CDS 430 - 1260

 /gene="1"

 /product="gp1"

 /function="hypothetical protein"

 /locus tag="Anaysia\_1"

 /note=Original Glimmer call @bp 430 has strength 4.84; Genemark calls start at 430

 /note=SSC: 430-1260 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BIZ67\_gp001 [Gordonia phage Remus] ],,NCBI, q1:s1 100.0% 0.0 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.943, -5.050866358565014, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ67\_gp001 [Gordonia phage Remus] ],,YP\_009281615,100.0,0.0 SIF-HHPRED: DUF4417 ; Domain of unknown function (DUF4417),,,PF14386.9,62.3188,100.0 SIF-Syn:

CDS 1335 - 1985

 /gene="2"

 /product="gp2"

 /function="VIP2-like ADP-ribosyltransferase toxin"

 /locus tag="Anaysia\_2"

 /note=Original Glimmer call @bp 1335 has strength 8.92; Genemark calls start at 1335

 /note=SSC: 1335-1985 CP: yes SCS: both ST: NA BLAST-Start: [ADP-ribosyltransferase [Gordonia phage Remus] ],,NCBI, q1:s80 100.0% 1.70049E-160 GAP: 74 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.046, -4.833322097261781, no F: VIP2-like ADP-ribosyltransferase toxin SIF-BLAST: ,,[ADP-ribosyltransferase [Gordonia phage Remus] ],,YP\_009281616,73.2203,1.70049E-160 SIF-HHPRED: d.166.1.1 (A:) Exoenzyme c3 {Clostridium botulinum C bacteriophage [TaxId: 12336]},,,d1r45a\_,97.6852,99.6 SIF-Syn:

CDS 1982 - 2281

 /gene="3"

 /product="gp3"

 /function="hypothetical protein"

 /locus tag="Anaysia\_3"

 /note=Original Glimmer call @bp 1982 has strength 12.53; Genemark calls start at 1982

 /note=SSC: 1982-2281 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp003 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 4.50653E-66 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.439, -3.790975366313636, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp003 [Gordonia phage Rosalind] ],,YP\_009268927,100.0,4.50653E-66 SIF-HHPRED: SIF-Syn:

 /note=HHPRED not informative

CDS 2278 - 2574

 /gene="4"

 /product="gp4"

 /function="HNH endonuclease"

 /locus tag="Anaysia\_4"

 /note=Original Glimmer call @bp 2368 has strength 5.46; Genemark calls start at 2368

 /note=SSC: 2278-2574 CP: yes SCS: both-cs ST: NA BLAST-Start: [HNH endonuclease [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 2.17733E-65 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.758, -5.2334963460608455, yes F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Gordonia phage Rosalind] ],,YP\_009268928,100.0,2.17733E-65 SIF-HHPRED: SIF-Syn:

CDS 2610 - 3065

 /gene="5"

 /product="gp5"

 /function="terminase, small subunit"

 /locus tag="Anaysia\_5"

 /note=Original Glimmer call @bp 2610 has strength 12.97; Genemark calls start at 2610

 /note=SSC: 2610-3065 CP: yes SCS: both ST: NA BLAST-Start: [terminase small subunit [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 4.38357E-106 GAP: 35 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.934, -2.6013996449736907, yes F: terminase, small subunit SIF-BLAST: ,,[terminase small subunit [Gordonia phage Rosalind] ],,YP\_009268929,100.0,4.38357E-106 SIF-HHPRED: Terminase\_4 ; Phage terminase, small subunit,,,PF05119.15,46.3576,98.7 SIF-Syn:

CDS 3082 - 3417

 /gene="6"

 /product="gp6"

 /function="hypothetical protein"

 /locus tag="Anaysia\_6"

 /note=Original Glimmer call @bp 3082 has strength 11.98; Genemark calls start at 3082

 /note=SSC: 3082-3417 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp006 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 1.75689E-74 GAP: 16 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.25, -2.0111200136961407, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp006 [Gordonia phage Rosalind] ],,YP\_009268930,100.0,1.75689E-74 SIF-HHPRED: SIF-Syn:

CDS 3414 - 4406

 /gene="7"

 /product="gp7"

 /function="hypothetical protein"

 /locus tag="Anaysia\_7"

 /note=Original Glimmer call @bp 3414 has strength 10.64; Genemark calls start at 3414

 /note=SSC: 3414-4406 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BIZ70\_gp007 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.806, -5.0535707005373816, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp007 [Gordonia phage JSwag] ],,YP\_009285951,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 4403 - 5071

 /gene="8"

 /product="gp8"

 /function="hypothetical protein"

 /locus tag="Anaysia\_8"

 /note=Original Glimmer call @bp 4403 has strength 4.26; Genemark calls start at 4403

 /note=SSC: 4403-5071 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein BIZ70\_gp008 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 6.77336E-148 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.089, -4.4713484557894425, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp008 [Gordonia phage JSwag] ],,YP\_009285952,100.0,6.77336E-148 SIF-HHPRED: SIF-Syn:

tRNA 5142 - 5217

 /gene="9"

 /product="tRNA-Asn(gtt)"

 /locus tag="ANAYSIA\_9"

 /note=tRNA-Asn(gtt)

tRNA 5219 - 5292

 /gene="10"

 /product="tRNA-Lys(ctt)"

 /locus tag="ANAYSIA\_10"

 /note=tRNA-Lys(ctt)

tRNA 5294 - 5366

 /gene="11"

 /product="tRNA-Gln(ctg)"

 /locus tag="ANAYSIA\_11"

 /note=tRNA-Gln(ctg)

CDS 5392 - 6432

 /gene="12"

 /product="gp12"

 /function="lysin A"

 /locus tag="Anaysia\_12"

 /note=Original Glimmer call @bp 5392 has strength 10.46; Genemark calls start at 5392

 /note=SSC: 5392-6432 CP: yes SCS: both ST: NI BLAST-Start: [lysin A [Gordonia phage Soups] ],,NCBI, q1:s1 100.0% 0.0 GAP: 320 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.24, -2.033982896655645, yes F: lysin A SIF-BLAST: ,,[lysin A [Gordonia phage Soups] ],,YP\_009269310,100.0,0.0 SIF-HHPRED: d.118.1.1 (A:1-157) N-acetylmuramoyl-L-alanine amidase PlyG {Anthrax bacillus (Bacillus anthracis) [TaxId: 1392]},,,d1yb0a1,40.1734,99.7 SIF-Syn:

CDS 6443 - 6670

 /gene="13"

 /product="gp13"

 /function="holin"

 /locus tag="Anaysia\_13"

 /note=Original Glimmer call @bp 6443 has strength 10.11; Genemark calls start at 6482

 /note=SSC: 6443-6670 CP: yes SCS: both-gl ST: SS BLAST-Start: [holin [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 1.07429E-44 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.087, -2.8035499123971284, yes F: holin SIF-BLAST: ,,[holin [Gordonia phage Rosalind] ],,YP\_009268934,100.0,1.07429E-44 SIF-HHPRED: Phage\_holin\_7\_1 ; Mycobacterial 2 TMS Phage Holin (M2 Hol) Family,,,PF16081.8,82.6667,99.6 SIF-Syn:

CDS 6686 - 8383

 /gene="14"

 /product="gp14"

 /function="terminase, large subunit"

 /locus tag="Anaysia\_14"

 /note=Original Glimmer call @bp 6686 has strength 10.24; Genemark calls start at 6686

 /note=SSC: 6686-8383 CP: yes SCS: both ST: SS BLAST-Start: [terminase [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 0.0 GAP: 15 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.24, -2.033982896655645, yes F: terminase, large subunit SIF-BLAST: ,,[terminase [Gordonia phage Rosalind] ],,YP\_009268935,100.0,0.0 SIF-HHPRED: Terminase large subunit; genome packaging, bacteriophage, ATPase, nuclease, VIRAL PROTEIN; HET: BR; 2.2A {Enterobacteria phage HK97},,,6Z6D\_A,91.3274,100.0 SIF-Syn:

CDS 8380 - 9840

 /gene="15"

 /product="gp15"

 /function="portal protein"

 /locus tag="Anaysia\_15"

