**Emmaloid Complete Genome**

Morphology: Siphoviridae

Subcluster: F1

ORFs: 104

Orphams: 3

G&C content: 61.2%

tRNAs: 0

Genome length: 57713

Phage ends: 3’ sticky overhangs

Lytic or lysogenic: Lysogenic

Gene 1

Original GeneMark call @bp 184

SSC: [184-2]

CP: [yes]

SCS: [GeneMark]

ST: [NA]

Blast-Start: [NKF] no hits on NCBI

Gap: [0]

LO: [no]

RBS: [Kibler6, Karlin Medium, 1.670, -5.435, no]

F: [NKF]

SIF-BLAST: [NKF] no hits on NCBI

SIF-HHPred: [NKF, no matches with a probability above 90%]

SIF-Syn: [Endonuclease, downstream terminase small subunit, just like Totinger]

Gene 2

Original Glimmer call @bp 41 has strength 3.03 \*\* not called by GeneMark

SSC: [41-333]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Rialto, gene 1, NCBI, Q1:S1, 99%, 6e-74]

Gap: [-143]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.290, -4.133, no]

F: [HNH endonuclease]

SIF-BLAST: [HNH endonuclease, GenBank, Rialto gp1, [WNM65567.1](https://www.ncbi.nlm.nih.gov/protein/WNM65567.1?report=genbank&log$=protalign&blast_rank=1&RID=UW8REXPX013), 99%, 6e-74]

SIF-HHPRED: [HNH endonuclease, RCSB PDB, Geobacillus virus E2, [5H0M\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=5H0M), 62.16%, 97.69]

SIF-Syn: [Terminase small subunit, upstream endonuclease, downstream terminase large subunit, just like Totinger]

Gene 3

Original Glimmer call @bp 446 has strength 13.29

SSC: [446-700]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Boomer, gene 2, NCBI, Q1:S1, 99%, 4e-51]

Gap: [113]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.852, -2.985, yes]

F: [Terminase small subunit]

SIF-BLAST: [Terminase small subunit, NCBI, Boomer gp2, YP\_002014218.1, 99%, 4e-51]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [Terminase large subunit, upstream terminase small subunit, downstream portal protein, just like Starcevich]

Gene 4

SSC: [672-2159]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Ramsey, gene 3, NCBI, Q1:S1, 100%, 0]

Gap: [-28]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.335, -4, no]

F: [Terminase]

SIF-BLAST: [Terminase, NCBI, Ramsey gp3, YP\_002241790.1, 100%, 0]

SIF-HHPRED: [Terminase large subunit, RCSB PDB, Byrnievirus HK97, [6Z6D\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=6Z6D), 82.86%, 100]

SIF-Syn: [Portal protein, upstream terminase large subunit, downstream NKF, just like Starcevich]

Gene 5

Original Glimmer call @bp 2200 has strength 11.94

SSC: [2200-3621]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Job42, gene 4, NCBI, Q1:S1, 100%, 0]

Gap: [41]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.483, -3.812, yes]

F: [Portal protein]

SIF-BLAST: [Portal protein, NCBI, Job42 gp4, YP\_008126594.1, 100%, 0]

SIF-HHPRED: [Portal protein, RCSB PDB, Mycobacterium phage Bxb1, [9D94\_Fd](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D94), 86.50%, 100]

SIF-Syn: [NKF, upstream portal protein, downstream NKF, just like Starcevich]

Gene 6

Original Glimmer call @bp 4161 has strength 8.73 \*\* not called by GeneMark

SSC: [4161-4045]

CP: [yes]

SCS: [Glimmer]

ST: [NA]

Blast-Start: [NKF] no hits on NCBI

Gap: [424]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.294, -4.143, yes]

F: [NKF]

SIF-BLAST: [NKF] no hits on NCBI

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream scaffolding protein, just like Starcevich]

Gene 7

Original Glimmer call @bp 4208 has strength 6.69; GeneMark calls start at 3605

SSC: [3605-4330]

CP: [yes]

SCS: [Both-GM]

ST: [SS]

Blast-Start: [Boomer, gene 5, NCBI, Q1:S1, 100%, 2e-176]

Gap: [-116]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.464, -3.709, yes]

F: [Capsid maturation protease]

SIF-BLAST: [Capsid maturation protease, NCBI, Boomer gp5, YP\_002014221.1, 100%, 2e-176]

SIF-HHPred: [Minor capsid protein 2, InterPro Pfam, [PF06152.16](https://www.ebi.ac.uk/interpro/entry/pfam/PF06152), 21.07%, 97.74]

SIF-Syn: [Scaffolding protein, upstream NKF, downstream major capsid protein, just like Starcevich]

Gene 8

Original Glimmer call @bp 4409 has strength 10.59

SSC: [4409-4945]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Bobi, gene 6, NCBI, Q1:S1, 99%, 4e-122]

Gap: [79]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.180, -4.440, yes]

F: [Capsid scaffolding protein]

SIF-BLAST: [Capsid scaffolding protein, NCBI, Bobi gp6, YP\_008408963.1, 99%, 4e-122]

SIF-HHPRED: [Capsid scaffolding protein, InterPro Pfam, Staphylococcus phage 80alpha gp46, [PF14265.11](https://www.ebi.ac.uk/interpro/entry/pfam/PF14265), 56.98%, 99.24]

SIF-Syn: [major capsid protein, upstream scaffolding protein, downstream head to tail adaptor, just like Starcevich]

Gene 9

Original Glimmer call @bp 5008 has strength 13.15

SSC: [5008-5916]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Boomer, gene 7, NCBI, Q1:S1, 100%, 0]

Gap: [63]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 3.213, -2.219, yes]

F: [Major capsid protein]

SIF-BLAST: [Hypothetical protein, NCBI, Boomer gp7, YP\_002014223.1, 100%, 0]

SIF-HHPRED: [Major capsid protein, RCSB PDB, Gordonia phage Ziko, [8EB4\_E](http://www.rcsb.org/pdb/explore/explore.do?structureId=8EB4), 96.70%, 100]

SIF-Syn: [head-to-tail adaptor, upstream major capsid protein, downstream head-to-tail stopper, just like Starcevich]

Gene 10

Original Glimmer call @bp 5929 has strength 4.66

SSC: [5929-6300]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Frankie, gene 8, NCBI, Q1:S1, 99%, 8e-81]

Gap: [13]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.300, -4.190, no]

F: [Head to tail adaptor]

SIF-BLAST: [Head to tail adaptor, GenBank, Frankie gp8, AUX81934.1, 99%, 8e-81]

SIF-HHPRED: [Head to tail adaptor, RCSB PDB, Mycobacterium phage Bxb1, [9D94\_Ga](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D94), 92.74%, 99.85]

SIF-Syn: [head-to-tail stopper, upstream head-to-tail adaptor, downstream NKF, just like Starcevich]

Gene 11

Original Glimmer call @bp 6297 has strength 9.14

SSC: [6297-6626]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Rialto, gene 9, NCBI, Q1:S1, 99%, 3e-71]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.700, -3.220, yes]

F: [Head to tail stopper]

SIF-BLAST: [Head to tail stopper, GenBank, Rialto gp9, WNM65575.1, 99%, 3e-71]

SIF-HHPRED: [Head to tail stopper, RCSB PDB, Mycobacterium phage Bxb1, [9D94\_Hc](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D94), 88.18%, 99.61]

SIF-Syn: [NKF, upstream head-to-tail stopper, downstream tail terminator, just like Starcevich]

Gene 12

Original Glimmer call @bp 6663 has strength 11.04; GeneMark calls start at 6633

SSC: [6633-6959]

CP: [yes]

SCS: [Both-GM]

ST: [SS]

Blast-Start: [Inventum, gene 9, NCBI, Q1:S1, 99%, 2e-73]

Gap: [7]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.638, -3.699, no]

F: [Portal protein]

SIF-BLAST: [Portal protein, NCBI, Inventum gp9, YP\_009125290.1, 99%, 2e-73]

SIF-HHPred: [NKF, Interpro Pfam, [PF17395.7](https://www.ebi.ac.uk/interpro/entry/pfam/PF17395), 62.39%, 99.25]

SIF-Syn: [tail terminator, upstream NKF, downstream major tail protein, just like Starcevich]

Gene 13

Original Glimmer call @bp 6949 has strength 8.16; GeneMark calls start at 7030

SSC: [6949-7353]

CP: [yes]

SCS: [Both-GL]

ST: [SS]

Blast-Start: [Boomer, gene 11, NCBI, Q1:S1, 99%, 3e-89]

Gap: [-10]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.243, -6.241, no]

F: [tail terminator portal protein]

SIF-BLAST: [Head tail adaptor, NCBI, Boomer gp11, YP\_002014227.1, 99%, 3e-89]

SIF-HHPRED: [Tail terminator portal protein, RCSB PDB, Mycobacterium phage Bxb1, [9D94\_Ic](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D94), 91.85%, 99.81]

SIF-Syn: [Major tail protein, upstream tail terminator, downstream Hypothetical protein, just like Starcevich]

Gene 14

Original Glimmer call @bp 7463 has strength 14.80

SSC: [7463-8272]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [DeadP, gene 11, NCBI, Q1:S1, 100%, 0]

Gap: [110]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 3.155, -2.339, yes]

F: [major tail protein]

SIF-BLAST: [Major tail protein, NCBI, DeadP gp11, YP\_009016901.1, 100%, 0]

SIF-HHPRED: [Major tail protein, RCSB PDB, Mycobacterium phage Bxb1, [9D9L\_J](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D9L), 63.70%, 99.82]

SIF-Syn: [Hypothetical protein, upstream major tail protein, downstream NKF, just like Starcevich]

Gene 15

Original Glimmer call @bp 8386 has strength 9.79

SSC: [8386-8937]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Pacc40, gene 12, NCBI, Q1:S1, 99%, 8e-130]

Gap: [114]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.977, -2.708, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Pacc40 gp12, YP\_002241597.1, 99%, 8e-130]

SIF-HHPRED: [Mycobacteriophage tail assembly protein, InterPro Pfam, [PF17388.7](https://www.ebi.ac.uk/interpro/entry/pfam/PF17388), 28.80%, 95.85]

SIF-Syn: [NKF, upstream Hypothetical protein, downstream tape measure protein, just like Starcevich]

Gene 16

Original Glimmer call @bp 8996 has strength 10.28

SSC: [8996-9322]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Byougenkin, gene 13, NCBI, Q1:S204, 99%, 6e-67]

Gap: [59]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.259, -4.197, no]

F: [tail assembly protein]

SIF-BLAST: [tail assembly protein, NCBI, Byougenkin gp13, YP\_009955319.1, 99%, 6e-67]

SIF-HHPRED: [NKF, InterPro Pfam, [PF17318.7](https://www.ebi.ac.uk/interpro/entry/pfam/PF17318), 32.11%, 97.60]

SIF-Syn: [tape measure protein, upstream NKF, downstream minor tail protein, just like Starcevich]

Gene 17

Original Glimmer call @bp 9341 has strength 9.22

SSC: [9341-12829]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Starcevich, gene 15, NCBI, Q1:S1, 100%, 0]

Gap: [19]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.483, -3.812, yes]

F: [tape measure protein]

SIF-BLAST: [tape measure protein, GenBank, Starcevich gp15, WNM68406.1, 100%, 0]

SIF-HHPRED: [Tape measure protein, RCSB PDB, Chivirus chi, [8VJH\_Q](http://www.rcsb.org/pdb/explore/explore.do?structureId=8VJH), 34.57%, 97.57]

SIF-Syn: [minor tail protein, upstream tape measure protein, downstream minor tail protein, just like Starcevich]

Gene 18

Original Glimmer call @bp 12830 has strength 13.06

SSC: [12830-14539]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Starcevich, gene 16, NCBI, Q1:S1, 100%, 0]

Gap: [1]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.966, -4.821, no]

F: [Minor tail protein]

SIF-BLAST: [minor tail protein, GenBank, Starcevich gp16, WNM68407.1, 100%, 0

SIF-HHPRED: [Minor tail protein, RCSB PDB, Mycobacterium phage Bxb1, [9D93\_Mf](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D93), 26.84%, 99.65]

SIF-Syn: [minor tail protein, upstream minor tail protein, downstream minor tail protein, just like Starcevich]

Gene 19

Original Glimmer call @bp 14596 has strength 9.32

SSC: [14596-16305]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Pacc40, gene 16, NCBI, Q1:S1, 100%, 0]

Gap: [57]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 3.310, -2.606, yes]

F: [minor tail protein]

SIF-BLAST: [Minor tail protein, NCBI, Pacc40 gp16, YP\_002241600.1, 100%, 0]

SIF-HHPRED: [Minor tail protein, RCSB PDB, Mycobacterium phage Bxb1, [9D93\_Oa](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D93), 91.93%, 100]

SIF-Syn: [minor tail protein, upstream minor tail protein, downstream minor tail protein, just like Starcevich]

Gene 20

Original Glimmer call @bp 16362 has strength 11.50

SSC: [16362-17192]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Saal, gene 17, NCBI, Q1:S6, 100%, 0]

Gap: [57]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.884, -3.190, yes]

F: [minor tail protein]

SIF-BLAST: [Minor tail protein, NCBI, Saal gp17, YP\_009007484.1, 100%, 0]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [minor tail protein, upstream minor tail protein, downstream minor tail protein D-ala-D-ala carboxypeptidase, just like Starcevich]

Gene 21

Original Glimmer call @bp 17189 has strength 13.37

SSC: [17189-19726]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Mantra, gene 18, NCBI, Q1:S1, 100%, 0]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.426, -4.695, no]

F: [minor tail protein]

SIF-BLAST: [Minor tail protein, NCBI, Mantra gp18, YP\_009959382.1, 100%, 0]

SIF-HHPRED: [Minor tail protein, RCSB PDB, Mycobacterium phage Bxb1, [9D93\_Pb](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D93), 68.68%, 100]

SIF-Syn: [minor tail protein D-ala-D-ala carboxypeptidase, upstream minor tail protein, downstream minor tail protein, just like Starcevich]

Gene 22

Original Glimmer call @bp 19723 has strength 7.00

SSC: [19723-21618]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Rialto, gene 21, NCBI, Q1:S1, 100%, 0]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.818, -3.626, no]

F: [Minor tail protein]

SIF-BLAST: [Minor tail protein, GenBank, Rialto gp21, WNM65587.1, 100%, 0]

SIF-HHPred: [Minor tail protein, RCSB PDB, Mycobacterium phage Bxb1, [9D93\_Sa](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D93), 63.92%, 100]

SIF-Syn: [Minor tail protein, upstream minor tail protein D-ala-D-ala carboxypeptidase, downstream NKF, just like Starcevich]

Gene 23

Original Glimmer call @bp 21621 has strength 6.55

SSC: [21621-22781]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Rialto, gene 22, NCBI, Q1:S3, 100%, 0]

Gap: [3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 1.620, -5.539, no]

F: [Minor tail protein]

SIF-BLAST: [Minor tail protein, GenBank, Rialto gp22, WNM65588.1, 100%, 0]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream minor tail protein, downstream NKF, just like Starcevich]

Gene 24

Original Glimmer call @bp 22799 has strength 5.92

SSC: [22799-23140]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Omega, gene 41, NCBI, Q1:S1, 99%, 1e-69]

Gap: [18]

LO: [no]

RBS: [Kibler6, Karlin Medium, 3.213, -2.156, yes]

F: [Virion-associated phage protein fiber tail adaptor]

SIF-BLAST: [capsid protein, NCBI, Omega gp41, NP\_818342.1, 99%, 1e-69]

SIF-HHPred: [Virion associated phage protein fiber tail adaptor, RCSB PDB, Ralstonia phage GP4, [8JOU\_i](http://www.rcsb.org/pdb/explore/explore.do?structureId=8JOU), 95.61%, 99.92]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Starcevich]

Gene 25

Original Glimmer call @bp 23163 has strength 8.30

SSC: [23163-23417]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Omega, gene 42, NCBI, Q1:S1, 99%, 4e-54]

Gap: [23]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.026, -4.699, yes]

F: [Minor tail protein]

SIF-BLAST: [Minor tail protein, NCBI, Omega gp42, NP\_818343.1, 99%, 4e-54]

SIF-HHPRED: [NKF, RCSB PDB, Rhodopseudomonas palustris CGA009, [5JN6\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=5JN6), 48.23%, 94.31]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Starcevich]

Gene 26

Original Glimmer call @bp 23431 has strength 9.41

SSC: [23431-24069]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Rialto, gene 25, NCBI, Q1:S1, 100%, 5e-149]

Gap: [14]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.503, -3.691, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Rialto gp25, WNM65591.1, 100%, 5e-149]

SIF-HHPRED: [Minor tail protein, RCSB PDB, Mycobacterium phage Bxb1, [9D93\_Lb](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D93), 87.32%, 99.36]

SIF-Syn: [NKF, upstream NKF, downstream helix-turn-helix DNA binding domain protein, just like LittleShirley]

Gene 27

Original Glimmer call @bp 24066 has strength 2.99

SSC: [24066-25007]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Rialto, gene 26, NCBI, Q1:S1, 100%, 0]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.303, -4.123, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Rialto gp26, WNM65592.1, 100%, 0]

SIF-HHPRED: [Minor tail protein tail tip, RCSB PDB, Mycobacterium phage Bxb1, [9D93\_Qa](http://www.rcsb.org/pdb/explore/explore.do?structureId=9D93), 36.94%, 98.92]

SIF-Syn: [helix-turn-helix DNA binding domain protein, upstream NKF, downstream NKF, just like LittleShirley]

Gene 28

Original Glimmer call @bp 25209 has strength 10.68

SSC: [25209-25012]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Pacc40, gene 25, NCBI, Q1:S1, 98%, 2e-38]

Gap: [5]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.478, -6.661, no]

F: [Hepatocyte nuclear factor 1-beta]

SIF-BLAST: [HTH DNA binding protein, NCBI, Pacc40 gp25, YP\_002241609.1, 98%, 2e-38]

SIF-HHPRED: [Hepatocyte nuclear factor 1-beta, RCSB PDB, Homo Sapiens, [2H8R\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=2H8R), 87.88%, 97.05]

SIF-Syn: [NKF, upstream helix-turn-helix DNA binding domain protein, downstream NKF, just like LittleShirley]

Gene 29

Original Glimmer call @bp 25358 has strength 8.59

SSC: [25358-25654]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Boomer, gene 27, NCBI, Q1:S1, 99%, 3e-64]

Gap: [149]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 3.234, -2.253, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Boomer gp27, YP\_002014243.1, 99%, 3e-64]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 30

Original Glimmer call @bp 25661 has strength 4.94 \*\* not called by GeneMark

SSC: [25661-25810]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Boomer, gene 28, NCBI, Q1:S1, 98%, 5e-26]

Gap: [7]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.135, -4.454, yes]

F: [Hypothetical protein]

SIF-BLAST: [hypothetical protein, NCBI, Boomer gp28, YP\_002014244.1, 98%, 5e-26]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream DNA endonuclease, just like LittleShirley]

Gene 31

Original Glimmer call @bp 25807 has strength 11.97

SSC: [25807-25944]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Rialto, gene 30, NCBI, Q1:S1, 98%, 1e-21]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 3,245, -2.090, yes]

F: [Membrane protein]

SIF-BLAST: [Membrane protein, GenBank, Rialto gp30, WNM65596.1, 98%, 1e-21]

SIF-HHPred: [NKF, no matches with a probability above 90%]

SIF-Syn: [DNA endonuclease, upstream NKF, downstream NKF, just like LittleShirley]

Gene 32

Original Glimmer call @bp 25978 has strength 8.40

SSC: [25978-27324]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Rialto, gene 31, NCBI, Q1:S1, 100%, 0]

Gap: [34]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.649, -5.480, no]

F: [Transposase]

SIF-BLAST: [Transposase, GenBank, Rialto gp31, WNM65597.1, 100%, 0]

SIF-HHPRED: [RNA-guided DNA endonuclease TnpB, RCSB PDB, [Deinococcus radiodurans R1 = ATCC 13939 = DSM 20539](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Deinococcus%20radiodurans%20R1%20=%20ATCC%2013939%20=%20DSM%2020539)), [8H1J\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=8H1J), 81.29%, 100]

SIF-Syn: [NKF, upstream DNA endonuclease, downstream lysin A, just like LittleShirley]

Gene 33

Original Glimmer call @bp 27477 has strength 11.50

SSC: [27477-27710]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Che8, gene 31, NCBI, Q1:S1, 99%, 3e-42]

Gap: [153]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.824, -3.104, yes]

F: [Lysin A]

SIF-BLAST: [Hypothetical protein, NCBI, Che8 gp31, NP\_817369.1, 99%, 3e-42]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [Lysin A, upstream NKF, downstream Lysin B, just like LittleShirley]

Gene 34

Original Glimmer call @bp 27707 has strength 8.83

SSC: [27707-28900]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [GUmbie, gene 30, NCBI, Q1:S1, 100%, 0]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.213, -4.229, no]

F: [Endolysin]

SIF-BLAST: [Endolysin, NCBI, GUmbie gp30, YP\_009018906.1, 100%, 0]

SIF-HHPRED: [N-acetylmuramoyl-L-alanine amidase amiD, RCSB PDB, [Escherichia coli str. K-12 substr. MG1655](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Escherichia%20coli%20str.%20K-12%20substr.%20MG1655), [3D2Y\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=3D2Y), 33.17%, 99.29]

SIF-Syn: [Lysin B, upstream Lysin A, downstream holin, just like LittleShirley]

Gene 35

Original Glimmer call @bp 28900 has strength 7.89

SSC: [28900-29901]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Drago, gene 32, NCBI, Q1:S1, 100%, 0]

Gap: [0]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.172, -4.456, yes]

F: [Lysin B]

SIF-BLAST: [Endolysin, NCBI, Drago gp32, YP\_009016110.1, 100%, 0]

SIF-HHPRED: [Crystal structure of lysin B, RCSB PDB, [Fromanvirus D29](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Fromanvirus%20D29) and Mycobacteriophage D29 gp12, [3HC7\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=3HC7), 72.16%, 100]

SIF-Syn: [Holin, upstream lysin B, downstream NKF, just like LittleShirley]

Gene 36

Original Glimmer call @bp 29915 has strength 6.48

SSC: [29915-30148]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Hamulus, gene 33, NCBI, Q1:S4, 99%, 3e-43]

Gap: [14]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.905, -3.145, yes]

F: [Holin]

SIF-BLAST: [Holin, NCBI, Hamulus gp33, YP\_008409097.1, 99%, 3e-43]

SIF-HHPRED: [Phage r1t holin, InterPro Pfam, lactococcus, [PF16945.10](https://www.ebi.ac.uk/interpro/entry/pfam/PF16945), 89.74%, 99.89]

SIF-Syn: [NKF, upstream Holin, downstream NKF, just like LittleShirley]

Gene 37

Original Glimmer call @bp 30145 has strength 7.01

SSC: [30145-30519]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [SiSi, gene 33, NCBI, Q1:S1, 99%, 3e-79]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.675, -5.486, no]

F: [Minor tail protein]

SIF-BLAST: [Minor tail protein, NCBI, SiSi gp33, YP\_008051159.1, 99%, 3e-79]

SIF-HHPRED: [NKF, InterPro Pfam, [PF10874.13](https://www.ebi.ac.uk/interpro/entry/pfam/PF10874), 76.80%, 99.91]

SIF-Syn: [NKF, upstream NKF, downstream DnaQ-like DNA polymerase III subunit, just like LittleShirley]

Gene 38

Original Glimmer call @bp 30543 has strength 4.27 \*\* not called by GeneMark

SSC: [30543-30776]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Ramsey, gene 37, NCBI, Q1:S1, 99%, 2e-48]

Gap: [24]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.797, -3.082, yes]

F: [DnaQ-like DNA polymerase III subunit]

SIF-BLAST: [Hypothetical protein, NCBI, Ramsey gp37, YP\_002241824.1, 99%, 2e-48]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [DnaQ-like DNA polymerase III subunit, upstream NKF, downstream NKF, just like LittleShirley]

Gene 39

Original Glimmer call @bp 30763 has strength 11.46; GeneMark calls start at 30808

SSC: [30763-31584]

CP: [yes]

SCS: [Both-GL]

ST: [SS]

Blast-Start: [DotProduct, gene 35, NCBI, Q1:S1, 100%, 0]

Gap: [-13]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.977, -2.725, yes]

F: [DNA polymerase exonuclease subunit]

SIF-BLAST: [DNA polymerase exonuclease subunit, NCBI, DotProduct gp35, YP\_009638396.1, 100%, 0]

SIF-HHPRED: [Exonuclease MrfB, RCSB PDB, [Bacillus subtilis](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Bacillus%20subtilis), [8UN9\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=8UN9), 62.77%, 99.49]

SIF-Syn: [NKF, upstream DnaQ-like DNA polymerase III subunit, downstream NKF, just like LittleShirley]

Gene 40

SSC: [31581-31892]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Totinger, gene 37, NCBI, Q1:S1, 99%, 7e-68]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.739, -4.445, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Totinger gp37, XIJ70784.1, 99%, 7e-68]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 41

Original GeneMark call @bp 31885

SSC: [31885-31977]

CP: [yes]

SCS: [GeneMark]

ST: [SS]

Blast-Start: [Che8, gene 39, NCBI, Q1:S1, 97%, 4e-10]

Gap: [-7]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.294, -4.970, no]

F: [Putative uncharacterized protein RNAI]

SIF-BLAST: [Hypothetical protein, NCBI, Che8 gp39, NP\_817377.2, 97%, 4e-10]

SIF-HHPRED: [Putative uncharacterized protein RNAI, RCSB PDB, [Enterococcus faecalis](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Enterococcus%20faecalis), [2KV5\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=2KV5), 74.19%, 90.01]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 42

Original Glimmer call @bp 32351 has strength 1.15

SSC: [32351-32082]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Totinger, gene 39, NCBI, Q1:S1, 99%, 7e-59]

Gap: [105]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.215, -4.367, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Totinger gp39, XIJ70786.1, 99%, 7e-59]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 43

Original Glimmer call @bp 32535 has strength 2.14 \*\* not called by GeneMark

SSC: [32535-32344]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Velveteen, gene 34, NCBI, Q1:S4, 98%, 1e-40]

Gap: [-7]

LO: [no]

RBS: [Kibler6, Karlin Medium, 1.565, -5.574, no]

F: [1st lim domain of pinch protein]

SIF-BLAST: [Hypothetical protein, NCBI, Velveteen gp34, YP\_008409571.1, 98%, 1e-40]

SIF-HHPRED: [1st lim domain of pinch protein, SCOPE, Homo sapiens, [SCOP\_d1g47a1](http://scop.berkeley.edu/sid%3Dd1g47a1), 39.06%, 95.21]

SIF-Syn: [NKF, upstream NKF, downstream tyrosine integrase, just like LittleShirley]

Gene 44

Original Glimmer call @bp 32735 has strength 5.28

SSC: [32735-32535]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Totinger, gene 41, NCBI, Q1:S1, 99%, 4e-40]

Gap: [0]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.772, -3.900, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Totinger gp41, XIJ70788.1, 99%, 4e-40]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [Tyrosine integrase, upstream NKF, downstream membrane protein, just like LittleShirley]

Gene 45

Original Glimmer call @bp 33131 has strength 10.90

SSC: [33131-34420]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Phatniss, gene 41, NCBI, Q1:S1, 100%, 0]

Gap: [396]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.405, -3.911, no]

F: [Endonuclease]

SIF-BLAST: [Endonuclease, NCBI, Phatniss gp41, YP\_009202558.1, 100%, 0]

SIF-HHPred: [Integrase; PROTEIN-DNA COMPLEX, DNA BINDING PROTEIN-DNA COMPLEX, RCSB PDB, Enterobacteria phage lambda, [1Z1B\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=1Z1B), 76.05%, 100]

SIF-Syn: [Membrane protein, upstream tyrosine integrase, downstream immunity repressor, just like Starcevich]

Gene 46

Original Glimmer call @bp 34947 has strength 7.32; GeneMark calls start at 34908

SSC: [34947-34501]

CP: [yes]

SCS: [Both-GL]

ST: [SS]

Blast-Start: [Phatniss, gene 42, NCBI, Q1:S1, 99%, 5e-100]

Gap: [81]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.983, -5.809, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Phatniss gp42, YP\_009202559.1, 99%, 5e-100]

SIF-HHPred: [Uncharacterized lipoprotein YifL; Lipopolysaccharide, Lipoprotein, LptDE, MEMBRANE PROTEIN, RCSB PDB, [Pseudomonas aeruginosa PAO1](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Pseudomonas%20aeruginosa%20PAO1), [Escherichia coli K-12](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Escherichia%20coli%20K-12), [8H1R\_F](http://www.rcsb.org/pdb/explore/explore.do?structureId=8H1R), 34.90%, 92.14]

SIF-Syn: [Immunity repressor, upstream membrane protein, downstream NKF, just like Starcevich]

Gene 47

Original Glimmer call @bp 35695 has strength 6.14; GeneMark calls start at 35713

SSC: [35713-35210]

CP: [yes]

SCS: [Both-GM]

ST: [SS]

Blast-Start: [Tweety, gene 45, NCBI, Q1:S11, 99%, 3e-115]

Gap: [263]

LO: [no]

RBS: [Kibler6, Karlin Medium, 1.175, -6.464, no]

F: [Transcriptional repressor]

SIF-BLAST: [transcriptional repressor, NCBI, Tweety gp45, YP\_001469278.1, 99%, 3e-115]

SIF-HHPRED: [P22 C2 transcriptional repressor, SCOPE, Salmonella bacteriophage P2, [SCOP\_d3jxbc\_](http://scop.berkeley.edu/sid%3Dd3jxbc_), 36.90%, 98.08]

SIF-Syn: [NKF, upstream immunity repressor, downstream antirepressor, just like Starcevich]

Gene 48

SSC: [35855-36202]

CP: [yes]

SCS: [Both-GM]

ST: [NI]

Blast-Start: [Wee, gene 49, NCBI, Q1:S1, 99%, 4e-79]

Gap: [142]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 0.612, -8.078, no]

F: [Transcriptional repressor]

SIF-BLAST: [Transcriptional repressor, NCBI, Wee gp49, YP\_004123871.1, 99%, 4e-79]

SIF-HHPred: [Transcriptional Repressor protein C2, SCOPE, [SCOP\_d3jxbc\_](http://scop.berkeley.edu/sid%3Dd3jxbc_), 52.59%, 98.63]

SIF-Syn: [Antirepressor, upstream NKF, downstream NKF, just like LittleShirley]

Gene 49

Original Glimmer call @bp 36261 has strength 8.49

SSC: [36261-37265]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [DotProduct, gene 44, NCBI, Q1:S1, 100%, 0]

Gap: [55]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.822, -3.319, yes]

F: [Anti-repressor ANT]

SIF-BLAST: [Anti-repressor ANT, NCBI, DotProduct gp44, YP\_009638405.1, 100%, 0]

SIF-HHPRED: [Antirepressor ANT, InterPro Pfam, phages P1 and P7, [PF03374.19](https://www.ebi.ac.uk/interpro/entry/pfam/PF03374), 32.84%, 97.32]

SIF-Syn: [NKF, upstream antirepressor, downstream NKF, just like LittleShirley]

Gene 50

Original Glimmer call @bp 37319 has strength 9.89; GeneMark calls start at 37262

SSC: [37262-37477]

CP: [yes]

SCS: [Both-GM]

ST: [SS]

Blast-Start: [Kersh, gene 51, NCBI, Q1:S1, 99%, 4e-43]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 0.855, -7.127, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Kersh gp51, YP\_009958593.1, 99%, 4e-43]

SIF-HHPred: [NKF, Interpro Pfam, [PF19887.4](https://www.ebi.ac.uk/interpro/entry/pfam/PF19887), 31.94%, 93.85]

SIF-Syn: [NKF, upstream NKF, downstream helix-turn-helix DNA binding domain, just like LittleShirley]

Gene 51

Original GeneMark call @bp 37474

SSC: [37474-37566]

CP: [yes]

SCS: [GeneMark]

ST: [SS]

Blast-Start: [LittleShirley, gene 49, NCBI, Q1:S1, 97%, 1e-10]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.652, -3.319, yes]

F: [helix-turn-helix DNA binding domain]

SIF-BLAST: [Hypothetical protein, GenBank, LittleShirley gp49, XEN19619.1, 97%, 1e-10]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [helix-turn-helix DNA binding domain, upstream NKF, downstream NKF, just like LittleShirley]

Gene 52

Original Glimmer call @bp 37563 has strength 5.39

SSC: [37563-37760]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Inventum, gene 45, NCBI, Q1:S31, 98%, 3e-39]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.772, -3.151, yes]

F: [Terminase gpNU1 subunit domain]

SIF-BLAST: [Hypothetical protein, NCBI, Inventum gp45, YP\_009125326.1, 98%, 3e-39]

SIF-HHPRED: [Terminase gpNU1 subunit domain, SCOPE, Escherichia phage TaxId: 10710, [SCOP\_d6hn7b1](http://scop.berkeley.edu/sid%3Dd6hn7b1), 78.79%, 99.03]

SIF-Syn: [NKF, upstream helix-turn-helix DNA binding domain, downstream NKF, just like LittleShirley]

Gene 53

SSC: [37757-37948]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [LittleShirley, gene 51, NCBI, Q1:S1, 98%, 3e-36]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.996, -5.508, no]

F: [Geminin]

SIF-BLAST: [Hypothetical protein, GenBank, LittleShirley gp51, XEN19621.1, 98%, 3e-36]

SIF-HHPred: [Geminin, Interpro Pfam, [PF07412.17](https://www.ebi.ac.uk/interpro/entry/pfam/PF07412), 85.94%, 95.1]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 54

Original Glimmer call @bp 37945 has strength 7.19

SSC: [37945-38349]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Mattes, gene 57, NCBI, Q1:S1, 99%, 3e-93]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.123, -4.496, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Mattes gp57, YP\_009959523.1, 99%, 3e-93]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 55

Original Glimmer call @bp 38533 has strength 7.02

SSC: [38533-38868]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Wachhund, gene 55, NCBI, Q28:S118, 75%, 1e-49]

Gap: [184]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.228, -6.334, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Wachhund gp55, YP\_009963239.1, 75%, 1e-49]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 56

Original Glimmer call @bp 38946 has strength 10.20

SSC: [38946-39227]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Fruitloop, gene 52, NCBI, Q1:S1, 99%, 8e-60]

Gap: [78]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.824, -3.025, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Fruitloop gp52, YP\_002241737.1, 99%, 8e-60]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 57

Original Glimmer call @bp 39224 has strength 7.74

SSC: [39224-39376]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Cornie, gene 50, NCBI, Q1:S1, 98%, 1e-23]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.405, -3.972, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Cornie gp50, YP\_009856236.1, 98%, 1e-23]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream WhiB family transcription factor, just like LittleShirley]

Gene 58

Original Glimmer call @bp 39373 has strength 6.85; GeneMark calls start at 39391

SSC: [39373-39765]

CP: [yes]

SCS: [Both-GL]

ST: [NI]

Blast-Start: [Royals2015, gene 59, NCBI, Q1:S1, 99%, 3e-91]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.926, -4.905, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Royals2015 gp59, YP\_009961990.1, 99%, 3e-91]

SIF-HHPRED: [NKF, InterPro Pfam, [PF05305.19](https://www.ebi.ac.uk/interpro/entry/pfam/PF05305), 52.67%, 99.56]

SIF-Syn: [WhiB family transcription factor, upstream NKF, downstream helix-turn-helix DNA binding domain, just like LittleShirley]

Gene 59

Original Glimmer call @bp 39765 has strength 5.68

SSC: [39765-40259]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Jarcob, gene 57, NCBI, Q1:S2, 99%, 8e-118]

Gap: [0]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.102, -4.602, no]

F: [WhiB family transcription factor]

SIF-BLAST: [WhiB family transcription factor, GenBank, Jarcob gp57, UVK58524.1, 99%, 8e-118]

SIF-HHPred: [Redox- and pH-responsive transcriptional regulator WhiB3, RCSB PDB, [Mycobacterium tuberculosis](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Mycobacterium%20tuberculosis), [8CYF\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=8CYF), 52.73%, 99.83]

SIF-Syn: [helix-turn-helix DNA binding domain, upstream WhiB family transcription factor, downstream WhiB family transcription factor, just like LittleShirley]

Gene 60

Original Glimmer call @bp 40256 has strength 7.06; GeneMark calls start at 40229

SSC: [40229-40741]

CP: [yes]

SCS: [Both-GM]

ST: [NI]

Blast-Start: [Ochi17, gene 61, NCBI, Q1:S1, 99%, 2e-117]

Gap: [-30]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.320, -6.909, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Ochi17 gp61, YP\_010101075.1, 99%, 2e-117]

SIF-HHPred: [Hypoxic Response Regulator DosR, TRANSCRIPTIONAL REGULATORY PROTEIN DEVR, RCSB PDB, [Mycobacterium tuberculosis](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Mycobacterium%20tuberculosis), [3C3W\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=3C3W), 34.50%, 96.46]

SIF-Syn: [WhiB family transcription factor, upstream helix-turn-helix DNA binding domain, downstream helix-turn-helix DNA binding domain, just like LittleShirley]

Gene 61

Original Glimmer call @bp 40738 has strength 6.70

SSC: [40738-41022]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [LittleShirley, gene 58, NCBI, Q1:S1, 99%, 2e-61]

Gap: [-3]

LO: [no

RBS: [Kibler6, Karlin Medium, 2.807, -3.138, yes]

F: [WhiB family transcription factor]

SIF-BLAST: [WhiB family transcription factor, GenBank, LittleShirley gp58, XEN19628.1, 99%, 2e-61]

SIF-HHPred: [Transcriptional regulator WhiB, RCSB PDB, [Streptomyces venezuelae](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Streptomyces%20venezuelae), [8DY7\_H](http://www.rcsb.org/pdb/explore/explore.do?structureId=8DY7), 76.84%, 99.87]

SIF-Syn: [helix-turn-helix DNA binding domain, upstream WhiB family transcription factor, downstream NKF, just like LittleShirley]

Gene 62

Original Glimmer call @bp 41019 has strength 6.17

SSC: [41019-41384]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [SiSi, gene 58, NCBI, Q1:S1, 99%, 2e-84]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.863, -3.023, yes]

F: [DNA binding protein]

SIF-BLAST: [DNA binding protein, NCBI, SiSi gp58, YP\_008051184.1, 99%, 2e-84]

SIF-HHPred: [Putative uncharacterized protein; DNA BINDING PROTEIN, RCSB PDB, [Hyperthermus butylicus DSM 5456](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Hyperthermus%20butylicus%20DSM%205456), [2LVS\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=2LVS), 77.87%, 99.36]

SIF-Syn: [NKF, upstream helix-turn-helix DNA binding domain, downstream NKF, just like LittleShirley]

Gene 63

Original Glimmer call @bp 41384 has strength 3.12 \*\* not called by GeneMark

SSC: [41384-41539]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [SiSi, gene 59, NCBI, Q1:S1, 98%, 1e-29]

Gap: [0]

LO: [no]

RBS: [Kibler6, Karlin Medium, 1.740, -5.351, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, SiSi gp59, YP\_008051185.1, 98%, 1e-29]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 64

Original Glimmer call @bp 41539 has strength 8.80

SSC: [41539-41769]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [SiSi, gene 60, NCBI, Q1:S1, 99%, 2e-44]

Gap: [0]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.588, -3.593, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, SiSi gp60, YP\_008051186.1, 99%, 2e-44]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream HNH endonuclease, just like LittleShirley]

Gene 65

Original Glimmer call @bp 41766 has strength 9.58

SSC: [41766-42011]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [TDanisky, gene 69, NCBI, Q1:S4, 99%, 3e-50]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.797, -3.018, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, TDanisky gp69, QGH71479.1, 99%, 3e-50]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [HNH endonuclease, upstream NKF, downstream NKF, just like LittleShirley]

Gene 66

SSC: [42008-42490]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Plumbus, gene 66, NCBI, Q1:S29, 99%, 8e-116]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.609, -3.549, yes]

F: [HNH endonuclease]

SIF-BLAST: [HNH endonuclease, NCBI, Plumbus gp66, YP\_010113849.1, 99%, 8e-116]

SIF-HHPred: [Zinc-binding loop region of homing endonuclease, Interpro Pfam, [PF05551.16](https://www.ebi.ac.uk/interpro/entry/pfam/PF05551), 63.98%, 99.76]

SIF-Syn: [NKF, upstream HNH endonuclease, downstream DNA methyltransferase, just like LittleShirley]

Gene 67

Original Glimmer call @bp 42487 has strength 12.18

SSC: [42487-43065]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Plumbus, gene 67, NCBI, Q1:S1, 99%, 3e-135]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 3.068, -2.807, no]

F: [Single strand annealing protein]

SIF-BLAST: [Single strand annealing protein, NCBI, Plumbus gp67, YP\_010113850.1, 99%, 3e-135]

SIF-HHPRED: [DNA repair protein RAD52 homolog, RCSB PDB, [Homo sapiens](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Homo%20sapiens), [8H1P\_H](http://www.rcsb.org/pdb/explore/explore.do?structureId=8H1P), 63.73%, 99.80]

SIF-Syn: [DNA methyltransferase, upstream NKF, downstream NKF, just like Rialto]

Gene 68

Original Glimmer call @bp 43421 has strength 10.79

SSC: [43421-44344]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Rialto, gene 71, NCBI, Q1:S1, 100%, 0]

Gap: [356]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.739, -3.279, yes]

F: [DNA methyltransferase]

SIF-BLAST: [DNA methyltransferase, GenBank, Rialto gp71, WNM65636.1, 100%, 0]

SIF-HHPRED: [Modification Methylase RSRI, RCSB PDB, [Cereibacter sphaeroides](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Cereibacter%20sphaeroides), [1EG2\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=1EG2), 79.87%, 99.96]

SIF-Syn: [NKF, upstream DNA methyltransferase, downstream NKF, just like Rialto]

Gene 69

Original Glimmer call @bp 44558 has strength 1.65 \*\* not called by GeneMark

SSC: [44558-44713]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Wee, gene 73, NCBI, Q1:S1, 98%, 9e-30]

Gap: [214]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.001, -4.731, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Wee gp73, YP\_004123895.1, 98%, 9e-30]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Rialto]

Gene 70

Original Glimmer call @bp 44706 has strength 7.36

SSC: [44706-44894]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Rialto, gene 74, NCBI, Q1:S1, 98%, 3e-35]

Gap: [-7]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 3.155, -2.928, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Rialto gp74, WNM65639.1, 98%, 3e-35]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Rialto]

Gene 71

Original Glimmer call @bp 44891 has strength 9.54

SSC: [44891-45040]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [DotProduct, gene 69, NCBI, Q1:S1, 98%, 2e-27]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.658, -3.447, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, DotProduct gp69, YP\_009638430.1, 98%, 2e-27]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream PAPS reductase-like domain protein, downstream G-I-Y-Y-I-G endonuclease, just like Lorde]

Gene 72

Original Glimmer call @bp 45180 has strength 4.90

SSC: [45180-45058]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Modragons, gene 73, NCBI, Q1:S78, 98%, 3e-16]

Gap: [140]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.056, -5.463, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GeneBank, Modragons gp73, QFP96456.1, 98%, 3e-16]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Lorde]

Gene 73

Original Glimmer call @bp 45179 has strength 6.09

SSC: [45179-45730]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Bipolar, gene 69, NCBI, Q1:S1, 99%, 4e-131]

Gap: [-1]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 0.922, -6.970, no]

F: [DNA Methyltransferase]

SIF-BLAST: [DNA Methyltransferase, NCBI, Bipolar gp69, YP\_009200696.1, 99%, 4e-131]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Lorde]

Gene 74

Original Glimmer call @bp 46066 has strength 7.37

SSC: [46066-46188]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [OwlsT2W, gene 74, NCBI, Q1:S2, 98%, 9e-20]

Gap: [336]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.919, -2.845, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, OwlsT2W gp74, YP\_009960968.1, 98%, 9e-20]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Rialto]

Gene 75

Original Glimmer call @bp 46185 has strength 2.50; GeneMark calls start at 46302

SSC: [46185-46403]

CP: [yes]

SCS: [Both-GL]

ST: [SS]

Blast-Start: [Rialto, gene 80, NCBI, Q1:S1, 99%, 5e-46]

Gap: [-3]

LO: [no]

RBS: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Rialto gp80, WNM65644.1, 99%, 5e-46]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream RepA-like replication initiator, just like Rialto]

Gene 76

Original Glimmer call @bp 46400 has strength 0.54

SSC: [46400-47305]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Eish, gene 77, NCBI, Q1:S1, 100%, 0]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.926, -4.888, no]

F: [Replication initiation protein]

SIF-BLAST: [Replication initiation protein, NCBI, Eish gp77, YP\_009956419.1, 100%, 0]

SIF-HHPRED: [N-terminal phage replisome organiser, InterPro Pfam, [PF09681.15](https://www.ebi.ac.uk/interpro/entry/pfam/PF09681), 28.81%, 93.45]

SIF-Syn: [RepA-like replication initiator, upstream NKF, downstream NKF, just like Rialto]

Gene 77

Original Glimmer call @bp 47302 has strength 8.28

SSC: [47302-47664]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Pacc40, gene 68, NCBI, Q1:S1, 99%, 1e-80]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.191, -4.416, yes]

F: [Replisome organizer]

SIF-BLAST: [Hypothetical protein, NCBI, Pacc40 gp68, YP\_002241652.1, 99%, 1e-80]

SIF-HHPRED: [replisome organizer, RCSB PDB, Bacillus phage SPP1, [1NO1\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=1NO1), 57.02%, 99.37]

SIF-Syn: [NKF, upstream RepA-like replication initiator, downstream NKF, just like Rialto]

Gene 78

Original Glimmer call @bp 47657 has strength 4.21 \*\* not called by GeneMark

SSC: [47657-47881]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Ramsey, gene 79, NCBI, Q1:S1, 99%, 6e-45]

Gap: [-7]

LO: [no]

RBS: [Kibler6, Karlin Medium, 1.904 -5.779, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Ramsey gp79, YP\_002241866.1, 99%, 6e-45]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Starcevich]

Gene 79

Original Glimmer call @bp 47961 has strength 2.79 \*\* not called by GeneMark

SSC: [47961-48353]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Rita, gene 83, NCBI, Q1:S1, 99%, 2e-88]

Gap: [80]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.998, -2.664, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Rita gp83, UVG34704.1, 99%, 2e-88]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 80

Original Glimmer call @bp 48353 has strength 8.46 \*\* not called by GeneMark

SSC: [48353-48553]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Madiba, gene 82, NCBI, Q1:S1, 99%, 1e-38]

Gap: [0]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.562, -3.858, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Madiba gp82, UJE15627.1, 99%, 1e-38]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Lorde]

Gene 81

Original Glimmer call @bp 48537 has strength 6.64

SSC: [48537-48842]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Hades, gene 79, NCBI, Q1:S1, 99%, 6e-64]

Gap: [-16]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 3.075, -2.505, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Hades gp79, YP\_009125258.1, 99%, 6e-64]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Lorde]

Gene 82

Original GeneMark call @bp 48897

SSC: [48897-49085]

CP: [yes]

SCS: [GeneMark]

ST: [SS]

Blast-Start: [Tweety, gene 83, NCBI, Q1:S1, 98%, 1e-33]

Gap: [55]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.648, -3.390, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Tweety gp83, YP\_001469316.1, 98%, 1e-33]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream MPME 1 protein, just like Lorde]

Gene 83

Original Glimmer call @bp 49194 has strength 2.57; GeneMark calls start at 49185

SSC: [49185-49526]

CP: [yes]

SCS: [Both-GM]

ST: [NI]

Blast-Start: [Plumbus, gene 84, NCBI, Q1:S4, 99%, 2e-76]

Gap: [100]

LO: [no]

RBS: [Kibler6, Karlin Medium, 1.120, -6.577, no]

F: [Mobile element MPME]

SIF-BLAST: [Mobile element MPME, NCBI, Plumbus gp84, YP\_010113867.1, 99%, 2e-76]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [MPME 1 protein, upstream NKF, downstream NKF, just like Lorde]

Gene 84

Original Glimmer call @bp 49689 has strength 3.75 \*\* not called by GeneMark

SSC: [49689-49817]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Job42, gene 85, NCBI, Q1:S1, 98%, 5e-22]

Gap: [163]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.648, -3.328, yes]

F: [DNA-directed RNA polymerase subunit P]

SIF-BLAST: [Hypothetical protein, NCBI, Job42 gp85, YP\_008126675.1, 98%, 5e-22]

SIF-HHPRED: [DNA-directed RNA polymerase subunit P, RCSB PDB, [Thermococcus kodakarensis KOD1](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Thermococcus%20kodakarensis%20KOD1), [4QIW\_W](http://www.rcsb.org/pdb/explore/explore.do?structureId=4QIW), 74.42%, 96.93]

SIF-Syn: [NKF, upstream MPME 1 protein, downstream NKF, just like Rialto]

Gene 85

Original Glimmer call @bp 49814 has strength 6.14 \*\* not called by GeneMark

SSC: [49814-50005]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Saal, gene 82, NCBI, Q1:S1, 98%, 1e-38]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.096, -4.825, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Saal gp82, YP\_009007549.1, 98%, 1e-38]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Rialto]

Gene 86

Original Glimmer call @bp 50002 has strength 5.61

SSC: [5002-50415]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Kersh, gene 88, NCBI, Q1:S1, 98%, 2e-93]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 3.213, -2.684, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Kersh gp88, YP\_009958630.1, 98%, 2e-93]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Rialto]

Gene 87

Original Glimmer call @bp 50408 has strength 4.83

SSC: [50408-50977]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [DosHalletts, gene 84, NCBI, Q1:S1, 99%, 7e-138]

Gap: [-7]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.503, -4.281, no]

F: [Histidine triad nucleotide binding protein]

SIF-BLAST: [Histidine triad nucleotide binding protein, GenBank, DosHalletts gp84, XEN17562.1, 99%, 7e-138]

SIF-HHPRED: [AP-4-A phosphorylase, RCSB PDB, [Mycobacterium tuberculosis H37Rv](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Mycobacterium%20tuberculosis%20H37Rv), [3ANO\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=3ANO), 54.21%, 99.65]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Rialto]

Gene 88

Original Glimmer call @bp 50977 has strength 5.88 \*\* not called by GeneMark

SSC: [50977-51093]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [DosHalletts, gene 85, NCBI, Q1:S1, 95%, 1e-16]

Gap: [0]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.731, -3.155, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, DosHalletts gp85, XEN17563.1, 95%, 1e-16]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Rialto]

Gene 89

Original Glimmer call @bp 51131 has strength 12.78

SSC: [51131-51529]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Bipolar, gene 91, NCBI, Q1:S1, 99%, 2e-88]

Gap: [38]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.824, -3.043, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Bipolar gp91, YP\_009200718.1, 99%, 2e-88]

SIF-HHPRED: [NKF, InterPro Pfam, [PF11750.13](https://www.ebi.ac.uk/interpro/entry/pfam/PF11750), 69.92%, 99.72]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Rialto]

Gene 90

Original Glimmer call @bp 51526 has strength 0.43 \*\* not called by GeneMark

SSC: [51526-51648]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Eradicator, gene 83, NCBI, Q1:S1, 98%, 2e-20]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.056, -4.635, yes]

F: [DNA double-strand break repair rad50 ATPase]

SIF-BLAST: [Hypothetical protein, GenBank, Eradicator gp83, QYW01447.1, 98%, 2e-20]

SIF-HHPRED: [DNA double-strand break repair rad50 ATPase, RCSB PDB, [Pyrococcus furiosus](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Pyrococcus%20furiosus), [1L8D\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=1L8D), 68.29%, 90.06]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Starcevich]

Gene 91

Original Glimmer call @bp 51645 has strength 3.97

SSC: [51645-51977]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [MilleniumForce, gene 91, NCBI, Q1:S1, 99%, 4e-75]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.824, -3.025, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, MilleniumForce gp91, YP\_009959757.1, 99%, 4e-75]

SIF-HHPRED: [DNA-directed RNA polymerase II subunit RPB1, RCSB PDB, [Saccharomyces cerevisiae S288C](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Saccharomyces%20cerevisiae%20S288C), [7UI9\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=7UI9), 25.23%, 92.95]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Starcevich]

Gene 92

Original Glimmer call @bp 51970 has strength 7.28

SSC: [51970-52233]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Poenanya, gene 96, NCBI, Q1:S1, 100%, 1e-55]

Gap: [-7]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.998, -3.254, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Poenanya gp96, YP\_009961394.1, 100%, 1e-55]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like Lorde]

Gene 93

Original Glimmer call @bp 52230 has strength 7.82

SSC: [52230-52874]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Buzzlyseyear, gene 100, NCBI, Q1:S1, 100%, 3e-155]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.053, 4.702, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Buzzlyseyear gp100, YP\_009125093.1, 100%, 3e-155]

SIF-HHPRED: [Small CPxCG-related zinc finger protein, RCSB PDB, [Haloferax volcanii DS2](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Haloferax%20volcanii%20DS2), [8Q5B\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=8Q5B), 14.88%, 96.91]

SIF-Syn: [NKF, upstream NKF, downstream helix-turn-helix DNA binding domain, MerR-like, just like Starcevich]

Gene 94

Original Glimmer call @bp 53202 has strength 4.90

SSC: [53202-53053]

CP: [yes]

SCS: [Glimmer]

ST: [NA]

Blast-Start: [NKF] no hits on NCBI

Gap: [179]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.638, -3.411, yes]

F: [NKF]

SIF-BLAST: [NKF]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [helix-turn-helix DNA binding domain, MerR-like, upstream NKF, downstream NKF, just like Starcevich]

Gene 95

Original Glimmer call @bp 53205 has strength 6.15

SSC: [53205-53372]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Ardmore, gene 80, NCBI, Q1:S1, 98%, 1e-30]

Gap: [3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.803, -5.988, yes]

F: [FYVE-finger-containing Rab5 effector protein rabenosyn-5]

SIF-BLAST: [Hypothetical protein, NCBI, Ardmore gp80, YP\_003495221.1, 98%, 1e-30]

SIF-HHPRED: [FYVE-finger-containing Rab5 effector protein rabenosyn-5, RCSB PDB, [Mus musculus](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Mus%20musculus) and [Homo sapiens](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Homo%20sapiens), [1Z0J\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=1Z0J), 69.64%, 94.51]

SIF-Syn: [NKF, upstream helix-turn-helix DNA binding domain, MerR-like, downstream NKF, just like Starcevich]

Gene 96

Original Glimmer call @bp 53379 has strength 11.93

SSC: [53379-53588]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Velveteen, gene 92, NCBI, Q1:S1, 99%, 6e-41]

Gap: [7]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.998, -3.703, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Velveteen gp92, YP\_008409629.1, 99%, 6e-41]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 97

Original Glimmer call @bp 53588 has strength 3.17 \*\* not called by GeneMark

SSC: [53588-53785]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Wee, gene 100, NCBI, Q1:S1, 98%, 1e-39]

Gap: [0]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.145, -4.513, yes]

F: [DNA gyrase inhibitor YacG; Isomerase]

SIF-BLAST: [Hypothetical protein, NCBI, Wee gp100, YP\_004123922.1, 98%, 1e-39]

SIF-HHPred: [DNA gyrase inhibitor YacG; Isomerase, RCSB PDB, [Escherichia coli str. K-12 substr. MC4100](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Escherichia%20coli%20str.%20K-12%20substr.%20MC4100), [Escherichia coli K-12](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Escherichia%20coli%20K-12), [4TMA\_K](http://www.rcsb.org/pdb/explore/explore.do?structureId=4TMA), 86.36%, 90.23]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 98

Original Glimmer call @bp 53782 has strength 5.46

SSC: [53782-54195]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Jarcob, gene 101, NCBI, Q1:S1, 99%, 7e-91]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.477, -5.897, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Jarcob gp101, UVK58567.1, 99%, 7e-91]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 99

Original GeneMark call @bp 54192

SSC: [54192-54434]

CP: [yes]

SCS: [GeneMark]

ST: [SS]

Blast-Start: [Starcevich, gene 101, NCBI, Q1:S1, 99%, 1e-48]

Gap: [-3]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 1.438, -5.900, no]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, GenBank, Starcevich gp101, WNM68473.1, 99%, 1e-48]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 100

Original Glimmer call @bp 54427 has strength 4.15

SSC: [54427-54588]

CP: [yes]

SCS: [Glimmer]

ST: [SS]

Blast-Start: [Tweety, gene 101, NCBI, Q1:S1, 98%, 3e-30]

Gap: [-7]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.085, -4.557, yes]

F: [Hypothetical protein]

SIF-BLAST: [Hypothetical protein, NCBI, Tweety gp101, YP\_001469334.1, 98%, 3e-30]

SIF-HHPRED: [NKF, no matches with a probability above 90%]

SIF-Syn: [NKF, upstream NKF, downstream NKF, just like LittleShirley]

Gene 101

Original Glimmer call @bp 54894 has strength 11.93

SSC: [54894-56330]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Fastidio, gene 104, NCBI, Q1:S59, 100%, 0]

Gap: [306]

LO: [yes]

RBS: [Kibler6, Karlin Medium, 2.200, -4.608, no]

F: [Glycosyltransferase]

SIF-BLAST: [Glycosyltransferase, GenBank, Fastidio gp104, XKC18180.1, 100%, 0]

SIF-HHPRED: [Polypeptide N-acetylgalactosaminyltransferase 1, SCOPE, [Mus musculus](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Mus%20musculus), [SCOP\_d1xhba2](http://scop.berkeley.edu/sid%3Dd1xhba2), 46.14%, 99.77]

SIF-Syn: [NKF, upstream NKF, downstream glycosyltransferase, just like LittleShirley]

Gene 102

Original Glimmer call @bp 56348 has strength 6.79; GeneMark calls start at 56333

SSC: [56333-56806]

CP: [yes]

SCS: [GeneMark]

ST: [NI]

Blast-Start: [QuickMath, gene 103, NCBI, Q1:S6, 99%, 3e-108]

Gap: [3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.493, -4.751, yes]

F: [Kinase]

SIF-BLAST: [Kinase, NCBI, QuickMath gp103, YP\_009961826.1, 99%, 3e-108]

SIF-HHPred: [METHYLTRANSFERASE WBDD; TRANSFERASE, KINASE, RCSB PDB, [Escherichia coli](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Escherichia%20coli), [4AZS\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=4AZS), 86.27%, 98.82]

SIF-Syn: [glycosyltransferase, upstream NKF, downstream serine/threonine kinase, just like LittleShirley]

Gene 103

Original Glimmer call @bp 56809 has strength 3.81 \*\* not called by GeneMark

SSC: [56809-57015]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Dante, gene 102, NCBI, Q1:S23, 99%, 3e-43]

Gap: [3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 2.294, -4.414, no]

F: [RNA chaperone]

SIF-BLAST: [Hypothetical protein, NCBI, Dante gp102, YP\_009212744.1, 99%, 3e-43]

SIF-HHPRED: [RNA chaperone, RCSB PDB, [Escherichia coli K-12](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Escherichia%20coli%20K-12), [5NBB\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=5NBB), 53.62%, 97.62]

SIF-Syn: [serine/threonine kinase, upstream glycosyltransferase, downstream NKF, just like LittleShirley]

Gene 104

Original Glimmer call @bp 57012 has strength 3.09

SSC: [57012-57623]

CP: [yes]

SCS: [Glimmer]

ST: [NI]

Blast-Start: [Buzzlyseyear, gene 110, NCBI, Q1:S1, 100%, 5e-140]

Gap: [-3]

LO: [no]

RBS: [Kibler6, Karlin Medium, 1.814, -5.886, no]

F: [Glycosyltransferase]

SIF-BLAST: [Glucosyltransferase, NCBI, Buzzlyseyear, YP\_009125103.1, 100%, 5e-140]

SIF-HHPRED: [Glycosyltransferase, RCSB PDB, [Aggregatibacter actinomycetemcomitans NUM4039](https://www.rcsb.org/search?q=rcsb_entity_source_organism.taxonomy_lineage.name:Aggregatibacter%20actinomycetemcomitans%20NUM4039), [8XKD\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=8XKD), 86.76%, 99.88]

SIF-Syn: [NKF, upstream serine/threonine kinase, just like LittleShirley]