Supplementary

Characterization and Full Genome Sequence of Novel KPP-5 Lytic Phage Against Klebsiella Pneumoniae Responsible for Recalcitrant Infection

Ahmed R. Sofy 1*, Noha K. El-Dougdoug 2, Ehab E. Refaey 1, Rehab A. Dawoud 3,4 and Ahmed A. Hmed 1

1 Botany and Microbiology Department, Faculty of Science, Al-Azhar University, Nasr City, Cairo 11884, Egypt; ehabrefaey@azhar.edu.eg (E.E.R); ahmed_hmed@azhar.edu.eg (A.A.H.)
2 Botany and Microbiology Department, Faculty of Science, Benha University, Benha 13518, Egypt; nohaeldougdoug@gmail.com
3 Virus and Phytoplasma Research Department, Plant Pathology Research Institute, Agricultural Research Center (ARC), Giza 12619, Egypt; rdawood@jazanu.edu.sa
4 Department of Biology, Faculty of Science, Jazan University, Box 114, Jazan 45142, Saudi Arabia
* Correspondence: ahmed_sofy@azhar.edu.eg (A.R.S)

Table S1. Antibiotics resistance profiles of the K. pneumoniae host strain.

| Scientific Name | Disc Potency (mcg) | Trade Name | Symbol | Antibiotic-resistance profiles |
|-----------------|-------------------|------------|--------|-------------------------------|
| Ampicillin      | 10                | Ampicillin | Am     | I                             |
| Gentamicin      | 10                | Gentamicin | CN     | R                             |
| Ciprofloxacin   | 5                 | Tarivid    | CIP    | R                             |
| Ofloxacin       | 5                 | Tarivid    | OFX    | I                             |
| Oxacillin       | 1                 | Oxacillin  |OX      | S                             |
| Clindamycin     | 2                 | Augmentin  | DA     | R                             |
| Levofoxacin     | 5                 | Le flox    | LEV    | I                             |
| Flucloxacillin  | 5                 | Keflin     | FL     | R                             |
| Rifamycin       | 30                | Remactan   | RF     | R                             |
| Tobramycin      | 10                | Nebcin     | TOB    | S                             |
| Norfoxacin      | 10                | Noroxin    | NOR    | I                             |
| Gatifloxacin    | 5                 | Lincocein  | GAT    | S                             |
| Tetracycline    | 30                | Tetracycline | TE | I                             |
| Erythromycin    | 15                | Erythromycin | E | R                             |
| Aztreonam       | 1                 | Meronam    | ATM    | R                             |
| Vancomycin      | 30                | Vancocin   | VA     | I                             |
| Cephradine      | 30                | Velocef    | CE     | S                             |
| Gene accession | Location | Strand | Frame | Protein size (aa) | Molecule mass (KDa) | Isoelectric Point (pI) | Predicted protein function | BLASTp best match | E-value | Identities | Accession |
|----------------|----------|--------|-------|------------------|---------------------|-----------------------|--------------------------|--------------------------|----------|------------|-----------|
| gp1 (QSJ04721) | 16-1062  | +      | 1     | 348              | 39.54               | 4.99                  | DNA ligase               | Klebsiella phage vB_KpnP_Emp27 | 0        | 345/348 (99.14%) | QEG11869 |
| gp2 (QSJ04722) | 950-1126 | +      | 2     | 58               | 6.32                | 12.43                 | hypothetical protein     | -                        | -        | -          | -         |
| gp3 (QSJ04723) | 1232-1489| +      | 2     | 85               | 9.90                | 11.58                 | hypothetical protein     | Enterobacter phage E-3   | 6e-54    | 83/85 (97.65%) | YP_009198329 |
| gp4 (QSJ04724) | 1489-1959| +      | 1     | 156              | 17.67               | 9.65                  | DUF3310 domain-containing protein | Klebsiella phage vB_KpnP_Emp27 | 1e-111  | 154/156 (98.72%) | QEG11871 |
| gp5 (QSJ04725) | 2080-2316| +      | 1     | 78               | 8.85                | 4.56                  | Host RNA polymerase inhibitor, T7-like | Enterobacter phage E-3 | 8e-52    | 78/78 (100%) | YP_009198326 |
| gp6 (QSJ04726) | 3066-3527| +      | 3     | 153              | 17.37               | 10.15                 | endonuclease             | Enterobacter phage E-3   | 3e-107   | 153/153 (100%) | YP_009198324 |
| gp7 (QSJ04727) | 3520-3975| +      | 1     | 151              | 16.88               | 9.23                  | endolysin                | Klebsiella phage 31       | 2e-109   | 151/151 (100%) | QGH73730 |
| gp8 (QSJ04728) | 4154-5854| +      | 2     | 566              | 62.80               | 4.90                  | DNA primase/helicase     | Enterobacteria phage T3 | 0        | 563/566 (99.47%) | NP_523315 |
| gp9 (QSJ04729) | 5574-5903| +      | 3     | 109              | 11.93               | 7.18                  | hypothetical protein     | Citrobacter phage SH1    | 5e-71    | 106/109 (97.25%) | YP_009286649 |
| gp10 (QSJ04730) | 6176-6460| +      | 2     | 94               | 10.75               | 10.60                 | hypothetical protein     | Klebsiella phage 31       | 3e-63    | 94/94 (100%)  | QGH73734 |
| gp11 (QSJ04731) | 6528-8642| +      | 3     | 704              | 79.76               | 6.96                  | DNA polymerase           | Enterobacter phage E-3   | 0        | 701/704 (99.57%) | YP_009198319 |
| gp12 (QSJ04732) | 8662-8961| +      | 1     | 99               | 11.17               | 8.48                  | HNS binding protein      | Enterobacter phage E-3   | 3e-66    | 99/99 (100%)  | YP_009198318 |
| gp13 (QSJ04733) | 8961-9170| +      | 3     | 69               | 7.26                | 10.25                 | HNS binding protein      | Klebsiella phage vB_KpnP_Emp27 | 2e-42    | 69/69 (100%)  | QEG11882 |
| gp14 (QSJ04734) | 9167-9346| +      | 2     | 59               | 6.70                | 3.96                  | host recBCD nuclease inhibitor | Enterobacter phage E-3 | 3e-35    | 58/59 (98.31%) | YP_009198316 |
| gp15 (QSJ04735) | 9343-10254 | + | 1 | 303 | 34.77 | 4.75 | exonuclease | Klebsiella phage Patroon | 0 | 302/303 (99.67%) | QBQ72894 |
| gp16 (QSJ04736) | 10442-10687 | + | 2 | 81 | 9.37 | 6.24 | hypothetical protein | Yersinia phage phiYeO3-12 | 5e-53 | 81/81 (100%) | NP_052103 |
| gp17 (QSJ04739) | 10970-11290 | + | 2 | 106 | 11.0 | 10.58 | tail assembly protein | Klebsiella phage Patroon | 2e-63 | 105/106 (99.06%) | QBQ72898 |
| gp18 (QSJ04737) | 11301-12908 | + | 3 | 535 | 58.64 | 4.27 | head-to-tail joining protein | Yersinia phage phiYeO3-12 | 0 | 535/535 (100%) | NP_052106 |
| gp19 (QSJ04738) | 13010-13942 | + | 2 | 310 | 33.72 | 4.02 | capsid assembly protein | Salmonella phage phiSG-JL2 | 0 | 306/310 (99%) | NP_052110 |
| gp20 (QSJ04740) | 14099-15142 | + | 2 | 347 | 36.92 | 6.73 | major capsid protein | Klebsiella phage NL_ZS_3 | 0 | 346/347 (99.71%) | QNN97371 |
| gp21 (QSJ04741) | 15181-15414 | + | 1 | 77 | 7.44 | 4.14 | major tail protein | Enterobacter phage E-3 | 4e-41 | 74/77 (96.10%) | NP_052106 |
| gp22 (QSJ04742) | 15527-16117 | + | 2 | 196 | 22.23 | 4.21 | tail tubular protein A | Yersinia phage phiYeO3-12 | 1e-142 | 196/196 (100%) | NP_052110 |
| gp23 (QSJ04743) | 16133-18538 | + | 2 | 801 | 89.79 | 6.30 | tail tubular protein B | Citrobacter phage SH1 | 0 | 798/801 (99.50%) | NP_009286665 |
| gp24 (QSJ04744) | 18611-19021 | + | 2 | 136 | 15.80 | 5.67 | internal virion protein A | Klebsiella phage 31 | 7e-96 | 134/136 (98.53%) | QGH73749 |
| gp25 (QSJ04745) | 19024-19617 | + | 1 | 197 | 21.25 | 9.85 | internal virion protein B | Yersinia phage phiYeO3-12 | 2e-139 | 197/197 (100%) | NP_052114 |
| gp26 (QSJ04746) | 19620-21863 | + | 3 | 747 | 85.08 | 5.32 | internal virion protein C | Klebsiella phage NL_ZS_3 | 0 | 743/747 (99.46%) | QNN97377 |
| gp27 (QSJ04747) | 21882-25844 | + | 3 | 1320 | 143.52 | 8.61 | internal virion protein D | Enterobacter phage E-3 | 0 | 1306/1320 (98.94%) | NP_009198337 |
| gp28 (QSJ04748) | 25892-27622 | + | 2 | 576 | 63.15 | 5.22 | tail fiber protein | Klebsiella phage vB_KpnP_Emp27 | 0 | 537/569 (94.38%) | QEG11854 |
| gp29 (QSJ04749) | 27586-28050 | + | 1 | 154 | 17.86 | 4.51 | ssDNA binding protein | Klebsiella phage vB_KpnP_Emp27 | 2e-75 | 110/137 (80.29%) | QEG11855 |
| gp30 (QSJ04750) | 28091-28294 | + | 2 | 67 | 7.41 | 6.72 | holin class II | Klebsiella phage vB_KpnP_Emp27 | 3e-40 | 67/67 (100%) | QEG11856 |
| gp31 (QSJ04751) | 28298-28564 | + | 2 | 88 | 9.91 | 4.46 | DNA packaging protein A | Klebsiella phage Patroon | 2e-56 | 88/88 (100%) | QBQ72912 |
| gp | (QS) | Accession | Start | End | Score1 | Score2 | Description | Organism | E-value | Identity (%) | Accession |
|----|------|-----------|-------|-----|--------|--------|-------------|----------|---------|--------------|-----------|
| gp32 | (QS)04752 | 28642-29106 | + | 1 | 154 | 17.29 | 9.98 | endopeptidase (Rz-like lysis protein) | Citrobacter phage SH1 | 3e-110 | 154/154 (100%) | YP_009286673 |
| gp33 | (QS)04753 | 29081-30844 | + | 2 | 587 | 66.72 | 5.17 | DNA packaging protein B | Klebsiella phage vB_KpnP_Emp27 | 0 | 587/587 (100%) | QEG11859 |
| gp34 | (QS)04754 | 32419-32877 | + | 1 | 152 | 17.01 | 7.86 | S-adenosyl-L-methionine hydrolase | Klebsiella phage Patroon | 4e-111 | 152/152 (100%) | QBQ72866 |
| gp35 | (QS)04755 | 32687-32884 | + | 2 | 65 | 7.36 | 10.71 | hypothetical protein | - | - | - |
| gp36 | (QS)04756 | 32941-33099 | + | 1 | 52 | 6.01 | 9.23 | hypothetical protein | Citrobacter phage SH2 | 8e-26 | 49/52 (94.23%) | YP_009289297 |
| gp37 | (QS)04757 | 33465-34574 | + | 3 | 369 | 42.53 | 8.55 | protein kinase | Klebsiella phage NL_ZS_3 | 0 | 325/369 (88.08%) | QNN97343 |
| gp38 | (QS)04758 | 34645-37299 | + | 1 | 884 | 98.81 | 7.51 | RNA polymerase | Klebsiella phage 31 | 0 | 881/884 (99.66%) | QGH73719 |
| gp39 | (QS)04759 | 37386-37658 | + | 3 | 90 | 10.34 | 9.89 | hypothetical protein | Enterobacter phage E-2 | 8e-59 | 89/90 (98.89%) | YP_009226208 |
| gp40 | (QS)04760 | 37891-38166 | + | 1 | 91 | 10.48 | 8.50 | dGTP triphosphohydrolase inhibitor | Klebsiella phage 31 | 3e-60 | 89/91 (97.80%) | QGH73722 |
Table S3. KPP-5 phage gene products are involved in five different modules.

| Modules                        | Protein                                      | ORFs    | Location     |
|-------------------------------|----------------------------------------------|---------|--------------|
| **Replication, regulation, transcription, and translation** | DNA ligase                                  | ORF 01  | 16-1062      |
|                               | Host RNA polymerase inhibitor                | ORF 05  | 2080-2316    |
|                               | Endonuclease                                 | ORF 06  | 3066-3527    |
|                               | DNA primase/helicase                         | ORF 08  | 4154-5854    |
|                               | DNA polymerase                               | ORF 11  | 6528-8642    |
|                               | HNS binding protein                          | ORF 12  | 8662-8961    |
|                               | HNS binding protein                          | ORF 13  | 8961-9170    |
|                               | host recBCD nuclease inhibitor               | ORF 14  | 9167-9346    |
|                               | Exonuclease                                  | ORF 15  | 9343-10254   |
|                               | ssDNA binding protein                        | ORF 29  | 27586-28050  |
|                               | S-adenosyl-L-methionine hydrolase            | ORF 34  | 32419-32877  |
|                               | Protein kinase                               | ORF 37  | 33465-34574  |
|                               | RNA polymerase                               | ORF 38  | 34645-37299  |
|                               | dGTP triphosphohydrolase inhibitor           | ORF 40  | 37891-38166  |
| **Host cell lysis**           | Endolysin                                    | ORF 07  | 3520-3975    |
|                               | Holin class II                               | ORF 30  | 28091-28294  |
|                               | Endopeptidase                                | ORF 32  | 28642-29106  |
| **Phage structure**           | Tail assembly protein                        | ORF 17  | 10970-11290  |
|                               | Head-to-tail joining protein                 | ORF 18  | 11301-12908  |
|                               | Capsid assembly protein                      | ORF 19  | 13010-13942  |
|                               | Major capsid protein                         | ORF 20  | 14099-15142  |
|                               | Major tail protein                           | ORF 21  | 15181-15414  |
|                               | Tail tubular protein A                       | ORF 22  | 15527-16117  |
|                               | Tail tubular protein B                       | ORF 23  | 16133-18538  |
|                               | Internal virion protein A                    | ORF 24  | 18611-19021  |
|                               | Internal virion protein B                    | ORF 25  | 19024-19617  |
|                               | Internal virion protein C                    | ORF 26  | 19620-21863  |
|                               | Internal virion protein D                    | ORF 27  | 21882-25844  |
|                               | Tail fiber protein                           | ORF 28  | 25892-27622  |
| **DNA packaging**             | DNA packaging protein A                      | ORF 31  | 28298-28564  |
|                               | DNA packaging protein B                      | ORF 33  | 29081-30844  |
| **Unknown functions**         | hypothetical protein                         | ORF 02  | 950-1126     |
|                               | hypothetical protein                         | ORF 03  | 1232-1489    |
|                               | DUF3310 domain-containing protein            | ORF 04  | 1489-1959    |
|                               | hypothetical protein                         | ORF 09  | 5574-5903    |
|                               | hypothetical protein                         | ORF 10  | 6176-6460    |
|                               | hypothetical protein                         | ORF 16  | 10442-10687  |
|                               | hypothetical protein                         | ORF 35  | 32687-32884  |
|                               | hypothetical protein                         | ORF 36  | 32941-33099  |
|                               | hypothetical protein                         | ORF 39  | 37386-37658  |
Table S4. Comparison of phages with BLASTN scores against the KPP-5 phage genome.

| Phage name          | Host                              | Phage Family     | Genus             | Location   | Collection date | Genome Length (kb) | Accession No. | Query Coverage | E-value | Genome Identity   |
|---------------------|-----------------------------------|------------------|-------------------|------------|-----------------|--------------------|---------------|----------------|---------|-------------------|
| Klebsiella phage    | Klebsiella pneumoniae             | Autographiviridae| Teetrevirus       | USA        | 2017            | 38,603             | MN013074      | 99%            | 0       | 16665/17507 (95.19%) |
| vB_KpnP_Emp27       |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Klebsiella phage    | Klebsiella pneumoniae             | Autographiviridae| Teetrevirus       | USA        | 2016            | 39,442             | MK608335      | 95%            | 0       | 22172/23377 (94.85%) |
| Patroon             |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Yersinia phage      | Yersinia enterocolitica           | Autographiviridae| Teetrevirus       | China      | 2012            | 39,210             | NC_047755     | 94%            | 0       | 23744/24777 (95.83%) |
| phiYe-F10           |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Enterobacter phage  | Enterobacter cloacae              | Autographiviridae| Teetrevirus       | Portugal   | 2014            | 39,142             | KP791807      | 94%            | 0       | 13978/14751 (94.76%) |
| E-4                 |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Klebsiella phage    | Klebsiella pneumoniae             | Autographiviridae| Teetrevirus       | -          | -               | 38,741             | MT813142      | 94%            | 0       | 12490/12955 (96.41%) |
| NL_ZS_3             |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Citrobacter phage   | Citrobacter freundii              | Autographiviridae| Teetrevirus       | -          | -               | 39,158             | NC_031092     | 93%            | 0       | 15703/17435 (90.07%) |
| SH2                 |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Escherichia phage   | Escherichia coli                  | Autographiviridae| Teetrevirus       | USA        | -               | 39,382             | NC_048063     | 93%            | 0       | 10890/11340 (96.03%) |
| LL2                 |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Serratia phage      | Serratia marcescens               | Autographiviridae| Teetrevirus       | Germany    | 2018            | 39,933             | MT419366      | 93%            | 0       | 10726/11340 (94.59%) |
| SALSA               |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Yersinia phage      | Yersinia enterocolitica           | Autographiviridae| Teetrevirus       | Canada     | -               | 38,646             | NC_025451     | 93%            | 0       | 8263/8721 (94.75%)  |
| vB_YenP_AP5         |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Klebsiella phage    | Klebsiella pneumoniae             | Autographiviridae| Teetrevirus       | China      | -               | 39,600             | MN149904      | 93%            | 0       | 9419/10986 (85.74%)  |
| 31                  |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Yersinia phage      | Yersinia enterocolitica           | Autographiviridae| Teetrevirus       | -          | -               | 39,600             | NC_001271     | 93%            | 0       | 7168/7485 (95.76%)  |
| phiYeO3-12          |                                   |                  |                   |            |                 |                    |               |                |         |                   |
| Phage                  | Host                | Family               | Genus       | Species          | Viral taxon       | Country/Year | Length | Accession   | Identity | Matches | Alignment | I.D.     | Unique ID        |
|-----------------------|---------------------|----------------------|-------------|------------------|-------------------|---------------|--------|-------------|----------|---------|-----------|----------|-----------------|
| Leclercia phage       | Leclercia adecarboxylata | Autographiviridae    | Teetrevirus | -                | -                 | 39,300        | NC_047843 | 92%         | 0        | 10895/11338 | (96.09%) |                |
| Citrobacter phage     | Citrobacter freundii | Autographiviridae    | Teetrevirus | -                | -                 | 39,434        | NC_031066 | 92%         | 0        | 10463/10886 | (96.11%) |                |
| Salmonella phage      | Salmonella enterica  | Autographiviridae    | Teetrevirus | South Korea      | -                 | 38,815        | NC_010807 | 92%         | 0        | 10461/10886 | (96.10%) |                |
| Serratia phage        | Serratia marcescens  | Autographiviridae    | Teetrevirus | -                | -                 | 39,631        | NC_047774 | 91%         | 0        | 10555/10992 | (96.02%) |                |
| Citrobacter phage     | Citrobacter freundii | Autographiviridae    | Teetrevirus | China 2013       | 38,625            | NC_028880     | 90%     | 0           | 12489/12988| (96.16%) |            |          |                |
| Enterobacter phage    | Enterobacter cloacae | Autographiviridae    | Teetrevirus | Portugal 2014    | 36,051            | NC_029102     | 89%     | 0           | 13978/14751| (94.76%) |            |          |                |
| Enterobacter phage    | Enterobacter cloacae | Autographiviridae    | Teetrevirus | Portugal 2014    | 31,522            | NC_028795     | 79%     | 0           | 14035/14572| (96.31%) |            |          |                |
| Salmonella phage      | Salmonella enterica  | Autographiviridae    | Teseptimavirus | South Korea 2016 | 38,554            | MN026740      | 79%     | 0           | 7543/11026 | (68.41%) |            |          |                |
| Escherichia phage     | Escherichia coli     | Autographiviridae    | Teseptimavirus | China 30          | -                 | 39,266        | NC_048078 | 78%         | 0        | 5183/7599  | (68.21%) |            |                |
| Serratia phage        | Serratia marcescens  | Autographiviridae    | Teseptimavirus | USA 2018         | 38,678            | MN098329      | 78%     | 0           | 6588/9633  | (68.39%) |            |          |                |
| Escherichia phage     | Escherichia coli     | Autographiviridae    | Teseptimavirus | China 2016       | 39,919            | NC_047895     | 78%     | 0           | 5257/7648  | (68.74%) |            |          |                |
| Escherichia phage     | Escherichia coli     | Autographiviridae    | Teseptimavirus | -                | -                 | 39,938        | AY264774 | 78%         | 0        | 5192/7603  | (68.29%) |            |                |
| Escherichia phage     | Escherichia coli     | Autographiviridae    | Berlinvirus   | -                | -                 | 40,829        | NC_028822 | 71%         | 0        | 2926/4006  | (73.04%) |            |                |
| Phage            | Host              | Family          | Genus            | Species          | Strain/Year | Accession Number | Identity (%) | Sequences Matched | Complete Matches (%) |
|------------------|-------------------|-----------------|------------------|------------------|-------------|------------------|--------------|-------------------|----------------------|
| *Salmonella* phage BSP161 | *Salmonella* enterica | Autographiviridae | Berlinvirus | - | - | 39,688 | NC_048105 | 71% | 3060/4241 (72.15%) |
| *Shigella* phage VB_Ship_A7 | *Shigella flexneri* | Autographiviridae | Berlinvirus | China | - | 40,058 | NC_048180 | 71% | 2892/3974 (72.77%) |
| *Escherichia* phage PhiV-1 | *Escherichia coli* | Autographiviridae | Berlinvirus | - | 2019 | 39461 | MT542512 | 71% | 2884/3964 (72.75%) |
| *Salmonella* phage BP12A | *Salmonella* enterica | Autographiviridae | Berlinvirus | Canada | 2003 | 39,696 | KM366096 | 71% | 2899/3988 (72.69%) |
| *Klebsiella* phage Henu1 | *Klebsiella pneumoniae* | Autographiviridae | Przondovirus | China | 2017 | 40,352 | NC_048138 | 69% | 4619/6644 (69.52%) |
| *Klebsiella* phage KN1-1 | *Klebsiella pneumoniae* | Autographiviridae | Przondovirus | Taiwan | - | 40,236 | NC_048129 | 69% | 4523/6482 (69.78%) |
| *Klebsiella* phage vB_KpnP_IME335 | *Klebsiella pneumoniae* | Autographiviridae | Przondovirus | China | - | 40,361 | MN176574 | 69% | 4412/6303 (70.00%) |
| *Klebsiella* phage Kund-ULIP54 | *Klebsiella pneumoniae* | Autographiviridae | Przondovirus | France | 2015 | 41,109 | MK380016 | 69% | 3994/5641 (70.80%) |
| *Klebsiella* phage vB_KpnP_IL33 | *Klebsiella pneumoniae* | Autographiviridae | Przondovirus | Poland | 2014 | 41,335 | NC_047782 | 69% | 3995/5643 (70.80%) |
| *Enterobacteria* phage DE3 | *Escherichia coli* | Siphoviridae | Lambdavirus | - | - | 42,925 | NC_042057 | 76.50% | 2031/2655 (6%) |
Table S5. The core genes of *Klebsiella* phage KPP-5, *Klebsiella* phage vB_KpnP_Emp27, *Klebsiella* phage Patroon, *Klebsiella* phage NL_ZS_3, and *Klebsiella* phage 31.

| Gene accession | Product | Accession Number | Product [Identities] | Accession Number | Product [Identities] | Accession Number | Product [Identities] | Accession Number | Product [Identities] | Accession Number | Product [Identities] |
|----------------|---------|------------------|-----------------------|------------------|-----------------------|------------------|-----------------------|------------------|-----------------------|------------------|-----------------------|
| gp1 (QSJ04721) | DNA ligase | QEG11869         | putative DNA ligase [345/348(99.14%)] | QBQ72877         | ATP-dependent DNA ligase [309/348(88.79%)] | QNN97348         | ATP-dependent DNA ligase [324/348(93.10%)] | QGH73723         | hypothetical protein [343/348(98.56%)] |
| gp3 (QSJ04723) | hypothetical protein | QEG11870         | hypothetical protein [75/85(88.24%)] | QBQ72879         | hypothetical protein [82/85(96.47%)] | QNN97349         | hypothetical protein [76/85(89.41%)] | QGH73724         | hypothetical protein [75/85(88.24%)] |
| gp4 (QSJ04724) | DUF3310 domain-containing protein | QEG11871         | DUF3310 domain-containing protein [154/156(98.72%)] | QBQ72880         | hypothetical protein [129/163(79.14%)] | QNN97350         | nucleotide kinase [154/159(96.86%)] | QGH73725         | hypothetical protein [153/156(98.08%)] |
| gp5 (QSJ04725) | Host RNA polymerase inhibitor, T7-like | QEG11873         | putative host RNA polymerase inhibitor [77/78(98.72%)] | QBQ72881         | inhibitor of host bacterial RNA polymerase [49/50(98%)] | QNN97351         | bacterial RNA polymerase inhibitor [77/78(98.72%)] | QGH73727         | host RNA polymerase inhibitor [77/78(98.72%)] |
| gp6 (QSJ04726) | endonuclease | QEG11875         | putative endonuclease [152/153(99.35%)] | QBQ72884         | endonuclease I [111/141(78.72%)] | QNN97353         | endonuclease I [152/153(99.35%)] | -               | -                     |
| gp7 (QSJ04727) | endolysin | QEG11876         | putative N-acetylmuramoyl-L-alanine amidase [150/151(99.34%)] | QBQ72885         | endolysin [146/151(96.69%)] | QNN97354         | endolysin [144/151(95.36%)] | QGH73730         | lysis [151/151(100%)] |
| gp8 (QSJ04728) | DNA primase/helicase | QEG11877         | putative primase/helicase [559/566(98.76%)] | QBQ72887         | DNA primase/helicase [540/566(95.41%)] | QNN97357         | primase/helicase protein [499/504(99.01%)] | QGH73732         | hypothetical protein [498/504(98.81%)] |
| gp10 (QSJ04730)| hypothetical protein | QEG11879         | hypothetical protein [92/94(97.87%)] | QBQ72889         | hypothetical protein [93/94(98.94%)] | QNN97359         | inhibitor of host toxin/antitoxin system [92/94(97.87%)] | QGH73734         | hypothetical protein [94/94(100%)] |
| gp11 (QSJ04731)| DNA polymerase | QEG11880         | putative DNA polymerase [695/704(98.72%)] | QBQ72890         | DNA polymerase [699/704(99.29%)] | QNN97360         | DNA-directed DNA polymerase [698/704(99.15%)] | QGH73735         | DNA polymerase [698/704(99.15%)] |
| gp | (QSJ04732) | HNS binding protein QEG11881 | putative HNS binding protein [88/99(88.89%)] | QBQ72891 | HNS binding protein [47/101(46.53%)] | QNN97361 | suppressor of silencing [44/101(43.56%)] | QGH73736 | putative HNS binding protein [98/99(98.99%)] |
|----|------------|-----------------------------|----------------------------------------------|----------|---------------------------------------|----------|--------------------------------------------|----------|--------------------------------------------|
| gp13 | (QSJ04733) | HNS binding protein QEG11882 | hypothetical protein [69/69(100%)] | QBQ72892 | hypothetical protein [68/69(98.55%)] | QNN97362 | hypothetical protein [66/69(95.65%)] | QGH73738 | putative HNS binding protein [67/69(97.10%)] |
| gp14 | (QSJ04734) | host recBCD nuclease inhibitor QEG11883 | hypothetical protein [32/49(65.31%)] | QBQ72893 | host recBCD nuclease inhibitor [42/59(71.19%)] | QNN97363 | inhibitor of recBCD nuclease [42/59(71.19%)] | QGH73739 | inhibitor of recBCD nuclease [42/59(71.19%)] |
| gp15 | (QSJ04735) | exonuclease QEG11884 | putative exonuclease [295/303(97.36%)] | QBQ72894 | exonuclease [302/303(99.67%)] | QNN97364 | exonuclease [297/303(98.02%)] | QGH73740 | exonuclease [297/303(98.02%)] |
| gp16 | (QSJ04736) | hypothetical protein QEG11886 | hypothetical protein [62/64(96.88%)] | QBQ72896 | hypothetical protein [79/81(97.53%)] | QNN97366 | hypothetical protein [79/81(97.53%)] | QGH73741 | hypothetical protein [79/81(97.53%)] |
| gp17 | (QSJ04739) | tail assembly protein QEG11888 | putative tail assembly protein [97/113(85.84%)] | QBQ72898 | host specificity protein B [105/106(99.06%)] | QNN97368 | virion assembly protein [101/106(95.28%)] | QGH73743 | host specificity protein [97/106(91.51%)] |
| gp18 | (QSJ04737) | head-to-tail joining protein QEG11889 | putative head-to-tail joining protein [532/535(99.44%)] | QBQ72899 | head-to-tail joining protein [534/535(99.81%)] | QNN97369 | collar, head-to-tail connector protein [534/535(99.81%)] | QGH73744 | hypothetical protein [532/535(99.44%)] |
| gp19 | (QSJ04738) | capsid assembly protein QEG11890 | putative capsid assembly protein [293/310(94.52%)] | QBQ72900 | capsid assembly protein [299/310(96.45%)] | QNN97370 | capsid assembly scaffolding protein [305/310(98.39%)] | QGH73745 | hypothetical protein [303/310(97.74%)] |
| gp20 | (QSJ04740) | major capsid protein QEG11891 | putative minor capsid protein [335/344(97.38%)] | QBQ72901 | major capsid protein [342/349(97.99%)] | QNN97371 | major capsid protein [346/347(99.71%)] | QGH73746 | capsid and scaffold protein [334/343(97.38%)] |
| gp21 | (QSJ04741) | major tail protein QEG11847 | putative minor capsid protein [377/382(92.66%)] | - | - | - | - | - |
| gp22 | (QSJ04742) | tail tubular protein A QEG11848 | putative tail tubular protein A [193/196(98.47%)] | QBQ72903 | tail tubular protein A [193/196(98.47%)] | QNN97373 | non-contractile tail tubular protein [195/196(99.49%)] | QGH73747 | tail tubular protein A [194/196(98.98%)] |
| gp/23 (QSJ04743) | tail tubular protein B | QEG11849 | putative tail tubular protein B [781/801(97.50%)] | QBQ72904 | tail tubular protein B [792/801(98.63%)] | QNN97374 | non-contractile tail tubular protein [794/801(99.13%)] | QGH73748 | hypothetical protein [795/801(99.25%)] |
| gp/24 (QSJ04744) | internal virion protein A | QEG11850 | putative internal virion protein A [133/136(97.06%)] | QBQ72905 | internal virion protein A [132/136(97.06%)] | QNN97375 | scaffold protein [131/136(96.32%)] | QGH73749 | internal (core) protein [134/136(98.53%)] |
| gp/25 (QSJ04745) | internal virion protein B | QEG11851 | putative internal virion protein B [191/197(98.98%)] | QBQ72906 | internal virion protein B [195/197(98.98%)] | QNN97376 | DNA ejectosome component [193/197(97.97%)] | QGH73750 | protein inside capsid B [196/197(99.49%)] |
| gp/26 (QSJ04746) | internal virion protein C | QEG11852 | putative internal virion protein C [734/747(98.26%)] | QBQ72907 | internal virion protein C [737/747(98.66%)] | QNN97377 | DNA ejectosome component [743/747(99.46%)] | QGH73751 | hypothetical protein [596/747(79.79%)] |
| gp/27 (QSJ04747) | internal virion protein D | QEG11853 | putative internal virion protein D [1301/1320(98.56%)] | QBQ72908 | internal virion protein D [1297/1320(98.26%)] | QNN97332 | DNA ejectosome component [1282/1320(97.12%)] | QGH73752 | hypothetical protein [1080/1315(82.13%)] |
| gp/28 (QSJ04748) | tail fiber protein | QEG11854 | putative tail fiber protein [537/569(94.38%)] | QBQ72909 | tail fiber protein [274/528(51.89%)] | QNN97333 | non-contractile tail fiber protein [215/305(70.49%)] | QGH73753 | tail fiber protein [275/530(51.89%)] |
| gp/29 (QSJ04749) | ssDNA binding protein | QEG11855 | putative ssDNA binding protein [110/137(80.29%)] | QBQ72910 | hypothetical protein [40/107(37.38%)] | QNN97334 | hypothetical protein [46/105(43.81%)] | QGH73754 | hypothetical protein [41/107(38.32%)] |
| gp/30 (QSJ04750) | holin class II | QEG11856 | putative class II holin [67/67(100%)] | QBQ72911 | holin [60/67(89.55%)] | QNN97335 | class II holin [67/67(100%)] | QGH73755 | class II holin [67/67(100%)] |
| gp/31 (QSJ04751) | DNA packaging protein A | QEG11857 | putative DNA packaging protein [87/88(98.86%)] | QBQ72912 | DNA packaging protein A [88/88(100%)] | QNN97336 | terminase small subunit [87/88(98.86%)] | QGH73756 | DNA packaging protein A [88/88(100%)] |
| gp/32 (QSJ04752) | endopeptidase (Rz-like lysis protein) | QEG11858 | putative endopeptidase [132/132(100%)] | QBQ72913 | I-spanin [149/150(99.33%)] | QNN97337 | endopeptidase Rz [150/150(100%)] | QGH73757 | endopeptidase Rz [86/148(58.11%)] |
| gp/33 (QSJ04753) | DNA packaging protein B | QEG11859 | putative DNA packaging protein [587/587(100%)] | QBQ72915 | DNA packaging protein B [582/587(99.15%)] | QNN97338 | terminase large subunit [587/587(100%)] | QGH73759.1 | DNA packaging protein [578/587(98.47%)] |
| gp/34 (QSJ04754) | S-adenosyl-L-methionine hydrolase | QEG11860 | putative adenosyl-L-methionine | QBQ72866 | S-adenosyl-L-methionine | QNN97340 | S-adenosyl-L-methionine | QGH73714 | S-adenosyl-L-methionine |
| gp36 (QSJ04756) | hypothetical protein | QEG11861 | hypothetical protein [47/52(90.38%)] | QBQ72868 | hypothetical protein [48/52(92.31%)] | QNN97341 | hypothetical protein [45/52(86.54%)] | - | - |
| gp37 (QSJ04757) | protein kinase | QEG11864 | putative protein kinase [313/370(84.59%)] | QBQ72871 | protein kinase [314/370(84.86%)] | QNN97343 | serine/threonine kinase [325/369(88.08%)] | QGH73718 | hypothetical protein [297/370(80.27%)] |
| gp38 (QSJ04758) | RNA polymerase | QEG11865 | putative RNA polymerase [879/884(99.43%)] | QBQ72872 | RNA polymerase [875/884(98.98%)] | QNN97344 | DNA-directed RNA polymerase [879/884(99.43%)] | QGH73719 | DNA-directed RNA polymerase [881/884(99.66%)] |
| gp39 (QSJ04759) | hypothetical protein | QEG11866 | hypothetical protein [87/90(96.67%)] | QBQ72873 | hypothetical protein [86/90(95.56%)] | QNN97345 | hypothetical protein [28/74(37.84%)] | QGH73720 | hypothetical protein [87/90(96.67%)] |
| gp40 (QSJ04760) | dGTP triphosphohydrolase inhibitor | QEG11868 | putative dGTP triphosphohydrolase inhibitor [87/91(95.60%)] | QBQ72875 | host dGTP triphosphohydrolase inhibitor [86/90(95.56%)] | QNN97347 | hypothetical protein [89/91(97.80%)] | QGH73722 | dGTP triphosphohydrolase inhibitor [89/91(97.80%)] |