 /note=Original Glimmer call @bp 8380 has strength 9.81; Genemark calls start at 8380

 /note=SSC: 8380-9840 CP: yes SCS: both ST: SS BLAST-Start: [portal protein [Gordonia phage Soups] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.012, -4.696275508110696, no F: portal protein SIF-BLAST: ,,[portal protein [Gordonia phage Soups] ],,YP\_009269313,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 9837 - 10697

 /gene="16"

 /product="gp16"

 /function="capsid maturation protease"

 /locus tag="Anaysia\_16"

 /note=Original Glimmer call @bp 9837 has strength 10.85; Genemark calls start at 9837

 /note=SSC: 9837-10697 CP: yes SCS: both ST: SS BLAST-Start: [capsid maturation protease [Gordonia phage Soups] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.009, -2.583959800616441, yes F: capsid maturation protease SIF-BLAST: ,,[capsid maturation protease [Gordonia phage Soups] ],,YP\_009269314,100.0,0.0 SIF-HHPRED: Phage\_min\_cap2 ; Phage minor capsid protein 2,,,PF06152.14,56.6434,96.2 SIF-Syn:

CDS 10750 - 11262

 /gene="17"

 /product="gp17"

 /function="scaffolding protein"

 /locus tag="Anaysia\_17"

 /note=Original Glimmer call @bp 10750 has strength 16.8; Genemark calls start at 10750

 /note=SSC: 10750-11262 CP: yes SCS: both ST: SS BLAST-Start: [scaffolding protein [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 4.46165E-120 GAP: 52 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.934, -2.7423981586358774, yes F: scaffolding protein SIF-BLAST: ,,[scaffolding protein [Gordonia phage Rosalind] ],,YP\_009268938,100.0,4.46165E-120 SIF-HHPRED: SIF-Syn:

CDS 11295 - 12245

 /gene="18"

 /product="gp18"

 /function="major capsid protein"

 /locus tag="Anaysia\_18"

 /note=Original Glimmer call @bp 11295 has strength 13.05; Genemark calls start at 11295

 /note=SSC: 11295-12245 CP: yes SCS: both ST: SS BLAST-Start: [major capsid protein [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 0.0 GAP: 32 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.009, -2.583959800616441, yes F: major capsid protein SIF-BLAST: ,,[major capsid protein [Gordonia Phage Boohoo]],,UAJ15510,100.0,0.0 SIF-HHPRED: Major head protein; major capsid protein, HK97-like fold, scaffolding protein, procapsid, VIRUS; 3.72A {Staphylococcus phage 80alpha},,,6B0X\_G,92.0886,100.0 SIF-Syn:

CDS 12316 - 12486

 /gene="19"

 /product="gp19"

 /function="hypothetical protein"

 /locus tag="Anaysia\_19"

 /note=Original Glimmer call @bp 12316 has strength 10.07; Genemark calls start at 12316

 /note=SSC: 12316-12486 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_BOOHOO\_19 [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 1.73958E-31 GAP: 70 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.611, -4.113180079823027, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_BOOHOO\_19 [Gordonia Phage Boohoo]],,UAJ15511,100.0,1.73958E-31 SIF-HHPRED: SIF-Syn:

CDS 12490 - 12867

 /gene="20"

 /product="gp20"

 /function="head-to-tail adaptor"

 /locus tag="Anaysia\_20"

 /note=Original Glimmer call @bp 12490 has strength 14.37; Genemark calls start at 12490

 /note=SSC: 12490-12867 CP: yes SCS: both ST: SS BLAST-Start: [head-to-tail adaptor [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 5.33654E-84 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.934, -2.6013996449736907, yes F: head-to-tail adaptor SIF-BLAST: ,,[head-to-tail adaptor [Gordonia phage Rosalind] ],,YP\_009268941,100.0,5.33654E-84 SIF-HHPRED: SIF-Syn:

CDS 12864 - 13061

 /gene="21"

 /product="gp21"

 /function="hypothetical protein"

 /locus tag="Anaysia\_21"

 /note=Original Glimmer call @bp 12864 has strength 7.45; Genemark calls start at 12864

 /note=SSC: 12864-13061 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp090 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 7.56019E-40 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.089, -4.532304881730868, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp090 [Gordonia phage Rosalind] ],,YP\_009268942,100.0,7.56019E-40 SIF-HHPRED: SIF-Syn:

CDS 13048 - 13416

 /gene="22"

 /product="gp22"

 /function="head-to-tail stopper"

 /locus tag="Anaysia\_22"

 /note=Original Glimmer call @bp 13048 has strength 16.03; Genemark calls start at 13048

 /note=SSC: 13048-13416 CP: yes SCS: both ST: NA BLAST-Start: [head-to-tail stopper [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 1.26133E-84 GAP: -14 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.857, -2.827683592113848, yes F: head-to-tail stopper SIF-BLAST: ,,[head-to-tail stopper [Gordonia phage Rosalind] ],,YP\_009268943,100.0,1.26133E-84 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\_E,93.4426,99.4 SIF-Syn:

CDS 13416 - 13784

 /gene="23"

 /product="gp23"

 /function="hypothetical protein"

 /locus tag="Anaysia\_23"

 /note=Original Glimmer call @bp 13416 has strength 10.2; Genemark calls start at 13416

 /note=SSC: 13416-13784 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein BEN61\_gp088 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 4.65795E-84 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.175, -6.407191719987598, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp088 [Gordonia phage Rosalind] ],,YP\_009268944,100.0,4.65795E-84 SIF-HHPRED: DUF5403 ; Family of unknown function (DUF5403),,,PF17395.5,92.6229,99.9 SIF-Syn:

CDS 13797 - 14207

 /gene="24"

 /product="gp24"

 /function="tail terminator"

 /locus tag="Anaysia\_24"

 /note=Original Glimmer call @bp 13797 has strength 8.17; Genemark calls start at 13806

 /note=SSC: 13797-14207 CP: yes SCS: both-gl ST: NA BLAST-Start: [tail terminator [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 7.4735E-94 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.009, -2.523003374675015, yes F: tail terminator SIF-BLAST: ,,[tail terminator [Gordonia phage Rosalind] ],,YP\_009268945,100.0,7.4735E-94 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,93.3824,99.2 SIF-Syn:

CDS 14232 - 14834

 /gene="25"

 /product="gp25"

 /function="major tail protein"

 /locus tag="Anaysia\_25"

 /note=Original Glimmer call @bp 14232 has strength 12.68; Genemark calls start at 14253

 /note=SSC: 14232-14834 CP: yes SCS: both-gl ST: NA BLAST-Start: [major tail protein [Gordonia phage Remus] ],,NCBI, q1:s1 100.0% 5.35523E-145 GAP: 24 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.24, -1.953940808934884, yes F: major tail protein SIF-BLAST: ,,[major tail protein [Gordonia phage Remus] ],,YP\_009281636,100.0,5.35523E-145 SIF-HHPRED: YSD1\_22 major tail protein; Bacteriophage tail, helical assembly, VIRAL PROTEIN; 3.5A {Bacteriophage sp.},,,6XGR\_M,98.0,98.0 SIF-Syn:

CDS 14948 - 15331

 /gene="26"

 /product="gp26"

 /function="tail assembly chaperone"

 /locus tag="Anaysia\_26"

 /note=Original Glimmer call @bp 14948 has strength 16.82; Genemark calls start at 14948

 /note=SSC: 14948-15331 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 2.13072E-85 GAP: 113 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.516, -3.487629880782256, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Gordonia phage Rosalind] ],,YP\_009268948,100.0,2.13072E-85 SIF-HHPRED: GP24\_25 ; Mycobacteriophage tail assembly protein,,,PF17388.5,95.2756,100.0 SIF-Syn:

CDS join(14948..15307,15307..15852)

 /gene="27"

 /product="gp27"

 /function="tail assembly chaperone"

 /locus tag="Anaysia\_27"

 /note=

 /note=SSC: 14948-15852 CP: no SCS: neither ST: NI BLAST-Start: [tail assembly chaperone [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 0.0 GAP: -384 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.516, -3.487629880782256, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Gordonia phage Rosalind] ],,YP\_009268947,100.0,0.0 SIF-HHPRED: GP24\_25 ; Mycobacteriophage tail assembly protein,,,PF17388.5,40.1993,100.0 SIF-Syn:

CDS 15923 - 18112

 /gene="28"

 /product="gp28"

 /function="tape measure protein"

 /locus tag="Anaysia\_28"

 /note=Original Glimmer call @bp 15923 has strength 10.66; Genemark calls start at 15755

 /note=SSC: 15923-18112 CP: no SCS: both-gl ST: NA BLAST-Start: [tape measure protein [Gordonia phage Waits] ],,NCBI, q1:s1 100.0% 0.0 GAP: 69 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.576, -5.558419310177749, no F: tape measure protein SIF-BLAST: ,,[tape measure protein [Gordonia phage Waits] ],,YP\_009624543,100.0,0.0 SIF-HHPRED: Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_AF,13.0316,99.9 SIF-Syn:

CDS 18122 - 19099

 /gene="29"

 /product="gp29"

 /function="minor tail protein"

 /locus tag="Anaysia\_29"

 /note=Original Glimmer call @bp 18122 has strength 7.89; Genemark calls start at 18122

 /note=SSC: 18122-19099 CP: no SCS: both ST: SS BLAST-Start: [minor tail protein [Gordonia phage Soups] ],,NCBI, q1:s1 100.0% 0.0 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.12, -4.325675514574479, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Gordonia phage Soups] ],,YP\_009269327,100.0,0.0 SIF-HHPRED: Distal Tail Protein, gp58; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_BD,96.9231,99.9 SIF-Syn:

CDS 19096 - 20883

 /gene="30"

 /product="gp30"

 /function="minor tail protein"

 /locus tag="Anaysia\_30"

 /note=Original Glimmer call @bp 19072 has strength 10.46; Genemark calls start at 19072

 /note=SSC: 19096-20883 CP: yes SCS: both-cs ST: NA BLAST-Start: [minor tail protein [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.109, -4.349108688274226, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Gordonia phage Rosalind] ],,YP\_009268951,100.0,0.0 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,94.4538,99.0 SIF-Syn:

CDS 20968 - 21411

 /gene="31"

 /product="gp31"

 /function="hypothetical protein"

 /locus tag="Anaysia\_31"

 /note=Original Glimmer call @bp 20968 has strength 8.26; Genemark calls start at 20968

 /note=SSC: 20968-21411 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 2.04735E-105 GAP: 84 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.774, -3.019720185458058, no F: hypothetical protein SIF-BLAST: ,,[minor tail protein [Gordonia phage Rosalind] ],,YP\_009268952,100.0,2.04735E-105 SIF-HHPRED: DUF2744 ; Protein of unknown function (DUF2744),,,PF10910.11,90.4762,100.0 SIF-Syn:

CDS 21408 - 21749

 /gene="32"

 /product="gp32"

 /function="hypothetical protein"

 /locus tag="Anaysia\_32"

 /note=Original Glimmer call @bp 21408 has strength 13.32; Genemark calls start at 21408

 /note=SSC: 21408-21749 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 1.16972E-76 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.165, -2.1924212546750814, yes F: hypothetical protein SIF-BLAST: ,,[membrane protein [Gordonia Phage Boohoo]],,UAJ15523,100.0,1.16972E-76 SIF-HHPRED: DUF2746 ; Protein of unknown function (DUF2746),,,PF10874.11,92.0354,99.9 SIF-Syn:

CDS 21746 - 23458

 /gene="33"

 /product="gp33"

 /function="minor tail protein"

 /locus tag="Anaysia\_33"

 /note=Original Glimmer call @bp 21746 has strength 7.66; Genemark calls start at 21746

 /note=SSC: 21746-23458 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.581, -3.4283035164720754, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Gordonia phage Rosalind] ],,YP\_009268954,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 23538 - 23894

 /gene="34"

 /product="gp34"

 /function="Lsr2-like DNA bridging protein"

 /locus tag="Anaysia\_34"

 /note=Original Glimmer call @bp 23562 has strength 6.89; Genemark calls start at 23562

 /note=SSC: 23538-23894 CP: yes SCS: both-cs ST: SS BLAST-Start: [Lsr2-like DNA bridging protein [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 1.80945E-82 GAP: 79 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.735, -6.242699631495065, no F: Lsr2-like DNA bridging protein SIF-BLAST: ,,[Lsr2-like DNA bridging protein [Gordonia phage Rosalind] ],,YP\_009268955,100.0,1.80945E-82 SIF-HHPRED: Lsr2 ; Lsr2,,,PF11774.11,97.4576,100.0 SIF-Syn:

CDS 23891 - 24199

 /gene="35"

 /product="gp35"

 /function="hypothetical protein"

 /locus tag="Anaysia\_35"

 /note=Original Glimmer call @bp 23891 has strength 3.55; Genemark calls start at 23891

 /note=SSC: 23891-24199 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp076 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 7.50526E-68 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.791, -5.103155778211132, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp076 [Gordonia phage Rosalind] ],,YP\_009268956,100.0,7.50526E-68 SIF-HHPRED: SIF-Syn:

CDS 24673 - 25248

 /gene="36"

 /product="gp36"

 /function="ParA-like dsDNA partitioning protein"

 /locus tag="Anaysia\_36"

 /note=Original Glimmer call @bp 24673 has strength 13.67; Genemark calls start at 24673

 /note=SSC: 24673-25248 CP: yes SCS: both ST: SS BLAST-Start: [ParA-like dsDNA partitioning protein [Gordonia phage MinecraftSteve] ],,NCBI, q1:s1 100.0% 3.23152E-134 GAP: 473 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.619, -5.467555466772303, no F: ParA-like dsDNA partitioning protein SIF-BLAST: ,,[ParA-like dsDNA partitioning protein [Gordonia phage MinecraftSteve] ],,QFP95101,100.0,3.23152E-134 SIF-HHPRED: Plasmid partitioning protein ParF; deviant walker box, dna segregation, UNKNOWN FUNCTION; HET: ADP; 1.8A {Escherichia coli},,,4DZZ\_A,96.3351,99.9 SIF-Syn:

CDS 25241 - 25555

 /gene="37"

 /product="gp37"

 /function="ParB-like dsDNA partitioning protein"

 /locus tag="Anaysia\_37"

 /note=Original Glimmer call @bp 25241 has strength 13.87; Genemark calls start at 25241

 /note=SSC: 25241-25555 CP: yes SCS: both ST: SS BLAST-Start: [ParB [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 2.97312E-67 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.507, -4.158838642442031, no F: ParB-like dsDNA partitioning protein SIF-BLAST: ,,[ParB [Gordonia phage Rosalind] ],,YP\_009268958,100.0,2.97312E-67 SIF-HHPRED: ORF E73; VIRAL PROTEIN, EXTREMOPHILE, ARCHAEA, RIBBON-HELIX-HELIX PROTEINS, DNA-BINDING PROTEINS; NMR {SULFOLOBUS VIRUS RAGGED HILLS},,,4AAI\_B,43.2692,98.7 SIF-Syn:

CDS 25607 - 25846

 /gene="38"

 /product="gp38"

 /function="Imm-like superinfection immunity protein"

 /locus tag="Anaysia\_38"

 /note=Original Glimmer call @bp 25607 has strength 10.32; Genemark calls start at 25607

 /note=SSC: 25607-25846 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp073 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 5.58896E-49 GAP: 51 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.009, -2.523003374675015, yes F: Imm-like superinfection immunity protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp073 [Gordonia phage Rosalind] ],,YP\_009268959,100.0,5.58896E-49 SIF-HHPRED: Imm\_superinfect ; Superinfection immunity protein,,,PF14373.9,51.8987,99.7 SIF-Syn:

CDS 25843 - 26025

 /gene="39"

 /product="gp39"

 /function="hypothetical protein"

 /locus tag="Anaysia\_39"

 /note=Original Glimmer call @bp 25831 has strength 7.65; Genemark calls start at 25843

 /note=SSC: 25843-26025 CP: yes SCS: both-gm ST: SS BLAST-Start: [hypothetical protein BIZ70\_gp074 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 3.50552E-35 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.343, -3.852397050429479, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp074 [Gordonia phage JSwag] ],,YP\_009285980,100.0,3.50552E-35 SIF-HHPRED: SIF-Syn:

CDS complement (26176 - 26493)

 /gene="40"

 /product="gp40"

 /function="membrane protein"

 /locus tag="Anaysia\_40"

 /note=Original Glimmer call @bp 26493 has strength 7.26; Genemark calls start at 26493

 /note=SSC: 26493-26176 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 5.99382E-70 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.533, -4.103700314387452, yes F: membrane protein SIF-BLAST: ,,[membrane protein [Gordonia Phage Boohoo]],,UAJ15531,100.0,5.99382E-70 SIF-HHPRED: SIF-Syn:

 /note=one transmembrane domain found by two different programs TmHmm and SOSUI.

CDS complement (26490 - 26879)

 /gene="41"

 /product="gp41"

 /function="hypothetical protein"

 /locus tag="Anaysia\_41"

 /note=Original Glimmer call @bp 26879 has strength 13.34; Genemark calls start at 26879

 /note=SSC: 26879-26490 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_BOOHOO\_41 [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 7.96684E-87 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.464, -3.659876950936526, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_BOOHOO\_41 [Gordonia Phage Boohoo]],,UAJ15532,100.0,7.96684E-87 SIF-HHPRED: SIF-Syn:

CDS complement (26879 - 27013)

 /gene="42"

 /product="gp42"

 /function="hypothetical protein"

 /locus tag="Anaysia\_42"

 /note=Original Glimmer call @bp 27013 has strength 13.43; Genemark calls start at 27013

 /note=SSC: 27013-26879 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein BEN62\_gp067 [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 2.64302E-19 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.934, -2.6814417326944517, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN62\_gp067 [Gordonia phage KatherineG] ],,YP\_009269063,100.0,2.64302E-19 SIF-HHPRED: SIF-Syn:

CDS complement (27013 - 27246)

 /gene="43"

 /product="gp43"

 /function="hypothetical protein"

 /locus tag="Anaysia\_43"

 /note=Original Glimmer call @bp 27246 has strength 12.08; Genemark calls start at 27246

 /note=SSC: 27246-27013 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BIZ67\_gp066 [Gordonia phage Remus] ],,NCBI, q1:s1 100.0% 4.17138E-48 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.009, -2.5052746077145835, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ67\_gp066 [Gordonia phage Remus] ],,YP\_009281655,100.0,4.17138E-48 SIF-HHPRED: SIF-Syn:

CDS complement (27239 - 27487)

 /gene="44"

 /product="gp44"

 /function="hypothetical protein"

 /locus tag="Anaysia\_44"

 /note=Original Glimmer call @bp 27466 has strength 10.2; Genemark calls start at 27466

 /note=SSC: 27487-27239 CP: yes SCS: both-cs ST: SS BLAST-Start: [hypothetical protein BEN62\_gp065 [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 1.52994E-52 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.804, -5.822326712960318, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN62\_gp065 [Gordonia phage KatherineG] ],,YP\_009269065,100.0,1.52994E-52 SIF-HHPRED: SIF-Syn:

CDS complement (27487 - 27711)

 /gene="45"

 /product="gp45"

 /function="hypothetical protein"

 /locus tag="Anaysia\_45"

 /note=Original Glimmer call @bp 27711 has strength 14.13; Genemark calls start at 27711

 /note=SSC: 27711-27487 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN62\_gp064 [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 1.95588E-44 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.144, -2.8084998623841946, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN62\_gp064 [Gordonia phage KatherineG] ],,YP\_009269066,100.0,1.95588E-44 SIF-HHPRED: SIF-Syn:

CDS complement (27708 - 28163)

 /gene="46"

 /product="gp46"

 /function="hypothetical protein"

 /locus tag="Anaysia\_46"

 /note=Original Glimmer call @bp 28163 has strength 11.75; Genemark calls start at 28163

 /note=SSC: 28163-27708 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp066 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 4.26775E-108 GAP: 13 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.934, -2.6013996449736907, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp066 [Gordonia phage Rosalind] ],,YP\_009268966,100.0,4.26775E-108 SIF-HHPRED: SIF-Syn:

CDS complement (28177 - 29967)

 /gene="47"

 /product="gp47"

 /function="DNA polymerase I"

 /locus tag="Anaysia\_47"

 /note=Original Glimmer call @bp 29967 has strength 10.95; Genemark calls start at 29967

 /note=SSC: 29967-28177 CP: yes SCS: both ST: SS BLAST-Start: [DNA polymerase I [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 0.0 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.009, -2.523003374675015, yes F: DNA polymerase I SIF-BLAST: ,,[DNA polymerase I [Gordonia Phage Boohoo]],,UAJ15538,100.0,0.0 SIF-HHPRED: Prex DNA polymerase; DNA polymerase, TRANSFERASE; HET: SO4; 2.9A {Plasmodium falciparum},,,5DKT\_A,97.4832,100.0 SIF-Syn:

CDS complement (29968 - 30327)

 /gene="48"

 /product="gp48"

 /function="hypothetical protein"

 /locus tag="Anaysia\_48"

 /note=Original Glimmer call @bp 30327 has strength 14.16; Genemark calls start at 30327

 /note=SSC: 30327-29968 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_DEKHOCKEY33\_48 [Gordonia phage DekHockey33]],,NCBI, q1:s2 100.0% 1.27421E-79 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.351, -3.8366550365551095, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_DEKHOCKEY33\_48 [Gordonia phage DekHockey33]],,QWS67829,99.1667,1.27421E-79 SIF-HHPRED: DUF6197 ; Family of unknown function (DUF6197),,,PF19698.2,98.3193,99.9 SIF-Syn:

CDS complement (30327 - 30563)

 /gene="49"

 /product="gp49"

 /function="hypothetical protein"

 /locus tag="Anaysia\_49"

 /note=Original Glimmer call @bp 30563 has strength 17.63; Genemark calls start at 30563

 /note=SSC: 30563-30327 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN62\_gp060 [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 4.49375E-50 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.305, -4.28556153901447, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN62\_gp060 [Gordonia phage KatherineG] ],,YP\_009269070,100.0,4.49375E-50 SIF-HHPRED: SIF-Syn:

CDS complement (30560 - 30853)

 /gene="50"

 /product="gp50"

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

 /locus tag="Anaysia\_50"

 /note=Original Glimmer call @bp 30853 has strength 9.61; Genemark calls start at 30853

 /note=SSC: 30853-30560 CP: yes SCS: both ST: NA BLAST-Start: [HTH DNA binding domain protein [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 2.05014E-64 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.009, -3.095100142625534, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[HTH DNA binding domain protein [Gordonia phage KatherineG] ],,YP\_009269071,100.0,2.05014E-64 SIF-HHPRED: SIF-Syn:

CDS complement (30850 - 31080)

 /gene="51"

 /product="gp51"

 /function="hypothetical protein"

 /locus tag="Anaysia\_51"

 /note=Original Glimmer call @bp 31080 has strength 12.73; Genemark calls start at 31080

 /note=SSC: 31080-30850 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein BEN62\_gp058 [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 5.02101E-47 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.098, -2.7806870294376242, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN62\_gp058 [Gordonia phage KatherineG] ],,YP\_009269072,100.0,5.02101E-47 SIF-HHPRED: SIF-Syn:

CDS complement (31089 - 31787)

 /gene="52"

 /product="gp52"

 /function="ThyX-like thymidylate synthase"

 /locus tag="Anaysia\_52"

 /note=Original Glimmer call @bp 31787 has strength 13.96; Genemark calls start at 31787

 /note=SSC: 31787-31089 CP: yes SCS: both ST: NA BLAST-Start: [ThyX-like thymidylate synthase [Gordonia phage LastResort] ],,NCBI, q1:s1 100.0% 6.72516E-170 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.203, -4.211732089774149, no F: ThyX-like thymidylate synthase SIF-BLAST: ,,[ThyX-like thymidylate synthase [Gordonia phage LastResort] ],,AXH47849,100.0,6.72516E-170 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\_F,98.2759,100.0 SIF-Syn:

CDS complement (31784 - 32128)

 /gene="53"

 /product="gp53"

 /function="MazG-like nucleotide pyrophosphohydrolase"

 /locus tag="Anaysia\_53"

 /note=Original Glimmer call @bp 32128 has strength 8.48; Genemark calls start at 32032

 /note=SSC: 32128-31784 CP: yes SCS: both-gl ST: NA BLAST-Start: [MazG-like nucleotide pyrophosphohydrolase [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 1.37538E-76 GAP: 87 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.951, -4.746946755792842, yes F: MazG-like nucleotide pyrophosphohydrolase SIF-BLAST: ,,[MazG-like nucleotide pyrophosphohydrolase [Gordonia phage KatherineG] ],,YP\_009269074,100.0,1.37538E-76 SIF-HHPRED: a.204.1.2 (A:) automated matches {Bacillus cereus [TaxId: 1396]},,,d5ie9a\_,90.3509,99.7 SIF-Syn:

CDS complement (32216 - 32758)

 /gene="54"

 /product="gp54"

 /function="hypothetical protein"

 /locus tag="Anaysia\_54"

 /note=Original Glimmer call @bp 32758 has strength 6.34; Genemark calls start at 32758

 /note=SSC: 32758-32216 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BIZ70\_gp060 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 1.87883E-127 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.069, -2.314799364732351, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp060 [Gordonia phage JSwag] ],,YP\_009285994,100.0,1.87883E-127 SIF-HHPRED: SIF-Syn:

CDS complement (32755 - 32871)

 /gene="55"

 /product="gp55"

 /function="hypothetical protein"

 /locus tag="Anaysia\_55"

 /note=Original Glimmer call @bp 32871 has strength 8.12; Genemark calls start at 32859

 /note=SSC: 32871-32755 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein BIZ70\_gp059 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 6.18213E-17 GAP: -16 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.695, -6.532269488709362, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp059 [Gordonia phage JSwag] ],,YP\_009285995,100.0,6.18213E-17 SIF-HHPRED: SIF-Syn:

 /note=TmHm and SOSUI predict each one transmembrane sequence.

CDS complement (32856 - 34919)

 /gene="56"

 /product="gp56"

 /function="ribonucleotide reductase"

 /locus tag="Anaysia\_56"

 /note=Original Glimmer call @bp 34919 has strength 10.68; Genemark calls start at 34919

 /note=SSC: 34919-32856 CP: yes SCS: both ST: NA BLAST-Start: [ribonucleotide reductase [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.943, -3.4105598537121566, yes F: ribonucleotide reductase SIF-BLAST: ,,[ribonucleotide reductase [Gordonia phage JSwag] ],,YP\_009285996,100.0,0.0 SIF-HHPRED: RIBONUCLEOSIDE TRIPHOSPHATE REDUCTASE; 10-stranded alpha-beta barrel, central finger loop, OXIDOREDUCTASE; 1.75A {Lactobacillus leichmannii} SCOP: c.7.1.4,,,1L1L\_B,98.69,100.0 SIF-Syn:

CDS complement (34916 - 35107)

 /gene="57"

 /product="gp57"

 /function="hypothetical protein"

 /locus tag="Anaysia\_57"

 /note=Original Glimmer call @bp 35107 has strength 8.44; Genemark calls start at 35107

 /note=SSC: 35107-34916 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp055 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 1.01296E-38 GAP: 61 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.09, -6.507092109581598, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp055 [Gordonia phage Rosalind] ],,YP\_009268977,100.0,1.01296E-38 SIF-HHPRED: SIF-Syn:

CDS complement (35169 - 35351)

 /gene="58"

 /product="gp58"

 /function="hypothetical protein"

 /locus tag="Anaysia\_58"

 /note=Original Glimmer call @bp 35351 has strength 9.28; Genemark calls start at 35351

 /note=SSC: 35351-35169 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein BIZ70\_gp055 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 1.85288E-36 GAP: -17 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.395, -5.924411981974289, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp055 [Gordonia phage JSwag] ],,YP\_009285999,100.0,1.85288E-36 SIF-HHPRED: GP52 ; Phage gene product 52,,,PF17468.5,98.3333,100.0 SIF-Syn:

CDS complement (35335 - 35907)

 /gene="59"

 /product="gp59"

 /function="DNA binding protein"

 /locus tag="Anaysia\_59"

 /note=Original Glimmer call @bp 35907 has strength 12.53; Genemark calls start at 35892

 /note=SSC: 35907-35335 CP: yes SCS: both-gl ST: NA BLAST-Start: [DNA binding protein [Gordonia phage Soups] ],,NCBI, q1:s1 100.0% 6.82529E-139 GAP: -19 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.24, -2.0949393225970705, yes F: DNA binding protein SIF-BLAST: ,,[DNA binding protein [Gordonia phage Soups] ],,YP\_009269358,100.0,6.82529E-139 SIF-HHPRED: ECF RNA polymerase sigma factor SigK; sigma factor, transcription initiation, DNA binding, Promoter DNA binding and transcription initiation, anti-sigma factor, DNA BINDING; HET: CD; 2.4A {Mycobacterium tuberculosis},,,4NQW\_A,84.7368,99.8 SIF-Syn:

CDS complement (35889 - 36029)

 /gene="60"

 /product="gp60"

 /function="hypothetical protein"

 /locus tag="Anaysia\_60"

 /note=

 /note=SSC: 36029-35889 CP: yes SCS: neither ST: NI BLAST-Start: [hypothetical protein SEA\_BOOHOO\_60 [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 1.30272E-25 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.953, -4.679270584912496, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_BOOHOO\_60 [Gordonia Phage Boohoo]],,UAJ15551,100.0,1.30272E-25 SIF-HHPRED: SIF-Syn:

CDS complement (36033 - 36797)

 /gene="61"

 /product="gp61"

 /function="metallophosphoesterase"

 /locus tag="Anaysia\_61"

 /note=Original Glimmer call @bp 36797 has strength 12.69; Genemark calls start at 36797

 /note=SSC: 36797-36033 CP: yes SCS: both ST: SS BLAST-Start: [metallophosphoesterase [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.429, -3.75071250087134, no F: metallophosphoesterase SIF-BLAST: ,,[metallophosphoesterase [Gordonia phage KatherineG] ],,YP\_009269081,100.0,0.0 SIF-HHPRED: d.159.1.5 (A:) automated matches {Pyrococcus horikoshii OT3 [TaxId: 70601]},,,d2gjua\_,94.4882,99.9 SIF-Syn:

CDS complement (36794 - 37228)

 /gene="62"

 /product="gp62"

 /function="hypothetical protein"

 /locus tag="Anaysia\_62"

 /note=Original Glimmer call @bp 37228 has strength 12.21; Genemark calls start at 37228

 /note=SSC: 37228-36794 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN62\_gp048 [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 5.93923E-102 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.009, -2.583959800616441, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN62\_gp048 [Gordonia phage KatherineG] ],,YP\_009269082,100.0,5.93923E-102 SIF-HHPRED: DUF3310 ; Protein of unknwon function (DUF3310),,,PF11753.11,40.9722,99.8 SIF-Syn:

CDS complement (37225 - 37401)

 /gene="63"

 /product="gp63"

 /function="hypothetical protein"

 /locus tag="Anaysia\_63"

 /note=Original Glimmer call @bp 37401 has strength 15.18; Genemark calls start at 37401

 /note=SSC: 37401-37225 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BIZ67\_gp047 [Gordonia phage Remus] ],,NCBI, q1:s1 100.0% 3.69388E-33 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.806, -5.132255893439239, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ67\_gp047 [Gordonia phage Remus] ],,YP\_009281674,100.0,3.69388E-33 SIF-HHPRED: SIF-Syn:

CDS complement (37398 - 37667)

 /gene="64"

 /product="gp64"

 /function="NrdH-like glutaredoxin"

 /locus tag="Anaysia\_64"

 /note=Original Glimmer call @bp 37667 has strength 16.25; Genemark calls start at 37667

 /note=SSC: 37667-37398 CP: yes SCS: both ST: NA BLAST-Start: [NrdH-like glutaredoxin [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 2.28391E-58 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.334, -3.9531326986493704, yes F: NrdH-like glutaredoxin SIF-BLAST: ,,[NrdH-like glutaredoxin [Gordonia Phage Boohoo]],,UAJ15555,100.0,2.28391E-58 SIF-HHPRED: c.47.1.0 (A:1-84) automated matches {Mycobacterium tuberculosis [TaxId: 1773]},,,d2lqoa1,91.0112,99.6 SIF-Syn:

CDS complement (37664 - 37876)

 /gene="65"

 /product="gp65"

 /function="hypothetical protein"

 /locus tag="Anaysia\_65"

 /note=Original Glimmer call @bp 37876 has strength 12.7; Genemark calls start at 37876

 /note=SSC: 37876-37664 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp048 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 5.80561E-42 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.943, -3.4105598537121566, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp048 [Gordonia phage Rosalind] ],,YP\_009268984,100.0,5.80561E-42 SIF-HHPRED: SIF-Syn:

CDS complement (37873 - 38334)

 /gene="66"

 /product="gp66"

 /function="DNA primase"

 /locus tag="Anaysia\_66"

 /note=Original Glimmer call @bp 38334 has strength 8.84; Genemark calls start at 38319

 /note=SSC: 38334-37873 CP: yes SCS: both-gl ST: NA BLAST-Start: [DNA primase [Gordonia phage Epsocamisio]],,NCBI, q1:s27 100.0% 7.46578E-109 GAP: 1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.613, -5.47994862755136, no F: DNA primase SIF-BLAST: ,,[DNA primase [Gordonia phage Epsocamisio]],,QLF84936,85.4749,7.46578E-109 SIF-HHPRED: e.13.1.1 (A:) DNA primase DnaG catalytic core {Escherichia coli [TaxId: 562]},,,d1dd9a\_,98.0392,99.8 SIF-Syn:

CDS complement (38336 - 38716)

 /gene="67"

 /product="gp67"

 /function="DNA primase"

 /locus tag="Anaysia\_67"

 /note=Original Glimmer call @bp 38716 has strength 1.98

 /note=SSC: 38716-38336 CP: yes SCS: glimmer ST: NA BLAST-Start: [DNA primase [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 2.31226E-88 GAP: 25 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.934, -2.6814417326944517, yes F: DNA primase SIF-BLAST: ,,[DNA primase [Gordonia phage Rosalind] ],,YP\_009268986,100.0,2.31226E-88 SIF-HHPRED: g.41.3.2 (A:) Zinc-binding domain of DNA primase {Bacillus stearothermophilus [TaxId: 1422]},,,d1d0qa\_,65.0794,99.6 SIF-Syn:

CDS complement (38742 - 38921)

 /gene="68"

 /product="gp68"

 /function="hypothetical protein"

 /locus tag="Anaysia\_68"

 /note=Original Glimmer call @bp 38921 has strength 14.69; Genemark calls start at 38921

 /note=SSC: 38921-38742 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein SEA\_MINECRAFTSTEVE\_68 [Gordonia phage MinecraftSteve] ],,NCBI, q1:s1 100.0% 1.71616E-33 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.62, -4.572332879622887, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_MINECRAFTSTEVE\_68 [Gordonia phage MinecraftSteve] ],,QFP95132,100.0,1.71616E-33 SIF-HHPRED: SIF-Syn:

CDS complement (38921 - 39556)

 /gene="69"

 /product="gp69"

 /function="lysin B"

 /locus tag="Anaysia\_69"

 /note=Original Glimmer call @bp 39556 has strength 7.91; Genemark calls start at 39556

 /note=SSC: 39556-38921 CP: yes SCS: both ST: SS BLAST-Start: [lysin B [Gordonia phage Epsocamisio]],,NCBI, q1:s1 100.0% 1.51762E-151 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.035, -4.505076120213986, no F: lysin B SIF-BLAST: ,,[lysin B [Gordonia phage Epsocamisio]],,QLF84938,99.5261,1.51762E-151 SIF-HHPRED: SIF-Syn:

CDS complement (39553 - 40011)

 /gene="70"

 /product="gp70"

 /function="endonuclease VII"

 /locus tag="Anaysia\_70"

 /note=Original Glimmer call @bp 39921 has strength 6.26; Genemark calls start at 39921

 /note=SSC: 40011-39553 CP: yes SCS: both-cs ST: NA BLAST-Start: [EndoVII [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 8.04992E-107 GAP: -17 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.126, -4.965528251064928, yes F: endonuclease VII SIF-BLAST: ,,[EndoVII [Gordonia phage Rosalind] ],,YP\_009268989,100.0,8.04992E-107 SIF-HHPRED: SIF-Syn:

CDS complement (39995 - 40108)

 /gene="71"

 /product="gp71"

 /function="hypothetical protein"

 /locus tag="Anaysia\_71"

 /note=Original Glimmer call @bp 40108 has strength 10.15; Genemark calls start at 40108

 /note=SSC: 40108-39995 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp042 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 5.80948E-15 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.613, -7.006287904941204, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp042 [Gordonia phage Rosalind] ],,YP\_009268990,100.0,5.80948E-15 SIF-HHPRED: SIF-Syn:

CDS complement (40105 - 40203)

 /gene="72"

 /product="gp72"

 /function="hypothetical protein"

 /locus tag="Anaysia\_72"

 /note=Genemark calls start at 40203

 /note=SSC: 40203-40105 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein BEN61\_gp041 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 5.13845E-10 GAP: 42 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.24, -1.953940808934884, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp041 [Gordonia phage Rosalind] ],,YP\_009268991,100.0,5.13845E-10 SIF-HHPRED: SIF-Syn:

CDS complement (40246 - 40644)

 /gene="73"

 /product="gp73"

 /function="hypothetical protein"

 /locus tag="Anaysia\_73"

 /note=Original Glimmer call @bp 40644 has strength 19.46; Genemark calls start at 40644

 /note=SSC: 40644-40246 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN59\_gp038 [Gordonia phage Soups] ],,NCBI, q1:s1 100.0% 5.50244E-92 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.144, -4.4157344874810125, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN59\_gp038 [Gordonia phage Soups] ],,YP\_009269371,100.0,5.50244E-92 SIF-HHPRED: DUF5052 ; Domain of unknown function (DUF5052),,,PF16475.8,79.5455,99.4 SIF-Syn:

CDS complement (40641 - 40835)

 /gene="74"

 /product="gp74"

 /function="membrane protein"

 /locus tag="Anaysia\_74"

 /note=Original Glimmer call @bp 40835 has strength 5.77; Genemark calls start at 40835

 /note=SSC: 40835-40641 CP: no SCS: both ST: NA BLAST-Start: [membrane protein [Gordonia phage LastResort] ],,NCBI, q1:s1 100.0% 1.81911E-33 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.712, -3.2123487306667524, yes F: membrane protein SIF-BLAST: ,,[membrane protein [Gordonia phage LastResort] ],,AXH47869,100.0,1.81911E-33 SIF-HHPRED: SIF-Syn:

CDS complement (40838 - 41596)

 /gene="75"

 /product="gp75"

 /function="hypothetical protein"

 /locus tag="Anaysia\_75"

 /note=Original Glimmer call @bp 41596 has strength 14.22; Genemark calls start at 41596

 /note=SSC: 41596-40838 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LASTRESORT\_73 [Gordonia phage LastResort] ],,NCBI, q1:s1 100.0% 0.0 GAP: 32 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.879, -4.9157003279346805, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LASTRESORT\_73 [Gordonia phage LastResort] ],,AXH47870,100.0,0.0 SIF-HHPRED: DUF6197 ; Family of unknown function (DUF6197),,,PF19698.2,50.7937,99.7 SIF-Syn:

CDS complement (41629 - 42108)

 /gene="76"

 /product="gp76"

 /function="hypothetical protein"

 /locus tag="Anaysia\_76"

 /note=Original Glimmer call @bp 42108 has strength 14.43; Genemark calls start at 42108

 /note=SSC: 42108-41629 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LASTRESORT\_74 [Gordonia phage LastResort] ],,NCBI, q1:s1 100.0% 1.14377E-109 GAP: 42 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.069, -2.66590822473965, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LASTRESORT\_74 [Gordonia phage LastResort] ],,AXH47871,100.0,1.14377E-109 SIF-HHPRED: SIF-Syn:

CDS complement (42151 - 42981)

 /gene="77"

 /product="gp77"

 /function="DnaB-like dsDNA helicase"

 /locus tag="Anaysia\_77"

 /note=Original Glimmer call @bp 42981 has strength 12.97; Genemark calls start at 42894

 /note=SSC: 42981-42151 CP: yes SCS: both-gl ST: NA BLAST-Start: [DnaB-like dsDNA helicase [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 0.0 GAP: 64 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.398, -5.996305562975237, no F: DnaB-like dsDNA helicase SIF-BLAST: ,,[DnaB-like dsDNA helicase [Gordonia phage Rosalind] ],,YP\_009268996,100.0,0.0 SIF-HHPRED: c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase domain {Bacteriophage T7 [TaxId: 10760]},,,d1cr1a\_,94.2029,100.0 SIF-Syn:

CDS complement (43046 - 43219)

 /gene="78"

 /product="gp78"

 /function="hypothetical protein"

 /locus tag="Anaysia\_78"

 /note=Original Glimmer call @bp 43219 has strength 15.12; Genemark calls start at 43219

 /note=SSC: 43219-43046 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp035 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 4.85019E-33 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.351, -3.898968357315439, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp035 [Gordonia phage Rosalind] ],,YP\_009268997,100.0,4.85019E-33 SIF-HHPRED: SIF-Syn:

CDS complement (43230 - 43418)

 /gene="79"

 /product="gp79"

 /function="hypothetical protein"

 /locus tag="Anaysia\_79"

 /note=Original Glimmer call @bp 43418 has strength 7.53; Genemark calls start at 43418

 /note=SSC: 43418-43230 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein BEN61\_gp034 [Gordonia phage Rosalind] ],,NCBI, q1:s3 100.0% 4.60214E-35 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.009, -3.3503726477288405, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp034 [Gordonia phage Rosalind] ],,YP\_009268998,96.875,4.60214E-35 SIF-HHPRED: SIF-Syn:

CDS complement (43421 - 43699)

 /gene="80"

 /product="gp80"

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

 /locus tag="Anaysia\_80"

 /note=Original Glimmer call @bp 43699 has strength 12.78; Genemark calls start at 43699

 /note=SSC: 43699-43421 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein BEN61\_gp033 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 4.57168E-60 GAP: 26 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.098, -2.7806870294376242, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[hypothetical protein BEN61\_gp033 [Gordonia phage Rosalind] ],,YP\_009268999,100.0,4.57168E-60 SIF-HHPRED: GP68 ; Gp68-like predicted RNA polymerase component,,,PF17469.5,84.7826,100.0 SIF-Syn:

CDS complement (43726 - 44115)

 /gene="81"

 /product="gp81"

 /function="HNH endonuclease"

 /locus tag="Anaysia\_81"

 /note=Original Glimmer call @bp 44115 has strength 1.13; Genemark calls start at 44064

 /note=SSC: 44115-43726 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein BEN61\_gp032 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 2.68796E-91 GAP: 11 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.087, -2.356391881054909, yes F: HNH endonuclease SIF-BLAST: ,,[hypothetical protein BEN61\_gp032 [Gordonia phage Rosalind] ],,YP\_009269000,100.0,2.68796E-91 SIF-HHPRED: SIF-Syn:

CDS complement (44127 - 44975)

 /gene="82"

 /product="gp82"

 /function="Cas4 family exonuclease"

 /locus tag="Anaysia\_82"

 /note=Original Glimmer call @bp 44975 has strength 11.16; Genemark calls start at 44927

 /note=SSC: 44975-44127 CP: yes SCS: both-gl ST: NA BLAST-Start: [Cas4 family exonuclease [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.695, -3.7606820078281067, yes F: Cas4 family exonuclease SIF-BLAST: ,,[Cas4 family exonuclease [Gordonia Phage Boohoo]],,UAJ15572,100.0,0.0 SIF-HHPRED: Cas4\_I-A; CRISPR/Cas system-associated protein Cas4. CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) and associated Cas proteins comprise a system for heritable host defense by prokaryotic cells against phage and other foreign DNA.,,,cd09659,94.6809,99.9 SIF-Syn:

CDS complement (44972 - 45370)

 /gene="83"

 /product="gp83"

 /function="hypothetical protein"

 /locus tag="Anaysia\_83"

 /note=Original Glimmer call @bp 45370 has strength 6.37; Genemark calls start at 45340

 /note=SSC: 45370-44972 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein BEN61\_gp030 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 1.17356E-91 GAP: 15 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.11, -4.697746622201849, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp030 [Gordonia phage Rosalind] ],,YP\_009269002,100.0,1.17356E-91 SIF-HHPRED: GP70 ; Gene product 70,,,PF17429.5,38.6364,99.8 SIF-Syn:

CDS complement (45386 - 45925)

 /gene="84"

 /product="gp84"

 /function="immunity repressor"

 /locus tag="Anaysia\_84"

 /note=Original Glimmer call @bp 45925 has strength 14.45; Genemark calls start at 45925

 /note=SSC: 45925-45386 CP: yes SCS: both ST: NA BLAST-Start: [immunity repressor [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 2.6534E-123 GAP: 397 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.591, -3.389881189012514, no F: immunity repressor SIF-BLAST: ,,[immunity repressor [Gordonia phage KatherineG] ],,YP\_009269104,100.0,2.6534E-123 SIF-HHPRED: SIF-Syn:

CDS complement (46323 - 46571)

 /gene="85"

 /product="gp85"

 /function="hypothetical protein"

 /locus tag="Anaysia\_85"

 /note=Original Glimmer call @bp 46571 has strength 13.86; Genemark calls start at 46571

 /note=SSC: 46571-46323 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp028 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 2.99438E-53 GAP: -17 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.591, -3.4076099559729456, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp028 [Gordonia phage Rosalind] ],,YP\_009269004,100.0,2.99438E-53 SIF-HHPRED: SIF-Syn:

CDS complement (46555 - 46827)

 /gene="86"

 /product="gp86"

 /function="hypothetical protein"

 /locus tag="Anaysia\_86"

 /note=Original Glimmer call @bp 46851 has strength 9.97; Genemark calls start at 46827

 /note=SSC: 46827-46555 CP: no SCS: both-gm ST: NI BLAST-Start: [hypothetical protein BIZ70\_gp027 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 6.67864E-60 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.542, -4.53218352334679, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp027 [Gordonia phage JSwag] ],,YP\_009286027,100.0,6.67864E-60 SIF-HHPRED: SIF-Syn:

CDS complement (46824 - 47291)

 /gene="87"

 /product="gp87"

 /function="SprT-like protease"

 /locus tag="Anaysia\_87"

 /note=Original Glimmer call @bp 47291 has strength 6.79; Genemark calls start at 47291

 /note=SSC: 47291-46824 CP: no SCS: both ST: NA BLAST-Start: [SprT-like protein [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 8.42614E-111 GAP: 114 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.12, -4.6767843745817785, yes F: SprT-like protease SIF-BLAST: ,,[SprT-like protein [Gordonia phage KatherineG] ],,YP\_009269107,100.0,8.42614E-111 SIF-HHPRED: SprT-like domain-containing protein Spartan; DPC repair protease, DNA BINDING PROTEIN; HET: ADP, MLZ, FLC; 1.5A {Homo sapiens},,,6MDW\_A,86.4516,99.8 SIF-Syn:

CDS complement (47406 - 47702)

 /gene="88"

 /product="gp88"

 /function="hypothetical protein"

 /locus tag="Anaysia\_88"

 /note=Original Glimmer call @bp 47702 has strength 7.99; Genemark calls start at 47702

 /note=SSC: 47702-47406 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein BIZ70\_gp025 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 1.83799E-66 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.533, -3.5316035464369326, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp025 [Gordonia phage JSwag] ],,YP\_009286029,100.0,1.83799E-66 SIF-HHPRED: SIF-Syn:

CDS complement (47705 - 47890)

 /gene="89"

 /product="gp89"

 /function="hypothetical protein"

 /locus tag="Anaysia\_89"

 /note=Original Glimmer call @bp 47890 has strength 9.13; Genemark calls start at 47890

 /note=SSC: 47890-47705 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein BIZ70\_gp024 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 4.14448E-36 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.632, -5.711596282398514, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp024 [Gordonia phage JSwag] ],,YP\_009286030,100.0,4.14448E-36 SIF-HHPRED: SIF-Syn:

CDS complement (47890 - 48060)

 /gene="90"

 /product="gp90"

 /function="hypothetical protein"

 /locus tag="Anaysia\_90"

 /note=Original Glimmer call @bp 48060 has strength 13.15; Genemark calls start at 48060

 /note=SSC: 48060-47890 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp022 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 3.0506E-33 GAP: 43 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.144, -4.354778061539587, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp022 [Gordonia phage Rosalind] ],,YP\_009269010,100.0,3.0506E-33 SIF-HHPRED: SIF-Syn:

CDS complement (48104 - 48286)

 /gene="91"

 /product="gp91"

 /function="hypothetical protein"

 /locus tag="Anaysia\_91"

 /note=Original Glimmer call @bp 48286 has strength 10.32; Genemark calls start at 48286

 /note=SSC: 48286-48104 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BIZ70\_gp022 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 6.087E-33 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.533, -5.921045285829382, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp022 [Gordonia phage JSwag] ],,YP\_009286032,100.0,6.087E-33 SIF-HHPRED: SIF-Syn:

CDS complement (48290 - 48457)

 /gene="92"

 /product="gp92"

 /function="hypothetical protein"

 /locus tag="Anaysia\_92"

 /note=Original Glimmer call @bp 48457 has strength 7.27; Genemark calls start at 48388

 /note=SSC: 48457-48290 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein BEN62\_gp019 [Gordonia phage KatherineG] ],,NCBI, q1:s1 100.0% 1.73396E-29 GAP: 54 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.913, -5.11571101996485, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN62\_gp019 [Gordonia phage KatherineG] ],,YP\_009269111,100.0,1.73396E-29 SIF-HHPRED: SIF-Syn:

CDS complement (48512 - 48754)

 /gene="93"

 /product="gp93"

 /function="hypothetical protein"

 /locus tag="Anaysia\_93"

 /note=Original Glimmer call @bp 48754 has strength 13.9; Genemark calls start at 48754

 /note=SSC: 48754-48512 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_BOOHOO\_92 [Gordonia Phage Boohoo]],,NCBI, q1:s1 100.0% 6.84838E-49 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.681, -4.045504852447161, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_BOOHOO\_92 [Gordonia Phage Boohoo]],,UAJ15581,100.0,6.84838E-49 SIF-HHPRED: SIF-Syn:

CDS complement (48754 - 48873)

 /gene="94"

 /product="gp94"

 /function="hypothetical protein"

 /locus tag="Anaysia\_94"

 /note=Original Glimmer call @bp 48873 has strength 16.07; Genemark calls start at 48852

 /note=SSC: 48873-48754 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein BEN61\_gp018 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 6.99153E-18 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.607, -5.4744737427355155, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp018 [Gordonia phage Rosalind] ],,YP\_009269014,100.0,6.99153E-18 SIF-HHPRED: SIF-Syn:

CDS complement (48870 - 49283)

 /gene="95"

 /product="gp95"

 /function="hypothetical protein"

 /locus tag="Anaysia\_95"

 /note=Original Glimmer call @bp 49283 has strength 11.7; Genemark calls start at 49283

 /note=SSC: 49283-48870 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LASTRESORT\_93 [Gordonia phage LastResort] ],,NCBI, q1:s1 100.0% 1.15735E-93 GAP: 30 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.693, -5.293557664252809, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LASTRESORT\_93 [Gordonia phage LastResort] ],,AXH47890,100.0,1.15735E-93 SIF-HHPRED: SIF-Syn:

CDS complement (49314 - 50042)

 /gene="96"

 /product="gp96"

 /function="hypothetical protein"

 /locus tag="Anaysia\_96"

 /note=Original Glimmer call @bp 50042 has strength 8.62; Genemark calls start at 50027

 /note=SSC: 50042-49314 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein BEN61\_gp016 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 6.09363E-180 GAP: -11 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.934, -2.66371296573402, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp016 [Gordonia phage Rosalind] ],,YP\_009269016,100.0,6.09363E-180 SIF-HHPRED: SIF-Syn:

CDS complement (50032 - 50175)

 /gene="97"

 /product="gp97"

 /function="hypothetical protein"

 /locus tag="Anaysia\_97"

 /note=Original Glimmer call @bp 50175 has strength 9.65; Genemark calls start at 50175

 /note=SSC: 50175-50032 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN61\_gp015 [Gordonia phage Rosalind] ],,NCBI, q1:s1 100.0% 9.50152E-26 GAP: 76 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.009, -2.523003374675015, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN61\_gp015 [Gordonia phage Rosalind] ],,YP\_009269017,100.0,9.50152E-26 SIF-HHPRED: SIF-Syn:

CDS complement (50252 - 50449)

 /gene="98"

 /product="gp98"

 /function="hypothetical protein"

 /locus tag="Anaysia\_98"

 /note=Original Glimmer call @bp 50449 has strength 11.59; Genemark calls start at 50449

 /note=SSC: 50449-50252 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein BIZ70\_gp014 [Gordonia phage JSwag] ],,NCBI, q1:s1 100.0% 8.7481E-39 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.506, -3.588526034455651, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BIZ70\_gp014 [Gordonia phage JSwag] ],,YP\_009286040,100.0,8.7481E-39 SIF-HHPRED: SIF-Syn:

CDS complement (50452 - 50682)

 /gene="99"

 /product="gp99"

 /function="hypothetical protein"

 /locus tag="Anaysia\_99"

 /note=Original Glimmer call @bp 50682 has strength 7.53; Genemark calls start at 50682

 /note=SSC: 50682-50452 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_SHAYRA\_97 [Gordonia phage ShayRa] ],,NCBI, q1:s1 100.0% 9.0763E-50 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.601, -3.3861058366776207, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_SHAYRA\_97 [Gordonia phage ShayRa] ],,ASZ73973,100.0,9.0763E-50 SIF-HHPRED: SIF-Syn:

CDS complement (50685 - 50870)

 /gene="100"

 /product="gp100"

 /function="hypothetical protein"

 /locus tag="Anaysia\_100"

 /note=Original Glimmer call @bp 50870 has strength 11.0; Genemark calls start at 50870

 /note=SSC: 50870-50685 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LASTRESORT\_98 [Gordonia phage LastResort] ],,NCBI, q1:s1 100.0% 3.20418E-37 GAP: 1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.496, -4.182126921701495, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LASTRESORT\_98 [Gordonia phage LastResort] ],,AXH47895,100.0,3.20418E-37 SIF-HHPRED: SIF-Syn:

CDS complement (50872 - 51081)

 /gene="101"

 /product="gp101"

 /function="hypothetical protein"

 /locus tag="Anaysia\_101"

 /note=Original Glimmer call @bp 51081 has strength 4.24; Genemark calls start at 51081

 /note=SSC: 51081-50872 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BEN59\_gp010 [Gordonia phage Soups] ],,NCBI, q1:s1 100.0% 3.5889E-43 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.838, -3.15492870275902, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BEN59\_gp010 [Gordonia phage Soups] ],,YP\_009269399,100.0,3.5889E-43 SIF-HHPRED: SIF-Syn:

CDS complement (51085 - 51369)

 /gene="102"

 /product="gp102"

 /function="hypothetical protein"

 /locus tag="Anaysia\_102"

 /note=Original Glimmer call @bp 51369 has strength 13.85; Genemark calls start at 51369

 /note=SSC: 51369-51085 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LASTRESORT\_100 [Gordonia phage LastResort] ],,NCBI, q1:s1 100.0% 1.65218E-63 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.12, -4.4057176022952405, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LASTRESORT\_100 [Gordonia phage LastResort] ],,AXH47897,100.0,1.65218E-63 SIF-HHPRED: SIF-Syn: