CDS 109 - 612

 /gene="1"

 /product="gp1"

 /function="terminase, small subunit"

 /locus tag="radfad\_1"

 /note=Original Glimmer call @bp 64 has strength 5.79; Genemark calls start at 109

 /note=SSC: 109-612 CP: yes SCS: both-gm ST: SS BLAST-Start: [terminase small subunit [Arthrobacter phage Auxilium]],,NCBI, q2:s17 99.4012% 1.08024E-109 GAP: 0 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.27, -7.0507070447296165, no F: terminase, small subunit SIF-BLAST: ,,[terminase small subunit [Arthrobacter phage Auxilium]],,AYN55781,89.011,1.08024E-109 SIF-HHPRED: SIF-Syn: Synteny with Richie and Seahorse.

CDS 599 - 1678

 /gene="2"

 /product="gp2"

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

 /locus tag="radfad\_2"

 /note=Original Glimmer call @bp 599 has strength 9.98; Genemark calls start at 599

 /note=SSC: 599-1678 CP: yes SCS: both ST: SS BLAST-Start: [terminase large subunit, ATPase domain [Arthrobacter phage Faja]],,NCBI, q1:s1 100.0% 0.0 GAP: -14 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.133, -4.863452397416132, no F: terminase, large subunit (ATPase domain) SIF-BLAST: ,,[terminase large subunit, ATPase domain [Arthrobacter phage Faja]],,AYN57857,100.0,0.0 SIF-HHPRED: SIF-Syn: Synteny with Auxilium and Faja

CDS 1647 - 2258

 /gene="3"

 /product="gp3"

 /function="terminase, large subunit"

 /locus tag="radfad\_3"

 /note=Original Glimmer call @bp 1647 has strength 11.05; Genemark calls start at 1647

 /note=SSC: 1647-2258 CP: yes SCS: both ST: SS BLAST-Start: [terminase large subunit, nuclease domain [Arthrobacter phage Faja]],,NCBI, q1:s1 100.0% 2.13394E-149 GAP: -32 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.197, -4.344614665115397, no F: terminase, large subunit SIF-BLAST: ,,[terminase large subunit, nuclease domain [Arthrobacter phage Faja]],,AYN57858,100.0,2.13394E-149 SIF-HHPRED: SIF-Syn: Synteny with Faja and Richie

CDS 2262 - 3605

 /gene="4"

 /product="gp4"

 /function="portal protein"

 /locus tag="radfad\_4"

 /note=Original Glimmer call @bp 2274 has strength 11.1; Genemark calls start at 2274

 /note=SSC: 2262-3605 CP: yes SCS: both-cs ST: NA BLAST-Start: [portal protein [Arthrobacter phage Auxilium]],,NCBI, q1:s1 100.0% 0.0 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 0.74, -7.605062753366521, no F: portal protein SIF-BLAST: ,,[portal protein [Arthrobacter phage Auxilium]],,AYN55784,94.8775,0.0 SIF-HHPRED: SIF-Syn:

CDS 3608 - 4822

 /gene="5"

 /product="gp5"

 /function="capsid maturation protease"

 /locus tag="radfad\_5"

 /note=Original Glimmer call @bp 3608 has strength 4.87; Genemark calls start at 3608

 /note=SSC: 3608-4822 CP: yes SCS: both ST: SS BLAST-Start: [capsid maturation protease [Arthrobacter phage Faja]],,NCBI, q1:s1 100.0% 0.0 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.308, -4.033958934919761, no F: capsid maturation protease SIF-BLAST: ,,[capsid maturation protease [Arthrobacter phage Faja]],,AYN57860,99.505,0.0 SIF-HHPRED: SIF-Syn: synteny with Faja and Isolde.

CDS 4944 - 5447

 /gene="6"

 /product="gp6"

 /function="scaffolding protein"

 /locus tag="radfad\_6"

 /note=Original Glimmer call @bp 4944 has strength 11.07; Genemark calls start at 4944

 /note=SSC: 4944-5447 CP: yes SCS: both ST: SS BLAST-Start: [scaffolding protein [Arthrobacter phage Faja]],,NCBI, q1:s1 98.8024% 2.50028E-106 GAP: 121 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.0895162839948163, yes F: scaffolding protein SIF-BLAST: ,,[scaffolding protein [Arthrobacter phage Faja]],,AYN57861,97.5904,2.50028E-106 SIF-HHPRED: SIF-Syn: Synteny with Auxilium and Faja

CDS 5476 - 5871

 /gene="7"

 /product="gp7"

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

 /locus tag="radfad\_7"

 /note=Original Glimmer call @bp 5476 has strength 11.66; Genemark calls start at 5476

 /note=SSC: 5476-5871 CP: yes SCS: both ST: NI BLAST-Start: [capsid decoration protein [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 1.94407E-82 GAP: 28 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.038, -2.5052746077145835, yes F: terminase, large subunit (nuclease domain) SIF-BLAST: ,,[capsid decoration protein [Arthrobacter phage Auxilium] ],,AYN55787,95.4198,1.94407E-82 SIF-HHPRED: SIF-Syn: most likely to Richie and Auxilium

CDS 5887 - 6927

 /gene="8"

 /product="gp8"

 /function="major capsid protein"

 /locus tag="radfad\_8"

 /note=Original Glimmer call @bp 5887 has strength 11.37; Genemark calls start at 5887

 /note=SSC: 5887-6927 CP: yes SCS: both ST: SS BLAST-Start: [major capsid protein [Arthrobacter phage Faja]],,NCBI, q1:s1 100.0% 0.0 GAP: 15 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.636, -3.6360588251033645, yes F: major capsid protein SIF-BLAST: ,,[major capsid protein [Arthrobacter phage Faja]],,AYN57863,97.6879,0.0 SIF-HHPRED: SIF-Syn: Synteny with Faja and Auxillium

CDS 6939 - 7277

 /gene="9"

 /product="gp9"

 /function="hypothetical protein"

 /locus tag="radfad\_9"

 /note=Original Glimmer call @bp 6939 has strength 13.1; Genemark calls start at 6939

 /note=SSC: 6939-7277 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_ISOLDE\_10 [Arthrobacter phage Isolde]],,NCBI, q1:s1 100.0% 1.55985E-56 GAP: 11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.139, -4.466674028236667, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_ISOLDE\_10 [Arthrobacter phage Isolde]],,AYR00979,92.8571,1.55985E-56 SIF-HHPRED: SIF-Syn: Synteny with Isolde and Hestia

CDS 7292 - 7648

 /gene="10"

 /product="gp10"

 /function="head-to-tail adaptor"

 /locus tag="radfad\_10"

 /note=Original Glimmer call @bp 7292 has strength 6.97; Genemark calls start at 7292

 /note=SSC: 7292-7648 CP: yes SCS: both ST: SS BLAST-Start: [head-to-tail adaptor [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 3.16576E-71 GAP: 14 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.472, -3.708514821076885, yes F: head-to-tail adaptor SIF-BLAST: ,,[head-to-tail adaptor [Arthrobacter phage Richie]],,AYN58838,95.7627,3.16576E-71 SIF-HHPRED: SIF-Syn: Synteny with Auxilium and Isolde

CDS 7645 - 8046

 /gene="11"

 /product="gp11"

 /function="head-to-tail stopper"

 /locus tag="radfad\_11"

 /note=Original Glimmer call @bp 7645 has strength 8.58; Genemark calls start at 7645

 /note=SSC: 7645-8046 CP: yes SCS: both ST: SS BLAST-Start: [head-to-tail stopper [Arthrobacter phage Isolde]],,NCBI, q1:s1 100.0% 4.33812E-84 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.696, -3.2997855658338913, yes F: head-to-tail stopper SIF-BLAST: ,,[head-to-tail stopper [Arthrobacter phage Isolde]],,AYR00981,96.9697,4.33812E-84 SIF-HHPRED: SIF-Syn: Synteny with Isolde and Auxilium

 /note=Q16S15 with Isolde, Auxilium and Richie

CDS 8043 - 8426

 /gene="12"

 /product="gp12"

 /function="hypothetical protein"

 /locus tag="radfad\_12"

 /note=Original Glimmer call @bp 8043 has strength 6.7; Genemark calls start at 8043

 /note=SSC: 8043-8426 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_RICHIE\_12 [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 1.55099E-84 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.038, -2.583959800616441, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_12 [Arthrobacter phage Richie]],,AYN58840,100.0,1.55099E-84 SIF-HHPRED: SIF-Syn: Synteny with Richie and Auxilium.

CDS 8408 - 8821

 /gene="13"

 /product="gp13"

 /function="tail terminator"

 /locus tag="radfad\_13"

 /note=Original Glimmer call @bp 8408 has strength 7.79; Genemark calls start at 8423

 /note=SSC: 8408-8821 CP: yes SCS: both-gl ST: SS BLAST-Start: [tail terminator [Arthrobacter phage Richie]],,NCBI, q6:s1 96.3504% 1.34783E-91 GAP: -19 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.54, -5.092387591382226, no F: tail terminator SIF-BLAST: ,,[tail terminator [Arthrobacter phage Richie]],,AYN58841,100.0,1.34783E-91 SIF-HHPRED: SIF-Syn:

 /note=Synteny with Richie

CDS 8868 - 9053

 /gene="14"

 /product="gp14"

 /function="hypothetical protein"

 /locus tag="radfad\_14"

 /note=Original Glimmer call @bp 8868 has strength 12.66; Genemark calls start at 8868

 /note=SSC: 8868-9053 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_14 [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 2.09888E-33 GAP: 46 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.962, -2.6013996449736907, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_14 [Arthrobacter phage Auxilium] ],,AYN55794,98.3607,2.09888E-33 SIF-HHPRED: SIF-Syn: Synteny with Auxillium and Richie.

CDS 9046 - 9561

 /gene="15"

 /product="gp15"

 /function="major tail protein"

 /locus tag="radfad\_15"

 /note=Original Glimmer call @bp 9046 has strength 11.14; Genemark calls start at 9046

 /note=SSC: 9046-9561 CP: yes SCS: both ST: SS BLAST-Start: [major tail protein [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 6.59341E-121 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.588, -3.4463834536695686, no F: major tail protein SIF-BLAST: ,,[major tail protein [Arthrobacter phage Richie]],,AYN58843,100.0,6.59341E-121 SIF-HHPRED: SIF-Syn: Synteny with Richie and Auxilium

CDS 9651 - 10187

 /gene="16"

 /product="gp16"

 /function="tail assembly chaperone"

 /locus tag="radfad\_16"

 /note=Original Glimmer call @bp 9651 has strength 12.87; Genemark calls start at 9651

 /note=SSC: 9651-10187 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 9.59013E-129 GAP: 89 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.372, -3.8366550365551095, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Arthrobacter phage Auxilium] ],,AYN55796,100.0,9.59013E-129 SIF-HHPRED: SIF-Syn: Synteny with Richie and Auxilium

CDS 10046 - 10534

 /gene="17"

 /product="gp17"

 /function="tail assembly chaperone"

 /locus tag="radfad\_17"

 /note=Original Glimmer call @bp 10331 has strength 6.01; Genemark calls start at 10331

 /note=SSC: 10046-10534 CP: no SCS: both-cs ST: SS BLAST-Start: [tail assembly chaperone [Arthrobacter phage Auxilium]],,NCBI, q26:s158 84.5679% 1.19607E-94 GAP: -142 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.161, -6.451135853805349, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Arthrobacter phage Auxilium]],,AYN55873,46.2585,1.19607E-94 SIF-HHPRED: SIF-Syn:

CDS complement (10531 - 10770)

 /gene="18"

 /product="gp18"

 /function="hypothetical protein"

 /locus tag="radfad\_18"

 /note=Original Glimmer call @bp 10770 has strength 4.78; Genemark calls start at 10770

 /note=SSC: 10770-10531 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_RICHIE\_18 [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 2.30922E-47 GAP: 72 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.772, -5.092497832398658, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_18 [Arthrobacter phage Richie]],,AYN58926,100.0,2.30922E-47 SIF-HHPRED: SIF-Syn: Synteny with Richie and Auxilium

CDS 10843 - 14784

 /gene="19"

 /product="gp19"

 /function="tape measure protein"

 /locus tag="radfad\_19"

 /note=Original Glimmer call @bp 10843 has strength 7.54; Genemark calls start at 10843

 /note=SSC: 10843-14784 CP: yes SCS: both ST: SS BLAST-Start: [tape measure protein [Arthrobacter phage Auxilium]],,NCBI, q1:s1 100.0% 0.0 GAP: 72 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.139, -4.325675514574479, no F: tape measure protein SIF-BLAST: ,,[tape measure protein [Arthrobacter phage Auxilium]],,AYN55798,99.7715,0.0 SIF-HHPRED: SIF-Syn: Synteny with Auxillium and Richie

CDS 14784 - 15611

 /gene="20"

 /product="gp20"

 /function="minor tail protein"

 /locus tag="radfad\_20"

 /note=Original Glimmer call @bp 14784 has strength 11.07; Genemark calls start at 14784

 /note=SSC: 14784-15611 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.196, -2.17469248771465, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Richie]],,AYN58846,100.0,0.0 SIF-HHPRED: SIF-Syn: Synteny with Richie and Auxilium

CDS 15623 - 16924

 /gene="21"

 /product="gp21"

 /function="minor tail protein"

 /locus tag="radfad\_21"

 /note=Original Glimmer call @bp 15623 has strength 11.09; Genemark calls start at 15623

 /note=SSC: 15623-16924 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Arthrobacter phage Auxilium]],,NCBI, q1:s1 100.0% 0.0 GAP: 11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.139, -4.466674028236667, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Auxilium]],,AYN55800,100.0,0.0 SIF-HHPRED: SIF-Syn: Synteny with Auxilium and Richie

CDS 16933 - 17892

 /gene="22"

 /product="gp22"

 /function="minor tail protein"

 /locus tag="radfad\_22"

 /note=Original Glimmer call @bp 16933 has strength 4.69; Genemark calls start at 16942

 /note=SSC: 16933-17892 CP: yes SCS: both-gl ST: SS BLAST-Start: [minor tail protein [Arthrobacter phage Hestia]],,NCBI, q1:s1 100.0% 0.0 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.383, -3.893834241316366, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Hestia]],,AYR00900,99.6865,0.0 SIF-HHPRED: SIF-Syn: Synteny with Hestia and Richie

CDS 17892 - 18551

 /gene="23"

 /product="gp23"

 /function="minor tail protein"

 /locus tag="radfad\_23"

 /note=Original Glimmer call @bp 17892 has strength 7.81; Genemark calls start at 17892

 /note=SSC: 17892-18551 CP: no SCS: both ST: NI BLAST-Start: [minor tail protein [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 3.4577E-157 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.291, -4.005585920014169, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Auxilium] ],,AYN55802,100.0,3.4577E-157 SIF-HHPRED: SIF-Syn: synteny with Auxilium and Richie

CDS 18563 - 19006

 /gene="24"

 /product="gp24"

 /function="hypothetical protein"

 /locus tag="radfad\_24"

 /note=Original Glimmer call @bp 18563 has strength 5.06; Genemark calls start at 18563

 /note=SSC: 18563-19006 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_24 [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 6.1702E-102 GAP: 11 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.87, -2.8564937087383147, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_24 [Arthrobacter phage Auxilium] ],,AYN55803,100.0,6.1702E-102 SIF-HHPRED: SIF-Syn: most synteny with Richie

CDS 19003 - 19329

 /gene="25"

 /product="gp25"

 /function="hypothetical protein"

 /locus tag="radfad\_25"

 /note=Original Glimmer call @bp 19003 has strength 7.39; Genemark calls start at 19003

 /note=SSC: 19003-19329 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_25 [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 1.30891E-72 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.962, -2.6814417326944517, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_25 [Arthrobacter phage Auxilium] ],,AYN55804,100.0,1.30891E-72 SIF-HHPRED: SIF-Syn: Most synteny with virus Richie

CDS 19341 - 19466

 /gene="26"

 /product="gp26"

 /function="hypothetical protein"

 /locus tag="radfad\_26"

 /note=Original Glimmer call @bp 19341 has strength 9.97; Genemark calls start at 19341

 /note=SSC: 19341-19466 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_26 [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 6.60632E-21 GAP: 11 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.139, -4.466674028236667, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_26 [Arthrobacter phage Auxilium] ],,AYN55805,100.0,6.60632E-21 SIF-HHPRED: SIF-Syn: Most synteny with virus Richie and Isolde

CDS 19466 - 20428

 /gene="27"

 /product="gp27"

 /function="lysin A"

 /locus tag="radfad\_27"

 /note=Original Glimmer call @bp 19466 has strength 8.2; Genemark calls start at 19466

 /note=SSC: 19466-20428 CP: no SCS: both ST: SS BLAST-Start: [lysin A [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.005, -5.6562426662814325, no F: lysin A SIF-BLAST: ,,[lysin A [Arthrobacter phage Auxilium] ],,AYN55806,99.6875,0.0 SIF-HHPRED: d.118.1.1 (A:1-157) N-acetylmuramoyl-L-alanine amidase PlyG {Anthrax bacillus (Bacillus anthracis) [TaxId: 1392]},,,d1yb0a1,50.9375,99.7 SIF-Syn:

CDS 20421 - 20726

 /gene="28"

 /product="gp28"

 /function="hypothetical protein"

 /locus tag="radfad\_28"

 /note=Original Glimmer call @bp 20421 has strength 7.07; Genemark calls start at 20421

 /note=SSC: 20421-20726 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_28 [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 2.69072E-63 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.962, -2.66371296573402, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_28 [Arthrobacter phage Auxilium] ],,AYN55807,100.0,2.69072E-63 SIF-HHPRED: SIF-Syn: Most synteny with virus Richie

CDS 20745 - 21050

 /gene="29"

 /product="gp29"

 /function="hypothetical protein"

 /locus tag="radfad\_29"

 /note=Original Glimmer call @bp 20745 has strength 7.77; Genemark calls start at 20745

 /note=SSC: 20745-21050 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_29 [Arthrobacter phage Auxilium]],,NCBI, q1:s1 100.0% 9.98657E-65 GAP: 18 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.884, -2.7653702713535186, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_29 [Arthrobacter phage Auxilium]],,AYN55808,99.0099,9.98657E-65 SIF-HHPRED: SIF-Syn: Most synteny with virus Richie

CDS 21047 - 21421

 /gene="30"

 /product="gp30"

 /function="hypothetical protein"

 /locus tag="radfad\_30"

 /note=Original Glimmer call @bp 21047 has strength 6.42; Genemark calls start at 21047

 /note=SSC: 21047-21421 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_ISOLDE\_30 [Arthrobacter phage Isolde]],,NCBI, q1:s1 100.0% 7.15783E-81 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.230514797657003, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_ISOLDE\_30 [Arthrobacter phage Isolde]],,AYR00999,100.0,7.15783E-81 SIF-HHPRED: SIF-Syn: Most synteny with virus Richie

CDS 21425 - 21637

 /gene="31"

 /product="gp31"

 /function="hypothetical protein"

 /locus tag="radfad\_31"

 /note=Original Glimmer call @bp 21425 has strength 2.62; Genemark calls start at 21446

 /note=SSC: 21425-21637 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein PBI\_RICHIE\_31 [Arthrobacter phage Richie] ],,NCBI, q1:s1 100.0% 2.16526E-41 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.95, -4.862260131515226, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_31 [Arthrobacter phage Richie] ],,AYN58857,100.0,2.16526E-41 SIF-HHPRED: SIF-Syn: Most synteny with Richie and Isolde

CDS 21637 - 22890

 /gene="32"

 /product="gp32"

 /function="lipase, LipC-like"

 /locus tag="radfad\_32"

 /note=Original Glimmer call @bp 21637 has strength 12.66; Genemark calls start at 21637

 /note=SSC: 21637-22890 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU46\_gp30 [Arthrobacter phage Bridgette] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.94, -5.092387591382226, no F: lipase, LipC-like SIF-BLAST: ,,[hypothetical protein HOU46\_gp30 [Arthrobacter phage Bridgette] ],,YP\_009815232,100.0,0.0 SIF-HHPRED: GDSL-like Lipase/Acylhydrolase family protein; alpha/Beta fold, peptidoglycan hydrolase, HYDROLASE; HET: EPE; 1.968A {Neisseria meningitidis},,,4K7J\_A,82.494,100.0 SIF-Syn: Most synteny with Isolde and Richie

CDS complement (22887 - 23087)

 /gene="33"

 /product="gp33"

 /function="hypothetical protein"

 /locus tag="radfad\_33"

 /note=Original Glimmer call @bp 23087 has strength 6.5; Genemark calls start at 23087

 /note=SSC: 23087-22887 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Bridgette] ],,NCBI, q1:s1 100.0% 8.00771E-37 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.902, -5.47366350364755, yes F: hypothetical protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Bridgette] ],,YP\_009815233,100.0,8.00771E-37 SIF-HHPRED: SIF-Syn: Most synteny with Isolde

CDS complement (23084 - 23851)

 /gene="34"

 /product="gp34"

 /function="esterase"

 /locus tag="radfad\_34"

 /note=Original Glimmer call @bp 23611 has strength 7.17; Genemark calls start at 23851

 /note=SSC: 23851-23084 CP: no SCS: both-gm ST: NI BLAST-Start: [lipase [Arthrobacter phage Bridgette] ],,NCBI, q1:s1 100.0% 0.0 GAP: 19 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.222, -6.386092517351332, no F: esterase SIF-BLAST: ,,[lipase [Arthrobacter phage Bridgette] ],,YP\_009815234,100.0,0.0 SIF-HHPRED: SIF-Syn: Synteny with Isolde and Richie

 /note=Genemark start was chosen based on preferred e-value and Q1S1.

CDS complement (23871 - 24380)

 /gene="35"

 /product="gp35"

 /function="hypothetical protein"

 /locus tag="radfad\_35"

 /note=Original Glimmer call @bp 24380 has strength 3.53; Genemark calls start at 24380

 /note=SSC: 24380-23871 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein HOU47\_gp33 [Arthrobacter phage Constance] ],,NCBI, q1:s5 100.0% 9.58949E-125 GAP: 191 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.819, -7.087342399739116, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein HOU47\_gp33 [Arthrobacter phage Constance] ],,YP\_009815306,97.6879,9.58949E-125 SIF-HHPRED: SIF-Syn: no synteny

CDS 24572 - 25492

 /gene="36"

 /product="gp36"

 /function="hypothetical protein"

 /locus tag="radfad\_36"

 /note=Original Glimmer call @bp 24572 has strength 12.13; Genemark calls start at 24572

 /note=SSC: 24572-25492 CP: no SCS: both ST: SS BLAST-Start: [integrase [Arthrobacter phage Nandita]],,NCBI, q1:s1 100.0% 0.0 GAP: 191 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.615, -3.4076099559729456, no F: hypothetical protein SIF-BLAST: ,,[integrase [Arthrobacter phage Nandita]],,AYN58657,99.3464,0.0 SIF-HHPRED: SITE-SPECIFIC RECOMBINASE XERD; XERD, RECOMBINASE, DNA BINDING, DNA RECOMBINATION; 2.5A {Escherichia coli} SCOP: a.60.9.1, d.163.1.1,,,1A0P\_A,91.1765,100.0 SIF-Syn: no synteny

CDS 25503 - 25859

 /gene="37"

 /product="gp37"

 /function="hypothetical protein"

 /locus tag="radfad\_37"

 /note=Original Glimmer call @bp 25503 has strength 4.47; Genemark calls start at 25503

 /note=SSC: 25503-25859 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_SARGE\_27 [Arthrobacter phage Sarge]],,NCBI, q1:s1 100.0% 1.80185E-77 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.189, -6.964808423506407, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_SARGE\_27 [Arthrobacter phage Sarge]],,UDL14874,96.6102,1.80185E-77 SIF-HHPRED: SIF-Syn: no synteny

CDS complement (25848 - 26084)

 /gene="38"

 /product="gp38"

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

 /locus tag="radfad\_38"

 /note=Original Glimmer call @bp 26084 has strength 4.54; Genemark calls start at 26060

 /note=SSC: 26084-25848 CP: yes SCS: both-gl ST: SS BLAST-Start: [helix-turn-helix DNA-binding domain protein [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 2.65938E-46 GAP: 133 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.225, -6.299988513554353, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA-binding domain protein [Arthrobacter phage Richie]],,AYN58865,97.4359,2.65938E-46 SIF-HHPRED: DUF3263 ; Protein of unknown function (DUF3263),,,PF11662.11,91.0256,99.9 SIF-Syn: no synteny

CDS 26218 - 26697

 /gene="39"

 /product="gp39"

 /function="HNH endonuclease"

 /locus tag="radfad\_39"

 /note=Original Glimmer call @bp 26218 has strength 4.38; Genemark calls start at 26218

 /note=SSC: 26218-26697 CP: no SCS: both ST: SS BLAST-Start: [HNH endonuclease [Arthrobacter phage Persistence]],,NCBI, q1:s9 99.3711% 7.67802E-107 GAP: 133 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.038, -2.523003374675015, yes F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Arthrobacter phage Persistence]],,QWY79664,90.4192,7.67802E-107 SIF-HHPRED: zf-His\_Me\_endon ; Zinc-binding loop region of homing endonuclease,,,PF05551.14,46.5409,99.6 SIF-Syn: most synteny with virus Seahorse

CDS complement (26659 - 27831)

 /gene="40"

 /product="gp40"

 /function="tyrosine integrase"

 /locus tag="radfad\_40"

 /note=Original Glimmer call @bp 27831 has strength 7.01; Genemark calls start at 27831

 /note=SSC: 27831-26659 CP: yes SCS: both ST: SS BLAST-Start: [integrase [Arthrobacter phage Isolde]],,NCBI, q1:s1 96.6667% 0.0 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.009, -5.12434507728107, no F: tyrosine integrase SIF-BLAST: ,,[integrase [Arthrobacter phage Isolde]],,AYR01010,94.723,0.0 SIF-HHPRED: Int protein; transposase protein-DNA complex, tyrosine recombinase, Y-transposase, Tn916-like conjugative transposon, antibiotic resistance transfer, RECOMBINATION; 2.5A {Enterococcus faecalis},,,6EMY\_A,78.2051,100.0 SIF-Syn: Most synteny with Seahorse and Richie

CDS complement (27824 - 28078)

 /gene="41"

 /product="gp41"

 /function="hypothetical protein"

 /locus tag="radfad\_41"

 /note=Genemark calls start at 28078

 /note=SSC: 28078-27824 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein [Pseudarthrobacter sp. NIBRBAC000502772] ],,NCBI, q50:s53 35.7143% 1.3144E-6 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.962, -2.7423981586358774, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein [Pseudarthrobacter sp. NIBRBAC000502772] ],,WP\_141139450,27.957,1.3144E-6 SIF-HHPRED: SIF-Syn: no synteny

CDS complement (28075 - 28347)

 /gene="42"

 /product="gp42"

 /function="hypothetical protein"

 /locus tag="radfad\_42"

 /note=Original Glimmer call @bp 28347 has strength 3.78; Genemark calls start at 28347

 /note=SSC: 28347-28075 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein [Pseudarthrobacter chlorophenolicus] ],,NCBI, q1:s1 97.7778% 1.94998E-6 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.705, -3.2804507689989406, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein [Pseudarthrobacter chlorophenolicus] ],,WP\_012623225,57.1429,1.94998E-6 SIF-HHPRED: SIF-Syn: no synteny

CDS complement (28344 - 28856)

 /gene="43"

 /product="gp43"

 /function="hypothetical protein"

 /locus tag="radfad\_43"

 /note=Original Glimmer call @bp 28856 has strength 4.8; Genemark calls start at 28856

 /note=SSC: 28856-28344 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein [Pseudarthrobacter sp. NIBRBAC000502772] ],,NCBI, q43:s41 66.4706% 1.01159E-46 GAP: 217 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.038, -2.970161406017234, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein [Pseudarthrobacter sp. NIBRBAC000502772] ],,WP\_141139449,47.9592,1.01159E-46 SIF-HHPRED: SIF-Syn: no synteny

CDS complement (29074 - 29385)

 /gene="44"

 /product="gp44"

 /function="hypothetical protein"

 /locus tag="radfad\_44"

 /note=Original Glimmer call @bp 29385 has strength 5.0; Genemark calls start at 29385

 /note=SSC: 29385-29074 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein [Arthrobacter sp. ISL-69] ],,NCBI, q54:s1 48.5437% 7.33036E-8 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.941, -2.7254235724530456, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein [Arthrobacter sp. ISL-69] ],,WP\_214954038,30.4348,7.33036E-8 SIF-HHPRED: SIF-Syn: no synteny

CDS complement (29382 - 29522)

 /gene="45"

 /product="gp45"

 /function="hypothetical protein"

 /locus tag="radfad\_45"

 /note=Original Glimmer call @bp 29522 has strength 11.0; Genemark calls start at 29522

 /note=SSC: 29522-29382 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein [Pseudarthrobacter sp. NIBRBAC000502772]],,NCBI, q1:s1 100.0% 6.65844E-18 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.962, -2.7423981586358774, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein [Pseudarthrobacter sp. NIBRBAC000502772]],,WP\_168223485,82.6087,6.65844E-18 SIF-HHPRED: SIF-Syn: no synteny

CDS complement (29519 - 29758)

 /gene="46"

 /product="gp46"

 /function="hypothetical protein"

 /locus tag="radfad\_46"

 /note=Original Glimmer call @bp 29758 has strength 9.63; Genemark calls start at 29758

 /note=SSC: 29758-29519 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_44 [Arthrobacter phage Seahorse]],,NCBI, q8:s3 84.8101% 1.78697E-6 GAP: 418 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.3, -6.143436698069647, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_44 [Arthrobacter phage Seahorse]],,AYR01544,21.6374,1.78697E-6 SIF-HHPRED: SIF-Syn: no synteny

tRNA complement (29875 - 29944)

 /gene="47"

 /product="tRNA-Leu(caa)"

 /locus tag="RADFAD\_47"

 /note=tRNA-Leu(caa)

CDS 30177 - 30344

 /gene="48"

 /product="gp48"

 /function="hypothetical protein"

 /locus tag="radfad\_48"

 /note=Original Glimmer call @bp 30177 has strength 8.89; Genemark calls start at 30177

 /note=SSC: 30177-30344 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_46 [Arthrobacter phage Seahorse]],,NCBI, q1:s1 100.0% 2.82282E-23 GAP: 418 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.038, -2.5052746077145835, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_46 [Arthrobacter phage Seahorse]],,AYR01546,90.9091,2.82282E-23 SIF-HHPRED: SIF-Syn: no synteny

CDS 30341 - 30766

 /gene="49"

 /product="gp49"

 /function="hypothetical protein"

 /locus tag="radfad\_49"

 /note=Original Glimmer call @bp 30341 has strength 6.28; Genemark calls start at 30341

 /note=SSC: 30341-30766 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein M707\_02590 [Arthrobacter sp. AK-YN10]],,NCBI, q41:s25 70.922% 3.15722E-42 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.144, -4.665772780726076, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein M707\_02590 [Arthrobacter sp. AK-YN10]],,ERI39164,63.7097,3.15722E-42 SIF-HHPRED: SIF-Syn: most synteny with Isolde

CDS 30763 - 30885

 /gene="50"

 /product="gp50"

 /function="hypothetical protein"

 /locus tag="radfad\_50"

 /note=Original Glimmer call @bp 30763 has strength 9.29; Genemark calls start at 30763

 /note=SSC: 30763-30885 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_ISOLDE\_47 [Arthrobacter phage Isolde]],,NCBI, q1:s1 100.0% 1.32352E-18 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.644, -3.40798002383845, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_ISOLDE\_47 [Arthrobacter phage Isolde]],,AYR01016,92.5,1.32352E-18 SIF-HHPRED: SIF-Syn: no synteny

CDS 30882 - 31274

 /gene="51"

 /product="gp51"

 /function="hypothetical protein"

 /locus tag="radfad\_51"

 /note=Original Glimmer call @bp 30882 has strength 10.18; Genemark calls start at 30882

 /note=SSC: 30882-31274 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_44 [Arthrobacter phage Auxilium]],,NCBI, q1:s1 82.3077% 4.29546E-60 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.305, -3.976650358801626, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_44 [Arthrobacter phage Auxilium]],,AYN55823,51.6129,4.29546E-60 SIF-HHPRED: SIF-Syn: no synteny

CDS 31271 - 31621

 /gene="52"

 /product="gp52"

 /function="hypothetical protein"

 /locus tag="radfad\_52"

 /note=Original Glimmer call @bp 31271 has strength 8.82; Genemark calls start at 31301

 /note=SSC: 31271-31621 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein [Actinoplanes rectilineatus]],,NCBI, q1:s1 97.4138% 4.54633E-51 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.54, -3.627004739933808, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein [Actinoplanes rectilineatus]],,WP\_045740773,80.1724,4.54633E-51 SIF-HHPRED: SIF-Syn: Synteny with Seahorse and Richie

 /note=Glimmer start has better e-value and Q1S1.

CDS 31772 - 31969

 /gene="53"

 /product="gp53"

 /function="hypothetical protein"

 /locus tag="radfad\_53"

 /note=Original Glimmer call @bp 31772 has strength 3.89

 /note=SSC: 31772-31969 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein HYP98\_gp69 [Arthrobacter phage Zartrosa] ],,NCBI, q2:s8 98.4615% 4.3565E-19 GAP: 150 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.39, -4.151092687961526, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein HYP98\_gp69 [Arthrobacter phage Zartrosa] ],,YP\_009884290,66.1972,4.3565E-19 SIF-HHPRED: SIF-Syn: no synteny

CDS complement (32030 - 32245)

 /gene="54"

 /product="gp54"

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

 /locus tag="radfad\_54"

 /note=Original Glimmer call @bp 32245 has strength 2.03; Genemark calls start at 32284

 /note=SSC: 32245-32030 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_47 [Arthrobacter phage Auxilium]],,NCBI, q1:s14 100.0% 1.04691E-40 GAP: 175 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.817, -5.140579096418487, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_47 [Arthrobacter phage Auxilium]],,AYN55826,84.5238,1.04691E-40 SIF-HHPRED: SIF-Syn: no synteny

CDS complement (32421 - 32879)

 /gene="55"

 /product="gp55"

 /function="hypothetical protein"

 /locus tag="radfad\_55"

 /note=Original Glimmer call @bp 32879 has strength 3.49; Genemark calls start at 32789

 /note=SSC: 32879-32421 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_PERSISTENCE\_47 [Arthrobacter phage Persistence]],,NCBI, q1:s1 100.0% 8.49985E-103 GAP: 339 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.032, -4.690056473634766, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_PERSISTENCE\_47 [Arthrobacter phage Persistence]],,QWY79676,96.7105,8.49985E-103 SIF-HHPRED: SIF-Syn: synteny with persistence and richie.

CDS 33219 - 33413

 /gene="56"

 /product="gp56"

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

 /locus tag="radfad\_56"

 /note=Original Glimmer call @bp 33219 has strength 8.03; Genemark calls start at 33219

 /note=SSC: 33219-33413 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_FAJA\_53 [Arthrobacter phage Faja]],,NCBI, q1:s10 100.0% 6.6112E-38 GAP: 339 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.112, -6.474540158127503, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[hypothetical protein PBI\_FAJA\_53 [Arthrobacter phage Faja]],,AYN57905,87.6712,6.6112E-38 SIF-HHPRED: SIF-Syn: Synteny with Seahorse

CDS 33410 - 33871

 /gene="57"

 /product="gp57"

 /function="HNH endonuclease"

 /locus tag="radfad\_57"

 /note=Original Glimmer call @bp 33410 has strength 9.73; Genemark calls start at 33410

 /note=SSC: 33410-33871 CP: yes SCS: both ST: SS BLAST-Start: [HNH endonuclease [Arthrobacter phage Faja]],,NCBI, q1:s1 100.0% 6.22746E-109 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.895, -4.897971560974249, no F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Arthrobacter phage Faja]],,AYN57906,99.3464,6.22746E-109 SIF-HHPRED: zf-His\_Me\_endon ; Zinc-binding loop region of homing endonuclease,,,PF05551.14,46.4052,99.5 SIF-Syn: Synteny with Richie

CDS 33876 - 34100

 /gene="58"

 /product="gp58"

 /function="excise"

 /locus tag="radfad\_58"

 /note=Original Glimmer call @bp 33876 has strength 8.43; Genemark calls start at 33876

 /note=SSC: 33876-34100 CP: yes SCS: both ST: SS BLAST-Start: [excise [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 9.27777E-47 GAP: 4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.3, -7.131202241652635, no F: excise SIF-BLAST: ,,[excise [Arthrobacter phage Auxilium] ],,AYN55829,100.0,9.27777E-47 SIF-HHPRED: SIF-Syn: Synteny with Richie

CDS 34186 - 34449

 /gene="59"

 /product="gp59"

 /function="hypothetical protein"

 /locus tag="radfad\_59"

 /note=Original Glimmer call @bp 34186 has strength 10.03; Genemark calls start at 34186

 /note=SSC: 34186-34449 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_51 [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 1.36584E-50 GAP: 85 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.377, -4.176752302706706, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_51 [Arthrobacter phage Auxilium] ],,AYN55830,98.8506,1.36584E-50 SIF-HHPRED: SIF-Syn: no synteny

CDS 34520 - 34798

 /gene="60"

 /product="gp60"

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

 /locus tag="radfad\_60"

 /note=Original Glimmer call @bp 34520 has strength 9.43; Genemark calls start at 34520

 /note=SSC: 34520-34798 CP: yes SCS: both ST: SS BLAST-Start: [helix-turn-helix DNA-binding domain protein [Arthrobacter phage Isolde]],,NCBI, q1:s1 100.0% 1.33397E-60 GAP: 70 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.049, -4.654077828316241, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA-binding domain protein [Arthrobacter phage Isolde]],,AYR01024,100.0,1.33397E-60 SIF-HHPRED: SIF-Syn: no synteny

CDS 34795 - 34953

 /gene="61"

 /product="gp61"

 /function="oxidoreductase"

 /locus tag="radfad\_61"

 /note=Original Glimmer call @bp 34795 has strength 6.24; Genemark calls start at 34795

 /note=SSC: 34795-34953 CP: no SCS: both ST: SS BLAST-Start: [oxidoreductase [Arthrobacter phage Isolde]],,NCBI, q1:s1 100.0% 1.82075E-29 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.129, -4.408951082954879, no F: oxidoreductase SIF-BLAST: ,,[oxidoreductase [Arthrobacter phage Isolde]],,AYR01025,100.0,1.82075E-29 SIF-HHPRED: SIF-Syn: Synteny with Isolde

CDS 34950 - 35156

 /gene="62"

 /product="gp62"

 /function="hypothetical protein"

 /locus tag="radfad\_62"

 /note=Original Glimmer call @bp 34950 has strength 7.97; Genemark calls start at 34983

 /note=SSC: 34950-35156 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein [Arthrobacter sp. SLBN-83]],,NCBI, q1:s1 100.0% 1.50979E-27 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.461, -4.5573882134260355, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein [Arthrobacter sp. SLBN-83]],,TQJ60502,86.3636,1.50979E-27 SIF-HHPRED: SIF-Syn: Synteny with Isolde

CDS 35153 - 35305

 /gene="63"

 /product="gp63"

 /function="hypothetical protein"

 /locus tag="radfad\_63"

 /note=Original Glimmer call @bp 35153 has strength 9.87; Genemark calls start at 35153

 /note=SSC: 35153-35305 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_FAJA\_59 [Arthrobacter phage Faja]],,NCBI, q1:s1 100.0% 4.85358E-26 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.144, -4.455662434380964, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_FAJA\_59 [Arthrobacter phage Faja]],,AYN57911,96.0,4.85358E-26 SIF-HHPRED: SIF-Syn: Synteny with Hestia

CDS 35305 - 35448

 /gene="64"

 /product="gp64"

 /function="hypothetical protein"

 /locus tag="radfad\_64"

 /note=Original Glimmer call @bp 35305 has strength 8.06; Genemark calls start at 35305

 /note=SSC: 35305-35448 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_56 [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 5.23914E-26 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.203, -4.541779190262089, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_56 [Arthrobacter phage Auxilium] ],,AYN55835,100.0,5.23914E-26 SIF-HHPRED: SIF-Syn: Synteny with Hestia

CDS 35445 - 35570

 /gene="65"

 /product="gp65"

 /function="hypothetical protein"

 /locus tag="radfad\_65"

 /note=Original Glimmer call @bp 35445 has strength 13.44; Genemark calls start at 35445

 /note=SSC: 35445-35570 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_ISOLDE\_60 [Arthrobacter phage Isolde]],,NCBI, q1:s1 100.0% 3.49195E-19 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.433, -3.7891620722695425, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_ISOLDE\_60 [Arthrobacter phage Isolde]],,AYR01029,100.0,3.49195E-19 SIF-HHPRED: SIF-Syn:

CDS 35567 - 35713

 /gene="66"

 /product="gp66"

 /function="hypothetical protein"

 /locus tag="radfad\_66"

 /note=Original Glimmer call @bp 35567 has strength 10.46; Genemark calls start at 35567

 /note=SSC: 35567-35713 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_64 [Arthrobacter phage Seahorse]],,NCBI, q1:s1 100.0% 7.07974E-23 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.962, -2.7423981586358774, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_64 [Arthrobacter phage Seahorse]],,AYR01564,95.8333,7.07974E-23 SIF-HHPRED: SIF-Syn:

CDS 35710 - 35898

 /gene="67"

 /product="gp67"

 /function="hypothetical protein"

 /locus tag="radfad\_67"

 /note=Original Glimmer call @bp 35710 has strength 7.26; Genemark calls start at 35710

 /note=SSC: 35710-35898 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_65 [Arthrobacter phage Seahorse]],,NCBI, q1:s1 100.0% 1.56096E-31 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.038, -2.583959800616441, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_65 [Arthrobacter phage Seahorse]],,AYR01565,93.5484,1.56096E-31 SIF-HHPRED: SIF-Syn: Synteny with Seahorse.

 /note=Check syn with pham.

CDS 35895 - 36032

 /gene="68"

 /product="gp68"

 /function="hypothetical protein"

 /locus tag="radfad\_68"

 /note=Original Glimmer call @bp 35895 has strength 3.93; Genemark calls start at 35895

 /note=SSC: 35895-36032 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_66 [Arthrobacter phage Seahorse]],,NCBI, q1:s1 100.0% 1.67992E-21 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.451, -4.197870532213559, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_66 [Arthrobacter phage Seahorse]],,AYR01566,95.5556,1.67992E-21 SIF-HHPRED: SIF-Syn: Synteny with seahorse.

 /note=Check with pham.

CDS 36029 - 36250

 /gene="69"

 /product="gp69"

 /function="DNA binding protein"

 /locus tag="radfad\_69"

 /note=Original Glimmer call @bp 36029 has strength 10.28; Genemark calls start at 36029

 /note=SSC: 36029-36250 CP: no SCS: both ST: SS BLAST-Start: [helix-turn-helix DNA-binding domain protein [Arthrobacter phage Faja] ],,NCBI, q1:s1 100.0% 1.72173E-37 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.787, -3.0478325568523097, no F: DNA binding protein SIF-BLAST: ,,[helix-turn-helix DNA-binding domain protein [Arthrobacter phage Faja] ],,AYN57916,91.8919,1.72173E-37 SIF-HHPRED: SIF-Syn: Synteny with Faja.

 /note=check with pham.

CDS 36247 - 36534

 /gene="70"

 /product="gp70"

 /function="hypothetical protein"

 /locus tag="radfad\_70"

 /note=Original Glimmer call @bp 36247 has strength 11.95; Genemark calls start at 36247

 /note=SSC: 36247-36534 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_68 [Arthrobacter phage Seahorse]],,NCBI, q1:s1 100.0% 5.47451E-61 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.647, -3.2620870821365617, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_68 [Arthrobacter phage Seahorse]],,AYR01568,96.8421,5.47451E-61 SIF-HHPRED: SIF-Syn: Synteny with Seahorse.

 /note=check with pham.

CDS 36500 - 37000

 /gene="71"

 /product="gp71"

 /function="hypothetical protein"

 /locus tag="radfad\_71"

 /note=Original Glimmer call @bp 36500 has strength 3.35; Genemark calls start at 36500

 /note=SSC: 36500-37000 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_69 [Arthrobacter phage Seahorse]],,NCBI, q1:s1 90.9639% 1.834E-103 GAP: -35 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.787, -3.0301037898918786, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_69 [Arthrobacter phage Seahorse]],,AYR01569,93.125,1.834E-103 SIF-HHPRED: SIF-Syn: synteny with Seahorse.

 /note=check with pham.

CDS 37117 - 37293

 /gene="72"

 /product="gp72"

 /function="hypothetical protein"

 /locus tag="radfad\_72"

 /note=Original Glimmer call @bp 37018 has strength 6.92; Genemark calls start at 37018

 /note=SSC: 37117-37293 CP: no SCS: both-cs ST: SS BLAST-Start: [hypothetical protein PBI\_ISOLDE\_65 [Arthrobacter phage Isolde]],,NCBI, q1:s1 96.5517% 2.04127E-32 GAP: 116 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.268, -7.4540503109019225, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_ISOLDE\_65 [Arthrobacter phage Isolde]],,AYR01034,96.5517,2.04127E-32 SIF-HHPRED: SIF-Syn: Synteny with Isolde.

 /note=check with pham.

CDS 37290 - 38117

 /gene="73"

 /product="gp73"

 /function="exonuclease"

 /locus tag="radfad\_73"

 /note=Original Glimmer call @bp 37290 has strength 10.57; Genemark calls start at 37290

 /note=SSC: 37290-38117 CP: no SCS: both ST: SS BLAST-Start: [RecB-like exonuclease/helicase [Arthrobacter phage Persistence]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.878, -5.012465458034031, no F: exonuclease SIF-BLAST: ,,[RecB-like exonuclease/helicase [Arthrobacter phage Persistence]],,QWY79690,96.7273,0.0 SIF-HHPRED: SIF-Syn: Synteny with Persistence.

 /note=check with pham.

CDS 38114 - 38662

 /gene="74"

 /product="gp74"

 /function="hypothetical protein"

 /locus tag="radfad\_74"

 /note=Original Glimmer call @bp 38114 has strength 8.24; Genemark calls start at 38114

 /note=SSC: 38114-38662 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PERSISTENCE\_63 [Arthrobacter phage Persistence]],,NCBI, q1:s1 100.0% 2.14312E-104 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.411, -3.8970005018578204, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_PERSISTENCE\_63 [Arthrobacter phage Persistence]],,QWY79691,93.3702,2.14312E-104 SIF-HHPRED: SIF-Syn: Synteny with Persistence.

 /note=check with pham.

CDS 38659 - 38826

 /gene="75"

 /product="gp75"

 /function="hypothetical protein"

 /locus tag="radfad\_75"

 /note=Original Glimmer call @bp 38659 has strength 8.04; Genemark calls start at 38659

 /note=SSC: 38659-38826 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_67 [Arthrobacter phage Auxilium]],,NCBI, q1:s1 100.0% 5.63971E-23 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.021, -2.4787699911121788, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_67 [Arthrobacter phage Auxilium]],,AYN55843,92.7273,5.63971E-23 SIF-HHPRED: SIF-Syn:

CDS 38827 - 39300

 /gene="76"

 /product="gp76"

 /function="ssDNA binding protein"

 /locus tag="radfad\_76"

 /note=Original Glimmer call @bp 38827 has strength 8.98; Genemark calls start at 38827

 /note=SSC: 38827-39300 CP: yes SCS: both ST: SS BLAST-Start: [ssDNA-binding protein [Arthrobacter phage Auxilium]],,NCBI, q1:s1 94.9045% 4.56575E-81 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.941, -2.6453814847322845, yes F: ssDNA binding protein SIF-BLAST: ,,[ssDNA-binding protein [Arthrobacter phage Auxilium]],,AYN55844,84.2767,4.56575E-81 SIF-HHPRED: SIF-Syn: Synteny with Auxilium

CDS 39406 - 39702

 /gene="77"

 /product="gp77"

 /function="NrdH-like glutaredoxin"

 /locus tag="radfad\_77"

 /note=Original Glimmer call @bp 39406 has strength 10.17; Genemark calls start at 39406

 /note=SSC: 39406-39702 CP: no SCS: both ST: SS BLAST-Start: [glutaredoxin [Arthrobacter phage Auxilium]],,NCBI, q1:s1 100.0% 1.63886E-52 GAP: 105 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.129, -5.174867876921511, yes F: NrdH-like glutaredoxin SIF-BLAST: ,,[glutaredoxin [Arthrobacter phage Auxilium]],,AYN55847,89.7959,1.63886E-52 SIF-HHPRED: SIF-Syn: Synteny Auxilium

CDS 39699 - 40220

 /gene="78"

 /product="gp78"

 /function="phosphatase"

 /locus tag="radfad\_78"

 /note=Original Glimmer call @bp 39699 has strength 13.96; Genemark calls start at 39699

 /note=SSC: 39699-40220 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_79 [Arthrobacter phage Seahorse]],,NCBI, q1:s1 100.0% 3.39016E-86 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.851, -5.008614874058139, no F: phosphatase SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_79 [Arthrobacter phage Seahorse]],,AYR01579,84.5714,3.39016E-86 SIF-HHPRED: SIF-Syn:

CDS 40447 - 42978

 /gene="79"

 /product="gp79"

 /function="DNA helicase"

 /locus tag="radfad\_79"

 /note=Original Glimmer call @bp 40447 has strength 15.36; Genemark calls start at 40462

 /note=SSC: 40447-42978 CP: yes SCS: both-gl ST: SS BLAST-Start: [DNA helicase/methylase [Arthrobacter phage Faja] ],,NCBI, q3:s2 99.7627% 0.0 GAP: 226 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.271, -2.033982896655645, yes F: DNA helicase SIF-BLAST: ,,[DNA helicase/methylase [Arthrobacter phage Faja] ],,AYN57928,99.5249,0.0 SIF-HHPRED: SIF-Syn:

CDS 42975 - 43364

 /gene="80"

 /product="gp80"

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

 /locus tag="radfad\_80"

 /note=Original Glimmer call @bp 42975 has strength 6.36; Genemark calls start at 42975

 /note=SSC: 42975-43364 CP: no SCS: both ST: SS BLAST-Start: [helix-turn-helix DNA-binding domain protein [Arthrobacter phage Richie]],,NCBI, q3:s7 98.4496% 4.06512E-71 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.929, -4.844644247678312, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA-binding domain protein [Arthrobacter phage Richie]],,AYN58905,85.7143,4.06512E-71 SIF-HHPRED: SIF-Syn:

CDS 43361 - 44443

 /gene="81"

 /product="gp81"

 /function="DNA polymerase III sliding clamp (Beta)"

 /locus tag="radfad\_81"

 /note=Original Glimmer call @bp 43361 has strength 13.88; Genemark calls start at 43361

 /note=SSC: 43361-44443 CP: no SCS: both ST: SS BLAST-Start: [DNA polymerase III beta subunit [Arthrobacter phage Faja] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.196, -2.4634880269616195, yes F: DNA polymerase III sliding clamp (Beta) SIF-BLAST: ,,[DNA polymerase III beta subunit [Arthrobacter phage Faja] ],,AYN57930,98.8889,0.0 SIF-HHPRED: SIF-Syn:

CDS 44611 - 44859

 /gene="82"

 /product="gp82"

 /function="portal protein"

 /locus tag="radfad\_82"

 /note=Original Glimmer call @bp 44440 has strength 8.89; Genemark calls start at 44440

 /note=SSC: 44611-44859 CP: no SCS: both-cs ST: SS BLAST-Start: [hypothetical protein PBI\_SEAHORSE\_86 [Arthrobacter phage Seahorse]],,NCBI, q2:s62 98.7805% 7.55178E-27 GAP: 167 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.548, -3.469401707954294, yes F: portal protein SIF-BLAST: ,,[hypothetical protein PBI\_SEAHORSE\_86 [Arthrobacter phage Seahorse]],,AYR01586,43.3566,7.55178E-27 SIF-HHPRED: SIF-Syn: Synteny with seahorse

CDS 44856 - 46322

 /gene="83"

 /product="gp83"

 /function="DNA methyltransferase"

 /locus tag="radfad\_83"

 /note=Original Glimmer call @bp 44856 has strength 13.26; Genemark calls start at 44856

 /note=SSC: 44856-46322 CP: no SCS: both ST: SS BLAST-Start: [DNA methylase [Arthrobacter phage Faja] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.941, -2.7254235724530456, yes F: DNA methyltransferase SIF-BLAST: ,,[DNA methylase [Arthrobacter phage Faja] ],,AYN57932,100.0,0.0 SIF-HHPRED: c.66.1.26 (A:1137-1600) Methyltransferase domain from DNA methyltransferase 1 (DNMT1) {Mouse (Mus musculus) [TaxId: 10090]},,,d3pt9a3,39.3443,100.0 SIF-Syn: Synteny with Faja and Hestia

CDS 46339 - 46773

 /gene="84"

 /product="gp84"

 /function="DNA binding protein"

 /locus tag="radfad\_84"

 /note=Original Glimmer call @bp 46339 has strength 9.1; Genemark calls start at 46339

 /note=SSC: 46339-46773 CP: yes SCS: both ST: SS BLAST-Start: [DNA binding protein [Arthrobacter phage Auxilium] ],,NCBI, q1:s1 100.0% 3.75736E-100 GAP: 16 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.271, -2.033982896655645, yes F: DNA binding protein SIF-BLAST: ,,[DNA binding protein [Arthrobacter phage Auxilium] ],,AYN55853,100.0,3.75736E-100 SIF-HHPRED: SIF-Syn: Synteny with Auxilium

CDS 47006 - 47377

 /gene="85"

 /product="gp85"

 /function="hypothetical protein"

 /locus tag="radfad\_85"

 /note=Original Glimmer call @bp 47006 has strength 6.33; Genemark calls start at 47006

 /note=SSC: 47006-47377 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_RICHIE\_84 [Arthrobacter phage Richie]],,NCBI, q1:s1 99.187% 1.83469E-82 GAP: 232 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.941, -2.996490344739583, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_84 [Arthrobacter phage Richie]],,AYN58910,99.187,1.83469E-82 SIF-HHPRED: SIF-Syn:

CDS 47374 - 47820

 /gene="86"

 /product="gp86"

 /function="hypothetical protein"

 /locus tag="radfad\_86"

 /note=Original Glimmer call @bp 47374 has strength 8.99; Genemark calls start at 47374

 /note=SSC: 47374-47820 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_RICHIE\_85 [Arthrobacter phage Richie]],,NCBI, q1:s1 89.1892% 5.98944E-86 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.402, -3.8540125308361968, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_85 [Arthrobacter phage Richie]],,AYN58911,95.4545,5.98944E-86 SIF-HHPRED: SIF-Syn:

CDS 47827 - 48099

 /gene="87"

 /product="gp87"

 /function="hypothetical protein"

 /locus tag="radfad\_87"

 /note=Original Glimmer call @bp 47827 has strength 7.7; Genemark calls start at 47827

 /note=SSC: 47827-48099 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PERSISTENCE\_80 [Arthrobacter phage Persistence]],,NCBI, q1:s1 93.3333% 3.1832E-25 GAP: 6 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.325, -4.075451192669358, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_PERSISTENCE\_80 [Arthrobacter phage Persistence]],,QWY79708,68.4783,3.1832E-25 SIF-HHPRED: SIF-Syn: None

CDS 48096 - 48530

 /gene="88"

 /product="gp88"

 /function="MazG-like nucleotide pyrophosphohydrolase"

 /locus tag="radfad\_88"

 /note=Original Glimmer call @bp 48096 has strength 12.29; Genemark calls start at 48096

 /note=SSC: 48096-48530 CP: yes SCS: both ST: SS BLAST-Start: [MazG-like nucleotide pyrophosphohydrolase [Arthrobacter phage Auxilium]],,NCBI, q1:s1 100.0% 7.73859E-83 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.714, -3.201021426436999, yes F: MazG-like nucleotide pyrophosphohydrolase SIF-BLAST: ,,[MazG-like nucleotide pyrophosphohydrolase [Arthrobacter phage Auxilium]],,AYN55857,84.8101,7.73859E-83 SIF-HHPRED: SIF-Syn: Synteny with Auxilium

CDS 48533 - 48712

 /gene="89"

 /product="gp89"

 /function="hypothetical protein"

 /locus tag="radfad\_89"

 /note=Original Glimmer call @bp 48533 has strength 8.38; Genemark calls start at 48533

 /note=SSC: 48533-48712 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_RICHIE\_88 [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 5.41289E-36 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.895, -4.976656753876107, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_88 [Arthrobacter phage Richie]],,AYN58914,100.0,5.41289E-36 SIF-HHPRED: SIF-Syn: Synteny with Richie

CDS 48709 - 49134

 /gene="90"

 /product="gp90"

 /function="RusA-like resolvase (endonuclease)"

 /locus tag="radfad\_90"

 /note=Original Glimmer call @bp 48709 has strength 8.51; Genemark calls start at 48721

 /note=SSC: 48709-49134 CP: no SCS: both-gl ST: NI BLAST-Start: [RusA-like resolvase [Arthrobacter phage Hestia]],,NCBI, q1:s1 100.0% 1.30582E-94 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.626, -3.368377069717189, yes F: RusA-like resolvase (endonuclease) SIF-BLAST: ,,[RusA-like resolvase [Arthrobacter phage Hestia]],,AYR00956,100.0,1.30582E-94 SIF-HHPRED: SIF-Syn:

CDS 49131 - 49442

 /gene="91"

 /product="gp91"

 /function="Hypothetical Protein"

 /locus tag="radfad\_91"

 /note=Original Glimmer call @bp 49131 has strength 8.97; Genemark calls start at 49131

 /note=SSC: 49131-49442 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_85 [Arthrobacter phage Auxilium]],,NCBI, q1:s1 100.0% 9.55005E-70 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.196, -2.17469248771465, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_85 [Arthrobacter phage Auxilium]],,AYN55860,100.0,9.55005E-70 SIF-HHPRED: SIF-Syn: Most synteny with Richie and Auxilium

CDS 49451 - 49672

 /gene="92"

 /product="gp92"

 /function="Hypothetical Protein"

 /locus tag="radfad\_92"

 /note=Original Glimmer call @bp 49451 has strength 9.96; Genemark calls start at 49451

 /note=SSC: 49451-49672 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_RICHIE\_91 [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 4.00587E-47 GAP: 8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.139, -4.4057176022952405, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_91 [Arthrobacter phage Richie]],,AYN58917,100.0,4.00587E-47 SIF-HHPRED: SIF-Syn: Most synteny with Richie

CDS 49669 - 49896

 /gene="93"

 /product="gp93"

 /function="Hypothetical Protein"

 /locus tag="radfad\_93"

 /note=Original Glimmer call @bp 49669 has strength 6.65; Genemark calls start at 49669

 /note=SSC: 49669-49896 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_RICHIE\_92 [Arthrobacter phage Richie] ],,NCBI, q1:s1 100.0% 5.67115E-45 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.53, -3.6476983004329377, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_92 [Arthrobacter phage Richie] ],,AYN58918,98.6667,5.67115E-45 SIF-HHPRED: SIF-Syn: Most synteny with Hestia and Richie

CDS 49893 - 50348

 /gene="94"

 /product="gp94"

 /function="hypothetical protein"

 /locus tag="radfad\_94"

 /note=Original Glimmer call @bp 49893 has strength 8.94; Genemark calls start at 49893

 /note=SSC: 49893-50348 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_SHOYA\_65 [Arthrobacter phage Shoya]],,NCBI, q1:s1 100.0% 6.48056E-89 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.175, -2.6835611257758942, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_SHOYA\_65 [Arthrobacter phage Shoya]],,QIG57736,91.3907,6.48056E-89 SIF-HHPRED: SIF-Syn: no synteny

CDS 50345 - 51079

 /gene="95"

 /product="gp95"

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

 /locus tag="radfad\_95"

 /note=Original Glimmer call @bp 50345 has strength 4.31; Genemark calls start at 50345

 /note=SSC: 50345-51079 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_RICHIE\_94 [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 2.36007E-176 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.787, -3.108788982793736, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[hypothetical protein PBI\_RICHIE\_94 [Arthrobacter phage Richie]],,AYN58920,97.9508,2.36007E-176 SIF-HHPRED: SIF-Syn: most synteny with Richie

CDS 51286 - 51522

 /gene="96"

 /product="gp96"

 /function="Hypothetical Protein"

 /locus tag="radfad\_96"

 /note=Original Glimmer call @bp 51286 has strength 0.62

 /note=SSC: 51286-51522 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein PBI\_AUXILIUM\_90 [Arthrobacter phage Auxilium]],,NCBI, q3:s9 58.9744% 2.66068E-8 GAP: 206 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.504, -5.734826123116989, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_AUXILIUM\_90 [Arthrobacter phage Auxilium]],,AYN55872,51.5152,2.66068E-8 SIF-HHPRED: SIF-Syn: most synteny with Auxilia

CDS 51743 - 51904

 /gene="97"

 /product="gp97"

 /function="hypothetical protein"

 /locus tag="radfad\_97"

 /note=Original Glimmer call @bp 51743 has strength 10.09; Genemark calls start at 51743

 /note=SSC: 51743-51904 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_FAJA\_94 [Arthrobacter phage Faja] ],,NCBI, q1:s1 100.0% 9.23309E-32 GAP: 220 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.207, -2.1518296047551457, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_FAJA\_94 [Arthrobacter phage Faja] ],,AYN57943,100.0,9.23309E-32 SIF-HHPRED: SIF-Syn: most synteny with Hestia

CDS 51920 - 52309

 /gene="98"

 /product="gp98"

 /function="Hypothetical Protein"

 /locus tag="radfad\_98"

 /note=Original Glimmer call @bp 51920 has strength 8.44; Genemark calls start at 51920

 /note=SSC: 51920-52309 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU49\_gp63 [Arthrobacter phage Eileen] ],,NCBI, q1:s1 100.0% 1.56713E-70 GAP: 15 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.548, -3.8205105679615925, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU49\_gp63 [Arthrobacter phage Eileen] ],,YP\_009815477,90.6977,1.56713E-70 SIF-HHPRED: DUF3307 ; Protein of unknown function (DUF3307),,,PF11750.11,96.8992,99.8 SIF-Syn: no synteny

CDS 52313 - 52633

 /gene="99"

 /product="gp99"

 /function="HNH endonuclease"

 /locus tag="radfad\_99"

 /note=Original Glimmer call @bp 52313 has strength 3.47

 /note=SSC: 52313-52633 CP: yes SCS: glimmer ST: SS BLAST-Start: [HNH endonuclease [Arthrobacter phage Richie]],,NCBI, q1:s1 100.0% 6.04784E-69 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.472, -5.783200083209299, no F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Arthrobacter phage Richie]],,AYN58924,98.1132,6.04784E-69 SIF-HHPRED: HNH endonuclease; Thermophilic bacteriophage, HNH Endonuclease, DNA nicking, HYDROLASE; 1.52A {Geobacillus virus E2},,,5H0M\_A,96.2264,99.5 SIF-Syn: most synteny with Richie and Faya

tRNA complement (52566 - 52644)

 /gene="100"

 /product="tRNA-Gly(gcc)"

 /locus tag="RADFAD\_100"

 /note=tRNA-Gly(gcc)