Yubaba Annotation Notes : Students worked individually in DNA Master and then we entered their information in PEECAN to make the notes.

CDS 41 - 379

 /gene="1"

 /product="gp1"

 /function="hypothetical protein"

 /locus tag="Yubaba\_1"

 /note=Original Glimmer call @bp 41 has strength 15.52; Genemark calls start at 41

 /note=SSC: 41-379 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein JTF51\_gp01 [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 4.89532E-73 GAP: 0 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.064, -5.035742295039811, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein JTF51\_gp01 [Microbacterium phage PaoPu] ],,YP\_009996586,100.0,4.89532E-73 SIF-HHPRED: SIF-Syn:

CDS 376 - 1071

 /gene="2"

 /product="gp2"

 /function="hypothetical protein"

 /locus tag="Yubaba\_2"

 /note=Original Glimmer call @bp 376 has strength 9.26; Genemark calls start at 376

 /note=SSC: 376-1071 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_MINIMA\_2 [Microbacterium phage Minima] ],,NCBI, q1:s1 100.0% 4.97688E-161 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.333, -4.497802523441791, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_MINIMA\_2 [Microbacterium phage Minima] ],,AXQ64351,100.0,4.97688E-161 SIF-HHPRED: SIF-Syn:

CDS 1074 - 2534

 /gene="3"

 /product="gp3"

 /function="Terminase"

 /locus tag="Yubaba\_3"

 /note=Original Glimmer call @bp 1074 has strength 11.92; Genemark calls start at 1074

 /note=SSC: 1074-2534 CP: yes SCS: both ST: SS BLAST-Start: [terminase [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 0.0 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.866, -5.98696854491312, no F: Terminase SIF-BLAST: ,,[terminase [Microbacterium phage PaoPu] ],,YP\_009996588,100.0,0.0 SIF-HHPRED: Terminase large subunit; genome packaging, bacteriophage, ATPase, nuclease, VIRAL PROTEIN; HET: BR; 2.2A {Enterobacteria phage HK97},,,6Z6D\_A,92.7984,100.0 SIF-Syn:

CDS 2660 - 3787

 /gene="4"

 /product="gp4"

 /function="portal protein"

 /locus tag="Yubaba\_4"

 /note=Original Glimmer call @bp 2660 has strength 12.55; Genemark calls start at 2729

 /note=SSC: 2660-3787 CP: yes SCS: both-gl ST: SS BLAST-Start: [portal protein [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 0.0 GAP: 125 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.981, -5.756015422186926, no F: portal protein SIF-BLAST: ,,[portal protein [Microbacterium phage PaoPu] ],,YP\_009996589,100.0,0.0 SIF-HHPRED: Phage portal protein, HK97 family; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus},,,6TE9\_A,87.4667,100.0 SIF-Syn:

CDS 3784 - 5370

 /gene="5"

 /product="gp5"

 /function="major capsid and protease fusion protein"

 /locus tag="Yubaba\_5"

 /note=Original Glimmer call @bp 3784 has strength 14.82; Genemark calls start at 3784

 /note=SSC: 3784-5370 CP: no SCS: both ST: SS BLAST-Start: [major capsid and protease fusion protein [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.107, -3.5088110057482766, yes F: major capsid and protease fusion protein SIF-BLAST: ,,[major capsid and protease fusion protein [Microbacterium phage PaoPu] ],,YP\_009996590,100.0,0.0 SIF-HHPRED: Major capsid protein Rcc01687; "capsid", "jelly roll", "spike", "HK97", VIRUS; 3.42A {Rhodobacter capsulatus DE442},,,6TSU\_B5,54.7348,99.9 SIF-Syn:

CDS 5374 - 5727

 /gene="6"

 /product="gp6"

 /function="head-to-tail adaptor"

 /locus tag="Yubaba\_6"

 /note=Original Glimmer call @bp 5374 has strength 18.4; Genemark calls start at 5374

 /note=SSC: 5374-5727 CP: yes SCS: both ST: SS BLAST-Start: [head-to-tail adaptor [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 1.04638E-78 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.681, -4.552792845506871, yes F: head-to-tail adaptor SIF-BLAST: ,,[head-to-tail adaptor [Microbacterium phage PaoPu] ],,YP\_009996591,100.0,1.04638E-78 SIF-HHPRED: Gp6; 13-membered ring, VIRAL PROTEIN; HET: MPD, MSE; 2.1A {Enterobacteria phage HK97},,,3JVO\_H,94.0171,99.5 SIF-Syn:

CDS 5724 - 6104

 /gene="7"

 /product="gp7"

 /function="tail terminator"

 /locus tag="Yubaba\_7"

 /note=Original Glimmer call @bp 5724 has strength 17.95; Genemark calls start at 5724

 /note=SSC: 5724-6104 CP: yes SCS: both ST: SS BLAST-Start: [tail terminator [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 4.10679E-84 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.523, -6.591314556970386, no F: tail terminator SIF-BLAST: ,,[tail terminator [Microbacterium phage PaoPu] ],,YP\_009996592,100.0,4.10679E-84 SIF-HHPRED: Tail terminator protein Rcc01690; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus},,,6TE9\_F,97.619,98.1 SIF-Syn:

CDS 6143 - 6577

 /gene="8"

 /product="gp8"

 /function="major tail protein"

 /locus tag="Yubaba\_8"

 /note=Original Glimmer call @bp 6143 has strength 12.18; Genemark calls start at 6143

 /note=SSC: 6143-6577 CP: yes SCS: both ST: SS BLAST-Start: [major tail protein [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 4.96284E-100 GAP: 38 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.537, -5.796882727134779, no F: major tail protein SIF-BLAST: ,,[major tail protein [Microbacterium phage PaoPu] ],,YP\_009996593,100.0,4.96284E-100 SIF-HHPRED: Phage major tail protein, TP901-1 family; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus},,,6TE9\_G,96.5278,99.4 SIF-Syn:

CDS 6590 - 6973

 /gene="9"

 /product="gp9"

 /function="minor tail protein"

 /locus tag="Yubaba\_9"

 /note=Original Glimmer call @bp 6590 has strength 15.26; Genemark calls start at 6590

 /note=SSC: 6590-6973 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein JTF51\_gp09 [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 2.93542E-85 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.259, -4.294054598558697, no F: minor tail protein SIF-BLAST: ,,[hypothetical protein JTF51\_gp09 [Microbacterium phage PaoPu] ],,YP\_009996594,100.0,2.93542E-85 SIF-HHPRED: HK97-gp10\_like ; Bacteriophage HK97-gp10, putative tail-component,,,PF04883.15,55.9055,99.1 SIF-Syn:

 /note=Phages DB minor tail protein

CDS 6987 - 7340

 /gene="10"

 /product="gp10"

 /function="tail assembly chaperone"

 /locus tag="Yubaba\_10"

 /note=Original Glimmer call @bp 6987 has strength 19.33; Genemark calls start at 6987

 /note=SSC: 6987-7340 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Microbacterium phage Gardevoir]],,NCBI, q1:s1 100.0% 8.30815E-75 GAP: 13 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.494, -3.8256434426994073, yes F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Microbacterium phage Gardevoir]],,UDL14923,100.0,8.30815E-75 SIF-HHPRED: Phage\_TAC\_12 ; Phage tail assembly chaperone protein, TAC,,,PF12363.11,46.1538,93.1 SIF-Syn:

CDS 7355 - 7456

 /gene="11"

 /product="gp11"

 /function="tail assembly chaperone"

 /locus tag="Yubaba\_11"

 /note=Genemark calls start at 7367

 /note=SSC: 7355-7456 CP: yes SCS: genemark-cs ST: NI BLAST-Start: [tail assembly chaperone [Microbacterium phage Bri160] ],,NCBI, q1:s113 100.0% 6.29587E-13 GAP: 14 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.37, -4.423424636048095, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Microbacterium phage Bri160] ],,YP\_009996645,22.7586,6.29587E-13 SIF-HHPRED: SIF-Syn:

CDS 7574 - 9679

 /gene="12"

 /product="gp12"

 /function="tape measure protein"

 /locus tag="Yubaba\_12"

 /note=Original Glimmer call @bp 7574 has strength 15.46; Genemark calls start at 7574

 /note=SSC: 7574-9679 CP: yes SCS: both ST: SS BLAST-Start: [tape measure protein [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 0.0 GAP: 117 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.765, -4.386181351886765, yes F: tape measure protein SIF-BLAST: ,,[tape measure protein [Microbacterium phage PaoPu] ],,YP\_009996597,100.0,0.0 SIF-HHPRED: Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_AF,22.2539,100.0 SIF-Syn:

tRNA 9436 - 9510

 /gene="13"

 /product="tRNA-Leu(gag)"

 /locus tag="YUBABA\_13"

 /note=tRNA-Leu(gag)

CDS 9676 - 10635

 /gene="14"

 /product="gp14"

 /function="minor tail protein"

 /locus tag="Yubaba\_14"

 /note=Original Glimmer call @bp 9676 has strength 9.72; Genemark calls start at 9676

 /note=SSC: 9676-10635 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.014, -4.924073590240254, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Microbacterium phage PaoPu] ],,YP\_009996598,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 10635 - 12704

 /gene="15"

 /product="gp15"

 /function="minor tail protein"

 /locus tag="Yubaba\_15"

 /note=Original Glimmer call @bp 10635 has strength 14.81; Genemark calls start at 10635

 /note=SSC: 10635-12704 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Microbacterium phage JoBros] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.311, -5.097661467667712, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Microbacterium phage JoBros] ],,QPX62224,100.0,0.0 SIF-HHPRED: SIF-Syn:

CDS 12706 - 13254

 /gene="16"

 /product="gp16"

 /function="minor tail protein"

 /locus tag="Yubaba\_16"

 /note=Original Glimmer call @bp 12706 has strength 14.72; Genemark calls start at 12706

 /note=SSC: 12706-13254 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 1.38337E-127 GAP: 1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.282, -2.394485424036831, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Microbacterium phage PaoPu] ],,YP\_009996600,100.0,1.38337E-127 SIF-HHPRED: d.231.1.1 (A:) Receptor-binding domain of short tail fibre protein gp12 {Bacteriophage T4 [TaxId: 10665]},,,d1ocya\_,35.7143,98.1 SIF-Syn:

CDS 13291 - 13578

 /gene="17"

 /product="gp17"

 /function="Hypothetical Protein"

 /locus tag="Yubaba\_17"

 /note=Original Glimmer call @bp 13291 has strength 14.34; Genemark calls start at 13267

 /note=SSC: 13291-13578 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein JTF51\_gp16 [Microbacterium phage PaoPu] ],,NCBI, q1:s9 100.0% 4.7907E-56 GAP: 36 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.653, -3.588526034455651, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein JTF51\_gp16 [Microbacterium phage PaoPu] ],,YP\_009996601,92.233,4.7907E-56 SIF-HHPRED: SIF-Syn:

CDS 13597 - 14283

 /gene="18"

 /product="gp18"

 /function="endolysin"

 /locus tag="Yubaba\_18"

 /note=Original Glimmer call @bp 13597 has strength 13.99; Genemark calls start at 13597

 /note=SSC: 13597-14283 CP: yes SCS: both ST: SS BLAST-Start: [endolysin [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 1.25401E-165 GAP: 18 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.488, -3.9776535502172963, yes F: endolysin SIF-BLAST: ,,[endolysin [Microbacterium phage PaoPu] ],,YP\_009996602,100.0,1.25401E-165 SIF-HHPRED: SIF-Syn:

CDS 14250 - 14513

 /gene="19"

 /product="gp19"

 /function="membrane protein"

 /locus tag="Yubaba\_19"

 /note=Original Glimmer call @bp 14250 has strength 10.24; Genemark calls start at 14250

 /note=SSC: 14250-14513 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein SEA\_BRADLEY2\_18 [Microbacterium phage Bradley2] ],,NCBI, q1:s1 100.0% 3.68167E-57 GAP: -34 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.594, -6.723716915074367, no F: membrane protein SIF-BLAST: ,,[hypothetical protein SEA\_BRADLEY2\_18 [Microbacterium phage Bradley2] ],,QFP94613,98.8506,3.68167E-57 SIF-HHPRED: SIF-Syn:

CDS 14510 - 14734

 /gene="20"

 /product="gp20"

 /function="holin"

 /locus tag="Yubaba\_20"

 /note=Original Glimmer call @bp 14510 has strength 13.17; Genemark calls start at 14510

 /note=SSC: 14510-14734 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein JTF51\_gp19 [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 1.18717E-43 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.853, -3.170856472917156, yes F: holin SIF-BLAST: ,,[hypothetical protein JTF51\_gp19 [Microbacterium phage PaoPu] ],,YP\_009996604,100.0,1.18717E-43 SIF-HHPRED: Phage\_holin\_7\_1 ; Mycobacterial 2 TMS Phage Holin (M2 Hol) Family,,,PF16081.8,59.4595,97.4 SIF-Syn:

CDS complement (14803 - 15015)

 /gene="21"

 /product="gp21"

 /function="Lsr2-like DNA bridging protein"

 /locus tag="Yubaba\_21"

 /note=Original Glimmer call @bp 15015 has strength 13.31; Genemark calls start at 15015

 /note=SSC: 15015-14803 CP: yes SCS: both ST: NI BLAST-Start: [Lsr2-like DNA bridging protein [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 1.13692E-41 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.664, -3.627004739933808, yes F: Lsr2-like DNA bridging protein SIF-BLAST: ,,[Lsr2-like DNA bridging protein [Microbacterium phage PaoPu] ],,YP\_009996605,100.0,1.13692E-41 SIF-HHPRED: Protein lsr2; anti-parallel beta sheet, dimer, DNA BINDING PROTEIN; 1.728A {Mycobacterium tuberculosis},,,4E1P\_B,84.2857,99.9 SIF-Syn:

CDS complement (15018 - 15455)

 /gene="22"

 /product="gp22"

 /function="helix-turn-helix DNA binding domain, MerR-like"

 /locus tag="Yubaba\_22"

 /note=Original Glimmer call @bp 15455 has strength 12.7; Genemark calls start at 15518

 /note=SSC: 15455-15018 CP: no SCS: both-gl ST: SS BLAST-Start: [MerR-like helix-turn-helix DNA binding domain protein [Microbacterium phage Minima]],,NCBI, q1:s26 100.0% 9.12717E-99 GAP: 142 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.006, -3.15492870275902, yes F: helix-turn-helix DNA binding domain, MerR-like SIF-BLAST: ,,[MerR-like helix-turn-helix DNA binding domain protein [Microbacterium phage Minima]],,AXQ64369,85.2941,9.12717E-99 SIF-HHPRED: AM32; Repressor, Protein-DNA complex, Type IV secretion system, DNA BINDING PROTEIN; HET: EPE; 1.93A {Enterococcus faecalis},,,6G1T\_A,91.0345,99.4 SIF-Syn:

CDS complement (15598 - 15828)

 /gene="23"

 /product="gp23"

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

 /locus tag="Yubaba\_23"

 /note=Original Glimmer call @bp 15828 has strength 5.05; Genemark calls start at 15828

 /note=SSC: 15828-15598 CP: yes SCS: both ST: SS BLAST-Start: [helix-turn-helix DNA binding domain protein [Microbacterium phage Gardevoir]],,NCBI, q1:s1 100.0% 1.82892E-45 GAP: 509 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 0.938, -7.838780790165433, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA binding domain protein [Microbacterium phage Gardevoir]],,UDL14934,100.0,1.82892E-45 SIF-HHPRED: Endothelial differentiation-related factor 1; EDF1, HMBF1alpha, helix-turn-helix, Structural Genomics, NPPSFA, National Project on Protein Structural and Functional Analyses, RIKEN Structural; NMR {Homo sapiens} SCOP: l.1.1.1, a.35.1.12,,,1X57\_A,89.4737,99.2 SIF-Syn:

CDS 16338 - 16724

 /gene="24"

 /product="gp24"

 /function="Hypothetical Protein"

 /locus tag="Yubaba\_24"

 /note=Original Glimmer call @bp 16338 has strength 6.51; Genemark calls start at 16542

 /note=SSC: 16338-16724 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_DONGWON\_23 [Microbacterium phage Dongwon] ],,NCBI, q1:s1 100.0% 2.98094E-83 GAP: 509 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.756, -5.824635795707105, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_DONGWON\_23 [Microbacterium phage Dongwon] ],,AYJ73787,100.0,2.98094E-83 SIF-HHPRED: SIF-Syn:

CDS 16808 - 17026

 /gene="25"

 /product="gp25"

 /function="helix-turn-helix DNA binding domain, MerR-like"

 /locus tag="Yubaba\_25"

 /note=Original Glimmer call @bp 16808 has strength 11.65; Genemark calls start at 16817

 /note=SSC: 16808-17026 CP: yes SCS: both-gl ST: SS BLAST-Start: [MerR-like helix-turn-helix DNA binding domain protein [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 7.18573E-44 GAP: 83 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.292, -6.574698744401119, no F: helix-turn-helix DNA binding domain, MerR-like SIF-BLAST: ,,[MerR-like helix-turn-helix DNA binding domain protein [Microbacterium phage PaoPu] ],,YP\_009996609,100.0,7.18573E-44 SIF-HHPRED: Putative DNA-binding protein; BldC, S. coelicolor, developmental switch, MerR-like, DNA BINDING PROTEIN-DNA complex; 3.09A {Streptomyces venezuelae},,,6AMA\_A,75.0,99.4 SIF-Syn:

CDS 17023 - 17322

 /gene="26"

 /product="gp26"

 /function="HNH endonuclease"

 /locus tag="Yubaba\_26"

 /note=Original Glimmer call @bp 17023 has strength 8.75; Genemark calls start at 17023

 /note=SSC: 17023-17322 CP: yes SCS: both ST: NI BLAST-Start: [HNH endonuclease [Microbacterium phage PaoPu] ],,NCBI, q1:s1 100.0% 5.34689E-68 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.419, -6.050814105256152, no F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Microbacterium phage PaoPu] ],,YP\_009996610,100.0,5.34689E-68 SIF-HHPRED: d.4.1.8 (A:775-907) CRISPR-associated endonuclease Cas9/Csn1, HNH domain {Streptococcus pyogenes [TaxId: 301447]},,,d4oo8a2,78.7879,98.4 SIF-Syn: 4 SIF-Syn: 0,5.34689E-68 SIF-HHPRED: SIF-Syn: