CDS 601 - 753

/gene="1"

/product="gp1"

/function="Hypothetical Protein"

/locus tag="Slagathor\_1"

/note=Original Glimmer call @bp 601 has strength 8.28; Genemark calls start at 601

/note=SSC: 601-753 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_U2\_1 [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 2.5351E-27 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.217, -4.070957012376616, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_U2\_1 [Mycobacterium phage U2] ],,YP\_001491571,100.0,2.5351E-27 SIF-HHPRED: SIF-Syn:

CDS 750 - 1046

/gene="2"

/product="gp2"

/function="HNH endonuclease"

/locus tag="Slagathor\_2"

/note=Original Glimmer call @bp 750 has strength 5.05; Genemark calls start at 750

/note=SSC: 750-1046 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_RUFUS\_2 [Mycobacterium phage Rufus] ],,NCBI, q1:s1 100.0% 1.41378E-63 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.569, -4.234979229026771, yes F: HNH endonuclease SIF-BLAST: ,,[hypothetical protein PBI\_RUFUS\_2 [Mycobacterium phage Rufus] ],,YP\_009199516,100.0,1.41378E-63 SIF-HHPRED: HNH endonuclease; Thermophilic bacteriophage, HNH Endonuclease, DNA nicking, HYDROLASE; 1.52A {Geobacillus virus E2},,,5H0M\_A,62.2449,97.8 SIF-Syn:

CDS 1081 - 1521

/gene="3"

/product="gp3"

/function="terminase, small subunit"

/locus tag="Slagathor\_3"

/note=Original Glimmer call @bp 1081 has strength 10.78; Genemark calls start at 1081

/note=SSC: 1081-1521 CP: yes SCS: both ST: NI BLAST-Start: [gp2 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 5.0353E-102 GAP: 34 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.912, -2.6814417326944517, yes F: terminase, small subunit SIF-BLAST: ,,[gp2 [Mycobacterium phage Bxb1] ],,NP\_075269,100.0,5.0353E-102 SIF-HHPRED: Terminase\_4 ; Phage terminase, small subunit,,,PF05119.15,45.2055,98.1 SIF-Syn:

CDS 1541 - 1852

/gene="4"

/product="gp4"

/function="hypothetical protein"

/locus tag="Slagathor\_4"

/note=

/note=SSC: 1541-1852 CP: yes SCS: neither ST: NI BLAST-Start: [hypothetical protein SEA\_ARCANINE\_4 [Mycobacterium phage Arcanine]],,NCBI, q1:s1 100.0% 2.9171E-65 GAP: 19 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.365, -6.702607070028507, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_ARCANINE\_4 [Mycobacterium phage Arcanine]],,AYD80980,100.0,2.9171E-65 SIF-HHPRED: SIF-Syn:

/note=This gene was added, because there was a big gap between this gene and gene number 3. It was also found in other phages, so that is why we decided to add it.

CDS 1849 - 2919

/gene="5"

/product="gp5"

/function="minor tail protein"

/locus tag="Slagathor\_5"

/note=Original Glimmer call @bp 1849 has strength 9.4; Genemark calls start at 1849

/note=SSC: 1849-2919 CP: yes SCS: both ST: NI BLAST-Start: [minor tail protein [Mycobacterium phage Arcanine]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.296, -6.101211774336551, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Arcanine]],,AYD80981,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 2929 - 3639

/gene="6"

/product="gp6"

/function="Hypothetical Protein"

/locus tag="Slagathor\_6"

/note=Original Glimmer call @bp 2929 has strength 5.59; Genemark calls start at 2929

/note=SSC: 2929-3639 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein SEA\_ARCANINE\_6 [Mycobacterium phage Arcanine]],,NCBI, q1:s1 100.0% 1.20635E-162 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.328, -3.8366550365551095, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ARCANINE\_6 [Mycobacterium phage Arcanine]],,AYD80982,99.5763,1.20635E-162 SIF-HHPRED: SIF-Syn:

CDS 3653 - 3913

/gene="7"

/product="gp7"

/function="Hypothetical Protein"

/locus tag="Slagathor\_7"

/note=Original Glimmer call @bp 3653 has strength 10.04; Genemark calls start at 3653

/note=SSC: 3653-3913 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein FDG63\_gp07 [Mycobacterium phage Marcell] ],,NCBI, q1:s1 100.0% 1.0141E-53 GAP: 13 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.333, -4.352843561762388, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein FDG63\_gp07 [Mycobacterium phage Marcell] ],,YP\_009591847,100.0,1.0141E-53 SIF-HHPRED: SIF-Syn:

CDS 3921 - 4178

/gene="8"

/product="gp8"

/function="Hypothetical Protein"

/locus tag="Slagathor\_8"

/note=Original Glimmer call @bp 3921 has strength 14.3; Genemark calls start at 3921

/note=SSC: 3921-4178 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_U2\_7 [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 6.91155E-52 GAP: 7 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.752, -3.7679082124642584, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_U2\_7 [Mycobacterium phage U2] ],,YP\_001491577,100.0,6.91155E-52 SIF-HHPRED: SIF-Syn:

CDS 4178 - 5611

/gene="9"

/product="gp9"

/function="lysin A"

/locus tag="Slagathor\_9"

/note=Original Glimmer call @bp 4178 has strength 8.54; Genemark calls start at 4178

/note=SSC: 4178-5611 CP: yes SCS: both ST: SS BLAST-Start: [lysin A [Mycobacterium phage Fushigi]],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.022, -7.428818319087355, no F: lysin A SIF-BLAST: ,,[lysin A [Mycobacterium phage Fushigi]],,QAY05661,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 5601 - 6569

/gene="10"

/product="gp10"

/function="lysin B"

/locus tag="Slagathor\_10"

/note=Original Glimmer call @bp 5601 has strength 8.17; Genemark calls start at 5601

/note=SSC: 5601-6569 CP: yes SCS: both ST: SS BLAST-Start: [lysin B [Mycobacterium phage Pinto] ],,NCBI, q1:s1 100.0% 0.0 GAP: -11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.704, -5.220380545373514, no F: lysin B SIF-BLAST: ,,[lysin B [Mycobacterium phage Pinto] ],,YP\_009043796,100.0,0.0 SIF-HHPRED: Gene 12 protein; alpha/beta sandwich, CELL ADHESION; 2.0A {Mycobacterium phage D29},,,3HC7\_A,75.1553,100.0 SIF-Syn:

CDS 6591 - 6905

/gene="11"

/product="gp11"

/function="Hypothetical Protein"

/locus tag="Slagathor\_11"

/note=Original Glimmer call @bp 6591 has strength 10.97; Genemark calls start at 6591

/note=SSC: 6591-6905 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein JMN89\_gp10 [Mycobacterium phage Rajelicia] ],,NCBI, q1:s1 100.0% 1.56636E-69 GAP: 21 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.74, -5.160958035523474, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN89\_gp10 [Mycobacterium phage Rajelicia] ],,YP\_009980345,100.0,1.56636E-69 SIF-HHPRED: Regulator of ribonuclease activity A protein 1; structural genomics, unknown function; HET: MSE; 1.87A {Vibrio cholerae} SCOP: c.8.7.1, l.1.1.1,,,1VI4\_A,28.8462,93.4 SIF-Syn:

CDS 6925 - 8613

/gene="12"

/product="gp12"

/function="terminase, large subunit"

/locus tag="Slagathor\_12"

/note=Original Glimmer call @bp 6925 has strength 9.62; Genemark calls start at 6925

/note=SSC: 6925-8613 CP: yes SCS: both ST: SS BLAST-Start: [terminase [Mycobacterium phage Solon] ],,NCBI, q1:s1 100.0% 0.0 GAP: 19 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.834, -2.8454123590742793, yes F: terminase, large subunit SIF-BLAST: ,,[terminase [Mycobacterium phage Solon] ],,YP\_002223952,100.0,0.0 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,90.9253,100.0 SIF-Syn:

CDS 8610 - 10052

/gene="13"

/product="gp13"

/function="portal protein"

/locus tag="Slagathor\_13"

/note=Original Glimmer call @bp 8610 has strength 9.76; Genemark calls start at 8610

/note=SSC: 8610-10052 CP: yes SCS: both ST: SS BLAST-Start: [portal protein [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.81, -4.423424636048095, no F: portal protein SIF-BLAST: ,,[portal protein [Mycobacterium phage U2] ],,YP\_001491582,100.0,0.0 SIF-HHPRED: PORTAL PROTEIN; BACTERIOPHAGE SPP1, DNA TRANSLOCATION, MOLECULAR MOTOR, VIRAL PORTAL PROTEIN, VIRAL PROTEIN; HET: CA, HG; 3.4A {BACTERIOPHAGE SPP1},,,2JES\_Q,89.5833,100.0 SIF-Syn:

CDS 10049 - 10930

/gene="14"

/product="gp14"

/function="capsid maturation protease"

/locus tag="Slagathor\_14"

/note=Original Glimmer call @bp 10049 has strength 7.54; Genemark calls start at 10049

/note=SSC: 10049-10930 CP: no SCS: both ST: SS BLAST-Start: [capsid maturation protease [Mycobacterium phage Museum] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.121, -4.62669054194548, no F: capsid maturation protease SIF-BLAST: ,,[capsid maturation protease [Mycobacterium phage Museum] ],,YP\_009637263,99.6587,0.0 SIF-HHPRED: Phage\_min\_cap2 ; Phage minor capsid protein 2,,,PF06152.14,57.3379,96.0 SIF-Syn:

CDS 10989 - 11501

/gene="15"

/product="gp15"

/function="scaffolding protein"

/locus tag="Slagathor\_15"

/note=Original Glimmer call @bp 10989 has strength 8.03; Genemark calls start at 10989

/note=SSC: 10989-11501 CP: no SCS: both ST: SS BLAST-Start: [scaffolding protein [Mycobacterium phage Lopton] ],,NCBI, q1:s1 100.0% 4.51548E-115 GAP: 58 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.912, -2.6013996449736907, yes F: scaffolding protein SIF-BLAST: ,,[scaffolding protein [Mycobacterium phage Lopton] ],,YP\_009978897,100.0,4.51548E-115 SIF-HHPRED: DUF4355 ; Domain of unknown function (DUF4355),,,PF14265.9,57.6471,98.0 SIF-Syn:

CDS 11512 - 12513

/gene="16"

/product="gp16"

/function="major capsid protein"

/locus tag="Slagathor\_16"

/note=Original Glimmer call @bp 11512 has strength 11.36; Genemark calls start at 11512

/note=SSC: 11512-12513 CP: no SCS: both ST: NI BLAST-Start: [major capsid protein [Mycobacterium phage Bob3] ],,NCBI, q1:s1 100.0% 0.0 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.229, -1.9310779259753799, yes F: major capsid protein SIF-BLAST: ,,[major capsid protein [Mycobacterium phage Bob3] ],,YP\_009977409,100.0,0.0 SIF-HHPRED: major capsid protein; acne, bacteriophage, HK97-like, VIRUS; 3.7A {Propionibacterium phage PA6},,,3JB5\_C,93.3934,100.0 SIF-Syn:

CDS 12592 - 12828

/gene="17"

/product="gp17"

/function="head-to-tail adaptor"

/locus tag="Slagathor\_17"

/note=Original Glimmer call @bp 12592 has strength 10.6; Genemark calls start at 12592

/note=SSC: 12592-12828 CP: no SCS: both ST: NI BLAST-Start: [gp15 [Mycobacterium phage Bethlehem] ],,NCBI, q1:s1 100.0% 1.0008E-47 GAP: 78 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.494, -3.486006226271621, yes F: head-to-tail adaptor SIF-BLAST: ,,[gp15 [Mycobacterium phage Bethlehem] ],,YP\_001491667,100.0,1.0008E-47 SIF-HHPRED: Coronin-1A; coiled coil, coronin 1, PROTEIN BINDING; 1.2A {N/A},,,2AKF\_C,25.641,92.2 SIF-Syn:

/note=this is the best fit for name of function, head-to-tail connector protein was what evidence suggested this gene to be.

CDS 12828 - 13277

/gene="18"

/product="gp18"

/function="head-to-tail adaptor"

/locus tag="Slagathor\_18"

/note=Original Glimmer call @bp 12828 has strength 12.54; Genemark calls start at 12828

/note=SSC: 12828-13277 CP: no SCS: both ST: NI BLAST-Start: [head-to-tail adaptor [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 9.6448E-104 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.95, -4.778071418780228, yes F: head-to-tail adaptor SIF-BLAST: ,,[head-to-tail adaptor [Mycobacterium phage U2] ],,YP\_001491587,100.0,9.6448E-104 SIF-HHPRED: Phage\_Gp19 ; Phage protein Gp19/Gp15/Gp42,,,PF09355.13,70.4698,99.8 SIF-Syn:

CDS 13322 - 13639

/gene="19"

/product="gp19"

/function="head-to-tail stopper"

/locus tag="Slagathor\_19"

/note=Original Glimmer call @bp 13322 has strength 7.04; Genemark calls start at 13277

/note=SSC: 13322-13639 CP: no SCS: both-gl ST: SS BLAST-Start: [head-to-tail stopper [Mycobacterium phage PattyP] ],,NCBI, q1:s16 100.0% 1.27309E-68 GAP: 44 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.966, -7.069481327841444, no F: head-to-tail stopper SIF-BLAST: ,,[head-to-tail stopper [Mycobacterium phage PattyP] ],,YP\_008050785,87.5,1.27309E-68 SIF-HHPRED: Minor\_capsid\_1 ; Minor capsid protein,,,PF10665.12,91.4286,99.3 SIF-Syn:

CDS 13639 - 14034

/gene="20"

/product="gp20"

/function="Hypothetical Protein"

/locus tag="Slagathor\_20"

/note=Original Glimmer call @bp 13639 has strength 8.94; Genemark calls start at 13639

/note=SSC: 13639-14034 CP: no SCS: both ST: SS BLAST-Start: [gp17 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 3.02849E-91 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.793, -4.968394496817548, no F: Hypothetical Protein SIF-BLAST: ,,[gp17 [Mycobacterium phage Bxb1] ],,NP\_075284,100.0,3.02849E-91 SIF-HHPRED: DUF5403 ; Family of unknown function (DUF5403),,,PF17395.5,84.7328,100.0 SIF-Syn:

/note=function unknown or unidentified

CDS 14038 - 14484

/gene="21"

/product="gp21"

/function="tail terminator"

/locus tag="Slagathor\_21"

/note=Original Glimmer call @bp 14038 has strength 5.86; Genemark calls start at 14038

/note=SSC: 14038-14484 CP: no SCS: both ST: SS BLAST-Start: [gp18 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 2.06428E-102 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.658, -3.2017655760970833, yes F: tail terminator SIF-BLAST: ,,[gp18 [Mycobacterium phage Bxb1] ],,NP\_075285,100.0,2.06428E-102 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,94.5946,99.1 SIF-Syn:

CDS 14493 - 15344

/gene="22"

/product="gp22"

/function="major tail protein"

/locus tag="Slagathor\_22"

/note=Original Glimmer call @bp 14493 has strength 14.11; Genemark calls start at 14493

/note=SSC: 14493-15344 CP: no SCS: both ST: SS BLAST-Start: [major tail protein [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 0.0 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.133, -2.66069824281639, yes F: major tail protein SIF-BLAST: ,,[major tail protein [Mycobacterium phage PattyP] ],,YP\_008050788,100.0,0.0 SIF-HHPRED: Phage\_TTP\_1 ; Phage tail tube protein,,,PF04630.15,46.6431,96.7 SIF-Syn:

CDS 15366 - 15842

/gene="23"

/product="gp23"

/function="tail assembly chaperone"

/locus tag="Slagathor\_23"

/note=Original Glimmer call @bp 15465 has strength 15.14; Genemark calls start at 15465

/note=SSC: 15366-15842 CP: no SCS: both-cs ST: SS BLAST-Start: [tail assembly chaperone [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 1.03349E-109 GAP: 21 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.489, -6.139996578852057, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Mycobacterium phage PattyP] ],,YP\_008050790,99.3671,1.03349E-109 SIF-HHPRED: GP24\_25 ; Mycobacteriophage tail assembly protein,,,PF17388.5,75.3165,100.0 SIF-Syn:

CDS 15893 - 16264

/gene="24"

/product="gp24"

/function="tail assembly chaperone"

/locus tag="Slagathor\_24"

/note=Original Glimmer call @bp 15893 has strength 8.91; Genemark calls start at 15893

/note=SSC: 15893-16264 CP: no SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Mycobacterium phage Acme] ],,NCBI, q1:s144 100.0% 1.08483E-84 GAP: 50 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.704, -5.810157796447017, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Mycobacterium phage Acme] ],,YP\_009976252,46.2406,1.08483E-84 SIF-HHPRED: DUF5361 ; Family of unknown function (DUF5361),,,PF17318.5,36.5854,98.8 SIF-Syn:

/note=found the frame-shift

CDS 16276 - 18747

/gene="25"

/product="gp25"

/function="tape measure protein"

/locus tag="Slagathor\_25"

/note=Original Glimmer call @bp 16276 has strength 8.6; Genemark calls start at 16276

/note=SSC: 16276-18747 CP: no SCS: both ST: NI BLAST-Start: [tapemeasure [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 0.0 GAP: 11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.553, -3.888407369012715, no F: tape measure protein SIF-BLAST: ,,[tapemeasure [Mycobacterium phage PattyP] ],,YP\_008050791,100.0,0.0 SIF-HHPRED: Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_AF,10.3281,99.9 SIF-Syn:

CDS 18771 - 20828

/gene="26"

/product="gp26"

/function="minor tail protein"

/locus tag="Slagathor\_26"

/note=Original Glimmer call @bp 18771 has strength 10.36; Genemark calls start at 18771

/note=SSC: 18771-20828 CP: yes SCS: both ST: NI BLAST-Start: [minor tail protein [Mycobacterium phage Carlyle]],,NCBI, q1:s1 100.0% 0.0 GAP: 23 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.834, -3.2925703904164987, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Carlyle]],,QDM57761,99.854,0.0 SIF-HHPRED: Distal Tail Protein, gp58; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_BD,33.4307,99.6 SIF-Syn:

CDS 20847 - 21029

/gene="27"

/product="gp27"

/function="Hypothetical Protein"

/locus tag="Slagathor\_27"

/note=Original Glimmer call @bp 20847 has strength 13.01; Genemark calls start at 20847

/note=SSC: 20847-21029 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein CL80\_gp26 [Mycobacterium phage Euphoria] ],,NCBI, q1:s1 100.0% 3.23998E-32 GAP: 18 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.74, -5.143229268563043, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein CL80\_gp26 [Mycobacterium phage Euphoria] ],,YP\_009016721,100.0,3.23998E-32 SIF-HHPRED: SIF-Syn:

CDS 21029 - 22831

/gene="28"

/product="gp28"

/function="minor tail protein"

/locus tag="Slagathor\_28"

/note=Original Glimmer call @bp 21029 has strength 10.65; Genemark calls start at 21029

/note=SSC: 21029-22831 CP: yes SCS: both ST: NI BLAST-Start: [minor tail protein [Mycobacterium phage Treddle]],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.438, -5.72088676244897, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Treddle]],,AJA43510,100.0,0.0 SIF-HHPRED: Protein gp18; NP\_465809.1, prophage tail protein gp18, Structural Genomics, Joint Center for Structural Genomics, JCSG, Protein Structure Initiative; HET: MSE, MLY; 1.7A {Listeria monocytogenes EGD-e},,,3GS9\_A,89.8333,99.0 SIF-Syn:

CDS 22926 - 23372

/gene="29"

/product="gp29"

/function="Hypothetical Protein"

/locus tag="Slagathor\_29"

/note=Original Glimmer call @bp 22926 has strength 5.22; Genemark calls start at 22926

/note=SSC: 22926-23372 CP: yes SCS: both ST: NI BLAST-Start: [gp26 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 1.72358E-104 GAP: 94 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.935, -5.3211856022650945, no F: Hypothetical Protein SIF-BLAST: ,,[gp26 [Mycobacterium phage Bxb1] ],,NP\_075293,100.0,1.72358E-104 SIF-HHPRED: DUF2744 ; Protein of unknown function (DUF2744),,,PF10910.11,89.8649,100.0 SIF-Syn:

/note=Hypothetical or minor tail protein?

CDS 23384 - 23716

/gene="30"

/product="gp30"

/function="Hypothetical Protein"

/locus tag="Slagathor\_30"

/note=Original Glimmer call @bp 23384 has strength 10.93; Genemark calls start at 23384

/note=SSC: 23384-23716 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein TROUBLE\_30 [Mycobacterium phage Trouble] ],,NCBI, q1:s1 100.0% 1.36882E-71 GAP: 11 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.588, -5.4833670199227385, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein TROUBLE\_30 [Mycobacterium phage Trouble] ],,YP\_008409762,99.0909,1.36882E-71 SIF-HHPRED: SIF-Syn:

/note=Hypothetical or minor tail protein?

CDS 23713 - 24060

/gene="31"

/product="gp31"

/function="minor tail protein"

/locus tag="Slagathor\_31"

/note=Original Glimmer call @bp 23713 has strength 11.54; Genemark calls start at 23713

/note=SSC: 23713-24060 CP: yes SCS: both ST: NI BLAST-Start: [gp28 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 8.22839E-76 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.456, -6.730876284578336, no F: minor tail protein SIF-BLAST: ,,[gp28 [Mycobacterium phage Bxb1] ],,NP\_075295,100.0,8.22839E-76 SIF-HHPRED: SIF-Syn:

/note=Hypothetical or minor tail protein?

CDS 24085 - 25938

/gene="32"

/product="gp32"

/function="minor tail protein"

/locus tag="Slagathor\_32"

/note=Original Glimmer call @bp 24085 has strength 9.63; Genemark calls start at 24085

/note=SSC: 24085-25938 CP: yes SCS: both ST: NI BLAST-Start: [minor tail protein [Mycobacterium phage HarryOW] ],,NCBI, q1:s1 100.0% 0.0 GAP: 24 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.672, -3.1085431521568267, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage HarryOW] ],,YP\_009978165,99.8379,0.0 SIF-HHPRED: SIF-Syn:

CDS 25931 - 27409

/gene="33"

/product="gp33"

/function="minor tail protein"

/locus tag="Slagathor\_33"

/note=Original Glimmer call @bp 25931 has strength 10.41; Genemark calls start at 25931

/note=SSC: 25931-27409 CP: yes SCS: both ST: NI BLAST-Start: [minor tail protein [Mycobacterium phage Ohno789]],,NCBI, q1:s1 100.0% 0.0 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.142, -4.580504230403352, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Ohno789]],,QYW07394,99.5935,0.0 SIF-HHPRED: e.3.1.0 (A:) automated matches {Acinetobacter baumannii [TaxId: 470]},,,d4neta\_,74.3902,100.0 SIF-Syn:

CDS 27502 - 27822

/gene="34"

/product="gp34"

/function="hypothetical protein"

/locus tag="Slagathor\_34"

/note=Original Glimmer call @bp 27502 has strength 12.85; Genemark calls start at 27502

/note=SSC: 27502-27822 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_MAKEMAKE\_34 [Mycobacterium phage Makemake] ],,NCBI, q1:s1 100.0% 6.18789E-70 GAP: 92 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.723, -5.643021380044263, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_MAKEMAKE\_34 [Mycobacterium phage Makemake] ],,YP\_009286712,100.0,6.18789E-70 SIF-HHPRED: SIF-Syn:

CDS 27832 - 28023

/gene="35"

/product="gp35"

/function="Hypothetical Protein"

/locus tag="Slagathor\_35"

/note=Original Glimmer call @bp 27832 has strength 12.42; Genemark calls start at 27832

/note=SSC: 27832-28023 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein JMN45\_gp35 [Mycobacterium phage Anglerfish] ],,NCBI, q1:s1 100.0% 2.68128E-37 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.229, -2.0111200136961407, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN45\_gp35 [Mycobacterium phage Anglerfish] ],,YP\_009976610,100.0,2.68128E-37 SIF-HHPRED: Fiber Upper, gp68; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_DM,46.0317,97.9 SIF-Syn:

CDS 28020 - 28940

/gene="36"

/product="gp36"

/function="Hypothetical Protein"

/locus tag="Slagathor\_36"

/note=Genemark calls start at 28020

/note=SSC: 28020-28940 CP: yes SCS: genemark ST: NI BLAST-Start: [hypothetical protein JMN98\_gp34 [Mycobacterium phage Snazzy] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.512, -5.6439192539311875, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN98\_gp34 [Mycobacterium phage Snazzy] ],,YP\_009981196,99.3443,0.0 SIF-HHPRED: SIF-Syn:

CDS 29063 - 29359

/gene="37"

/product="gp37"

/function="Hypothetical Protein"

/locus tag="Slagathor\_37"

/note=Original Glimmer call @bp 29063 has strength 8.28; Genemark calls start at 29063

/note=SSC: 29063-29359 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein Jasper\_37 [Mycobacterium phage Jasper] ],,NCBI, q1:s1 100.0% 5.32077E-64 GAP: 122 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.89, -4.843798539558957, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein Jasper\_37 [Mycobacterium phage Jasper] ],,YP\_001994584,100.0,5.32077E-64 SIF-HHPRED: SIF-Syn:

CDS 29511 - 31013

/gene="38"

/product="gp38"

/function="serine integrase"

/locus tag="Slagathor\_38"

/note=Original Glimmer call @bp 29526 has strength 7.41; Genemark calls start at 29526

/note=SSC: 29511-31013 CP: yes SCS: both-cs ST: NI BLAST-Start: [integrase [Mycobacterium phage Arcanine]],,NCBI, q1:s28 100.0% 0.0 GAP: 151 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.159, -4.255713929532742, no F: serine integrase SIF-BLAST: ,,[integrase [Mycobacterium phage Arcanine]],,AYD81012,94.8767,0.0 SIF-HHPRED: SIF-Syn:

/note=I wasn`t for sure on this one because when I blasted it, it only came up with integrase. The only reason I choose serine integrase is because another phage had it, it would be tyrosine integrase, but I went with serine.

CDS complement (31136 - 31408)

/gene="39"

/product="gp39"

/function="Hypothetical Protein"

/locus tag="Slagathor\_39"

/note=Original Glimmer call @bp 31408 has strength 14.67; Genemark calls start at 31408

/note=SSC: 31408-31136 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_SARFIRE\_38 [Mycobacterium phage SarFire] ],,NCBI, q1:s1 100.0% 8.76038E-56 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.834, -3.59360038608048, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_SARFIRE\_38 [Mycobacterium phage SarFire] ],,YP\_008530503,100.0,8.76038E-56 SIF-HHPRED: SIF-Syn:

CDS complement (31405 - 31575)

/gene="40"

/product="gp40"

/function="Hypothetical Protein"

/locus tag="Slagathor\_40"

/note=Original Glimmer call @bp 31584 has strength 3.52; Genemark calls start at 31575

/note=SSC: 31575-31405 CP: yes SCS: both-gm ST: SS BLAST-Start: [hypothetical protein JMO00\_gp041 [Mycobacterium phage STLscum] ],,NCBI, q1:s1 100.0% 3.79297E-34 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.123, -4.622300575606491, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMO00\_gp041 [Mycobacterium phage STLscum] ],,YP\_009981382,82.3529,3.79297E-34 SIF-HHPRED: SIF-Syn:

CDS complement (31572 - 31667)

/gene="41"

/product="gp41"

/function="Hypothetical Protein"

/locus tag="Slagathor\_41"

/note=Genemark calls start at 31667

/note=SSC: 31667-31572 CP: yes SCS: genemark ST: NI BLAST-Start: [gp38 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 2.26231E-11 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.677, -3.098116455756734, yes F: Hypothetical Protein SIF-BLAST: ,,[gp38 [Mycobacterium phage Bxb1] ],,NP\_075305,100.0,2.26231E-11 SIF-HHPRED: SIF-Syn:

CDS complement (31664 - 31936)

/gene="42"

/product="gp42"

/function="Hypothetical Protein"

/locus tag="Slagathor\_42"

/note=Original Glimmer call @bp 31936 has strength 4.3; Genemark calls start at 31936

/note=SSC: 31936-31664 CP: yes SCS: both ST: SS BLAST-Start: [gp40 [Mycobacterium phage Bethlehem] ],,NCBI, q1:s1 100.0% 2.8495E-60 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.065, -4.534089041695007, yes F: Hypothetical Protein SIF-BLAST: ,,[gp40 [Mycobacterium phage Bethlehem] ],,YP\_001491692,100.0,2.8495E-60 SIF-HHPRED: SIF-Syn:

CDS complement (31933 - 32184)

/gene="43"

/product="gp43"

/function="Hypothetical Protein"

/locus tag="Slagathor\_43"

/note=Original Glimmer call @bp 32184 has strength 3.9; Genemark calls start at 32061

/note=SSC: 32184-31933 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_TRIPL3T\_43 [Mycobacterium phage Tripl3t]],,NCBI, q1:s9 100.0% 4.60307E-55 GAP: 35 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.781, -5.822326712960318, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_TRIPL3T\_43 [Mycobacterium phage Tripl3t]],,QBI97196,91.2088,4.60307E-55 SIF-HHPRED: SIF-Syn:

CDS complement (32220 - 32576)

/gene="44"

/product="gp44"

/function="Hypothetical Protein"

/locus tag="Slagathor\_44"

/note=Original Glimmer call @bp 32576 has strength 13.38; Genemark calls start at 32576

/note=SSC: 32576-32220 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein JMN69\_gp43 [Mycobacterium phage Killigrew] ],,NCBI, q1:s1 100.0% 5.1048E-79 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.834, -2.8454123590742793, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN69\_gp43 [Mycobacterium phage Killigrew] ],,YP\_009978744,100.0,5.1048E-79 SIF-HHPRED: SIF-Syn:

CDS complement (32576 - 32854)

/gene="45"

/product="gp45"

/function="Hypothetical Protein"

/locus tag="Slagathor\_45"

/note=Original Glimmer call @bp 32854 has strength 11.46; Genemark calls start at 32854

/note=SSC: 32854-32576 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein JMN76\_gp44 [Mycobacterium phage MaryBeth] ],,NCBI, q1:s1 100.0% 1.46111E-57 GAP: 20 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.122, -2.6835611257758942, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN76\_gp44 [Mycobacterium phage MaryBeth] ],,YP\_009979289,100.0,1.46111E-57 SIF-HHPRED: SIF-Syn:

CDS complement (32875 - 33360)

/gene="46"

/product="gp46"

/function="HNH endonuclease"

/locus tag="Slagathor\_46"

/note=Original Glimmer call @bp 33360 has strength 5.37; Genemark calls start at 33264

/note=SSC: 33360-32875 CP: no SCS: both-gl ST: NI BLAST-Start: [HNH endonuclease [Mycobacterium phage TheloniousMonk] ],,NCBI, q1:s1 100.0% 7.67046E-117 GAP: -23 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.51, -4.552792845506871, no F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Mycobacterium phage TheloniousMonk] ],,YP\_009201058,100.0,7.67046E-117 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,98.1366,100.0 SIF-Syn:

CDS complement (33338 - 35125)

/gene="47"

/product="gp47"

/function="DNA polymerase I"

/locus tag="Slagathor\_47"

/note=Original Glimmer call @bp 35125 has strength 8.55; Genemark calls start at 35125

/note=SSC: 35125-33338 CP: yes SCS: both ST: NI BLAST-Start: [DNA polymerase I [Mycobacterium phage Arcanine] ],,NCBI, q1:s1 100.0% 0.0 GAP: 36 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.483, -3.5707972674952195, no F: DNA polymerase I SIF-BLAST: ,,[DNA polymerase I [Mycobacterium phage Arcanine] ],,AYD81020,100.0,0.0 SIF-HHPRED: DNA polymerase theta; DNA polymerase, Transferase-DNA complex; HET: GOL, DG3; 3.9A {Homo sapiens},,,4X0Q\_B,97.6471,100.0 SIF-Syn:

CDS complement (35162 - 35392)

/gene="48"

/product="gp48"

/function="Hypothetical Protein"

/locus tag="Slagathor\_48"

/note=Original Glimmer call @bp 35392 has strength 13.19; Genemark calls start at 35392

/note=SSC: 35392-35162 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein Jasper\_48 [Mycobacterium phage Jasper] ],,NCBI, q1:s1 100.0% 1.49713E-48 GAP: 30 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.097, -4.387988835334809, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein Jasper\_48 [Mycobacterium phage Jasper] ],,YP\_001994595,100.0,1.49713E-48 SIF-HHPRED: SIF-Syn:

CDS complement (35423 - 35914)

/gene="49"

/product="gp49"

/function="Hypothetical Protein"

/locus tag="Slagathor\_49"

/note=Original Glimmer call @bp 35914 has strength 9.27; Genemark calls start at 35914

/note=SSC: 35914-35423 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein RIDGECB\_47 [Mycobacterium phage RidgeCB] ],,NCBI, q1:s1 100.0% 1.34948E-113 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.891, -2.7254235724530456, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein RIDGECB\_47 [Mycobacterium phage RidgeCB] ],,YP\_009014215,100.0,1.34948E-113 SIF-HHPRED: SIF-Syn:

CDS complement (35911 - 36093)

/gene="50"

/product="gp50"

/function="Hypothetical Protein"

/locus tag="Slagathor\_50"

/note=Original Glimmer call @bp 36093 has strength 9.39; Genemark calls start at 36093

/note=SSC: 36093-35911 CP: no SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_U2\_48 [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 3.49517E-37 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.746, -3.0149320667577513, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_U2\_48 [Mycobacterium phage U2] ],,YP\_001491618,100.0,3.49517E-37 SIF-HHPRED: GP52 ; Phage gene product 52,,,PF17468.5,96.6667,100.0 SIF-Syn:

CDS complement (36090 - 36881)

/gene="51"

/product="gp51"

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

/locus tag="Slagathor\_51"

/note=Original Glimmer call @bp 36881 has strength 8.0; Genemark calls start at 36881

/note=SSC: 36881-36090 CP: yes SCS: both ST: SS BLAST-Start: [helix-turn-helix DNA-binding domain protein [Mycobacterium phage Arcanine]],,NCBI, q1:s1 100.0% 0.0 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.736, -3.036436186053076, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA-binding domain protein [Mycobacterium phage Arcanine]],,AYD81024,100.0,0.0 SIF-HHPRED: RNA polymerase sigma factor; SSGCID, Bartonella quintana, sigma factor, anti-sigma factor, Structural Genomics, Seattle Structural Genomics Center for Infectious Disease; HET: MSE, SO4; 2.45A {Bartonella quintana},,,5UXX\_C,53.6122,98.8 SIF-Syn:

CDS complement (36874 - 37014)

/gene="52"

/product="gp52"

/function="Hypothetical Protein"

/locus tag="Slagathor\_52"

/note=Original Glimmer call @bp 37014 has strength 10.5; Genemark calls start at 37008

/note=SSC: 37014-36874 CP: yes SCS: both-gl ST: SS BLAST-Start: [gp46 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 1.06266E-23 GAP: 4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.232, -4.947056885847969, no F: Hypothetical Protein SIF-BLAST: ,,[gp46 [Mycobacterium phage Bxb1] ],,NP\_075313,100.0,1.06266E-23 SIF-HHPRED: SIF-Syn:

CDS complement (37019 - 38737)

/gene="53"

/product="gp53"

/function="phosphoesterase"

/locus tag="Slagathor\_53"

/note=Original Glimmer call @bp 38737 has strength 8.26; Genemark calls start at 38737

/note=SSC: 38737-37019 CP: yes SCS: both ST: SS BLAST-Start: [phosphoesterase [Mycobacterium phage KBG] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.483, -3.588526034455651, no F: phosphoesterase SIF-BLAST: ,,[phosphoesterase [Mycobacterium phage KBG] ],,YP\_001994511,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS complement (38734 - 38913)

/gene="54"

/product="gp54"

/function="Hypothetical Protein"

/locus tag="Slagathor\_54"

/note=Original Glimmer call @bp 38913 has strength 10.58; Genemark calls start at 38913

/note=SSC: 38913-38734 CP: yes SCS: both ST: SS BLAST-Start: [gp52 [Mycobacterium phage Bethlehem] ],,NCBI, q1:s1 100.0% 4.35539E-34 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.441, -3.738562143838384, yes F: Hypothetical Protein SIF-BLAST: ,,[gp52 [Mycobacterium phage Bethlehem] ],,YP\_001491704,100.0,4.35539E-34 SIF-HHPRED: SIF-Syn:

CDS complement (38910 - 39464)

/gene="55"

/product="gp55"

/function="Hypothetical Protein"

/locus tag="Slagathor\_55"

/note=Original Glimmer call @bp 39464 has strength 9.95; Genemark calls start at 39476

/note=SSC: 39464-38910 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_ARCANINE\_54 [Mycobacterium phage Arcanine] ],,NCBI, q1:s1 100.0% 2.48588E-130 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.647, -3.160956374632079, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ARCANINE\_54 [Mycobacterium phage Arcanine] ],,AYD81028,100.0,2.48588E-130 SIF-HHPRED: DUF6378 ; Domain of unknown function (DUF6378),,,PF19905.2,42.9348,99.9 SIF-Syn:

CDS complement (39461 - 39682)

/gene="56"

/product="gp56"

/function="Hypothetical Protein"

/locus tag="Slagathor\_56"

/note=Original Glimmer call @bp 39682 has strength 10.23; Genemark calls start at 39682

/note=SSC: 39682-39461 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein JMN46\_gp52 [Mycobacterium phage Arlo] ],,NCBI, q1:s1 100.0% 7.36817E-44 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.463, -3.630723714250106, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN46\_gp52 [Mycobacterium phage Arlo] ],,YP\_009976720,100.0,7.36817E-44 SIF-HHPRED: hypothetical protein PH0500; Rossmann fold, tRNA synthetase, nucleotide binding protein, Structural Genomics, RIKEN Structural Genomics/Proteomics Initiative, RSGI, UNKNOWN FUNCTION; HET: GOL; 1.75A {Pyrococcus horikoshii} SCOP: c.120.1.1,,,1V96\_A,49.3151,51.9 SIF-Syn:

CDS complement (39679 - 40140)

/gene="57"

/product="gp57"

/function="DNA primase"

/locus tag="Slagathor\_57"

/note=Original Glimmer call @bp 40140 has strength 6.32; Genemark calls start at 40326

/note=SSC: 40140-39679 CP: yes SCS: both-gl ST: SS BLAST-Start: [DNA primase [Mycobacterium phage Arcanine]],,NCBI, q1:s63 100.0% 1.49821E-106 GAP: 13 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.411, -5.839080406929234, no F: DNA primase SIF-BLAST: ,,[DNA primase [Mycobacterium phage Arcanine]],,AYD81030,71.1628,1.49821E-106 SIF-HHPRED: e.13.1.1 (A:) DNA primase DnaG catalytic core {Escherichia coli [TaxId: 562]},,,d1dd9a\_,98.6928,99.7 SIF-Syn:

CDS complement (40154 - 40564)

/gene="58"

/product="gp58"

/function="DNA primase"

/locus tag="Slagathor\_58"

/note=

/note=SSC: 40564-40154 CP: no SCS: neither ST: SS BLAST-Start: [DNA primase [Mycobacterium phage KBG] ],,NCBI, q1:s1 100.0% 9.8056E-93 GAP: -22 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.93, -4.759312672633257, no F: DNA primase SIF-BLAST: ,,[DNA primase [Mycobacterium phage KBG] ],,YP\_001994514,100.0,9.8056E-93 SIF-HHPRED: SIF-Syn:

/note=ADDED GENE

/note=(bp gap over 400)

CDS complement (40543 - 40692)

/gene="59"

/product="gp59"

/function="Hypothetical Protein"

/locus tag="Slagathor\_59"

/note=Original Glimmer call @bp 40692 has strength 19.36; Genemark calls start at 40707

/note=SSC: 40692-40543 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein PBI\_PATTYP\_57 [Mycobacterium phage PattyP] ],,NCBI, q1:s11 100.0% 8.0047E-28 GAP: 82 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.945, -5.29832271930559, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_PATTYP\_57 [Mycobacterium phage PattyP] ],,YP\_008050822,83.0508,8.0047E-28 SIF-HHPRED: SIF-Syn:

CDS complement (40775 - 40909)

/gene="60"

/product="gp60"

/function="Hypothetical Protein"

/locus tag="Slagathor\_60"

/note=Original Glimmer call @bp 40909 has strength 8.49; Genemark calls start at 40909

/note=SSC: 40909-40775 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein JMN47\_gp62 [Mycobacterium phage Atkinbua] ],,NCBI, q1:s2 100.0% 6.45044E-23 GAP: 25 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.891, -2.6453814847322845, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN47\_gp62 [Mycobacterium phage Atkinbua] ],,YP\_009976826,97.7778,6.45044E-23 SIF-HHPRED: SIF-Syn:

CDS complement (40935 - 42332)

/gene="61"

/product="gp61"

/function="DNA methyltransferase"

/locus tag="Slagathor\_61"

/note=Original Glimmer call @bp 42332 has strength 4.44; Genemark calls start at 42332

/note=SSC: 42332-40935 CP: yes SCS: both ST: SS BLAST-Start: [DNA methylase [Mycobacterium phage Museum] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.891, -2.996490344739583, yes F: DNA methyltransferase SIF-BLAST: ,,[DNA methylase [Mycobacterium phage Museum] ],,YP\_009637308,99.5699,0.0 SIF-HHPRED: Adenine specific DNA methyltransferase (Mod); DNA methyltransferase, sinefungin, DNA BINDING PROTEIN; HET: SFG; 2.65A {Helicobacter pylori 26695},,,6K0W\_B,20.8602,100.0 SIF-Syn:

CDS complement (42329 - 42823)

/gene="62"

/product="gp62"

/function="endonuclease VII"

/locus tag="Slagathor\_62"

/note=Original Glimmer call @bp 42823 has strength 4.69; Genemark calls start at 42823

/note=SSC: 42823-42329 CP: yes SCS: both ST: SS BLAST-Start: [endonuclease VII [Mycobacterium phage BaconJack] ],,NCBI, q1:s1 100.0% 5.29332E-115 GAP: -14 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.739, -3.0301037898918786, yes F: endonuclease VII SIF-BLAST: ,,[endonuclease VII [Mycobacterium phage BaconJack] ],,YP\_009976927,99.3902,5.29332E-115 SIF-HHPRED: Restriction endonuclease Hpy99I; ENDONUCLEASE-DNA COMPLEX, RESTRICTION ENZYME, HPY99I, PSEUDOPALINDROME, HYDROLASE-DNA COMPLEX; HET: 1PE; 1.5A {Helicobacter pylori},,,3GOX\_A,78.0488,99.8 SIF-Syn:

CDS complement (42810 - 42929)

/gene="63"

/product="gp63"

/function="Hypothetical Protein"

/locus tag="Slagathor\_63"

/note=Original Glimmer call @bp 42929 has strength 7.88; Genemark calls start at 42929

/note=SSC: 42929-42810 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein VIOLET\_59 [Mycobacterium phage Violet] ],,NCBI, q1:s1 100.0% 9.74248E-18 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.89, -4.904754965500383, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein VIOLET\_59 [Mycobacterium phage Violet] ],,YP\_009012747,100.0,9.74248E-18 SIF-HHPRED: SIF-Syn:

CDS complement (42926 - 43192)

/gene="64"

/product="gp64"

/function="NrdH-like glutaredoxin"

/locus tag="Slagathor\_64"

/note=Original Glimmer call @bp 43192 has strength 10.44; Genemark calls start at 43192

/note=SSC: 43192-42926 CP: yes SCS: both ST: SS BLAST-Start: [glutaredoxin [Mycobacterium phage Arcanine]],,NCBI, q1:s1 100.0% 3.64601E-58 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.932, -2.6395089437464523, yes F: NrdH-like glutaredoxin SIF-BLAST: ,,[glutaredoxin [Mycobacterium phage Arcanine]],,AYD81037,100.0,3.64601E-58 SIF-HHPRED: SIF-Syn:

CDS complement (43192 - 44013)

/gene="65"

/product="gp65"

/function="DnaB-like dsDNA helicase"

/locus tag="Slagathor\_65"

/note=Original Glimmer call @bp 44013 has strength 9.09; Genemark calls start at 44013

/note=SSC: 44013-43192 CP: yes SCS: both ST: NI BLAST-Start: [DnaB-like dsDNA helicase [Mycobacterium phage Anglerfish] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.65, -3.1550389437754522, yes F: DnaB-like dsDNA helicase SIF-BLAST: ,,[DnaB-like dsDNA helicase [Mycobacterium phage Anglerfish] ],,YP\_009976638,100.0,0.0 SIF-HHPRED: DNAB-Like Replicative Helicase; ATPase, REPLICATION; 3.91A {Bacillus phage SPP1},,,3BGW\_E,98.1685,100.0 SIF-Syn:

CDS complement (44013 - 44186)

/gene="66"

/product="gp66"

/function="Hypothetical Protein"

/locus tag="Slagathor\_66"

/note=Original Glimmer call @bp 44186 has strength 5.6; Genemark calls start at 44186

/note=SSC: 44186-44013 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein SEA\_DUSSY\_65 [Mycobacterium phage Dussy] ],,NCBI, q1:s1 98.2456% 3.53416E-33 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.834, -2.8454123590742793, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_DUSSY\_65 [Mycobacterium phage Dussy] ],,UJE15531,98.2456,3.53416E-33 SIF-HHPRED: SIF-Syn:

CDS complement (44183 - 44305)

/gene="67"

/product="gp67"

/function="Hypothetical Protein"

/locus tag="Slagathor\_67"

/note=Original Glimmer call @bp 44296 has strength 9.98; Genemark calls start at 44290

/note=SSC: 44305-44183 CP: yes SCS: both-cs ST: NI BLAST-Start: [hypothetical protein JMN89\_gp65 [Mycobacterium phage Rajelicia] ],,NCBI, q1:s1 100.0% 1.41085E-16 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.426, -3.628472733356124, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN89\_gp65 [Mycobacterium phage Rajelicia] ],,YP\_009980400,100.0,1.41085E-16 SIF-HHPRED: SIF-Syn:

CDS complement (44302 - 44595)

/gene="68"

/product="gp68"

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

/locus tag="Slagathor\_68"

/note=Original Glimmer call @bp 44595 has strength 12.02; Genemark calls start at 44595

/note=SSC: 44595-44302 CP: yes SCS: both ST: NI BLAST-Start: [helix-turn-helix DNA binding domain protein [Mycobacterium phage ILeeKay] ],,NCBI, q1:s1 100.0% 7.74779E-61 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.406, -3.8116689268127657, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA binding domain protein [Mycobacterium phage ILeeKay] ],,YP\_009978390,98.9691,7.74779E-61 SIF-HHPRED: SIF-Syn:

CDS complement (44592 - 44912)

/gene="69"

/product="gp69"

/function="Hypothetical Protein"

/locus tag="Slagathor\_69"

/note=Original Glimmer call @bp 44912 has strength 10.16; Genemark calls start at 44837

/note=SSC: 44912-44592 CP: no SCS: both-gl ST: NI BLAST-Start: [hypothetical protein SEA\_ARCANINE\_69 [Mycobacterium phage Arcanine]],,NCBI, q1:s1 100.0% 5.00732E-71 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.047, -2.9669382204036308, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ARCANINE\_69 [Mycobacterium phage Arcanine]],,AYD81042,100.0,5.00732E-71 SIF-HHPRED: SIF-Syn:

CDS complement (44916 - 45098)

/gene="70"

/product="gp70"

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

/locus tag="Slagathor\_70"

/note=Original Glimmer call @bp 45098 has strength 4.3; Genemark calls start at 45098

/note=SSC: 45098-44916 CP: yes SCS: both ST: NI BLAST-Start: [gp68 [Mycobacterium phage Bethlehem] ],,NCBI, q1:s1 100.0% 1.60964E-36 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.987, -2.523003374675015, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[gp68 [Mycobacterium phage Bethlehem] ],,YP\_001491720,100.0,1.60964E-36 SIF-HHPRED: Putative DNA-binding protein; BldC, S. coelicolor, developmental switch, MerR-like, DNA BINDING PROTEIN-DNA complex; 3.09A {Streptomyces venezuelae},,,6AMA\_D,93.3333,99.2 SIF-Syn:

CDS complement (45095 - 45253)

/gene="71"

/product="gp71"

/function="Hypothetical Protein"

/locus tag="Slagathor\_71"

/note=Original Glimmer call @bp 45253 has strength 10.36; Genemark calls start at 45253

/note=SSC: 45253-45095 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein SEA\_ARCANINE\_71 [Mycobacterium phage Arcanine]],,NCBI, q1:s1 100.0% 4.9437E-30 GAP: 29 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.218, -2.0162541296952132, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ARCANINE\_71 [Mycobacterium phage Arcanine]],,AYD81044,100.0,4.9437E-30 SIF-HHPRED: SIF-Syn:

CDS complement (45283 - 46101)

/gene="72"

/product="gp72"

/function="Cas4 family exonuclease"

/locus tag="Slagathor\_72"

/note=Original Glimmer call @bp 46101 has strength 8.79; Genemark calls start at 46089

/note=SSC: 46101-45283 CP: no SCS: both-gl ST: NI BLAST-Start: [Cas4 family exonuclease [Mycobacterium phage Museum] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.93, -4.820269098574683, no F: Cas4 family exonuclease SIF-BLAST: ,,[Cas4 family exonuclease [Mycobacterium phage Museum] ],,YP\_009637319,100.0,0.0 SIF-HHPRED: Csa1 ; CRISPR-associated exonuclease Csa1,,,PF06023.15,93.75,99.9 SIF-Syn:

CDS complement (46098 - 46265)

/gene="73"

/product="gp73"

/function="Hypothetical Protein"

/locus tag="Slagathor\_73"

/note=Original Glimmer call @bp 46265 has strength 0.42

/note=SSC: 46265-46098 CP: yes SCS: glimmer ST: NI BLAST-Start: [hypothetical protein PBI\_PATTYP\_72 [Mycobacterium phage PattyP] ],,NCBI, q1:s3 100.0% 1.04447E-31 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.244, -4.842073408680848, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_PATTYP\_72 [Mycobacterium phage PattyP] ],,YP\_008050837,96.4912,1.04447E-31 SIF-HHPRED: SH3\_18 ; CarS bacterial SH3 domain,,,PF18354.4,80.0,94.8 SIF-Syn:

CDS complement (46268 - 46573)

/gene="74"

/product="gp74"

/function="Imm-like superinfection immunity protein"

/locus tag="Slagathor\_74"

/note=Original Glimmer call @bp 46573 has strength 9.12; Genemark calls start at 46573

/note=SSC: 46573-46268 CP: yes SCS: both ST: NI BLAST-Start: [Imm-like protein [Mycobacterium phage Rajelicia] ],,NCBI, q1:s1 100.0% 6.34152E-64 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.065, -2.417348306996335, yes F: Imm-like superinfection immunity protein SIF-BLAST: ,,[Imm-like protein [Mycobacterium phage Rajelicia] ],,YP\_009980410,100.0,6.34152E-64 SIF-HHPRED: Imm\_superinfect ; Superinfection immunity protein,,,PF14373.9,40.5941,99.7 SIF-Syn:

CDS complement (46570 - 46965)

/gene="75"

/product="gp75"

/function="Hypothetical Protein"

/locus tag="Slagathor\_75"

/note=Original Glimmer call @bp 46974 has strength 9.92; Genemark calls start at 46965

/note=SSC: 46965-46570 CP: yes SCS: both-gm ST: NI BLAST-Start: [hypothetical protein SEA\_ARCANINE\_78 [Mycobacterium phage Arcanine]],,NCBI, q1:s4 100.0% 1.02635E-91 GAP: 41 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.075, -4.513234975742373, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ARCANINE\_78 [Mycobacterium phage Arcanine]],,AYD81051,97.7612,1.02635E-91 SIF-HHPRED: GP70 ; Gene product 70,,,PF17429.5,39.6947,99.8 SIF-Syn:

/note=Changed start site to 46965. Better z-score and final score, called in more phages in A1 cluster.

CDS complement (47007 - 47519)

/gene="76"

/product="gp76"

/function="immunity repressor"

/locus tag="Slagathor\_76"

/note=Original Glimmer call @bp 47519 has strength 8.6; Genemark calls start at 47477

/note=SSC: 47519-47007 CP: yes SCS: both-gl ST: NI BLAST-Start: [gp69 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 3.31033E-122 GAP: 261 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.987, -2.523003374675015, yes F: immunity repressor SIF-BLAST: ,,[gp69 [Mycobacterium phage Bxb1] ],,NP\_075336,100.0,3.31033E-122 SIF-HHPRED: DUF2774 ; Protein of unknown function (DUF2774),,,PF11242.11,20.5882,98.5 SIF-Syn:

CDS complement (47781 - 48080)

/gene="77"

/product="gp77"

/function="Hypothetical Protein"

/locus tag="Slagathor\_77"

/note=Original Glimmer call @bp 48080 has strength 8.27; Genemark calls start at 48080

/note=SSC: 48080-47781 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_ALSFRO\_83 [Mycobacterium phage Alsfro] ],,NCBI, q1:s1 100.0% 2.21207E-66 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.979, -5.402512189985548, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_ALSFRO\_83 [Mycobacterium phage Alsfro] ],,YP\_009021651,100.0,2.21207E-66 SIF-HHPRED: SIF-Syn:

CDS complement (48077 - 48349)

/gene="78"

/product="gp78"

/function="Hypothetical Protein"

/locus tag="Slagathor\_78"

/note=Original Glimmer call @bp 48349 has strength 6.7; Genemark calls start at 48244

/note=SSC: 48349-48077 CP: yes SCS: both-gl ST: NI BLAST-Start: [hypothetical protein FGG29\_gp78 [Mycobacterium phage Museum] ],,NCBI, q1:s1 100.0% 1.63925E-58 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.065, -2.2763497933341483, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein FGG29\_gp78 [Mycobacterium phage Museum] ],,YP\_009637326,98.8889,1.63925E-58 SIF-HHPRED: SIF-Syn:

CDS complement (48346 - 48540)

/gene="79"

/product="gp79"

/function="Hypothetical Protein"

/locus tag="Slagathor\_79"

/note=Original Glimmer call @bp 48540 has strength 10.08; Genemark calls start at 48540

/note=SSC: 48540-48346 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein SEA\_ARCANINE\_82 [Mycobacterium phage Arcanine]],,NCBI, q1:s1 100.0% 1.46382E-38 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.679, -5.272053544957485, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ARCANINE\_82 [Mycobacterium phage Arcanine]],,AYD81054,100.0,1.46382E-38 SIF-HHPRED: SIF-Syn:

CDS complement (48537 - 48725)

/gene="80"

/product="gp80"

/function="Hypothetical Protein"

/locus tag="Slagathor\_80"

/note=Original Glimmer call @bp 48725 has strength 10.18; Genemark calls start at 48725

/note=SSC: 48725-48537 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein JMN66\_gp17 [Mycobacterium phage JackSparrow] ],,NCBI, q1:s1 100.0% 1.1498E-34 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.942, -4.732489854405757, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN66\_gp17 [Mycobacterium phage JackSparrow] ],,YP\_009978493,100.0,1.1498E-34 SIF-HHPRED: SIF-Syn:

CDS complement (48725 - 48892)

/gene="81"

/product="gp81"

/function="Hypothetical Protein"

/locus tag="Slagathor\_81"

/note=Original Glimmer call @bp 48892 has strength 7.2; Genemark calls start at 48892

/note=SSC: 48892-48725 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein JMN96\_gp82 [Mycobacterium phage Sibs6] ],,NCBI, q1:s1 100.0% 1.89439E-27 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.834, -2.827683592113848, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN96\_gp82 [Mycobacterium phage Sibs6] ],,YP\_009981049,96.3636,1.89439E-27 SIF-HHPRED: SIF-Syn:

CDS complement (48889 - 49017)

/gene="82"

/product="gp82"

/function="Hypothetical Protein"

/locus tag="Slagathor\_82"

/note=Original Glimmer call @bp 49017 has strength 8.22; Genemark calls start at 49017

/note=SSC: 49017-48889 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_PAPEZ\_86 [Mycobacterium phage Papez] ],,NCBI, q1:s1 100.0% 3.57323E-15 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.834, -2.8454123590742793, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_PAPEZ\_86 [Mycobacterium phage Papez] ],,YP\_009283333,95.2381,3.57323E-15 SIF-HHPRED: SIF-Syn:

CDS complement (49014 - 49196)

/gene="83"

/product="gp83"

/function="Hypothetical Protein"

/locus tag="Slagathor\_83"

/note=Original Glimmer call @bp 49157 has strength 1.06

/note=SSC: 49196-49014 CP: yes SCS: glimmer-cs ST: NI BLAST-Start: [hypothetical protein JMN43\_gp80 [Mycobacterium phage AFIS] ],,NCBI, q1:s1 100.0% 3.00075E-34 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.27, -5.059653572764363, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN43\_gp80 [Mycobacterium phage AFIS] ],,YP\_009976483,96.7213,3.00075E-34 SIF-HHPRED: SIF-Syn:

/note=Changed start site to 49196. Is the longest ORF, scores not as good. Called in more phages in the A1 cluster.

CDS complement (49193 - 49414)

/gene="84"

/product="gp84"

/function="Hypothetical Protein"

/locus tag="Slagathor\_84"

/note=Original Glimmer call @bp 49414 has strength 12.14; Genemark calls start at 49414

/note=SSC: 49414-49193 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein JMN45\_gp86 [Mycobacterium phage Anglerfish] ],,NCBI, q1:s1 100.0% 2.54911E-43 GAP: 25 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.097, -4.325675514574479, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN45\_gp86 [Mycobacterium phage Anglerfish] ],,YP\_009976661,98.6301,2.54911E-43 SIF-HHPRED: SIF-Syn:

CDS complement (49440 - 49589)

/gene="85"

/product="gp85"

/function="Hypothetical Protein"

/locus tag="Slagathor\_85"

/note=Original Glimmer call @bp 49589 has strength 4.84; Genemark calls start at 49541

/note=SSC: 49589-49440 CP: yes SCS: both-gl ST: NI BLAST-Start: [hypothetical protein SEA\_TASP14\_82 [Mycobacterium phage Tasp14] ],,NCBI, q1:s10 100.0% 5.3295E-25 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.429, -4.7244367426328875, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_TASP14\_82 [Mycobacterium phage Tasp14] ],,YP\_009197660,84.4828,5.3295E-25 SIF-HHPRED: DUF6482 ; Family of unknown function (DUF6482),,,PF20090.2,65.3061,90.9 SIF-Syn:

CDS complement (49586 - 49813)

/gene="86"

/product="gp86"

/function="Hypothetical Protein"

/locus tag="Slagathor\_86"

/note=Original Glimmer call @bp 49813 has strength 10.6; Genemark calls start at 49813

/note=SSC: 49813-49586 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein FGG18\_gp12 [Mycobacterium phage BPBiebs31] ],,NCBI, q1:s1 100.0% 1.87764E-45 GAP: 68 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.097, -4.325675514574479, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein FGG18\_gp12 [Mycobacterium phage BPBiebs31] ],,YP\_009637619,100.0,1.87764E-45 SIF-HHPRED: SIF-Syn:

CDS complement (49882 - 49995)

/gene="87"

/product="gp87"

/function="Hypothetical Protein"

/locus tag="Slagathor\_87"

/note=

/note=SSC: 49995-49882 CP: no SCS: neither ST: NI BLAST-Start: [hypothetical protein JMN59\_gp79 [Mycobacterium phage Crispicous1] ],,NCBI, q1:s1 100.0% 2.21222E-14 GAP: -44 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.342, -6.574823874961161, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN59\_gp79 [Mycobacterium phage Crispicous1] ],,YP\_009977848,91.8919,2.21222E-14 SIF-HHPRED: SIF-Syn:

/note=Gene appears in other phages on Phamerator with same length and similar overlap (i.e. Arcanine)

CDS complement (49952 - 50083)

/gene="88"

/product="gp88"

/function="Hypothetical Protein"

/locus tag="Slagathor\_88"

/note=

/note=SSC: 50083-49952 CP: yes SCS: neither ST: NI BLAST-Start: [hypothetical protein JMN62\_gp87 [Mycobacterium phage GageAP] ],,NCBI, q1:s1 100.0% 4.16298E-22 GAP: 17 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.418, -6.591314556970386, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN62\_gp87 [Mycobacterium phage GageAP] ],,YP\_009978129,100.0,4.16298E-22 SIF-HHPRED: SIF-Syn:

/note=Added gene. Found in Arcanine, GageAP (both in A1).

CDS complement (50101 - 50784)

/gene="89"

/product="gp89"

/function="DNA methyltransferase"

/locus tag="Slagathor\_89"

/note=Original Glimmer call @bp 50784 has strength 11.01; Genemark calls start at 50769

/note=SSC: 50784-50101 CP: yes SCS: both-gl ST: NI BLAST-Start: [DNA methylase [Mycobacterium phage Hope4ever] ],,NCBI, q1:s3 100.0% 7.56795E-169 GAP: 19 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.834, -2.8454123590742793, yes F: DNA methyltransferase SIF-BLAST: ,,[DNA methylase [Mycobacterium phage Hope4ever] ],,AXH47545,99.1266,7.56795E-169 SIF-HHPRED: Cytosine-specific methyltransferase; METHYLTRANSFERASE, DNA-BINDING, NAD-BINDING, STRUCTURAL GENOMICS, PROTEIN STRUCTURE INITIATIVE, PSI, NEW YORK STRUCTURAL GENOMIX RESEARCH CONSORTIUM, NYSGXRC; HET: GOL; 1.75A {Escherichia coli O157:H7 EDL933},,,5GUT\_A,94.7137,100.0 SIF-Syn:

CDS complement (50804 - 50887)

/gene="90"

/product="gp90"

/function="Hypothetical Protein"

/locus tag="Slagathor\_90"

/note=

/note=SSC: 50887-50804 CP: no SCS: neither ST: NI BLAST-Start: [hypothetical protein JMN45\_gp91 [Mycobacterium phage Anglerfish] ],,NCBI, q1:s6 100.0% 3.0162E-6 GAP: 91 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.066, -5.492537754859381, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN45\_gp91 [Mycobacterium phage Anglerfish] ],,YP\_009976666,81.25,3.0162E-6 SIF-HHPRED: SIF-Syn:

/note=Added gene. Found in Arcanine and Gage AP.

CDS complement (50979 - 51233)

/gene="91"

/product="gp91"

/function="Hypothetical Protein"

/locus tag="Slagathor\_91"

/note=Original Glimmer call @bp 51233 has strength 6.04; Genemark calls start at 51233

/note=SSC: 51233-50979 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein JMN45\_gp92 [Mycobacterium phage Anglerfish] ],,NCBI, q1:s48 100.0% 2.53426E-54 GAP: 155 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.579, -3.4470622626190464, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JMN45\_gp92 [Mycobacterium phage Anglerfish] ],,YP\_009976667,63.3588,2.53426E-54 SIF-HHPRED: SIF-Syn:

CDS complement (51389 - 51592)

/gene="92"

/product="gp92"

/function="Hypothetical Protein"

/locus tag="Slagathor\_92"

/note=Original Glimmer call @bp 51592 has strength 10.93; Genemark calls start at 51592

/note=SSC: 51592-51389 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_PATTYP\_92 [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 2.15051E-38 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.122, -2.6835611257758942, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_PATTYP\_92 [Mycobacterium phage PattyP] ],,YP\_008050857,97.0149,2.15051E-38 SIF-HHPRED: SIF-Syn: