6},,,3JB5\_C,91.9505,100.0 SIF-Syn:

CDS 13278 - 13475

/gene="21"

/product="gp21"

/function="Hypothetical Protein"

/locus tag="Tucker\_21"

/note=Original Glimmer call @bp 13278 has strength 12.18; Genemark calls start at 13278

/note=SSC: 13278-13475 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein CL99\_gp095 [Mycobacterium phage Blue7] ],,NCBI, q1:s1 100.0% 5.31211E-38 GAP: 71 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.734, -3.7907710954237626, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein CL99\_gp095 [Mycobacterium phage Blue7] ],,YP\_009014508,100.0,5.31211E-38 SIF-HHPRED: SIF-Syn:

CDS 13478 - 13855

/gene="22"

/product="gp22"

/function="head-to-tail adaptor"

/locus tag="Tucker\_22"

/note=Original Glimmer call @bp 13478 has strength 10.25; Genemark calls start at 13478

/note=SSC: 13478-13855 CP: yes SCS: both ST: SS BLAST-Start: [Gp19/Gp15/Gp42 family protein [Mycobacterium phage Gladiator] ],,NCBI, q1:s1 100.0% 3.23617E-83 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.826, -2.8454123590742793, yes F: head-to-tail adaptor SIF-BLAST: ,,[Gp19/Gp15/Gp42 family protein [Mycobacterium phage Gladiator] ],,YP\_009635515,99.2,3.23617E-83 SIF-HHPRED: 15 PROTEIN; VIRAL PROTEIN, VIRAL INFECTION, TAILED BACTERIOPHAGE, SIPHOVIRIDAE, SPP1, VIRAL ASSEMBLY, HEAD-TO-TAIL INTERFACE, DNA GATEKEEPER, ALLOSTERIC MECHANISM; 7.2A {BACILLUS PHAGE SPP1},,,5A21\_D,84.0,98.6 SIF-Syn:

CDS 13852 - 14043

/gene="23"

/product="gp23"

/function="Hypothetical Protein"

/locus tag="Tucker\_23"

/note=Original Glimmer call @bp 13852 has strength 6.6; Genemark calls start at 13852

/note=SSC: 13852-14043 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp093 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 2.72849E-38 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.114, -6.516132674450062, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp093 [Mycobacterium phage CloudWang3] ],,YP\_008856792,100.0,2.72849E-38 SIF-HHPRED: SIF-Syn:

CDS 14043 - 14411

/gene="24"

/product="gp24"

/function="head-to-tail stopper"

/locus tag="Tucker\_24"

/note=Original Glimmer call @bp 14043 has strength 9.37; Genemark calls start at 14043

/note=SSC: 14043-14411 CP: no SCS: both ST: SS BLAST-Start: [head-to-tail stopper [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 2.77841E-85 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.865, -4.905314844093283, no F: head-to-tail stopper SIF-BLAST: ,,[head-to-tail stopper [Mycobacterium phage Artemis2UCLA] ],,YP\_008858447,100.0,2.77841E-85 SIF-HHPRED: HEAD COMPLETION PROTEIN GP16; VIRAL PROTEIN, VIRAL INFECTION, TAILED BACTERIOPHAGE, SIPHOVIRIDAE, SPP1, VIRAL ASSEMBLY, HEAD-TO-TAIL INTERFACE, DNA GATEKEEPER, ALLOSTERIC MECHANISM; 7.2A {BACILLUS PHAGE SPP1},,,5A21\_F,95.9016,99.4 SIF-Syn:

CDS 14411 - 14764

/gene="25"

/product="gp25"

/function="Hypothetical Protein"

/locus tag="Tucker\_25"

/note=Original Glimmer call @bp 14411 has strength 8.59; Genemark calls start at 14411

/note=SSC: 14411-14764 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X828\_gp090 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 6.7889E-80 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.025, -4.482213237254482, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp090 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858448,100.0,6.7889E-80 SIF-HHPRED: DUF5403 ; Family of unknown function (DUF5403),,,PF17395.5,93.1624,100.0 SIF-Syn:

CDS 14761 - 15180

/gene="26"

/product="gp26"

/function="tail terminator"

/locus tag="Tucker\_26"

/note=Original Glimmer call @bp 14761 has strength 6.96; Genemark calls start at 14761

/note=SSC: 14761-15180 CP: yes SCS: both ST: SS BLAST-Start: [tail terminator [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.17292E-96 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.731, -3.0301037898918786, yes F: tail terminator SIF-BLAST: ,,[tail terminator [Mycobacterium phage CloudWang3] ],,YP\_008856795,100.0,1.17292E-96 SIF-HHPRED: TAIL-TO-HEAD JOINING PROTEIN GP17; VIRAL PROTEIN, VIRAL INFECTION, TAILED BACTERIOPHAGE, SIPHOVIRIDAE, SPP1, VIRAL ASSEMBLY, HEAD-TO-TAIL INTERFACE, DNA GATEKEEPER, ALLOSTERIC MECHANISM; 7.2A {BACILLUS PHAGE SPP1},,,5A21\_G,91.3669,99.2 SIF-Syn:

CDS 15209 - 15811

/gene="27"

/product="gp27"

/function="major tail protein"

/locus tag="Tucker\_27"

/note=Original Glimmer call @bp 15209 has strength 11.21; Genemark calls start at 15233

/note=SSC: 15209-15811 CP: yes SCS: both-gl ST: SS BLAST-Start: [major tail protein [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 2.81951E-143 GAP: 28 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.557, -3.482870966776971, no F: major tail protein SIF-BLAST: ,,[major tail protein [Mycobacterium phage CloudWang3] ],,YP\_008856796,100.0,2.81951E-143 SIF-HHPRED: Phage\_TTP\_1 ; Phage tail tube protein,,,PF04630.15,68.0,97.2 SIF-Syn:

CDS 15923 - 16327

/gene="28"

/product="gp28"

/function="tail assembly chaperone"

/locus tag="Tucker\_28"

/note=Original Glimmer call @bp 15923 has strength 13.29; Genemark calls start at 15923

/note=SSC: 15923-16327 CP: no SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 9.37428E-89 GAP: 111 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.489, -4.014829999845237, yes F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Mycobacterium phage Artemis2UCLA] ],,YP\_008858452,100.0,9.37428E-89 SIF-HHPRED: GP24\_25 ; Mycobacteriophage tail assembly protein,,,PF17388.5,95.5224,100.0 SIF-Syn:

/note=There is a point for slippage here at 16300, the sequence GGGGGAA appears.

CDS 16279 - 16740

/gene="29"

/product="gp29"

/function="tail assembly chaperone"

/locus tag="Tucker\_29"

/note=Original Glimmer call @bp 16279 has strength 5.21; Genemark calls start at 16324

/note=SSC: 16279-16740 CP: yes SCS: both-gl ST: SS BLAST-Start: [tail assembly chaperone [Mycobacterium phage DaVinci]],,NCBI, q1:s1 100.0% 1.66703E-102 GAP: -49 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.865, -4.966271270034708, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Mycobacterium phage DaVinci]],,AEK08471,98.7013,1.66703E-102 SIF-HHPRED: SIF-Syn:

/note=This was a frameshift, 16300, GGGGGAA.

CDS 16733 - 18949

/gene="30"

/product="gp30"

/function="tape measure protein"

/locus tag="Tucker\_30"

/note=Original Glimmer call @bp 16733 has strength 11.04; Genemark calls start at 16733

/note=SSC: 16733-18949 CP: no SCS: both ST: SS BLAST-Start: [tapemeasure protein [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 0.0 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.204, -2.0162541296952132, yes F: tape measure protein SIF-BLAST: ,,[tapemeasure protein [Mycobacterium phage Zaka] ],,YP\_008859136,100.0,0.0 SIF-HHPRED: Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_AF,21.0027,99.9 SIF-Syn:

CDS 18976 - 19992

/gene="31"

/product="gp31"

/function="minor tail protein"

/locus tag="Tucker\_31"

/note=Original Glimmer call @bp 18976 has strength 8.28; Genemark calls start at 18976

/note=SSC: 18976-19992 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 0.0 GAP: 26 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.902, -2.66371296573402, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage CloudWang3] ],,YP\_008856800,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 19989 - 21761

/gene="32"

/product="gp32"

/function="minor tail protein"

/locus tag="Tucker\_32"

/note=Original Glimmer call @bp 19989 has strength 10.33; Genemark calls start at 19965

/note=SSC: 19989-21761 CP: no SCS: both-gl ST: NI BLAST-Start: [minor tail protein [Mycobacterium phage CloudWang3] ],,NCBI, q1:s9 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.087, -4.349108688274226, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage CloudWang3] ],,YP\_008856801,98.6622,0.0 SIF-HHPRED: SIF-Syn:

CDS 21777 - 22229

/gene="33"

/product="gp33"

/function="Hypothetical Protein"

/locus tag="Tucker\_33"

/note=Original Glimmer call @bp 21777 has strength 5.91; Genemark calls start at 21777

/note=SSC: 21777-22229 CP: yes SCS: both ST: SS BLAST-Start: [DUF2744 domain-containing protein [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 5.30031E-106 GAP: 15 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.122, -4.354778061539587, no F: Hypothetical Protein SIF-BLAST: ,,[DUF2744 domain-containing protein [Mycobacterium phage Artemis2UCLA] ],,YP\_008858456,100.0,5.30031E-106 SIF-HHPRED: DUF2744 ; Protein of unknown function (DUF2744),,,PF10910.11,88.6667,100.0 SIF-Syn:

CDS 22226 - 22522

/gene="34"

/product="gp34"

/function="Hypothetical Protein"

/locus tag="Tucker\_34"

/note=Original Glimmer call @bp 22226 has strength 10.36; Genemark calls start at 22226

/note=SSC: 22226-22522 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp082 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 2.7837E-64 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.826, -2.9063687850157054, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp082 [Mycobacterium phage CloudWang3] ],,YP\_008856803,100.0,2.7837E-64 SIF-HHPRED: DUF2746 ; Protein of unknown function (DUF2746),,,PF10874.11,95.9184,99.9 SIF-Syn:

CDS 22519 - 23940

/gene="35"

/product="gp35"

/function="minor tail protein"

/locus tag="Tucker\_35"

/note=Original Glimmer call @bp 22519 has strength 9.05; Genemark calls start at 22519

/note=SSC: 22519-23940 CP: no SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Zulu]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.11, -2.2364030944336752, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Zulu]],,AYD84849,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 23951 - 24235

/gene="36"

/product="gp36"

/function="Hypothetical Protein"

/locus tag="Tucker\_36"

/note=Original Glimmer call @bp 23951 has strength 7.05; Genemark calls start at 23951

/note=SSC: 23951-24235 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X821\_gp078 [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 2.96312E-63 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.718, -2.9966005857560156, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X821\_gp078 [Mycobacterium phage Zaka] ],,YP\_008859142,100.0,2.96312E-63 SIF-HHPRED: SIF-Syn:

CDS 24300 - 24494

/gene="37"

/product="gp37"

/function="Hypothetical Protein"

/locus tag="Tucker\_37"

/note=

/note=SSC: 24300-24494 CP: no SCS: neither ST: NA BLAST-Start: [hypothetical protein SEA\_WUNDERPHUL\_36 [Mycobacterium phage WunderPhul]],,NCBI, q1:s25 100.0% 2.69044E-38 GAP: 64 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.319, -5.157748419876103, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_WUNDERPHUL\_36 [Mycobacterium phage WunderPhul]],,ATW59781,72.7273,2.69044E-38 SIF-HHPRED: SIF-Syn:

/note=This gene was added manually.

CDS 24505 - 24693

/gene="38"

/product="gp38"

/function="Hypothetical Protein"

/locus tag="Tucker\_38"

/note=

/note=SSC: 24505-24693 CP: no SCS: neither ST: NA BLAST-Start: [hypothetical protein SEA\_INDRA\_38 [Mycobacterium phage Indra]],,NCBI, q1:s1 100.0% 3.31205E-17 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.962, -5.4473345649252005, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_INDRA\_38 [Mycobacterium phage Indra]],,QWT29780,63.8889,3.31205E-17 SIF-HHPRED: SIF-Syn:

/note=This gene was manually added.

CDS 24901 - 25443

/gene="39"

/product="gp39"

/function="ParA-like dsDNA partitioning protein"

/locus tag="Tucker\_39"

/note=Original Glimmer call @bp 24901 has strength 8.49; Genemark calls start at 24865

/note=SSC: 24901-25443 CP: no SCS: both-gl ST: SS BLAST-Start: [ParA-like dsDNA partitioning protein [Mycobacterium phage Priamo] ],,NCBI, q1:s1 100.0% 6.44855E-126 GAP: 207 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.92, -4.769809638752346, no F: ParA-like dsDNA partitioning protein SIF-BLAST: ,,[ParA-like dsDNA partitioning protein [Mycobacterium phage Priamo] ],,YP\_010061262,100.0,6.44855E-126 SIF-HHPRED: Plasmid partitioning protein ParF; deviant walker box, dna segregation, UNKNOWN FUNCTION; HET: ADP; 1.8A {Escherichia coli},,,4DZZ\_A,98.3333,99.8 SIF-Syn:

CDS 25436 - 25711

/gene="40"

/product="gp40"

/function="ParB-like dsDNA partitioning protein"

/locus tag="Tucker\_40"

/note=Original Glimmer call @bp 25436 has strength 9.49; Genemark calls start at 25436

/note=SSC: 25436-25711 CP: no SCS: both ST: SS BLAST-Start: [ParB-like dsDNA partitioning protein [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.87474E-56 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.718, -4.302337117698874, no F: ParB-like dsDNA partitioning protein SIF-BLAST: ,,[ParB-like dsDNA partitioning protein [Mycobacterium phage CloudWang3] ],,YP\_008856808,100.0,1.87474E-56 SIF-HHPRED: SIF-Syn:

CDS 25767 - 25928

/gene="41"

/product="gp41"

/function="Hypothetical Protein"

/locus tag="Tucker\_41"

/note=Original Glimmer call @bp 25767 has strength 8.74; Genemark calls start at 25797

/note=SSC: 25767-25928 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein X820\_gp076 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 4.19786E-30 GAP: 55 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.959, -3.1309088467834587, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp076 [Mycobacterium phage CloudWang3] ],,YP\_008856809,100.0,4.19786E-30 SIF-HHPRED: SIF-Syn:

CDS complement (26015 - 26404)

/gene="42"

/product="gp42"

/function="deoxycytidylate deaminase"

/locus tag="Tucker\_42"

/note=Original Glimmer call @bp 26173 has strength 6.85; Genemark calls start at 26173

/note=SSC: 26404-26015 CP: no SCS: both-cs ST: SS BLAST-Start: [deoxycytidylate deaminase [Mycobacterium phage Zulu]],,NCBI, q1:s1 100.0% 6.21859E-88 GAP: -11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.666, -3.188585239877588, yes F: deoxycytidylate deaminase SIF-BLAST: ,,[deoxycytidylate deaminase [Mycobacterium phage Zulu]],,AYD84854,100.0,6.21859E-88 SIF-HHPRED: SIF-Syn:

/note=Changed start site to 26173 to 26,404 to reduce the gap

CDS complement (26394 - 26756)

/gene="43"

/product="gp43"

/function="HNH endonuclease"

/locus tag="Tucker\_43"

/note=Original Glimmer call @bp 26756 has strength 3.51

/note=SSC: 26756-26394 CP: no SCS: glimmer ST: SS BLAST-Start: [HNH endonuclease [Microbacterium sp. JAI119] ],,NCBI, q7:s20 90.8333% 1.67616E-14 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.695, -5.330723697772664, no F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Microbacterium sp. JAI119] ],,WP\_218867778,42.3841,1.67616E-14 SIF-HHPRED: HNH homing endonuclease; HNH catalytic motif, Helix-turn-helix DNA binding domain, protein-DNA complex, DNA binding protein-DNA COMPLEX; HET: EDO; 2.92A {Bacillus phage SPO1} SCOP: d.4.1.3, d.285.1.1,,,1U3E\_M,57.5,99.3 SIF-Syn:

CDS complement (26753 - 27160)

/gene="44"

/product="gp44"

/function="Hypothetical Protein"

/locus tag="Tucker\_44"

/note=Original Glimmer call @bp 27160 has strength 16.27; Genemark calls start at 27160

/note=SSC: 27160-26753 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X821\_gp072 [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 1.49418E-94 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.976, -2.583959800616441, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X821\_gp072 [Mycobacterium phage Zaka] ],,YP\_008859148,100.0,1.49418E-94 SIF-HHPRED: SIF-Syn:

CDS complement (27157 - 27459)

/gene="45"

/product="gp45"

/function="Hypothetical Protein"

/locus tag="Tucker\_45"

/note=Original Glimmer call @bp 27459 has strength 10.4; Genemark calls start at 27459

/note=SSC: 27459-27157 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein FGG36\_gp62 [Mycobacterium phage Jeffabunny] ],,NCBI, q1:s1 100.0% 3.37143E-67 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.207, -4.4439998970339065, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein FGG36\_gp62 [Mycobacterium phage Jeffabunny] ],,YP\_009638213,100.0,3.37143E-67 SIF-HHPRED: SIF-Syn:

CDS complement (27456 - 27689)

/gene="46"

/product="gp46"

/function="terminase, large subunit (ATPase domain)"

/locus tag="Tucker\_46"

/note=Original Glimmer call @bp 27689 has strength 12.36; Genemark calls start at 27689

/note=SSC: 27689-27456 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X821\_gp070 [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 3.95685E-48 GAP: 20 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.943, -5.185777143476347, no F: terminase, large subunit (ATPase domain) SIF-BLAST: ,,[hypothetical protein X821\_gp070 [Mycobacterium phage Zaka] ],,YP\_008859150,100.0,3.95685E-48 SIF-HHPRED: TerL\_ATPase ; Terminase large subunit, ATPase domain,,,PF03354.18,70.1299,93.3 SIF-Syn:

CDS complement (27710 - 27928)

/gene="47"

/product="gp47"

/function="Hypothetical Protein"

/locus tag="Tucker\_47"

/note=Original Glimmer call @bp 27928 has strength 9.28; Genemark calls start at 27928

/note=SSC: 27928-27710 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp071 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 2.78941E-44 GAP: 22 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.976, -2.970161406017234, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp071 [Mycobacterium phage CloudWang3] ],,YP\_008856814,100.0,2.78941E-44 SIF-HHPRED: SIF-Syn:

CDS complement (27951 - 29792)

/gene="48"

/product="gp48"

/function="DNA polymerase I"

/locus tag="Tucker\_48"

/note=Original Glimmer call @bp 29792 has strength 14.09; Genemark calls start at 29792

/note=SSC: 29792-27951 CP: no SCS: both ST: SS BLAST-Start: [DNA polymerase I [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 0.0 GAP: 7 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.326, -4.36385515561809, no F: DNA polymerase I SIF-BLAST: ,,[DNA polymerase I [Mycobacterium phage CloudWang3] ],,YP\_008856815,100.0,0.0 SIF-HHPRED: DNA polymerase theta; DNA polymerase, Transferase-DNA complex; HET: GOL, DG3; 3.9A {Homo sapiens},,,4X0Q\_B,95.4323,100.0 SIF-Syn:

CDS complement (29800 - 29988)

/gene="49"

/product="gp49"

/function="Hypothetical Protein"

/locus tag="Tucker\_49"

/note=Original Glimmer call @bp 29988 has strength 10.43; Genemark calls start at 29988

/note=SSC: 29988-29800 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp069 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 5.70329E-37 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.11, -2.5074698667202133, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp069 [Mycobacterium phage CloudWang3] ],,YP\_008856816,100.0,5.70329E-37 SIF-HHPRED: SIF-Syn:

CDS complement (29985 - 30323)

/gene="50"

/product="gp50"

/function="Hypothetical Protein"

/locus tag="Tucker\_50"

/note=Original Glimmer call @bp 30323 has strength 8.95; Genemark calls start at 30323

/note=SSC: 30323-29985 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_ZULU\_48 [Mycobacterium phage Zulu]],,NCBI, q1:s1 100.0% 1.05951E-74 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.662, -4.217820759167949, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ZULU\_48 [Mycobacterium phage Zulu]],,AYD84862,100.0,1.05951E-74 SIF-HHPRED: SIF-Syn:

CDS complement (30323 - 30751)

/gene="51"

/product="gp51"

/function="helix-turn-helix DNA binding domain"

/locus tag="Tucker\_51"

/note=Original Glimmer call @bp 30778 has strength 9.8; Genemark calls start at 30751

/note=SSC: 30751-30323 CP: no SCS: both-gm ST: SS BLAST-Start: [MerR-like HTH DNA-binding protein [Mycobacterium phage Zulu]],,NCBI, q1:s1 100.0% 2.07052E-96 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.216, -4.423424636048095, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[MerR-like HTH DNA-binding protein [Mycobacterium phage Zulu]],,AYD84863,99.2958,2.07052E-96 SIF-HHPRED: SIF-Syn:

CDS complement (30751 - 30957)

/gene="52"

/product="gp52"

/function="Hypothetical Protein"

/locus tag="Tucker\_52"

/note=Original Glimmer call @bp 30957 has strength 10.61; Genemark calls start at 30957

/note=SSC: 30957-30751 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp065 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 4.85907E-41 GAP: 1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.676, -3.0856802691973226, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp065 [Mycobacterium phage CloudWang3] ],,YP\_008856820,100.0,4.85907E-41 SIF-HHPRED: Uncharacterized protein; NESG, Q8EI81\_SHEON, Structural Genomics, PSI-2, Protein Structure Initiative, Northeast Structural Genomics Consortium, UNKNOWN FUNCTION; HET: MSE; 2.5A {Shewanella oneidensis} SCOP: l.1.1.1, b.38.1.6,,,2RB6\_B,79.4118,96.9 SIF-Syn:

CDS complement (30959 - 31669)

/gene="53"

/product="gp53"

/function="ThyX-like thymidylate synthase"

/locus tag="Tucker\_53"

/note=Original Glimmer call @bp 31669 has strength 10.87; Genemark calls start at 31669

/note=SSC: 31669-30959 CP: no SCS: both ST: SS BLAST-Start: [ThyX-like thymidylate synthase [Mycobacterium phage Zulu]],,NCBI, q1:s1 100.0% 1.0736E-174 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.312, -4.395041241556842, no F: ThyX-like thymidylate synthase SIF-BLAST: ,,[ThyX-like thymidylate synthase [Mycobacterium phage Zulu]],,AYD84865,100.0,1.0736E-174 SIF-HHPRED: Thymidylate synthase thyX; ThyX, FAD, FdUMP, Flavoprotein, Methyltransferase, Nucleotide biosynthesis, Transferase, Structural Genomics, Seattle Structural Genomics Center for Infectious; HET: FAD, UFP; 1.9A {Mycobacterium tuberculosis},,,3GWC\_A,99.1525,100.0 SIF-Syn:

CDS complement (31666 - 32184)

/gene="54"

/product="gp54"

/function="RNA ligase"

/locus tag="Tucker\_54"

/note=Original Glimmer call @bp 32184 has strength 11.74; Genemark calls start at 32238

/note=SSC: 32184-31666 CP: no SCS: both-gl ST: SS BLAST-Start: [RNA ligase [Mycobacterium phage Zulu]],,NCBI, q1:s19 100.0% 1.20291E-122 GAP: 207 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.678, -5.3069602069835, no F: RNA ligase SIF-BLAST: ,,[RNA ligase [Mycobacterium phage Zulu]],,AYD84866,90.5263,1.20291E-122 SIF-HHPRED: d.142.2.4 (A:) RNA editing ligase MP52 {Trypanosome (Trypanosoma brucei) [TaxId: 5691]},,,d1xdna\_,95.9302,99.9 SIF-Syn:

CDS complement (32392 - 32940)

/gene="55"

/product="gp55"

/function="Hypothetical Protein"

/locus tag="Tucker\_55"

/note=Original Glimmer call @bp 32940 has strength 9.31; Genemark calls start at 32940

/note=SSC: 32940-32392 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein CL99\_gp061 [Mycobacterium phage Blue7] ],,NCBI, q1:s67 100.0% 3.11763E-130 GAP: 11 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.688, -3.1417032362307356, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein CL99\_gp061 [Mycobacterium phage Blue7] ],,YP\_009014542,73.3871,3.11763E-130 SIF-HHPRED: SIF-Syn:

CDS complement (32952 - 35006)

/gene="56"

/product="gp56"

/function="ribonucleotide reductase"

/locus tag="Tucker\_56"

/note=Original Glimmer call @bp 35006 has strength 9.61; Genemark calls start at 35006

/note=SSC: 35006-32952 CP: no SCS: both ST: SS BLAST-Start: [ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.11, -2.9845911214398755, yes F: ribonucleotide reductase SIF-BLAST: ,,[ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent [Mycobacterium phage Zaka] ],,YP\_008859161,99.7076,0.0 SIF-HHPRED: RIBONUCLEOSIDE TRIPHOSPHATE REDUCTASE; 10-stranded alpha-beta barrel, central finger loop, OXIDOREDUCTASE; 1.75A {Lactobacillus leichmannii} SCOP: c.7.1.4,,,1L1L\_A,99.269,100.0 SIF-Syn:

CDS complement (35003 - 35185)

/gene="57"

/product="gp57"

/function="Hypothetical Protein"

/locus tag="Tucker\_57"

/note=Original Glimmer call @bp 35185 has strength 11.98; Genemark calls start at 35185

/note=SSC: 35185-35003 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp060 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 3.28762E-36 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.215, -2.0720764396375664, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp060 [Mycobacterium phage CloudWang3] ],,YP\_008856825,100.0,3.28762E-36 SIF-HHPRED: SIF-Syn:

CDS complement (35182 - 35322)

/gene="58"

/product="gp58"

/function="Hypothetical Protein"

/locus tag="Tucker\_58"

/note=Original Glimmer call @bp 35322 has strength 11.69; Genemark calls start at 35322

/note=SSC: 35322-35182 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp059 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.7812E-23 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.13, -2.17469248771465, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp059 [Mycobacterium phage CloudWang3] ],,YP\_008856826,100.0,1.7812E-23 SIF-HHPRED: SIF-Syn:

CDS complement (35319 - 35987)

/gene="59"

/product="gp59"

/function="DNA binding protein"

/locus tag="Tucker\_59"

/note=Original Glimmer call @bp 35987 has strength 13.31; Genemark calls start at 35987

/note=SSC: 35987-35319 CP: no SCS: both ST: SS BLAST-Start: [DNA binding protein [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.03217E-161 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.084, -4.356861600513232, no F: DNA binding protein SIF-BLAST: ,,[DNA binding protein [Mycobacterium phage CloudWang3] ],,YP\_008856827,100.0,1.03217E-161 SIF-HHPRED: ECF RNA polymerase sigma factor SigW; Sigma-anti-sigma complex, zinc binding motif, METAL BINDING PROTEIN; 2.6A {Bacillus subtilis subsp. subtilis str. 168},,,5WUR\_A,71.6216,99.8 SIF-Syn:

CDS complement (35991 - 36761)

/gene="60"

/product="gp60"

/function="metallophosphoesterase"

/locus tag="Tucker\_60"

/note=Original Glimmer call @bp 36761 has strength 14.09; Genemark calls start at 36761

/note=SSC: 36761-35991 CP: no SCS: both ST: SS BLAST-Start: [metallophosphoesterase [Mycobacterium phage JewelBug] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.364, -3.8360440759163943, no F: metallophosphoesterase SIF-BLAST: ,,[metallophosphoesterase [Mycobacterium phage JewelBug] ],,YP\_010061191,99.6094,0.0 SIF-HHPRED: d.159.1.7 (A:4-196) Vacuolar protein sorting 29, VPS29 {Cryptosporidium parvum [TaxId: 5807]},,,d2a22a1,98.8281,99.8 SIF-Syn:

CDS complement (36758 - 37201)

/gene="61"

/product="gp61"

/function="Hypothetical Protein"

/locus tag="Tucker\_61"

/note=Original Glimmer call @bp 37201 has strength 9.63; Genemark calls start at 37201

/note=SSC: 37201-36758 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp056 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 6.6735E-103 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.976, -3.095100142625534, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp056 [Mycobacterium phage CloudWang3] ],,YP\_008856829,100.0,6.6735E-103 SIF-HHPRED: DUF6378 ; Domain of unknown function (DUF6378),,,PF19905.2,53.7415,99.9 SIF-Syn:

CDS complement (37198 - 37299)

/gene="62"

/product="gp62"

/function="Hypothetical Protein"

/locus tag="Tucker\_62"

/note=Genemark calls start at 37299

/note=SSC: 37299-37198 CP: no SCS: genemark ST: SS BLAST-Start: [hypothetical protein X820\_gp055 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.35459E-14 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.911, -3.4105598537121566, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp055 [Mycobacterium phage CloudWang3] ],,YP\_008856830,100.0,1.35459E-14 SIF-HHPRED: SIF-Syn:

CDS complement (37299 - 37931)

/gene="63"

/product="gp63"

/function="DNA primase"

/locus tag="Tucker\_63"

/note=Original Glimmer call @bp 37931 has strength 9.01; Genemark calls start at 37838

/note=SSC: 37931-37299 CP: no SCS: both-gl ST: SS BLAST-Start: [toprim domain-containing protein [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 9.1284E-155 GAP: 213 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.054, -2.338663114094478, yes F: DNA primase SIF-BLAST: ,,[toprim domain-containing protein [Mycobacterium phage CloudWang3] ],,YP\_008856831,100.0,9.1284E-155 SIF-HHPRED: e.13.1.1 (A:) DNA primase DnaG catalytic core {Escherichia coli [TaxId: 562]},,,d1dd9a\_,95.2381,99.9 SIF-Syn:

CDS complement (38145 - 38300)

/gene="64"

/product="gp64"

/function="Hypothetical Protein"

/locus tag="Tucker\_64"

/note=Original Glimmer call @bp 38300 has strength 14.54; Genemark calls start at 38300

/note=SSC: 38300-38145 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X828\_gp051 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 1.82443E-27 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.064, -2.7806870294376242, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp051 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858487,100.0,1.82443E-27 SIF-HHPRED: SIF-Syn:

CDS complement (38293 - 38793)

/gene="65"

/product="gp65"

/function="endonuclease VII"

/locus tag="Tucker\_65"

/note=Original Glimmer call @bp 38793 has strength 8.18; Genemark calls start at 38793

/note=SSC: 38793-38293 CP: no SCS: both ST: SS BLAST-Start: [endonuclease VII domain-containing protein [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 1.43484E-119 GAP: -29 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.826, -3.4175091270247986, yes F: endonuclease VII SIF-BLAST: ,,[endonuclease VII domain-containing protein [Mycobacterium phage Artemis2UCLA] ],,YP\_008858488,100.0,1.43484E-119 SIF-HHPRED: Endonuclease\_7 ; Recombination endonuclease VII,,,PF02945.18,42.7711,99.6 SIF-Syn:

CDS complement (38765 - 38887)

/gene="66"

/product="gp66"

/function="Hypothetical Protein"

/locus tag="Tucker\_66"

/note=Original Glimmer call @bp 38887 has strength 9.63; Genemark calls start at 38905

/note=SSC: 38887-38765 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein X820\_gp049 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s7 100.0% 2.70324E-17 GAP: 14 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.479, -3.859592806742189, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp049 [Mycobacterium phage CloudWang3] ],,YP\_008856836,84.7826,2.70324E-17 SIF-HHPRED: SIF-Syn:

CDS complement (38902 - 39051)

/gene="67"

/product="gp67"

/function="Hypothetical Protein"

/locus tag="Tucker\_67"

/note=Original Glimmer call @bp 39051 has strength 7.32; Genemark calls start at 39051

/note=SSC: 39051-38902 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp048 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 6.55774E-28 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.865, -4.825272756372522, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp048 [Mycobacterium phage CloudWang3] ],,YP\_008856837,97.9592,6.55774E-28 SIF-HHPRED: SIF-Syn:

CDS complement (39048 - 39281)

/gene="68"

/product="gp68"

/function="Hypothetical Protein"

/locus tag="Tucker\_68"

/note=Original Glimmer call @bp 39281 has strength 9.37; Genemark calls start at 39281

/note=SSC: 39281-39048 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_GRUUNAGA\_67 [Mycobacterium phage Gruunaga] ],,NCBI, q1:s1 100.0% 2.74292E-49 GAP: 153 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.11, -2.297359520375101, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_GRUUNAGA\_67 [Mycobacterium phage Gruunaga] ],,AOQ28081,100.0,2.74292E-49 SIF-HHPRED: SIF-Syn:

CDS complement (39435 - 39821)

/gene="69"

/product="gp69"

/function="Hypothetical Protein"

/locus tag="Tucker\_69"

/note=Original Glimmer call @bp 39821 has strength 13.94; Genemark calls start at 39821

/note=SSC: 39821-39435 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein CL99\_gp046 [Mycobacterium phage Blue7] ],,NCBI, q1:s1 100.0% 3.78263E-88 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.404, -3.75071250087134, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein CL99\_gp046 [Mycobacterium phage Blue7] ],,YP\_009014557,100.0,3.78263E-88 SIF-HHPRED: DUF5052 ; Domain of unknown function (DUF5052),,,PF16475.8,84.375,99.5 SIF-Syn:

CDS complement (39818 - 40174)

/gene="70"

/product="gp70"

/function="Hypothetical Protein"

/locus tag="Tucker\_70"

/note=Original Glimmer call @bp 40174 has strength 11.71; Genemark calls start at 40174

/note=SSC: 40174-39818 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp045 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 2.56976E-81 GAP: 14 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.745, -3.5918169534085775, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp045 [Mycobacterium phage CloudWang3] ],,YP\_008856840,100.0,2.56976E-81 SIF-HHPRED: DUF6197 ; Family of unknown function (DUF6197),,,PF19698.2,99.1525,99.9 SIF-Syn:

/note=Original Glimmer call @bp 40174 has strength 11.71

/note=

/note=SSC: 39818-40174

/note=CP: yes

/note=SCS: Glimmer and GeneMark called at 40174

/note=ST: Artemis2UCLA\_69, BABullseye\_61, Blue7\_70

/note=Blast-start: Phagesdb.org: Wiks\_68, Koko\_71, Jeffabunny\_69, Evalue: 9e-63, Function: hypothetical protein NCBI: CloudWang3, Artemis2UCLA, Blue7, Evalue: 3e-81, 2e-80, 8e-80, Function: hypothetical protein

/note=Gap: 3 bp overlap between 63 and 64, 15bp gap between 64 and 65

/note=LO: no

/note=RBS: Zvalue: 2.771 Final Score: -3.592

/note=F: hypothetical protein

/note=SIF-HHPRED: NA

CDS complement (40189 - 40368)

/gene="71"

/product="gp71"

/function="hypothetical protein"

/locus tag="Tucker\_71"

/note=Original Glimmer call @bp 40368 has strength 13.07; Genemark calls start at 40368

/note=SSC: 40368-40189 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp044 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 3.87043E-31 GAP: 32 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.92, -4.848494831654204, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X820\_gp044 [Mycobacterium phage CloudWang3] ],,YP\_008856841,100.0,3.87043E-31 SIF-HHPRED: SIF-Syn:

/note=Original Glimmer call @bp 40368 has strength 13.07

/note=

/note=SSC: 40189-40368

/note=CP: yes

/note=SCS: Glimmer and GeneMark called at 40368

/note=ST: Artemis2UCLA\_70, BaBullseye\_62, Cookiedough\_69

/note=Blast-start: Phagesdb.org: Zulu, Zaka, Yokurt, Evalue: 7e-29, Function: unknown NCBI: Blue7, CloudWang3, Gruunaga, Evalue: 3e-15, 5e-15, Function: hypothetical protein

/note=Gap: 15bp gap between 64 and 65, 44 bp gap between 65 and 66

/note=LO: yes

/note=RBS: Zvalue: 1.938 Final Score: -4.848

/note=F: hypothetical protein

/note=SIF-HHPRED: NA

CDS complement (40401 - 41147)

/gene="72"

/product="gp72"

/function="DnaB-like dsDNA helicase"

/locus tag="Tucker\_72"

/note=Original Glimmer call @bp 41147 has strength 12.95; Genemark calls start at 41147

/note=SSC: 41147-40401 CP: yes SCS: both ST: SS BLAST-Start: [AAA family ATPase [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 4.56007E-180 GAP: 72 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 0.595, -7.550715894035402, no F: DnaB-like dsDNA helicase SIF-BLAST: ,,[AAA family ATPase [Mycobacterium phage Zaka] ],,YP\_008859178,99.1936,4.56007E-180 SIF-HHPRED: DNAB-Like Replicative Helicase; ATPase, REPLICATION; 3.91A {Bacillus phage SPP1},,,3BGW\_E,99.1936,100.0 SIF-Syn:

/note=Original Glimmer call @bp 41147 has strength 12.95

/note=

/note=SSC: 40401-41147

/note=CP: yes

/note=SCS: Glimmer and GeneMark called at 41147

/note=ST: Blue7\_72, Hammer\_71, Indra\_74

/note=Blast-start: Phagesdb.org: Zulu, Zaka, Yokurt, Evalue: e-139, Function: DnaB-like dsDNA helicase NCBI: Zaka, CloudWang3, Gladiator, Evalue: 5e-180, 2e-178, 2e-177, Function: AAA Family ATPase

/note=Gap: 44 bp gap between 65 and 66, 73bp gap between 66 and 67

/note=LO: yes

/note=RBS: Zvalue: 0.598 Final Score: -7.551

/note=F: DnaB-like dsDNA helicase

/note=SIF-HHPRED: NA

CDS complement (41220 - 41357)

/gene="73"

/product="gp73"

/function="Hypothetical Protein"

/locus tag="Tucker\_73"

/note=Original Glimmer call @bp 41357 has strength 12.23; Genemark calls start at 41357

/note=SSC: 41357-41220 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X821\_gp041 [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 1.09324E-24 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.083, -6.502765885351857, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X821\_gp041 [Mycobacterium phage Zaka] ],,YP\_008859179,100.0,1.09324E-24 SIF-HHPRED: SIF-Syn:

/note=Original Glimmer call @bp 41357 has strength 12.23

/note=

/note=SSC: 41220-41357

/note=CP: yes

/note=SCS: Glimmer and Genemark call at 41357

/note=ST: Artemis2UCLA\_69, BABullseye\_61, Blue7\_70

/note=Blast-start: Phagesdb.org: Wiks\_68, Tucker\_Draft\_67, Koko\_71, Evalue: 9e-63, Function: hypothetical protein, NCBI: CloudWang3, Artemis2UCLA, Blue7, Evalue: 3e-81, 2e-80, 8e-80, Function: hypothetical protein

/note=Gap: 73bp gap between 66 and 67, 3bp overlap between 67 and 68

/note=LO: yes

/note=RBS: Zvalue:( 1.092) Final Score:(-6.053)

/note=F: antimicrobial protein

/note=SIF-HHPRED: Subtillisin A, Evalue: 420, Function: Antimicrobial protein

/note=

/note=

/note=Additional Notes:

CDS complement (41354 - 41611)

/gene="74"

/product="gp74"

/function="hypothetical protein"

/locus tag="Tucker\_74"

/note=Original Glimmer call @bp 41611 has strength 8.75; Genemark calls start at 41611

/note=SSC: 41611-41354 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein CL99\_gp041 [Mycobacterium phage Blue7] ],,NCBI, q1:s1 100.0% 2.19005E-54 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.339, -3.8100388651815202, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein CL99\_gp041 [Mycobacterium phage Blue7] ],,YP\_009014562,100.0,2.19005E-54 SIF-HHPRED: GP68 ; Gp68-like predicted RNA polymerase component,,,PF17469.5,88.2353,100.0 SIF-Syn:

/note=Original Glimmer call @bp 41611 has strength 8.75

/note=

/note=SSC: 41354-41611

/note=CP: yes

/note=SCS: Glimmer and Genemark called at 41611

/note=ST: Addzy, Artemis2UCLA, Blue7

/note=Blast-start: Phagesdb.org: Blue7, Zulu, Zaka, Evalue: 3e-45, 9e-45, 3e-44, Function: MerR-like HTH binding protein NCBI: Blue7, Zaka, Gruunaga, Evalue: 2e-54, 2e-53, 4e-49, Function: hypothetical protein

/note=Gap: 3bp overlap between 67 and 68, 3bp overlap between 68 and 69

/note=LO: yes

/note=RBS: Zvalue: 2.361 Final Score: -3.810

/note=F: MerR-like HTH Binding protein

/note=SIF-BLAST: 5VJ7\_B, Evalue: 1400, Function: Ferredoxin NADP+ Reductase Subunit Alpha

/note=SIF-HHPRED:

CDS complement (41608 - 41907)

/gene="75"

/product="gp75"

/function="Hypothetical Protein"

/locus tag="Tucker\_75"

/note=Original Glimmer call @bp 41907 has strength 4.6; Genemark calls start at 41907

/note=SSC: 41907-41608 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp041 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 6.05446E-67 GAP: 5 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.826, -2.9063687850157054, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp041 [Mycobacterium phage CloudWang3] ],,YP\_008856844,100.0,6.05446E-67 SIF-HHPRED: SIF-Syn:

/note=Original Glimmer call @bp 41907 has strength 4.60; GeneMark calls start at 41856

/note=

/note=SSC: 41608-41907

/note=CP: yes

/note=SCS: Glimmer called at 41907, GeneMark called at 41856

/note=ST: Artemis2UCLA\_73, Blue7\_75, Gladiator\_71

/note=Blast-start: Phagesdb.org: Zulu, Zaka, Yokurt, Evalue: 2e-54, Function: hypthetical protein NCBI: CloudWang3, Indra, Gladiator, Evalue: 6e-67, 2e-66, 6e-66, Function: hypothetical protein

/note=Gap: 3bp overlap between 68 and 69, 6bp gap between 69 and 70

/note=LO: no

/note=RBS: Zvalue: -2.853 Final Score: -2.906

/note=F: hypothetical protein

/note=SIF-BLAST: 6QK5\_A, Evalue: 1400, Function: metal binding protein

/note=SIF-HHPRED:

CDS complement (41913 - 42287)

/gene="76"

/product="gp76"

/function="Hypothetical Protein"

/locus tag="Tucker\_76"

/note=Original Glimmer call @bp 42287 has strength 11.17; Genemark calls start at 42287

/note=SSC: 42287-41913 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp040 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.67874E-83 GAP: 48 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.122, -4.274735973818826, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp040 [Mycobacterium phage CloudWang3] ],,YP\_008856845,100.0,1.67874E-83 SIF-HHPRED: SIF-Syn:

/note=Original Glimmer call @bp 42287 has strength 11.17

/note=

/note=SSC: 41913-42287

/note=CP: yes

/note=SCS: Glimmer and GeneMark called at 42287

/note=ST: Artemis2UCLA, Blue7, CloudWang3

/note=Blast-start: Phagesdb.org: Zulu, Zaka, Yokurt, Evalue: 1e-69, Function: hypothetical protein NCBI: Gladiator, CloudWang3, Roksolana, Evalue: 8e-50, 1e-49, 1e-48, Function: hypothetical protein

/note=Gap: 6bp gap between 69 and 70, 49bp gap between 70 and 71

/note=LO: no

/note=RBS: Zvalue: 2.142 Final Score:-4.275

/note=F: hypothetical protein

/note=SIF-HHPRED: 6MSL\_C, Evalue: 5500, Function: Cystine knot protein

CDS complement (42336 - 43157)

/gene="77"

/product="gp77"

/function="Cas4 family exonuclease"

/locus tag="Tucker\_77"

/note=Original Glimmer call @bp 43157 has strength 10.88; Genemark calls start at 43157

/note=SSC: 43157-42336 CP: no SCS: both ST: SS BLAST-Start: [Cas4 family exonuclease [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.364, -3.8183153089559627, no F: Cas4 family exonuclease SIF-BLAST: ,,[Cas4 family exonuclease [Mycobacterium phage CloudWang3] ],,YP\_008856846,100.0,0.0 SIF-HHPRED: Csa1 ; CRISPR-associated exonuclease Csa1,,,PF06023.15,96.337,99.9 SIF-Syn:

CDS complement (43154 - 43540)

/gene="78"

/product="gp78"

/function="Hypothetical Protein"

/locus tag="Tucker\_78"

/note=Original Glimmer call @bp 43540 has strength 3.81; Genemark calls start at 43540

/note=SSC: 43540-43154 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein KIP56\_gp036 [Mycobacterium phage Koko] ],,NCBI, q1:s1 100.0% 5.4043E-90 GAP: 48 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.621, -6.001789403574632, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein KIP56\_gp036 [Mycobacterium phage Koko] ],,YP\_010061400,100.0,5.4043E-90 SIF-HHPRED: GP70 ; Gene product 70,,,PF17429.5,37.5,99.8 SIF-Syn:

CDS complement (43589 - 44104)

/gene="79"

/product="gp79"

/function="immunity repressor"

/locus tag="Tucker\_79"

/note=Original Glimmer call @bp 44104 has strength 11.53; Genemark calls start at 44080

/note=SSC: 44104-43589 CP: no SCS: both-gl ST: SS BLAST-Start: [immunity repressor [Mycobacterium phage ToneTone] ],,NCBI, q1:s1 100.0% 9.63481E-125 GAP: 235 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.564, -3.3275678682521845, no F: immunity repressor SIF-BLAST: ,,[immunity repressor [Mycobacterium phage ToneTone] ],,ANT42265,100.0,9.63481E-125 SIF-HHPRED: SIF-Syn:

CDS complement (44340 - 44492)

/gene="80"

/product="gp80"

/function="Hypothetical Protein"

/locus tag="Tucker\_80"

/note=Original Glimmer call @bp 44492 has strength 11.17; Genemark calls start at 44492

/note=SSC: 44492-44340 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp036 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.4376E-24 GAP: 4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.309, -3.9531326986493704, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp036 [Mycobacterium phage CloudWang3] ],,YP\_008856849,100.0,1.4376E-24 SIF-HHPRED: SIF-Syn:

CDS complement (44497 - 44838)

/gene="81"

/product="gp81"

/function="Hypothetical Protein"

/locus tag="Tucker\_81"

/note=Original Glimmer call @bp 44838 has strength 8.75; Genemark calls start at 44838

/note=SSC: 44838-44497 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein KIP56\_gp033 [Mycobacterium phage Koko] ],,NCBI, q1:s1 100.0% 1.55006E-78 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.554, -3.4892599424135016, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein KIP56\_gp033 [Mycobacterium phage Koko] ],,YP\_010061403,100.0,1.55006E-78 SIF-HHPRED: SIF-Syn:

CDS complement (44838 - 45047)

/gene="82"

/product="gp82"

/function="Hypothetical Protein"

/locus tag="Tucker\_82"

/note=Original Glimmer call @bp 45047 has strength 13.83; Genemark calls start at 45047

/note=SSC: 45047-44838 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X828\_gp034 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 2.86042E-40 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.933, -4.820269098574683, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp034 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858504,100.0,2.86042E-40 SIF-HHPRED: SIF-Syn:

/note=Saw a few RNA polymerase inhibitors in the HHPRED data.

/note=

/note=Original Glimmer call @bp 45047 has strength 13.83

/note=

/note=SSC: 44838-45047

/note=CP: yes

/note=SCS: Glimmer and GeneMark called at 45047

/note=ST: Artemis2UCLA\_80, Blue7\_82, Indra\_84

/note=Blast-start: Phagesdb.org: Zulu, Zaka, Yokurt, Evalue: 2e-32, Function: hypothetical protein NCBI: Artemis2UCLA, GaugeLDP, IronMan Evalue: 3e-40, 1e-22, Function: hypothetical protein

/note=Gap: 0bp gap between 78 and 79, 3bp overlap between 79 and 80

/note=LO: yes

/note=RBS: Zvalue: 1.951 Final Score: -4.820

/note=F: hypothetical protein

/note=SIF-HHPRED: 5WBS\_E, Evalue: 2400, Function: signaling protein

CDS complement (45044 - 45313)

/gene="83"

/product="gp83"

/function="Hypothetical Protein"

/locus tag="Tucker\_83"

/note=Original Glimmer call @bp 45313 has strength 11.69; Genemark calls start at 45313

/note=SSC: 45313-45044 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X828\_gp033 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 2.50787E-57 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.098, -4.4057176022952405, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp033 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858505,98.8764,2.50787E-57 SIF-HHPRED: SIF-Syn:

CDS complement (45322 - 45444)

/gene="84"

/product="gp84"

/function="Hypothetical Protein"

/locus tag="Tucker\_84"

/note=Original Glimmer call @bp 45444 has strength 8.26; Genemark calls start at 45444

/note=SSC: 45444-45322 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X828\_gp032 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 1.0151E-19 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.003, -5.358904934826584, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp032 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858506,100.0,1.0151E-19 SIF-HHPRED: SIF-Syn:

CDS complement (45441 - 45704)

/gene="85"

/product="gp85"

/function="Hypothetical Protein"

/locus tag="Tucker\_85"

/note=Original Glimmer call @bp 45692 has strength 5.83; Genemark calls start at 45704

/note=SSC: 45704-45441 CP: no SCS: both-gm ST: NI BLAST-Start: [hypothetical protein X828\_gp031 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 2.97205E-56 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.081, -7.608323496372297, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp031 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858507,100.0,2.97205E-56 SIF-HHPRED: SIF-Syn:

CDS complement (45701 - 45832)

/gene="86"

/product="gp86"

/function="Hypothetical Protein"

/locus tag="Tucker\_86"

/note=Original Glimmer call @bp 45832 has strength 12.28; Genemark calls start at 45790

/note=SSC: 45832-45701 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein X828\_gp030 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 5.95223E-22 GAP: -46 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.683, -3.5985503360675457, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp030 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858508,100.0,5.95223E-22 SIF-HHPRED: SIF-Syn:

CDS complement (45787 - 46248)

/gene="87"

/product="gp87"

/function="SprT-like protease"

/locus tag="Tucker\_87"

/note=Original Glimmer call @bp 46248 has strength 6.44; Genemark calls start at 46248

/note=SSC: 46248-45787 CP: yes SCS: both ST: SS BLAST-Start: [SprT-like protein [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 3.15806E-110 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.356, -3.773970443115436, yes F: SprT-like protease SIF-BLAST: ,,[SprT-like protein [Mycobacterium phage Artemis2UCLA] ],,YP\_008858509,100.0,3.15806E-110 SIF-HHPRED: SprT-like domain-containing protein Spartan; DPC repair protease, DNA BINDING PROTEIN; HET: ADP, MLZ, FLC; 1.5A {Homo sapiens},,,6MDW\_A,88.8889,99.8 SIF-Syn:

CDS complement (46252 - 46383)

/gene="88"

/product="gp88"

/function="Hypothetical Protein"

/locus tag="Tucker\_88"

/note=Original Glimmer call @bp 46383 has strength 7.43; Genemark calls start at 46383

/note=SSC: 46383-46252 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X828\_gp028 [Mycobacterium phage Artemis2UCLA] ],,NCBI, q1:s1 100.0% 8.50648E-21 GAP: 8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.623, -4.300637332820981, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X828\_gp028 [Mycobacterium phage Artemis2UCLA] ],,YP\_008858510,100.0,8.50648E-21 SIF-HHPRED: SIF-Syn:

CDS complement (46392 - 46550)

/gene="89"

/product="gp89"

/function="Hypothetical Protein"

/locus tag="Tucker\_89"

/note=Original Glimmer call @bp 46550 has strength 13.07; Genemark calls start at 46550

/note=SSC: 46550-46392 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein AXJ19\_gp026 [Mycobacterium phage VohminGhazi] ],,NCBI, q1:s1 100.0% 8.56383E-30 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.309, -4.701320725655571, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein AXJ19\_gp026 [Mycobacterium phage VohminGhazi] ],,YP\_009224208,100.0,8.56383E-30 SIF-HHPRED: SIF-Syn:

CDS complement (46553 - 46762)

/gene="90"

/product="gp90"

/function="Hypothetical Protein"

/locus tag="Tucker\_90"

/note=Original Glimmer call @bp 46762 has strength 12.99; Genemark calls start at 46762

/note=SSC: 46762-46553 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp026 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 8.37969E-43 GAP: 20 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.11, -2.9845911214398755, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp026 [Mycobacterium phage CloudWang3] ],,YP\_008856859,100.0,8.37969E-43 SIF-HHPRED: GP79 ; Gene product 79,,,PF17463.5,71.0145,100.0 SIF-Syn:

CDS complement (46783 - 47319)

/gene="91"

/product="gp91"

/function="methylase"

/locus tag="Tucker\_91"

/note=Original Glimmer call @bp 47025 has strength 3.8; Genemark calls start at 47319

/note=SSC: 47319-46783 CP: no SCS: both-gm ST: NA BLAST-Start: [methylase [Mycobacterium phage Hammer] ],,NCBI, q1:s1 100.0% 4.24587E-124 GAP: -68 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.065, -7.370345837000447, no F: methylase SIF-BLAST: ,,[methylase [Mycobacterium phage Hammer] ],,YP\_009636605,99.4382,4.24587E-124 SIF-HHPRED: SIF-Syn:

/note=These two DNA Methylase in a row are shared by other phages in the cluster, but start and stops may be off (?).

/note=

/note=Original Glimmer call @bp 47025 has strength 3.80; GeneMark calls start at 47319

/note=

/note=SSC: 46783-47319

/note=CP: yes, extends beyond gene region

/note=SCS: Glimmer called at 47025, GeneMark called at 47319

/note=ST: Indra\_93, Jeffabunny\_78 at 47025

/note=Blast-start: Phagesdb.org: ToneTone\_87, Roksolana\_90, Rifter\_90, Evalue: 4e-42, 1e-41, Function: DNA methylase NCBI: Hammer, CloudWang3, Gladiator, Evalue: 5e-50, 2e-49, Function: DNA methylase

/note=Gap: 21bp gap between 87 and 88, 68bp overlap between 88 and 89

/note=LO: no

/note=RBS: Zvalue:1.065 Final Score: -7.370

/note=F: DNA Methylase

/note=SIF-BLAST:

CDS complement (47252 - 47779)

/gene="92"

/product="gp92"

/function="methylase"

/locus tag="Tucker\_92"

/note=Original Glimmer call @bp 47785 has strength 5.02; Genemark calls start at 47779

/note=SSC: 47779-47252 CP: no SCS: both-gm ST: SS BLAST-Start: [DNA methylase [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 2.59874E-123 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.826, -2.9063687850157054, yes F: methylase SIF-BLAST: ,,[DNA methylase [Mycobacterium phage CloudWang3] ],,YP\_008856861,100.0,2.59874E-123 SIF-HHPRED: c.66.1.26 (A:) automated matches {Haemophilus aegyptius [TaxId: 197575]},,,d3ubta\_,98.2857,100.0 SIF-Syn:

/note=Original Glimmer call @bp 47785 has strength 5.02; GeneMark calls start at 47779

/note=

/note=SSC: 47252-47779

/note=CP: yes

/note=SCS: Glimmer called at 47785 and GeneMark called at 47779

/note=ST: SS92 confirmed by ToneTone\_88, Blue7\_92, and McFly\_89

/note=Blast-start: Phagesdb.org: ToneTone\_88, Rokosolana\_91, Rifter\_91, Evalue: 3e-97, Function: DNA methylase NCBI: CloudWang3, Hammer, Gladiator, Evalue: 7e-123, 9e-123, 1e-121, Function: DNA methylase

/note=Gap: 68bp overlap between 88 and 89, 4bp overlap between 89 and 90

/note=LO: no

/note=RBS: Zvalue: 2.853 Final Score: -2.906

/note=F: DNA methylase

/note=SIF-BLAST:

CDS complement (47776 - 48132)

/gene="93"

/product="gp93"

/function="ParB-like nuclease domain"

/locus tag="Tucker\_93"

/note=Original Glimmer call @bp 48132 has strength 11.09; Genemark calls start at 48132

/note=SSC: 48132-47776 CP: yes SCS: both ST: NI BLAST-Start: [ParB-like nuclease domain protein [Mycobacterium phage ToneTone]],,NCBI, q1:s1 100.0% 1.40903E-80 GAP: 25 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.122, -4.274735973818826, no F: ParB-like nuclease domain SIF-BLAST: ,,[ParB-like nuclease domain protein [Mycobacterium phage ToneTone]],,ANT42277,100.0,1.40903E-80 SIF-HHPRED: ParB\_N\_like\_MT; ParB N-terminal-like domain, some attached to C-terminal S-adenosylmethionine-dependent methyltransferase domain.,,,cd16844,43.2203,99.0 SIF-Syn:

CDS complement (48158 - 48517)

/gene="94"

/product="gp94"

/function="hypothetical protein"

/locus tag="Tucker\_94"

/note=Original Glimmer call @bp 48517 has strength 10.38; Genemark calls start at 48538

/note=SSC: 48517-48158 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_ROKSOLANA\_93 [Mycobacterium phage Roksolana]],,NCBI, q1:s1 100.0% 7.6628E-82 GAP: 17 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.257, -6.656829154529785, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_ROKSOLANA\_93 [Mycobacterium phage Roksolana]],,QYC54090,100.0,7.6628E-82 SIF-HHPRED: SIF-Syn:

CDS complement (48535 - 48732)

/gene="95"

/product="gp95"

/function="hypothetical protein"

/locus tag="Tucker\_95"

/note=Original Glimmer call @bp 48732 has strength 11.68; Genemark calls start at 48732

/note=SSC: 48732-48535 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp021 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 2.2303E-38 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.902, -3.5088110057482766, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X820\_gp021 [Mycobacterium phage CloudWang3] ],,YP\_008856864,100.0,2.2303E-38 SIF-HHPRED: DUF5713 ; Family of unknown function (DUF5713),,,PF18977.3,80.0,65.8 SIF-Syn:

CDS complement (48729 - 48821)

/gene="96"

/product="gp96"

/function="hypothetical protein"

/locus tag="Tucker\_96"

/note=Genemark calls start at 48821

/note=SSC: 48821-48729 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein X820\_gp020 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 3.38593E-11 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.545, -5.5915060314559355, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X820\_gp020 [Mycobacterium phage CloudWang3] ],,YP\_008856865,100.0,3.38593E-11 SIF-HHPRED: DUF5490 ; Family of unknown function (DUF5490),,,PF17593.5,36.6667,50.4 SIF-Syn:

CDS complement (48818 - 49021)

/gene="97"

/product="gp97"

/function="hypothetical protein"

/locus tag="Tucker\_97"

/note=Original Glimmer call @bp 49021 has strength 13.59; Genemark calls start at 49021

/note=SSC: 49021-48818 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp019 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.0556E-40 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.479, -4.16062280240617, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X820\_gp019 [Mycobacterium phage CloudWang3] ],,YP\_008856866,100.0,1.0556E-40 SIF-HHPRED: SIF-Syn:

CDS complement (49021 - 49197)

/gene="98"

/product="gp98"

/function="hypothetical protein"

/locus tag="Tucker\_98"

/note=Original Glimmer call @bp 49197 has strength 9.65; Genemark calls start at 49188

/note=SSC: 49197-49021 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein X820\_gp018 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.80374E-34 GAP: -13 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.959, -3.3861813518867647, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X820\_gp018 [Mycobacterium phage CloudWang3] ],,YP\_008856867,100.0,1.80374E-34 SIF-HHPRED: DUF5419 ; Family of unknown function (DUF5419),,,PF17441.5,84.4828,99.9 SIF-Syn:

CDS complement (49185 - 49313)

/gene="99"

/product="gp99"

/function="hypothetical protein"

/locus tag="Tucker\_99"

/note=Original Glimmer call @bp 49313 has strength 13.24; Genemark calls start at 49313

/note=SSC: 49313-49185 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X821\_gp015 [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 1.1786E-21 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.882, -3.1725816037952645, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X821\_gp015 [Mycobacterium phage Zaka] ],,YP\_008859205,100.0,1.1786E-21 SIF-HHPRED: SIF-Syn:

CDS complement (49313 - 49426)

/gene="100"

/product="gp100"

/function="hypothetical protein"

/locus tag="Tucker\_100"

/note=Original Glimmer call @bp 49426 has strength 11.64; Genemark calls start at 49426

/note=SSC: 49426-49313 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein CL99\_gp015 [Mycobacterium phage Blue7] ],,NCBI, q1:s1 100.0% 1.60026E-18 GAP: 1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.364, -3.8183153089559627, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein CL99\_gp015 [Mycobacterium phage Blue7] ],,YP\_009014588,100.0,1.60026E-18 SIF-HHPRED: SIF-Syn:

/note=SSC: 46.426-49,313 (R)

/note=CP: yes

/note=SCS: Glimmer and GeneMark called at 49426

/note=ST: Artemis2UCLA\_98, BABullseye\_88, Blue7\_100

/note=Blast-start: Phagesdb.org: SuperCallie99\_93, Rifter\_99, 1ndra\_101, Evalue: 2e-19, Function: hypothetical protein NCBI: Blue7, CloudWang3, Zaka, Evalue: 2e-18, 5e-18, 6e-18, Function: hypothetical protein

/note=Gap: 0bp gap between 96 and 97, 2bp gap between 97 and 98

/note=LO: yes

/note=RBS: Zvalue: 2.386 Final Score: -3.818

/note=F: hypothetical protein

/note=SIF-BLAST: NA

CDS complement (49428 - 49700)

/gene="101"

/product="gp101"

/function="hypothetical protein"

/locus tag="Tucker\_101"

/note=Original Glimmer call @bp 49625 has strength 16.26; Genemark calls start at 49625

/note=SSC: 49700-49428 CP: yes SCS: both-cs ST: NI BLAST-Start: [hypothetical protein X820\_gp015 [Mycobacterium phage CloudWang3] ],,NCBI, q22:s1 76.6667% 1.061E-41 GAP: -67 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.025, -4.5445265580148115, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X820\_gp015 [Mycobacterium phage CloudWang3] ],,YP\_008856870,100.0,1.061E-41 SIF-HHPRED: SIF-Syn:

/note=Start changed to 49700 because this includes all of the coding potential and has a higher z value and final score, despite the large gap

/note=

/note=SSC: 49700-49428 (R)

/note=CP: yes

/note=SCS: Glimmer and GeneMark called at 49426

/note=ST: Artemis2UCLA\_98, BABullseye\_88, Blue7\_100

/note=Blast-start: Phagesdb.org: SuperCallie99\_93, Rifter\_99, 1ndra\_101, Evalue: 2e-19, Function: hypothetical protein NCBI: Blue7, CloudWang3, Zaka, Evalue: 2e-18, 5e-18, 6e-18, Function: hypothetical protein

/note=Gap: 0bp gap between 97 and 98, 2bp gap between 98 and 99

/note=LO: yes

/note=RBS: Zvalue: 2.386 Final Score: -3.818

/note=F: hypothetical protein

/note=SIF-BLAST: NA

CDS complement (49634 - 50344)

/gene="102"

/product="gp102"

/function="hypothetical protein"

/locus tag="Tucker\_102"

/note=Original Glimmer call @bp 50344 has strength 9.85; Genemark calls start at 50344

/note=SSC: 50344-49634 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X821\_gp012 [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 1.45974E-174 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.788, -5.0535707005373816, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X821\_gp012 [Mycobacterium phage Zaka] ],,YP\_008859208,100.0,1.45974E-174 SIF-HHPRED: SIF-Syn:

CDS complement (50347 - 50544)

/gene="103"

/product="gp103"

/function="hypothetical protein"

/locus tag="Tucker\_103"

/note=Original Glimmer call @bp 50544 has strength 10.96; Genemark calls start at 50544

/note=SSC: 50544-50347 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X821\_gp011 [Mycobacterium phage Zaka] ],,NCBI, q1:s1 100.0% 1.16647E-38 GAP: 29 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.479, -3.588526034455651, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X821\_gp011 [Mycobacterium phage Zaka] ],,YP\_008859209,100.0,1.16647E-38 SIF-HHPRED: SIF-Syn:

CDS complement (50574 - 50654)

/gene="104"

/product="gp104"

/function="Hypothetical Protein"

/locus tag="Tucker\_104"

/note=

/note=SSC: 50654-50574 CP: yes SCS: neither ST: NA BLAST-Start: [hypothetical protein X820\_gp010 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 2.64909E-9 GAP: 32 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.415, -3.6460682388016923, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp010 [Mycobacterium phage CloudWang3] ],,YP\_008856875,100.0,2.64909E-9 SIF-HHPRED: SIF-Syn:

/note=This gene was manually added.

CDS complement (50687 - 51019)

/gene="105"

/product="gp105"

/function="Hypothetical Protein"

/locus tag="Tucker\_105"

/note=Original Glimmer call @bp 51019 has strength 6.46; Genemark calls start at 51019

/note=SSC: 51019-50687 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein X820\_gp009 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.11111E-71 GAP: -333 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.734, -3.0425830684175623, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp009 [Mycobacterium phage CloudWang3] ],,YP\_008856876,100.0,1.11111E-71 SIF-HHPRED: SIF-Syn:

CDS complement (50687 - 51019)

/gene="106"

/product="gp106"

/function="Hypothetical Protein"

/locus tag="Tucker\_106"

/note=

/note=SSC: 51019-50687 CP: yes SCS: neither ST: SS BLAST-Start: [hypothetical protein X820\_gp009 [Mycobacterium phage CloudWang3] ],,NCBI, q1:s1 100.0% 1.115E-71 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.734, -3.0425830684175623, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein X820\_gp009 [Mycobacterium phage CloudWang3] ],,YP\_008856876,100.0,1.115E-71 SIF-HHPRED: SIF-Syn: