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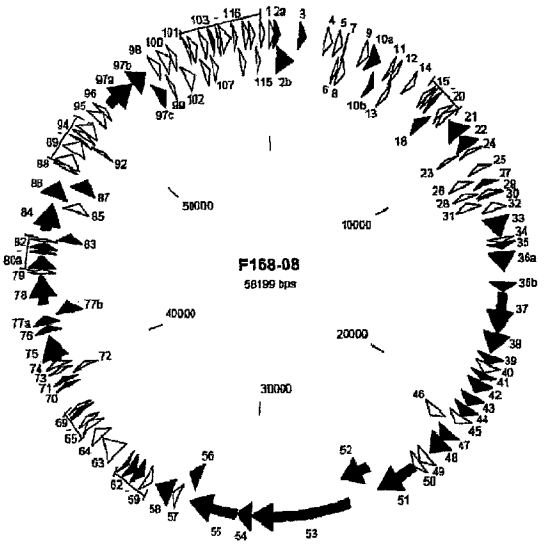

orf	Putative function
2a-2b	RNA ligase
3	regulation of muramidase-2 export
18	endodeoxyribonuclease
22	endonuclease
27	ribonucleoside-diphosphate reductase class Ib glutaredoxin subunit
33	terminase small subunit
35	holin
36a-36b	terminase large subunit
37	portal protein
38	virion morphogenesis
39	ribonuclease phage related protein
41	major head protein
42	major capsid protein
43	major tail protein
48	major tail protein
51	tail length tape measure protein
52	minor capsid protein

orf	Putative function
53	tail component
54	phage minor structural protein
55	minor structural protein
56	host interaction protein
58	CHAP endolysin
61	endonuclease
67	tRNA-Trp
68	tRNA-Ser
75	DNA primase
76	DNA binding protein
77a-77b	DNA replication
78	DNA helicase
80a-80b	C5 methylase
83	endonuclease
86	crossover junction endodeoxyribonuclease
87	nucleoside/nucleotide kinase
97a-97c	DNA polymerase I

(57) Abrégé/Abstract:
The present invention is directed to the field of phage therapy for the treatment and control of bacterial infections. In particular, the present invention is directed to the novel bacteriophages F1245/05, F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06 and F91a/06, isolated polypeptides thereof, compositions comprising one or more of the novel bacteriophages and/or isolated polypeptides and methods for the treatment and prevention of bacterial infection, either alone or in combination with other antibacterial therapies, e.g., antibiotics or other phage therapies.

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ABSTRACT

The present invention is directed to the field of phage therapy for the treatment and control of bacterial infections. In particular, the present invention is directed to the novel bacteriophages F1245/05, F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06 and F91a/06, isolated polypeptides thereof, compositions comprising one or more of the novel bacteriophages and/or isolated polypeptides and methods for the treatment and prevention of bacterial infection, either alone or in combination with other antibacterial therapies, e.g., antibiotics or other phage therapies.

ANTIBACTERIAL PHAGE, PHAGE PEPTIDES AND METHODS OF USE THEREOF

1. RELATED APPLICATIONS

[0001] This International Application claims priority to U.S. Provisional Application Ser. No. 61/150,585, filed February 6, 2009, entitled "Antibacterial Phage and Uses Thereof" and to U.S. Provisional Application Ser. No. 61/218,345, filed June 18, 2009, entitled "Antibacterial Phage, Phage Peptides and Methods of Use Thereof".

2. FIELD OF THE INVENTION

[0002] The present invention is directed to the field of phage therapy for the treatment and control of bacterial infections. In particular, the present invention is directed to the novel bacteriophages F1245/05, F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06 and F91a/06, isolated polypeptides thereof, compositions comprising one or more of the novel bacteriophages and/or isolated polypeptides and methods for the treatment and prevention of bacterial infections caused by *Acinetobacter baumannii*, *Enterococcus faecalis*, *E. faecium*, *Pseudomonas aeruginosa*, and/or *Staphylococcus aureus*, either alone or in combination with other antibacterial therapies, *e.g.*, antibiotics or other phage therapies.

3. BACKGROUND

[0003] Bacteriophages (phage) are viruses that specifically infect and lyse bacteria. Phage therapy, a method of using whole phage viruses for the treatment of bacterial infectious diseases, was introduced in the 1920s by Felix d'Herelle. Initially, phage therapy was vigorously investigated and numerous studies were undertaken to asses the potential of phage therapy for the treatment of bacterial infection in humans and animals. Early success prompted the development of multiple commercial phage preparations. For example, in 1940 Eli Lilly Company produced 7 phage products for human use, including phage preparations for treating different sicknesses caused by *Staphylococcus* sp., *E. coli* and other pathogenic bacteria. These preparations were used to treat infections that cause abscesses, purulent wounds, vaginitis, acute chronic upper-respiratory tract infections and mastoid infections.

[0004] However, with the development of antibiotics in the 1940s, interest in phage-based therapeutics declined in the Western world. One of the most important factors that contributed to this decline was the lack of standardized testing protocols and methods of production. The failure to develop industry wide standards for the testing of phage therapies interfered with the documentation of study results, leading to a perceived lack of efficacy as well as problems of credibility regarding the value of phage therapy. Further, problems related to the production of phage samples/specimens complicated initial study and research. Diverse stabilizers and preservatives were initially used in attempts to increase the viability of the phage therapeutics. However, because the biology of both the phage and the various stabilizers were poorly understood, many of the ingredients added in an attempt to prolong the viability of phage preparations proved to be either toxic to humans or to negatively impact long term storage. Another problem related to phage production was the purity grade of the commercial preparations of these viruses. At the time, phage therapy preparations generally consisted of raw lysates of host bacteria that had been treated with the phage of interest. Thus, many preparations contained what are now recognized as undesired bacterial components, *e.g.*, endotoxins. Accordingly, adverse events were often associated with the preparations, particularly in patients receiving them intravenously. Nevertheless, in Eastern Europe and the former Soviet Union, where access to antibiotics was limited, the development and use of phage therapy continued jointly with, or in place of, antibiotics.

[0005] With the rise of antibiotic resistant strains of bacteria, however, interest in phage-based therapeutics has returned in the Western world. Even though novel classes of antibiotics may be developed, the prospect that bacteria will eventually develop resistance to the new drugs has intensified the search for non-chemotherapeutic means for controlling, preventing, and treating bacterial infections. There are three main phage-based strategies for using phage therapy in a clinical environment: 1) the administration of virulent phages; 2) the use of endolysins or purified lysins encoded by bacteriophages 3) the use of structural proteins of the identified phages as metabolic inhibitors of key enzymes for the synthesis of bacterial peptidoglycan.

[0006] There is therefore a need to develop novel bacteriophages and phage products as potential therapeutic and prophylactic agents for use *in vivo* to eliminate pathogenic bacteria. In particular, there is a need for bacteriophages capable of lysing nosocomial bacteria, including *Acinetobacter baumannii*, *Enterococcus faecalis*, *E. faecium*, *Pseudomonas aeruginosa*, and/or

Staphylococcus aureus. Because most phage and phage peptides studied to date exhibit activity often restricted to the related species, or subspecies, of bacteria from which they are isolated, the novel phage-based therapies may find particular use in the hospital setting, selectively targeting nosocomial pathogens without affecting the normal surrounding flora.

4. SUMMARY OF THE INVENTION

[0007] The present invention is directed to isolated bacteriophages and to isolated antibacterial polypeptides of bacteriophage origin for the treatment, prevention, or management of conditions associated with infection by Gram-positive or Gram-negative bacteria. In particular, the isolated bacteriophage or polypeptides of the invention may be used in pharmaceutical compositions for the treatment, prophylaxis, or management of infection by nosocomial pathogens, *e.g.*, Gram-positive bacteria including but not limited to *Enterococcus faecalis, E. faecium, E. hirae, E. avium, Staphylococcus aureus, S. epidermidis, S. auricularis, S. capitis, S. haemolyticus, S. hominis, S. saprophyticus, S. simulans,* and *S. xylosis*; and/or Gram-negative bacteria including but not limited to *Acinetobacter baumannii*, and *Pseudomonas aeruginosa*. In certain embodiments, the pharmaceutical compositions of the invention are of use in the treatment of conditions associated with infection by antibiotic resistant strains of bacteria, *e.g.*, methicillin resistant strains of *Staphylococcus aureus* (MRSA). In particular embodiments, the isolated bacteriophages or polypeptides of the invention are used for the topical treatment of infection by nosocomial pathogens in a subject in need thereof. In other embodiments, the isolated bacteriophages or polypeptides of the invention are used for the diagnosis of the infective agent in a sample (*e.g.*, tissue, blood, urine, sputum sample) derived from a patient. In other embodiments, the isolated bacteriophages or polypeptides of the invention are used as a prophylactic disinfectant or anti-infective for the preparation of solid surfaces, including skin or other epidermal surfaces.

[0008] In certain embodiments, the invention provides an isolated bacteriophage, F168/08 or F170/08, having a genome comprising the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, respectively, and exhibiting antibacterial activity against one or more strains of *Enterococcus faecalis* and/or *E. faecium*. In other embodiments, the invention provides an isolated bacteriophage, F770/05, having a genome comprising the nucleic acid sequence of SEQ ID NO:3 and exhibiting antibacterial activity against one or more strains of *Pseudomonas aeruginosa*. In yet other embodiments, the invention provides the isolated bacteriophage

F197/08, F86/06, F87s/06 or F91a/06 having a genome comprising the nucleic acid sequence of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7, respectively, and exhibiting antibacterial activity against one or more strains of *Staphylococcus aureus*. In still yet other embodiments, the invention provides an isolated bacteriophage, F1245/05, having a genome comprising the nucleic acid sequence of SEQ ID NO:760 and exhibiting antibacterial activity against one or more strains of *Acinetobacter baumannii*.

[0009] The invention also encompasses isolated bacteria infected with one or more bacteriophage of the invention. In specific embodiments, the invention provides an isolated *E. faecalis* infected with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:1 and/or SEQ ID NO:2. In other embodiments, the invention provides an isolated *E. faecium* infected with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:1 and/or SEQ ID NO:2. In still other embodiments, the invention provides an isolated *P. aeruginosa* infected with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:3. In yet other embodiments, the invention provides an isolated *S. aureus* infected with one or more bacteriophages having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and/or SEQ ID NO:7. In still yet other embodiments, the invention provides an isolated *A. baumannii* infected with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:760.

[0010] The present invention encompasses polypeptides isolated from bacteriophage F1245/05, F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06 and/or F91a/06, which polypeptides exhibit antibacterial activity against one or more species or strains of Gram-positive or Gram-negative bacterium, *e.g.*, *A. baumannii*, *E. faecalis*, *E. faecium*, *P. aeruginosa* and/or *S. aureus*. In specific embodiments, the polypeptides of the invention isolated or derived from F168/08 or F/170/08 exhibit antibacterial or antimicrobial activity, *e.g.*, lytic killing activity, against at least *E. faecalis* and/or *E. faecium*; those isolated or derived from F770/05 against at least *P. aeruginosa*; those isolated or derived from F197/08, F86/06, F87s/06 or F91a/06 against at least *S. aureus*; and those isolated or derived from F1245/05 against at least *A. baumannii*.

[0011] In certain embodiments, a polypeptide of the invention comprises or consists of an isolated endolysin or fragment thereof (*e.g.*, a CHAP domain) that exhibits antibacterial activity against one or more species or strains of bacteria, *e.g.*, Gram-positive bacteria and/or Gram-

negative bacteria such as *A. baumannii*, *E. faecalis*, *E. faecium*, *P. aeruginosa* and/or *S. aureus*. In specific embodiments, the polypeptide of the invention is an isolated lysin protein, *e.g.*, an endolysin or tail lysin, comprising or consisting of the amino acid sequence SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712. In yet still other embodiments, the invention provides a polypeptide comprising or consisting of an amino acid sequence selected from the group consisting of SEQ ID NO: 761 to SEQ ID NO: 816.

[0012] In other embodiments, a polypeptide of the invention comprises a fragment, variant or derivative of SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712, wherein said fragment, variant or derivative has antibacterial activity or antimicrobial activity, *e.g.*, lytic killing activity, against one or more strains of *E. faecalis*, *E. faecium*, *P. aeruginosa* and/or *S. aureus*. In specific examples in accordance with this embodiment, the variant, fragment or derivative of the amino acid sequence of SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202 and/or SEQ ID NO:203 exhibits antibacterial or antimicrobial activity (*e.g.*, lytic killing activity) against one or more strains of *E. faecalis* and/or *E. faecium*. In other examples in accordance with this embodiment, the variant, fragment or derivative of the amino acid sequence of SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641 and/or SEQ ID NO:712 exhibits antibacterial or antimicrobial activity (*e.g.*, lytic killing activity) against one or more strains of *S. aureus*.

[0013] In specific embodiments, the isolated polypeptide of the invention comprises or consists of the CHAP domain of SEQ ID NO:68, SEQ ID NO:446, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712. In certain embodiments, the isolated polypeptide comprises or consists of the CHAP domain of SEQ ID NO:68, SEQ ID NO:446, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712, e.g., having the amino acid sequence of SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758 or SEQ ID NO:759, respectively. In other embodiments, a polypeptide of the invention comprises a fragment, variant or derivative of SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758 or SEQ ID NO:759, wherein said fragment, variant or derivative has antibacterial activity or antimicrobial activity, *e.g.*, lytic killing activity, against at least one or more strains of *E. faecalis*, *E. faecium*, *P. aeruginosa* and/or *S. aureus*. In yet still other embodiments, a polypeptide of the invention comprises a fragment, variant or

derivative of SEQ ID NO: 761 to SEQ ID NO: 816, wherein said fragment, variant or derivative has antibacterial activity or antimicrobial activity, *e.g.*, lytic killing activity, against at least one or more strains of *A. baumannii*.

[0014] In other embodiments, a polypeptide of the invention comprises or consists of an isolated tail length tape measure protein or tail protein (*e.g.*, tail component, tail fiber protein, adsorption associated tail protein), or fragment thereof, having a biologic function associated with the bacteriophage from which it is derived, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against at least one or more species or strains of *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii*. In specific embodiments, the polypeptide of the invention is an isolated tail length tape measure protein or tail proteins comprising or consisting of the amino acid sequence SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704 or SEQ ID NO:795. In other embodiments, a polypeptide of the invention comprises a fragment, variant or derivative of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704 or SEQ ID NO:795, wherein said fragment, variant or derivative exhibits a biologic function associated with the bacteriophage from which it is derived, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii*.

[0015] In certain embodiments, the invention encompasses a variant, fragment or derivative of the amino acid sequence of SEQ ID NO:61 or SEQ ID NO:63 that exhibits a biologic function associated with the bacteriophage having a genome comprising or consisting of the nucleic acid

sequence SEQ ID NO:1, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *E. faecalis* and/or *E. faecium*. In other embodiments, the invention encompasses a variant, fragment or derivative of the amino acid sequence of SEQ ID NO:204 or SEQ ID NO:214 that exhibits a biologic function associated with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:2, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *E. faecalis* and/or *E. faecium*.

[0016] In certain embodiments, the invention encompasses a variant, fragment or derivative of the amino acid sequence of SEQ ID NO:435 or SEQ ID NO:438 that exhibits a biologic function associated with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:3, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *P. aeruginosa*.

[0017] In certain embodiments, the invention encompasses a variant, fragment or derivative of the amino acid sequence of SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538 or SEQ ID NO:539 that exhibits a biologic function associated with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:4, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *S. aureus*. In other embodiments, the invention encompasses a variant, fragment or derivative of the amino acid sequence of SEQ ID NO:567 or SEQ ID NO:568 that exhibits a biologic function associated with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:5, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *S. aureus*. In yet other embodiments, the invention encompasses a variant, fragment or derivative of the amino acid sequence of SEQ ID NO:632 or SEQ ID NO:633 that exhibits a biologic function associated with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:6, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *S. aureus*. In yet other embodiments, the invention encompasses a variant, fragment or derivative of the amino acid sequence of SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703 or

SEQ ID NO:704 that exhibits a biologic function associated with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:7, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *S. aureus*.

[0018] In certain embodiments, the invention encompasses a variant, fragment or derivative of the amino acid sequence of SEQ ID NOS: 761-816 that exhibits a biologic function associated with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:760, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), which function is directed against one or more strains of *A. baumannii*.

[0019] In certain embodiments, the invention provides for isolated polypeptides that exhibit antimicrobial or antibacterial activity (*e.g.*, lytic killing activity) against one or more strains of bacteria (*e.g.*, Gram-positive bacteria (*e.g.*, *E. faecalis*, *E. faecium*, *S. aureus*), Gram-negative bacteria (*e.g.*, of *A. baumannii*, *P. aeruginosa*) or bacteria not classified as either Gram-positive or Gram-negative), wherein the isolated polypeptides have an amino acid sequence with at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity to a second amino acid sequence of the same length (*i.e.*, consisting of the same number of residues), which second amino acid sequence is SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:575, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:641, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:712, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NOS:761-816, and/or a fragment thereof.

[0020] The invention further provides isolated polypeptides comprising or consisting of the amino acid sequence of any of SEQ ID NOS:8-130, SEQ ID NOS:131-343, SEQ ID NOS:344-438, SEQ ID NOS:439-553, SEQ ID NOS:554-616, SEQ ID NOS:617-681, SEQ ID NOS:682-759, and SEQ ID NOS:761-816. In other embodiments, isolated polypeptides of the invention

recombinantly fused or chemically conjugated (*e.g.*, covalent or non-covalent conjugation) to therapeutic agents (*e.g.*, heterologous polypeptides or small molecules) are provided.

[0021] The invention also encompasses polynucleotides that encode the polypeptides of the invention. In a specific embodiment, the invention provides an isolated nucleic acid comprising a nucleic acid sequence encoding the polypeptide of any of SEQ ID NOS:8-130, SEQ ID NOS:131-343, SEQ ID NOS:344-438, SEQ ID NOS:439-553, SEQ ID NOS:554-616, SEQ ID NOS:617-681, SEQ ID NOS:682-759, and SEQ ID NOS 761-816. In other embodiments, the invention provides an isolated nucleic acid comprising a nucleic acid sequence encoding the polypeptide of any of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:575, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:641, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:712, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NOS 761-816, or active fragment, variant or derivative thereof, which polypeptide or active fragment, variant or derivative exhibits a biologic function associated with the bacteriophage from which it is isolated and/or derived, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity). The invention also relates to a vector comprising said nucleic acid. In one specific embodiment, said vector is an expression vector. The invention further provides host cells containing a vector comprising polynucleotides encoding the polypeptides of the invention.

[0022] The present invention encompasses methods for the production of polypeptides of the invention or active fragments thereof, in particular for use in pharmaceutical compositions, *i.e.*, antimicrobial compositions. For example, the polypeptides of the invention may be isolated directly from cell cultures (e.g., bacterial cell cultures) infected with bacteriophage F1245/05, F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06 or F91a/06. Alternatively, the polypeptides of the present invention may be derived by recombinant means using expression vectors comprising nucleic acid sequence encoding polypeptides of the invention, *e.g.*, SEQ ID

NO:61, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:575, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:641, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:712, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NOS:761-816, or active fragments, derivatives or variants thereof. The polypeptides of the invention or fragments thereof can be produced by any method known in the art for the production of a polypeptide, in particular, by chemical synthesis or by recombinant expression techniques. In specific embodiments, the invention relates to a method for recombinantly producing a phage protein, *e.g.*, a lysin protein, tail protein or active fragment, variant or derivative thereof, said method comprising: (i) culturing under conditions suitable for the expression of said protein in a medium, a host cell containing a vector comprising a nucleic acid sequence encoding the amino acid sequence SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:575, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:641, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:712, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NOS:761-816, or fragment thereof; and (ii) recovery of said protein from said medium. In certain embodiments, the nucleic acid sequence encoding the polypeptide of the invention is operably linked to a heterologous promoter.

[0023] The invention also encompasses methods for the diagnosis of the causative agent in a clinical presentation of bacterial infection. The isolated bacteriophages or polypeptides of the invention may be used to aid in the determination of species of bacteria in a patient sample by

establishing susceptibility of the bacteria in the sample to the bacteriophages and/or polypeptides of the invention. Such methods further encompass methods of evaluation of antibacterial activity of the isolated bacteriophages and/or polypeptides of the invention. Antibacterial activity of the bacteriophages or the polypeptides of the invention, or susceptibility of an unknown sample to such activity, may be assessed by any method known in the art and/or described herein. In certain embodiments, antibacterial activity and/or susceptibility is assessed by culturing known bacteria and/or patient tissue, blood, fluid or swab samples according to standard techniques (*e.g.*, in liquid culture or on agar plates), contacting the culture with bacteriophages and/or polypeptides of the invention and monitoring cell growth after said contacting. For example, in a liquid culture, the bacteria (*e.g.*, *A. baumannii*, *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*) may be grown to a optical density ("OD") representative of a mid-point in exponential growth of the culture; the culture is exposed to one or more concentrations of one or more bacteriophages and/or polypeptides of the invention and the OD is monitored relative to a control culture. Decreased OD relative to a control culture is representative of a bacteriophage and/or polypeptide exhibiting antibacterial activity (*e.g.*, exhibits lytic killing activity) against the tested sample or bacterial species and/or strain in the culture. Similarly, bacterial colonies can be allowed to form on an agar plate, the plate exposed to a bacteriophage or polypeptide of the invention, and subsequent growth of the colonies evaluated relative to control plates. Decreased size of colonies, or decreased total numbers of colonies, indicates a bacteriophage and/or polypeptide with antibacterial activity against the tested sample and/or cultured species or strain.

[0024] The present invention is also directed to pharmaceutical compositions comprising or consisting of a bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7, or SEQ ID NO:760. In certain embodiments, the pharmaceutical composition of the invention comprises a bacteriophage having the genome comprising or consisting of the nucleic acid sequence SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7, or SEQ ID NO:760 in addition to one or more other bacteriophages. The one or more other bacteriophages may be one or more bacteriophages of the invention (*e.g.*, having a genome comprising or consisting of a nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7, or SEQ ID NO:760), one or more strains thereof, or may be one or

more bacteriophages known in the art. Further, the one or more bacteriophages in the pharmaceutical composition of the invention may target the same or different species or strains of bacteria. In certain embodiments, the pharmaceutical compositions comprising one or more bacteriophages of the invention further comprise one or more polypeptides of the invention and/or other phage products as described herein or known in the art.

[0025] In certain embodiments, the invention provides pharmaceutical compositions comprising polypeptides, or active fragments thereof, in particular those having anti-microbial and/or antibacterial activity, isolated from bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 SEQ ID NO:7, and/or SEQ ID NO:760. In specific embodiments, the pharmaceutical compositions of the invention comprise one or more polypeptides having an amino acid sequence of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:575, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:641, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:712, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759 or SEQ ID NOS:761-816. In other embodiments, the pharmaceutical compositions of the invention comprise a polypeptide that is a variant, derivative or fragment of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:575, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:641, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:712, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID

NO:759, or SEQ ID NOS:761-816 wherein the variant, derivative or fragment retains a biologic function of the polypeptide from which it is derived, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), preferably against one or more strains of *A. baumannii, E. faecalis, E. faecium, P. aeruginosa* and/or *S. aureus.*

[0026] The pharmaceutical compositions of the invention may additionally comprise a pharmaceutically acceptable carrier, excipient, or stabilizer. In certain embodiments, the pharmaceutical compositions of the invention are antibiotic compositions (in that they exhibit antibacterial activity) or therapeutic compositions for the treatment, prevention, and/or amelioration of symptoms of a disease or disorder associated with infection by bacteria in a subject in need thereof. In specific embodiments, the pharmaceutical compositions of the invention are antibacterial compositions or therapeutic compositions for the treatment, prevention, and/or amelioration of symptoms of a disease or disorder associated with infection by *A. baumannii, E. faecalis, E. faecium, P. aeruginosa* and/or *S. aureus.* In certain embodiments, the subject receiving a pharmaceutical composition of the invention is a mammal (*e.g.*, bovine, ovine, caprine, equid, primate (*e.g.*, human), rodent, lagomorph or avian (*e.g.*, chicken, duck, goose)).

[0027] The present invention provides for methods for the treatment or prevention of bacterial infection comprising administering to a subject in need thereof a pharmaceutical composition comprising one or more bacteriophages or phage products (*e.g.*, an isolated bacteriophage polypeptide or active fragment, variant or derivative thereof), optionally in addition to one or more other bacteriophages or other phage products, as described herein. In the context of the present invention, "treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to eliminate, lessen, decrease the severity of, slow the progression of or delay or prevent the symptoms or underlying cause (*e.g.*, bacterial infection) associated with the pathological condition or disorder. The pharmaceutical compositions of the present invention may be used in the treatment or management of infections associated with any bacterial infection, including, but not limited to *A. baumanni, S. aureus, S. epidermidis, S. auricularis, S. capitis, S. haemolyticus, S. hominis, S. saprophyticus, S. simulans, S. xylosis, M. luteus, B. subtilis, B. pumilus, E. faecalis, E. hirae, E. faecium, E. avium, P. aeruginosa* and combinations thereof. In certain embodiments, the pharmaceutical compositions may be used to treat conditions or disorders associated with bacterial infections including, but

not limited to, post-operative endophtalmitis, endocarditis, infections of the central nervous system, pneumonia, osteomylelitis, wound infections (*e.g.*, diabetic foot ulcers), mastitis, septicemia, food poisoning and meningitis and/or other conditions associated with nosocomial bacterial infections.

[0028] In certain embodiments, the invention provides for the use of a bacteriophage or an isolated phage product (*e.g.*, an isolated phage polypeptide or active fragment, variant or derivative thereof) as a single agent therapy. In other embodiments, the invention provides for the use of a bacteriophage, or phage product (*e.g.*, an isolated phage polypeptide or active fragment, variant or derivative thereof), in combination with a standard or experimental treatment for bacterial infection. Such combination therapy may enhance the efficacy of the standard or experimental treatment. Examples of therapeutic agents that are particularly useful in combination with a polypeptide of the invention are anti-inflammatory agents, standard chemotherapeutic antibiotic agents (*e.g.*, penicillin, synthetic penicillins, bacitracin, methicillin, cephalosporin, polymyxin, cefaclor, Cefadroxil, cefamandole nafate, cefazolin, cefixime, cefmetazole, cefonioid, cefoperazone, ceforanide, cefotanme, cefotaxime, cefotetan, cefoxitin, cefpodoxime proxetil, ceftazidime, ceftizoxime, ceftriaxone, cefriaxone moxalactam, cefuroxime, cephalexin, cephalosporin C, cephalosporin C sodium salt, cephalothin, cephalothin sodium salt, cephapirin, cephradine, cefuroximeaxetil, dihydratecephalothin, moxalactam, loracarbef mafate and chelating agents), local anesthetic agents, and/or corticosteroids. In yet another embodiment, the compositions of the present invention may be combined with one or more bacteriophages or phage products known in the art. The combination therapies encompassed by the invention may be formulated into a single pharmaceutical composition or may be administered in separate compositions, but as part of an overall treatment regimen.

[0029] The pharmaceutical compositions of the invention may be administered by any method known in the art suitable for administration of an antibacterial compound (*e.g.*, via oral or parenteral (*e.g.*, inhalation, intramuscular, intravenous, or epidermal)) delivery. In preferred embodiments, the pharmaceutical compositions of the invention are administered topically, e.g., in a topical formulation. The compositions of the invention may be used topically to treat and/or prevent common nosocomial infections, such as infections at surgical incision sites or associated with catheters or drains. In other embodiments, the compositions of the invention are use to treat

bacterial infections of the skin or upper dermal layers (e.g., infections of diabetic ulcers of the foot).

[0030] The pharmaceutical compositions of the present invention may also be used for traditionally non-therapeutic uses such as antibacterial agents in cosmetics, or in sprays or solutions for use on solid surfaces to prevent the colonization of bacteria (i.e., as disinfectants).

[0031] The present invention is also directed to methods for screening peptides for antibacterial activity. In one embodiment the method comprises screening contiguous amino acid sequences of at least 6, 10, 15, 20 or 25 residues in length that are encoded by the open reading frames of the nucleic acid sequence SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:760 for antibacterial activity, said antibacterial activity measured by the peptides ability to inhibit bacterial growth in agar or liquid culture.

Various embodiments of the present invention relate to a purified bacteriophage having a genome which comprises at least 99% sequence identity to the nucleotide sequence of SEQ ID NO:760, and having antibacterial activity against *Acinetobacter baumannii*, or a pharmaceutical composition comprising the bacteriophage and a pharmaceutically acceptable carrier. The composition may be used for treating or reducing the incidence of an *Acinetobacter baumannii* bacterial infection in a subject in need thereof. The bacteriophage may be used for reducing or inhibiting colonization of *Acinetobacter baumannii* on a biological surface contacted therewith. The bacteriophage may be used in a method for reducing or inhibiting colonization or growth of *Acinetobacter baumannii* on a non-biological solid surface comprising contacting said surface with the bacteriophage. The bacteriophage may be used for the preparation of a medicament for reducing or inhibiting colonization of *Acinetobacter baumannii* on a biological surface contacted therewith. Various embodiments of the present invention relate to a method for diagnosing the causative agent of a bacterial infection comprising: (i) culturing a sample from a patient; (ii) contacting the culture of step (i) with the bacteriophage; and (iii) monitoring for evidence of growth or lysis of the culture; wherein evidence of lysis of the culture indicates that the culture comprises a species or strain of *Acinetobacter baumannii* bacteria susceptible to the bacteriophage used in step (ii).

4.1 DEFINITIONS

[0032] As used herein, the term "fragment" refers to a peptide or polypeptide comprising an amino acid sequence of at least 5 contiguous amino acid residues, at least 10 contiguous amino acid residues, at least 15 contiguous amino acid residues, at least 20 contiguous amino acid residues, at least 25

contiguous amino acid residues, at least 40 contiguous amino acid residues, at least 50 contiguous amino acid residues, at least 60 contiguous amino residues, at least 70 contiguous amino acid residues, at least contiguous 80 amino acid residues, at least contiguous 90 amino acid residues, at least contiguous 100 amino acid residues, at least contiguous 125 amino acid residues, at least 150 contiguous amino acid residues, at least contiguous 175 amino acid residues, at least contiguous 200 amino acid residues, or at least contiguous 250 amino acid residues of the amino acid sequence of a protein. In a specific embodiment, the fragment is a functional fragment in that it retains at least one function of the protein from which it is isolated (e.g., antimicrobial or antibacterial activity (e.g., lytic cell killing)).

[0033] As used herein the terms "active bacteriophage products" and "bacteriophage products" refer to polypeptides, or fragments, variants or derivatives thereof, isolated from a bacteriophage of the invention, which polypeptide, or fragment, variant or derivative thereof, exhibits a biological function or activity associated with the bacteriophage from which it was isolated or derived (e.g., antimicrobial or antibacterial activity (e.g., lytic cell killing)).

[0034] As used herein, the term "isolated" in the context of a peptide, polypeptide, or fusion protein or refers to a peptide, polypeptide or fusion protein that is substantially free of cellular material or contaminating proteins from the cell or tissue source from which it is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of a peptide, polypeptide or fusion protein in which the peptide, polypeptide or fusion protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, a peptide, polypeptide or fusion protein that is substantially free of cellular material includes preparations of a peptide, polypeptide or fusion protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the peptide, polypeptide or fusion protein is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the peptide, polypeptide or fusion protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, *i.e.*, it is separated from chemical precursors or other chemicals which are involved in the synthesis of the peptide, polypeptide or fusion protein. Accordingly such preparations of a peptide, polypeptide, fusion protein or antibody have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the peptide, polypeptide or fusion protein of interest.

[0035] As used herein, the term "isolated" in the context of nucleic acid molecules refers to a nucleic acid molecule which is separated from other nucleic acid molecules which are present in the natural source of the first nucleic acid molecule. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized and may be free of cDNA or other genomic DNA molecules, *e.g.*, has been isolated from other clones in a nucleic acid library.

[0036] The term "purified" means that the peptide, polypeptide, fusion protein or nucleic acid molecule has been measurably increased in concentration by any purification process, including but not limited to, column chromatography, HPLC, precipitation, electrophoresis, etc., thereby partially, substantially, or completely removing impurities such as precursors or other chemicals involved in preparing the peptide, polypeptide, fusion protein or nucleic acid molecule. One of

skill in the art will appreciate the amount of purification necessary for a given use. For example, isolated protein meant for use in therapeutic compositions intended for administration to humans ordinarily must be of high purity in accordance with regulatory standards and good manufacturing processes.

[0037] As used herein, the term "derivative" in the context of polypeptides refers to a polypeptide that comprises an amino acid sequence which has been altered by the introduction of amino acid residue substitutions, deletions or additions. The term "derivative" as used herein also refers to a polypeptide that has been modified, *i.e.*, by the covalent attachment of any type of molecule to the polypeptide. For example, but not by way of limitation, a polypeptide may be modified, *e.g.*, by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. A derivative polypeptide may be produced by chemical modifications using techniques known to those of skill in the art, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Further, a derivative polypeptide may contain one or more non-classical amino acids. A polypeptide derivative possesses a similar or identical function as the polypeptide from which it was derived. The term "derived" as used in reference to a polypeptide "derived" from an organism may also refer to isolation of a polypeptide directly from said organism (e.g. bacterial cells or phage).

[0038] As used herein, the term "host cell" refers to the particular subject cell transfected with a nucleic acid molecule and the progeny or potential progeny of such a cell that contain the nucleic acid molecule or chromosomally integrated version thereof. Progeny of such a cell may not be identical to the parent cell transfected with the nucleic acid molecule due to mutations or environmental influences that may occur in succeeding generations or integration of the nucleic acid molecule into the host cell genome. For the expression of bacteriophage proteins and polypeptides, the host cell is preferably not of the same species or strain from which the bacteriophage was isolated or cultured.

[0039] As used herein, the term "in combination" refers to the use of more than one prophylactic and/or therapeutic agent. The use of the term "in combination" does not restrict the order in which prophylactic and/or therapeutic agents are administered to a subject with a disease or disorder. A first prophylactic or therapeutic agent can be administered prior to (*e.g.*, 5 minutes,

15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 4 hours, 6 hours, 12 hours, 24 hours, 48 hours, 72 hours, 96 hours, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 8 weeks, or 12 weeks before), concomitantly with, or subsequent to (*e.g.*, 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 4 hours, 6 hours, 12 hours, 24 hours, 48 hours, 72 hours, 96 hours, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 8 weeks, or 12 weeks after) the administration of a second prophylactic or therapeutic agent (different from the first prophylactic or therapeutic agent) to a subject with a disease or disorder.

[0040] As used herein, the terms "nucleic acids" and "nucleotide sequences" include single-stranded and double-stranded DNA and/or RNA molecules, or combinations thereof. As used herein, the term "encoded by the nucleic acid" refers to an amino acid sequence that results from the translation of the forward, reverse, complementary or reverse-complementary sequence of the referenced nucleic acid sequence using the standard genetic code (*i.*e., standard codon triplets) as well known in the art.

[0041] As used herein, the terms "prophylactic agent" and "prophylactic agents" refer to bacteriophages and/or polypeptides of the invention, which can be used in the prevention, treatment, management or amelioration of one or more symptoms associated with infection by a bacterium.

[0042] As used herein, the terms "therapeutic agent" and "therapeutic agents" refer to bacteriophages and/or polypeptides of the invention that can be used in the prevention, treatment, management or amelioration of one or more symptoms of a disease or disorder, in particular, a disease or disorder associated with a bacterial infection.

[0043] As used herein, the term "therapeutically effective amount" refers to that amount of a therapeutic agent sufficient to result in amelioration of one or more symptoms of a disease or disorder, in particular, a disease or disorder associated with a bacterial infection.

[0044] As used herein, the terms "treat", "treatment" and "treating" refer to the amelioration of one or more symptoms associated with a bacterial infection that results from the administration of one or more bacteriophages and/or polypeptides of the invention. As noted above, "treatment" and related terms refer to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to eliminate, lessen, decrease the severity of, slow the progression of, or delay or prevent the symptoms or underlying cause (*e.g.*, bacterial infection) associated with the pathological condition or disorder.

[0045] As used herein, the terms "antibacterial activity" and "antimicrobial activity" with reference to a bacteriophage, isolated bacteriophage protein (or variant, derivative or fragment thereof), or bacteriophage product, are used interchangeably to refer to the ability to kill and/or inhibit the growth or reproduction of a microorganism, in particular, the bacteria of the species or strain that the bacteriophage infects. In certain embodiments, antibacterial or antimicrobial activity is assessed by culturing bacteria (*e.g.*, Gram-positive bacteria (*e.g.*, *E. faecalis*, *E. faecium*, *S. aureus*), Gram-negative bacteria (*e.g.*, *A. baumannii*, *P. aeruginosa*) or bacteria not classified as either Gram-positive or Gram-negative) according to standard techniques (*e.g.*, in liquid culture or on agar plates), contacting the culture with a bacteriophage or polypeptide of the invention and monitoring cell growth after said contacting. For example, in a liquid culture, the bacteria may be grown to an optical density ("OD") representative of a mid-point in exponential growth of the culture; the culture is exposed to one or more concentrations of one or more bacteriophages or polypeptides of the invention and the OD is monitored relative to a control culture. Decreased OD relative to a control culture is representative of a bacteriophage or polypeptide exhibiting antibacterial activity (*e.g.*, exhibits lytic killing activity). Similarly, bacterial colonies can be allowed to form on an agar plate, the plate exposed to a bacteriophage or polypeptide of the invention, and subsequent growth of the colonies evaluated related to control plates. Decreased size of colonies, or decreased total numbers of colonies, indicate a bacteriophage or polypeptide with antibacterial activity.

[0046] As used herein, a "CHAP domain" refers to a conserved amidase domain found in several phage-encoded peptidoglycan hydrolases and stands for for "cysteine, histidine-dependent amidohydrolases/peptidases." See, e.g., Rigden D, et. al., Trends Biochem Sci. 2003 May 28(5): 230-4. It is found in a superfamily of amidases, including GSP amidase and peptidoglycan hydrolases. The family includes at least two different types of peptidoglycan cleavage activities: L-muramoyl-L-alanine amidase and D-alanyl-glycyl endopeptidase activity. CHAP domains generally contain conserved cysteine and histidine residues and hydrolyze γ-glutamyl-containing substrates. These cysteine residues are believed to be essential for the activity of several of these amidases, and their thiol groups appear to function as the nucleophiles in the catalytic mechanisms of all enzymes containing this domain. CHAP domains are often found in association with other domains that cleave peptidoglycan, e.g., acting in a cooperative manner to

cleave specialized substrates. See also, Bateman A, et al., Trends Biochem Sci. 2003 May 28(5): 234-7.

5. BRIEF DESCRIPTION OF THE FIGURES

[0047] FIG. 1: Schematic of the organization of the F168/08 genome, comprising the nucleic acid sequence of SEQ ID NO:1. The open reading frames ("ORFs") predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 2.

[0048] FIGS. 2A-X: Features of the bacteriophage F168/08 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded polypeptide and (iv) an assignment of putative function. ORFs 1-116 listed in FIG. 2 encode the amino acid sequences of SEQ ID NO:8-130, respectively.

[0049] FIGS. 3A-B: The host range of F168/08 as determined by the spot test in 105 *Enterococcus faecalis* (EFS) (3A) and 56 *Enterococcus faecium* (EFM) (3B) strains isolated from clinical samples. Each spot contained 5 µl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0050] FIG. 4: Schematic of the organization of the F170/08 genome, comprising the nucleic acid sequence of SEQ ID NO:2. The ORFs predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase

letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 5.

[0051] FIGS. 5A-AR: Features of the bacteriophage F170/08 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded polypeptide and (iv) an assignment of putative function. ORFs 1-213 listed in FIG. 5 encode the amino acid sequences of SEQ ID NO:131-343, respectively.

[0052] FIGS. 6A-B: The host range of F170/08 as determined by the spot test in 105 *Enterococcus faecalis* (EFS) (6A) and 56 *Enterococcus faecium* (EFM) (6B) strains isolated from clinical samples. Each spot contained 5 µl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0053] FIG. 7: Schematic of the organization of the F770/05 genome, comprising the nucleic acid sequence of SEQ ID NO:3. The ORFs predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 8.

[0054] FIGS. 8A-AC: Features of the bacteriophage F770/05 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded

polypeptide and (iv) an assignment of putative function. ORFs 1-95 listed in FIG. 8 encode the amino acid sequences of SEQ ID NO:344-438, respectively.

[0055] FIG. 9: The host range of F770/05 as determined by the spot test in 100 *Pseudomonas aeruginosa* (PSA) strains isolated from clinical samples. Each spot contained 5 µl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0056] FIG. 10: Schematic of the organization of the F197/08 genome, comprising the nucleic acid sequence of SEQ ID NO:4. The ORFs predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 11.

[0057] FIGS. 11A-AA: Features of the bacteriophage F197/08 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded polypeptide and (iv) an assignment of putative function. ORFs 1-66 listed in FIG. 11 encode the amino acid sequences of SEQ ID NO:439-553, respectively.

[0058] FIG. 12: The host range of F197/08 as determined by the spot test in 100 *Staphylococcus aureus* (STA) strains isolated from clinical samples. Each spot contained 5 µl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0059] FIG. 13: Schematic of the organization of the F86/06 genome, comprising the nucleic acid sequence of SEQ ID NO:5. The ORFs predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color

coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 14.

[0060] FIGS. 14A-S: Features of the bacteriophage F86/06 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded polypeptide and (iv) an assignment of putative function. ORFs 1-63 listed in FIG. 14 encode the amino acid sequences of SEQ ID NO:554-616, respectively.

[0061] FIG. 15: The host range of F86/06 as determined by the spot test in 100 *Staphylococcus aureus* (STA) strains isolated from clinical samples. Each spot contained 5 µl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0062] FIG. 16: Schematic of the organization of the F87s/06 genome, comprising the nucleic acid sequence of SEQ ID NO:6. The ORFs predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 17.

[0063] FIGS. 17A-U: Features of the bacteriophage F87s/06 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid

sequence, (iii) a listing of homologous proteins and conserved domains within its encoded polypeptide and (iv) an assignment of putative function. ORFs 1-61 listed in FIG. 17 encode the amino acid sequences of SEQ ID NO:617-681, respectively.

[0064] FIG. 18: The host range of F87s/06 as determined by the spot test in 100 *Staphylococcus aureus* (STA) strains isolated from clinical samples. Each spot contained 5 µl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0065] FIG. 19: Schematic of the organization of the F91a/06 genome, comprising the nucleic acid sequence of SEQ ID NO:7. The ORFs predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 20.

[0066] FIGS. 20A-U: Features of the bacteriophage F91a/06 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded polypeptide and (iv) an assignment of putative function. ORFs 1-64 listed in FIG. 20 encode the amino acid sequences of SEQ ID NO:682-754, respectively.

[0067] FIG. 21: The host range of F91a/06 as determined by the spot test in 100 *Staphylococcus aureus* (STA) strains isolated from clinical samples. Each spot contained 5 µl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0068] FIG. 22: Schematic organization of the F1245/05 genome, comprising the nucleic acid sequence of SEQ ID NO:760. The ORFs predicted in the 43kb genome are represented by

arrows and numbered in black. For the ORFs functionally assigned, the number is substituted by the predicted function. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for whose products a functional assignment could be made based on homologous proteins; Gray - ORFs coding for products that are similar to proteins of unknown function; Striped – ORFs with an assigned function based on its relative genome position and on the presence of putative transmembrane domains in the encoded product; Empty arrows – ORFs coding for proteins that share no significant homology with proteins in databases.

[0069] FIGS. 23A-I: Features of bacteriophage F1245/05 genome, including gene products and assignment of putative functions are provided.

[0070] FIGS. 24A-E: The host range of F1245/05 as determined by the spot test in 100 *Acinetobacter baumannii* strains isolated from clinical samples is provided. Each spot contained 5 µl bacteriophage suspensions with indicated titers (prepared from CsCl purified lysate). Sensitivity to the phage is presented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

6. DETAILED DESCRIPTION

[0071] The present invention is directed to isolated bacteriophages, and their isolated polypeptide products, having antibacterial activity against one or more species or strains of the nosocomial pathogens *A. baumannii, E. faecalis, E. faecium, P. aeruginosa* and *S. aureus*. In one embodiment, isolated bacteriophages or polypeptides are provided that exhibit antimicrobial and/or antibacterial activity against methicillin resistant strains of *S. aureus* (MRSA). In addition, the bacteriophages and polypeptides of the invention may exhibit antibacterial or antimicrobial activity against one or more species or strains of pathogenic bacteria including, but not limited to, S. *epidermidis, S. auricularis, S. capitis, S. haemolyticus, S. hominis, S. saprophyticus, S. simulans, S. xylosis, Micrococcus luteus, Bacilus subtilis, B. pumilus, E. hirae* and *E. avium*.

[0072] In one embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:1. A specific example in accordance with this embodiment is the isolated bacteriophage F168/08, which targets a number of strains of *E. faecalis* and *E. faecium*. Open reading frames (ORFs) in the F168/08 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino

acid sequences (*i.e.*, encoded proteins and/or polypeptides) are provided in FIG. 2 (also providing the amino acid sequences SEQ ID NOS:8-130).

[0073] *Enterococci* are gram-positive, spherical bacteria that form colonies in groups or chains. They are found as part of the digestive tract flora in many mammals, including humans. *Enterococcus* infections account for 12% of all nosocomial infections. An *Enterococcus* infection can cause complicated abdominal infections, skin and skin structure infections, urinary tract infections and infections of the blood stream, which can be difficult to treat, particularly in cases where the strain involved has developed resistance to several antibiotics. In such instances, infection can be life threatening, especially where the patient is already immunodeficient.

[0074] *Enterococcus faecalis* accounts for the majority of *Enterococci* infections and is a Gram-positive commensal bacterium inhabiting the gastrointestinal tracts of humans and other mammals. It is non-motile and facultatively anaerobic. *E. faecalis* can cause endocarditis, as well as bladder, prostate, and epididymal infections, including life threatening infections in humans, especially in the nosocomial environment. *E. faecalis* is resistant to many commonly used antimicrobial agents (such as, e.g., aminoglycosides, aztreonam, cephalosporins, clindamycin, the semi-synthetic penicillins nafcillin and oxacillin, trimethoprim-sulfamethoxazole, and the like).

[0075] *Enterococcus faecium* is known to have a resistance to several types of antibiotics including quinolones and aminoglycosides. Vancomycin-resistant strains of *E. faecium* are also known. Resistance to several antibiotics and tolerance for adverse conditions makes *E. faecium* a major concern for the medical community, which has dubbed this microbe a "supergerm".In another embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:2. A specific example in accordance with this embodiment is the isolated bacteriophage F170/08, which targets a number of strains of *E. faecalis* and *E. faecium*. Open reading frames (ORFs) in the F178/08 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino acid sequences (*i.e.*, encoded proteins and/or polypeptides) are provided in FIG. 5 (also providing the amino acid sequences SEQ ID NOS:131-343).

[0076] In still another embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:3. A specific example in accordance with this embodiment is the isolated bacteriophage F770/05, which targets a number

of strains of *P. aeruginosa*. Open reading frames (ORFs) in the F770/05 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino acid sequences (*i.e.*, encoded proteins and/or polypeptides) are provided in FIG. 8 (also providing the amino acid sequences SEQ ID NOS:344-438).

[0077] *Pseudomonas aeruginosa* is a common Gram-negative rod-shaped bacterium found in soil, water, skin flora and most man-made environments. It thrives not only in normal atmospheres, but also with little oxygen as a facultative anaerobe, and can infect damaged tissues or immunocomromised inidviduals. When such colonisations occur in critical body organs such as the lungs, the urinary tract, and kidneys, the results can be fatal. Because it thrives on surfaces, this bacterium is also found on and in medical equipment including catheters, causing cross infections in hospitals and clinics. *P. aeruginosa* is one of the most relevant opportunistic, nosocomial pathogens, and it has been estimated that one in ten hosptical-acquired infections are from Pseudomonas. P. aeruginosa is also the most common cause of burn injury infections and the most frequent colonizer of medical devices, such as catheters.

[0078] In yet another embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:4. A specific example in accordance with this embodiment is the isolated bacteriophage F197/08, which targets a number of strains of *S. aureus*. Open reading frames (ORFs) in the F197/08 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino acid sequences (*i.e.*, encoded proteins and/or polypeptides) are provided in FIG. 11 (also providing the amino acid sequences SEQ ID NOS:439-553).

[0079] In yet another embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:5. A specific example in accordance with this embodiment is the isolated bacteriophage F86/06, which targets a number of strains of *S. aureus*. Open reading frames (ORFs) in the F86/06 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino acid sequences (*i.e.*, encoded proteins and/or polypeptides) are provided in FIG. 14 (also providing the amino acid sequences SEQ ID NOS:554-616).

[0080] In yet another embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:6. A specific example in accordance with this embodiment is the isolated bacteriophage F87s/06, which targets a number

of strains of *S. aureus*. Open reading frames (ORFs) in the F87s/06 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino acid sequences (*i.e.*, encoded proteins and/or polypeptides) are provided in FIG. 17 (also providing the amino acid sequences SEQ ID NOS:617-681).

[0081] In still another embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:7. A specific example in accordance with this embodiment is the isolated bacteriophage F91a/06, which targets a number of strains of *S. aureus*. Open reading frames (ORFs) in the F91a/06 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino acid sequences (*i.e.*, encoded proteins and/or polypeptides) are provided in FIG. 20 (also providing the amino acid sequences SEQ ID NOS:682-754).

[0082] *S. aureus* is a spherical, facultatively-anaerobic, Gram-positive bacterium, often part of the skin flora found in the nose and on skin. *S. aureus* can cause a range of illnesses from minor skin infections, such as pimples, to gastroenteritis, to life-threatening diseases such as pneumonia, meningitis, osteomyelitis, endocarditis, toxic shock syndrome (TSS), bacteremia, and sepsis. It is one of the five most common causes of nosocomial infections, and often the cause of postsurgical wound infections. Today, *S. aureus* has become resistant to many commonly used antibiotics, and it has been estimated that only 2% of all *S. a*ureus isolates are sensitive to penicillin. Second-generation penicillins, such s methicillin, oxacillin, cloxacillin and flucloxacillin, were developed to treat penicillin-resistant *S. aureus*. Methicillin was the first antibiotic in this class to be used, but only two years later, the first case of methicillin-resistant *S. aureus* (MRSA) was reported. Since the 1990s, there has been an explosion in MRSA prevalence in hospitals, where it is now considered an endemic.

[0083] In still another embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:760. A specific example in accordance with this embodiment is the isolated bacteriophage F1245/05, which targets a number of strains of *A. baumannii*. Open reading frames (ORFs) in the F1245/05 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino acid sequences (*i.e.*, encoded proteins and/or polypeptides) are provided in FIG. 23 (also providing the amino acid sequences SEQ ID NOS:761-816).

[0084] *Acinetobacter baumannii* is a species of bacteria that causes a number of severe clinical infections, particularly in individuals with compromised immune systems. *Acinetobacter baumannii* is a pleomorphic aerobic gram-negative bacillus that is commonly isolated from the hospital environment and from hospitalized patients. The bacterium often enters the body open wounds, catheters, or breathing tubes. *Acinetobacter baumannii* usually colonizes aquatic environments and is often cultured from hospitalized patients' sputum or respiratory secretions, wounds, and urine. In a hospital setting, *Acinetobacter baumannii* commonly colonizes irrigating solutions and intravenous solutions. It is also known to be resistant to multiple antibiotics and the number of nosocomial infections caused by *A. baumanni* has increased in recent years.

[0085] In certain embodiments, the bacteriophage of the invention comprises or consists of a genome having a sequence identity of at least 85%, 90%, 95%, 96%, 97%, 98% or at least 99% with the nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:760, which bacteriophage exhibits at least one biological, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity), of one or more of bacteriophage F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06, F91a/06 and F1245/05. Alternatively or in addition, the bacteriophage of the invention may have a genome comprising a functional fragment of the nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:760, including the sequences of any of the open reading frames described in FIGS. 2, 5, 8, 11, 14, 17, 20, and 23.

[0086] The invention also provides for isolated bacteria infected with one or more of the bacteriophages of the invention. In certain embodiments, the invention provides isolated *E. faecalis* or *E. faecium* infected with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:1 and/or SEQ ID NO:2. In other embodiments, the invention provides isolated *P. aeruginosa* infected with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:3. In still other embodiments, the invention provides isolated *S. aureus* infected with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and/or SEQ ID NO:7. In yet still other embodiments, the invention provides isolated *A. baumannii* infected with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:760.

[0087] The invention provides for methods of production and isolation of a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:760. In certain embodiments, the invention provides for a method of producing and/or isolating a bacteriophage having a genome that comprises or consists of the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2 comprising (i) obtaining a culture of *E. faecalis* or *E. faecium*, (ii) infecting it with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2; (iii) culturing until significant lysis of the culture is observed and (iv) isolating from the culture the bacteriophage. In other embodiments, the invention provides for a method of producing and/or isolating a bacteriophage having a genome that comprises or consists of the nucleic acid sequence of SEQ ID NO:3 comprising (i) obtaining a culture of *P. aeruginosa*, (ii) infecting it with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:3; (iii) culturing until significant lysis of the culture is observed and (iv) isolating from the culture the bacteriophage. In still other embodiments, the invention provides for a method of producing and/or isolating a bacteriophage having a genome that comprises or consists of the nucleic acid sequence of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7 comprising (i) obtaining a culture of *S. aureus*, (ii) infecting it with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence of ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7; (iii) culturing until significant lysis of the culture is observed and (iv) isolating from the culture the bacteriophage. In yet still other embodiments, the invention provides for a method of producing and/or isolating a bacteriophage having a genome that comprises or consists of the nucleic acid sequence of SEQ ID NO:760 comprising (i) obtaining a culture of *A. baumannii*, (ii) infecting it with the bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:760; (iii) culturing until significant lysis of the culture is observed and (iv) isolating from the culture the bacteriophage.

[0088] Bacteriophage may be isolated from a bacterial sample using any method described herein or known in the art (see, *e.g.*, Carlson, "Working with bacteriophages: common techniques and methodological approaches," *In,* Kutter and Sulakvelidze (Eds) Bacteriophages: Biology and Applications, 5th ed. CRC Press (2005)).

[0089] The invention also provides for polypeptides isolated from bacteriophages of the invention. The isolated polypeptides may be full length bacteriophage proteins or may be fragments, variants or derivatives of the bacteriophage proteins provided that the fragment, variant or derivative exhibit at least one biological activity associated with the bacteriophage or polypeptide from which it is derived. In certain embodiments, the polypeptides of the invention are isolated from bacteriophage F1245/05 (which typically infects *A. baumannii*), F168/08 or F170/08 (which typically infects *E. faecalis* and/or *E. faecium*), bacteriophage F770/05 (which typically infects *P. aeruginosa*) or bacteriophage F197/08, F86/06, F87s/06 or F91a/06 (which typically infect *S. aureus*).

[0090] In specific embodiments, the polypeptide of the invention is an endolysin or lysin isolated from a bacteriophage having a genome comprising or consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:760 (*e.g.*, bacteriophage F168/08, F170/08, F197/08, F86/06, F87s/06, F91a/06, or F1245/05 respectively). In specific embodiments, the polypeptide of the invention is an endolysin or lysin having the amino acid sequence comprising or consisting of SEQ ID NO:797, SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712. In other embodiments, the isolated polypeptide of the invention is a fragment, variant or derivative of an endolysin or lysin isolated from a bacteriophage of the invention, which fragment, variant or derivative exhibits at least one biological activity, preferably antibacterial activity (*e.g.*, lytic killing activity), of the endolysin, lysin or bacteriophage from which it is isolated or derived. Accordingly, in certain embodiments, the invention provides isolated polypeptides that are fragments, variants or derivatives of endolysins or lysins isolated from bacteriophages of the invention, which fragments, variants or derivatives exhibit antibacterial or antimicrobial activity (*e.g.*, lytic killing activity) against one or more of *A. baumannii, E. faecalis, E. faecium* or *S. aureus*. In other embodiments, the isolated polypeptides that are fragments, variants or derivatives of endolysins or lysins isolated from bacteriophages of the invention that exhibit antibacterial or antimicrobial activity (*e.g.*, lytic killing activity) against one or more species of bacteria other than *A. baumannii, E. faecalis, E. faecium* or *S. aureus* (*e.g.*, *P. aeruginosa*). In certain embodiments, the polypeptide of the invention comprises or consists of the amino acid sequence SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202 or SEQ ID NO:203, or a fragment, variant or

derivative thereof, which polypeptide exhibits antibacterial or antimicrobial activity against *E. faecalis* or *E. faecium*. In other embodiments, the polypeptide of the invention comprises or consists of the amino acid sequence SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712, or a fragment, variant or derivative thereof, which polypeptide exhibits antibacterial or antimicrobial activity against *S. aureus*. In yet still other embodiments, the polypeptide of the invention comprises or consists of the amino acid sequence SEQ ID NO:797, or a fragment, variant or derivative thereof, which polypeptide exhibits antibacterial or antimicrobial activity against *A. baumanni*.

[0091] In certain embodiments, the polypeptide of the invention comprises or consists of a CHAP domain isolated from an endolysin or lysin of bacteriophage F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06 or F91a/06. Isolated CHAP domains have been demonstrated to retain the antibacterial activity, *e.g.*, lytic killing activity, of the endolysin or lysin from which they are derived; CHAP domains may be identified and isolated by methods routine in the art (see, *e.g.*, Rigden et al., 2003, *Trends Biochem. Sci.* 28:230-234; Bateman et al., 2003, *Trends Biochem. Sci.* 28:234-237). In specific embodiments, the polypeptide of the invention comprises or consists of a CHAP domain isolated from a polypeptide having an amino acid sequence of SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712. In specific embodiments, the invention provides for an isolated polypeptide that comprises or consists of the CHAP domain derived from a second polypeptide having the amino acid sequence of SEQ ID NO:68, SEQ ID NO:446, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712, wherein the CHAP domain has the amino acid sequence of SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758 or SEQ ID NO:759, respectively. That is, SEQ ID NO:755 corresponds to a CHAP domain derived from the polypeptide having amino acid sequence of SEQ ID NO:68; SEQ ID NO:756 corresponds to a CHAP domain derived from the polypeptide having amino acid sequence of SEQ ID NO:446, and so forth. In other embodiments the invention provides for a fragment, variant or derivative of a CHAP domain of isolated from an endolysin or lysin of bacteriophage F 168/08, F 170/08, F770/05, F197/08, F86/06, F87s/06 or F91a/06, which fragment, variant or derivative exhibits at least one biological activity, *e.g.*, lytic cell killing, of the CHAP domain from which it was derived and wherein said CHAP domain has an amino acid sequence of SEQ ID NO:755, SEQ

ID NO:756, SEQ ID NO:757, SEQ ID NO:758 or SEQ ID NO:759. The amino acid sequences of SEQ ID NO:755-SEQ ID NO:759 are provided in Table 1.

Table 1: Amino acid sequences of CHAP domains isolated from bacteriophages of the invention

SEQ ID NO	Sequence	Phage
755	NGLVGKGVDADGWYGTQCMDLTVDVMQRFFGWRPYGNAIALV DQPIPAGFQRIRTTSSTQIKAGDVMIWGLGYYAQYGHTGIATEDG RADGTFVSVDQNWINPSLEVGSPAAAIHHNMDGVWGVIR	F168/08
756	DNSLGKQFNPDLFYGFQCYDYANMFFMIATGERLQGLYAYNIPF DNKARIEKYGQIIKNYDSFLPQKLDIVVFPSKYGGGAGHVEIVESA NLNTFTSYGQNWNGKGWTNGVAQPGWGPETVTRHVHYYDDPM YFIR	F197/08
757	RWYQGRYIDFDGWYGYQCADLAVDYIYWLLEIRMWGNAKDAI NNDFKNMATVYENTPSFVPQIGDVAVFTKGIYKQYGHIGLVFNG GNTNQFLILEQNYDGNANTPAKLRWDNYYGCTHFIR	F86/06
758	RWYQGRYIDFDGWYGYQCADLAVDYIYWLLEIRMWGNAKDAI NNDFKNMATVYENTPSFVPQIGDVAVFTKGIYKQYGHIGLVFNG GNTNQFLILEQNYDGNANTPAKLRWDNYYGCTHFIR	F87s/06
759	RWYQGRYIDFDGWYGYQCADLAVDYIYWLLEIRMWGNAKDAI NNDFKNMATVYENTPSFVPQIGDVAVFTKGIYKQYGHIGLVFNG GNTNQFLILEQNYDGNANTPAKLRWDNYYGCTHFIR	F91a/06

[0092] In certain embodiments, a polypeptide of the invention comprises or consists of a tail length tape measure protein or tail protein (*e.g.*, tail component, tail fiber protein, adsorption associated tail protein), or fragment thereof, isolated from a bacteriophage having a genome comprising or consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:760 (*e.g.*, bacteriophage F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06, F91a/06, or F1245/05, respectively), wherein the tail length tape measure protein or tail protein, or fragment thereof has a biologic function associated with the bacteriophage from which it is derived, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity). In specific embodiments, the antimicrobial or antibacterial activity of the tail length tape measure protein or tail protein is directed against at least one or more species or strains of *A. baumannii*, *E. faecalis*, *E. faecium*, *P. aeruginosa* and/or *S. aureus*. In specific embodiments, the polypeptide of the invention is a tail tape measure protein or tail protein having the amino acid sequence comprising or consisting of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID

NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, or SEQ ID NO:795. In other embodiments, the isolated polypeptide of the invention is a fragment, variant or derivative of the amino acid sequence of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, , or SEQ ID NO:795, which fragment variant or derivative exhibits at least one biological activity or function of the bacteriophage from which it is isolated or derived, *e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity). In preferred embodiments, the at least one biological activity or function of the fragment, variant or derivative is directed against one or more strains of *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii*.

[0093] In certain embodiments, the isolated polypeptide of the invention is a variant of a bacteriophage polypeptide, which variant comprises or consists of a amino acid sequence having at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity to a second amino acid sequence of the same length (*i.e.*, consisting of the same number of residues), which second amino acid sequence is SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:575, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:641, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:712, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:795, or SEQ ID NO:797, and/or a fragment thereof, and wherein the

variant exhibits at least one biological function or activity of the bacteriophage from which it was derived (*e.g.*, antimicrobial or antibacterial activity (*e.g.*, lytic killing activity)) against one or more strains of bacteria (*e.g.*, Gram-positive bacteria (*e.g.*, *E. faecalis*, *E. faecium*, *S. aureus*), Gram-negative bacteria (*e.g.*, *P. aeruginosa, A baumannii*) or bacteria not classified as either Gram-positive or Gram-negative).

[0094] In certain embodiments, the invention provides an isolated polypeptide having an amino acid sequence of any of SEQ ID NOS:2-124, SEQ ID NOS: 126-338, SEQ ID NOS:340-434, SEQ ID NOS:436-550, SEQ ID NOS:552-614, SEQ ID NOS:616-680, SEQ ID NOS:682-759, SEQ ID NOS:761-816, and active biologic fragments thereof. In preferred embodiments, the variant polypeptide of the invention exhibits at least one biologic activity associated with the polypeptide or bacteriophage from which it was isolated or derived directed against at least one or more strains of *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus,* and/or *A. baumannii.*

[0095] In other embodiments, the invention provides an isolated nucleic acid sequence encoding the amino acid sequence of one of SEQ ID NOS:8-130, SEQ ID NOS:131-343, SEQ ID NOS:344-438, SEQ ID NOS:439-553, SEQ ID NOS:554-616, SEQ ID NOS:617-681, SEQ ID NOS:682-759, SEQ ID NOS:761-816, and active fragments thereof. In other embodiments the invention provides the nucleic acid sequence of any of the open reading frames identified in FIGS. 2, 5, 8, 11, 14, 17, 20, and 23.

[0096] In certain embodiments, the polypeptides of the present invention are recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugations) to therapeutic agents, *e.g.*, heterologous polypeptides or small molecules, to generate fusion proteins or chimeric polypeptides. The fusion does not necessarily need to be direct, but may occur through linker sequences or through chemical conjugation. Non-limiting examples of therapeutic agents to which the polypeptides of the invention may be conjugated are peptide or non-peptide cytotoxins (including antimicrobials and/or antibiotics), tracer/marker molecules (*e.g.*, radionuclides and fluorphores) and other antibiotic or antibacterial compounds known in the art.

6.1 ANTIBIOTIC COMPOSITIONS

[0097] The isolated bacteriophages or polypeptides of the present invention may be administered alone or incorporated into a pharmaceutical composition for the use in treatment or prophylaxis of bacterial infections, *e.g.*, infections caused by bacteria including, but not limited to, *A.*

baumannii, E. faecalis, E. faecium, P. aeruginosa and *S. aureus*. The polypeptides may be combined with a pharmaceutically acceptable carrier, excipient, or stabilizer. Examples of pharmaceutically acceptable carriers, excipients and stabilizers include, but are not limited to, buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight polypeptides; proteins, such as serum albumin and gelatin; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™. The pharmaceutical composition of the present invention (*e.g.*, antibacterial composition) can also include a lubricant, a wetting agent, a sweetener, a flavoring agent, an emulsifier, a suspending agent, and a preservative, in addition to the above ingredients.

[0098] The bacteriophages and/or polypeptides of the present invention may also be combined with one or more therapeutic and or prophylactic agents useful for the treatment of bacterial infection as described herein and/or known in the art (*e.g.* one or more lysins). The pharmaceutical compositions of the invention may therefore comprise two or more isolated bacteriophages of the invention (with antibacterial activity against the same or different bacterial species or strains), the combination of a bacteriophage and a polypeptide of the invention or the combination of a bacteriophage and/or polypeptide of the invention and a bacteriophage and/or therapeutic polypeptide known in the art. In specific embodiments, the therapeutic components of a combination target two or more species or strains of bacteria or exhibit differing enzymatic activity. For example, lysins, in general, exhibit one of amidase, endopeptidase, muramidase or glucosamidase activity. Accordingly, the combination of lysins exhibiting different activities may provide synergistic enhancement to the therapeutic activity of the pharmaceutical composition of the invention.

[0099] Examples of other therapeutic agents that may be used in combination with the polypeptide of the invention include, but are not limited to, standard antibiotic agents, anti-inflammatory agents, antiviral agents, local anesthetic agents, and corticosteroids.

[0100] Standard antibiotics that maybe used with pharmaceutical compositions comprising polypeptides of the invention include, but are not limited to, amikacin, gentamicin, kanamycin,

neomycin, netilmicin, paromomycin, rhodostreptomycin, streptomycin, tobramycin, apramycin, rifamycin, naphthomycin, mupirocin, geldanamycin, ansamitocin, carbacephems, imipenem, meropenem, ertapenem, faropenem, doripenem, panipenem/betamipron, biapenem, PZ-601, cephalosporins, cefacetrile, cefadroxil, cefalexin, cefaloglycin, cefalonium, cefaloridine, cefalotin, cefapirin, cefatrizine, cefazaflur, cefazedone, cefazolin, cefradine, cefroxadine, ceftezole, cefaclor, cefonicid, cefprozil, cefuroxime, cefuzonam, cefmetazole, cefotetan, cefoxitin, cefcapene, cefdaloxime, cefdinir, cefditoren, cefetamet, cefixime, cefmenoxime, cefteram, ceftibuten, ceftiofur, ceftiolene, ceftizoxime, ceftriaxone, cefoperazone, ceftazidime latamoxef, cefclidine, cefepime, cefluprenam, cefoselis, cefozopran, cefpirome, cefquinome, flomoxef. ceftobiprole, azithromycin, clarithromycin, dirithromycin, erythromycin, roxithromycin, aztreonam, pencillin and penicillin derivatives, actinomycin, bacitracin, colistin, polymyxin B, cinoxacin, flumequine, nalidixic acid, oxolinic acid, piromidic acide, pipemidic acid, rosoxacin, ciprofloxacin, enoxacin, fleroxacin, lomefloxacin, nadifloxacin, norfloxacin, ofloxacin, pefloxacin, rufloxacin, balofloxacin, gatifloxacin, grepafloxacin, levofloxacin, moxifloxacin, pazufloxacin, sparfloxacin, temafloxacin, tosufloxacin, clinafloxacin, garenoxacin, gemifloxacin, stifloxacin, trovalfloxacin, prulifloxacin, acetazolamide, benzolamide, bumetanide, celecoxib, chlorthalidone, clopamide, dichlorphenamide, dorzolamide, ethoxyzolamide, furosemide, hydrochlorothiazide, indapamide, mafendide, mefruside, metolazone, probenecid, sulfacetamide, sulfadimethoxine, sulfadoxine, sulfanilamides, sulfamethoxazole, sulfasalazine, sultiame, sumatriptan, xipamide, tetracycline, chlortetracycline, oxytetracycline, doxycycline, lymecycline, meclocycline, methacycline, minocycline, rolitetracycline and any combination thereof in amounts that are effective to additively or synergistically enhance the therapeutic effect of the bacteriophage or polypeptide of the invention for a given infection.

[0101] Local anesthetics that may be used in pharmaceutical compositions of the present invention include tetracaine, tetracaine hydrochloride, lidocain, lidocaine hydrochloride, dimethisoquin hydrochloride, dibucaine, dibucaine hydrochloride, butambenpicrate, and pramoxine hydrochloride. An exemplary concentration of local anesthetic is about 0.025% to about 5% by weight of the total composition.

[0102] Corticosteroids that may be useful in combination with the polypeptides, phage, and/or pharmaceutical compositions of the invention include betamethasone, dipropionate,

fluocinolone, actinide, betamethasone valerate, triamcinolone actinide, clobetasol propionate, desoximetasone, diflorasone diacetate, amcinonide, flurandrenolide, hydrocortisone valerate, hydrocortisone butyrate, and desonide. An exemplary concentration of corticosteroid is about 0.01% to about 1% by weight of the total composition.

[0103] In certain embodiments, a formulation comprising a bacteriophage and/or polypeptide of the invention further comprises SM buffer (0.05 M Tris-HCl (pH 7.4-7.5); 0.1 M NaCl; 10 mM $MgSO_4$). In other embodiments, the formulation further comprises SM buffer and 10 mM $MgCl_2$. In still other embodiments, the formulation further comprises SM buffer and about 20% or about 30% ethanol.

[0104] Pharmaceutical compositions comprising a bacteriophage and/or polypeptide of the present invention can be formulated in a unit dose or multi-dose formulation. Suitable formulations can be selected from the group consisting of ointments, solutions, suspensions or emulsions, extracts, powders, granules, sprays, lozenges, tablets or capsules and additionally include a dispersing agent or a stabilizing agent.

[0105] The pharmaceutical compositions of the invention can be administered by inhalation, in the form of a suppository or pessary, topically (*e.g.*, in the form of a lotion, solution, cream, ointment or dusting powder), epi- or transdermally (*e.g.*, by use of a skin patch), orally (*e.g.*, as a tablet, which may contain excipients such as starch or lactose), as a capsule, ovule, elixirs, solutions or suspensions (each optionally containing flavoring, coloring agents and/or excipients), or they can be injected parenterally (*e.g.*, intravenously, intramuscularly or subcutaneously). For parenteral administration, the compositions may be best used in the form of a sterile aqueous solution which may contain other substances, for example enough salts or monosaccharides to make the solution isotonic with blood. For buccal or sublingual administration the compositions may be administered in the form of tablets or lozenges which can be formulated in a conventional manner. In a preferred embodiment, a bacteriophage and/or polypeptide of the present invention is administered topically, either as a single agent, or in combination with other antibiotic treatments as described herein or known in the art.

[0106] A bacteriophage and/or polypeptide of the present invention may also be dermally or transdermally administered. For topical application to the skin, the bacteriophages and/or polypeptides of the present invention may be combined with one, or a combination of carriers, which include but are not limited to, an aqueous liquid, an alcohol base liquid, a water soluble

gel, a lotion, an ointment, a nonaqueous liquid base, a mineral oil base, a blend of mineral oil and petrolatum, lanolin, liposomes, proteins carriers such as serum albumin or gelatin, powdered cellulose carmel, and combination thereof. A topical mode of delivery may include a smear, a spray, a time-release patch, a liquid absorbed wipe, and combinations thereof. The bacteriophage and/or polypeptide of the invention may be applied to a patch or bandage either directly or in one of the carriers. The patches may be damp or dry, wherein the phage and/or polypeptide (e.g., a lysin) is in a lyophilized form on the patch. The carriers of topical compositions may comprise semi-solid and gel-like vehicles that include a polymer thickener, water, preservatives, active surfactants, or emulsifiers, antioxidants, sun screens, and a solvent or mixed solvent system. U.S. Patent No. 5,863,560 discloses a number of different carrier combinations that can aid in the exposure of skin to a medicament.

[0107] For intranasal or administration by inhalation, the bacteriophage and/or polypeptide of the invention is conveniently delivered in the form of a dry powder inhaler or an aerosol spray presentation from a pressurized container, pump, spray or nebuliser with the use of a suitable propellant, e.g. dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, a hydrofluoroalkane such as 1,1,1,2-tetrafluoroethane (HFA 134A.TM.) or 1,1,1,2,3,3,3-heptafluoropropane (HFA 227EA.TM.), carbon dioxide or other suitable gas. In the case of a pressurized aerosol, the dosage unit may be determined by providing a valve to deliver a metered amount. The pressurized container, pump, spray or nebuliser may contain a solution or suspension of the active compound, e.g. using a mixture of ethanol and the propellant as the solvent, which may additionally contain a lubricant, e.g. sorbitan trioleate. Capsules and cartridges (made, for example, from gelatin) for use in an inhaler or insufflator may be formulated to contain a powder mix of the bacteriophage and/or polypeptide of the invention and a suitable powder base such as lactose or starch.

[0108] For administration in the form of a suppository or pessary, the therapeutic compositions may be applied topically in the form of a gel, hydrogel, lotion, solution, cream, ointment or dusting powder. Compositions of the invention may also be administered by the ocular route. For ophthalmic use, the compositions of the invention can be formulated as micronized suspensions in isotonic, pH adjusted, sterile saline, or, preferably, as solutions in isotonic, pH

adjusted, sterile saline, optionally in combination with a preservative such as a benzylalkonium chloride. Alternatively, they may be formulated in an ointment such as petrolatum.

[0109] Dosages and desired drug concentrations of the pharmaceutical compositions of the present invention may vary depending on the particular use. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments can provide reliable guidance for the determination of effective doses in human therapy. Interspecies scaling of effective doses can be performed by one of ordinary skill in the art following the principles described by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" in Toxicokinetics and New Drug Development, Yacobi et al., Eds., Pergamon Press, New York 1989, pp42-96.

6.2 THERAPEUTIC USE

[0110] The bacteriophages and polypeptides of the present invention have activity against a plurality of strains of *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii*-, as described in FIGS. 3A-B, 6A-B, 9, 12, 15, 18, 21, and 23. Therefore, the compositions of the present invention may used in methods of preventing and treating infections associated with *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii* in both humans and animals. In other embodiments, the compositions of the present invention may be used to treat infection associated with related species or strains of these bacteria, including, but not limited to *S. epidermidis, S. auricularis, S. capitis, S. haemolyticus, S. hominis, S. saprophyticus, S. simulans, S. xylosis, Micrococcus luteus, Bacilus subtilis, B. pumilus, E. hirae*, and/or one or more of the strains of *A. baumannii*, e..g, one or more of the strains described in FIG. 24.

[0111] In specific embodiments, the subject receiving a pharmaceutical composition of the invention is a mammal (e.g., bovine, ovine, caprine, equid, primate (e.g., human), rodent, lagomorph or avian (e.g., chicken, duck, goose)). In the context of the present invention, "treatment" refers to therapeutic treatment and wherein the object is to eliminate, lessen, decrease the severity of, ameliorate, slow the progression of or prevent the symptoms or underlying cause (e.g., bacterial infection) associated with the pathological condition or disorder. "Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to eliminate, lessen, decrease the severity of, slow the progression of or delay or prevent the symptoms or underlying cause (*e.g.*, bacterial infection) associated with the pathological condition or disorder. It is also contemplated that a bacteriophage and/or

polypeptide of the invention acts as a prophylactic or preventative measure, preventing the onset of infection caused by one or more bacteria.

[0112] *A. baumannii, E. faecalis, E. faecium, P. aeruginosa* and *S. aureus* are responsible for many severe opportunistic infections, particularly in individuals with compromised immune systems. The pharmaceutical compositions of the present invention are contemplated for treating any infection associated with *A. baumannii, E. faecalis, E. faecium, P. aeruginosa* or *S. aureus*, or associated with other species or strains of bacteria, including, but not limited to, infections of the skin (including but not limited to skin ulcers, bed sores and diabetic foot ulcers), infections in and around wounds, post-operative infections, infections associated with catheters and surgical drains and infections of the blood.

[0113] *A. baumannii, E. faecalis, E. faecium, P. aeruginosa* and *S. aureus* are also associated with infections that involve organ systems that have a high fluid content, and it is contemplated that the bacteriophages and/or polypeptides of the invention have therapeutic use in the prevention and treatment of these infections. For example, the pharmaceutical compositions of the invention may be used for the prevention or treatment of infections of the respiratory tract, of the cerebrospinal fluid, of peritoneal fluid, and of the urinary tract. The compositions of the invention may also be used to prevent and/or treat nosocomial pneumonia, infections associated with continuous ambulatory peritoneal dialysis (CAPD), catheter-associated bacteruria, and nosocomial meningitis.

[0114] In a preferred embodiment, a bacteriophage and/or polypeptide of the invention is used prophylactically in hospital setting, particularly to prevent infections associated with wounds, ulcers, and openings in the skin due to catheterization, and any other medical procedures or devices.

[0115] In certain embodiments, a bacteriophage and/or polypeptide of the invention is used as a single agent for treating or preventing infections associated with *A. baumannii, E. faecalis, E. faecium, P. aeruginosa, S. aureus* or other bacterial species. In other embodiments of the invention, a bacteriophage and/or polypeptide of the invention is used in combination with other agents, including other bacteriophages (for example, that target a different species or strain of bacteria), or with antibiotics that target the same or different kinds of bacteria, including bacteria selected from any gram-positive bacteria, any gram-negative bacteria, and any other groups of bacteria that is not classified as gram-positive or gram-negative. The compositions of the

invention may also be used in combination with any other means of treating bacterial infection known to one of skill in the art.

[0116] Also contemplated by the invention are methods of preventing and methods of treating an infection caused by bacteria including, but not limited to, *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii*, comprising administering to a mammal in need thereof a composition comprising a lysin comprising or consisting of the amino acid sequence of SEQ ID NO:68, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641, I.D. NO:712, and/or SEQ ID NO:797, or a fragment, variant or derivative thereof, wherein the fragment, variant or derivative exhibits antibacterial or antimicrobial activity against the species of bacteria from which the parent bacteriophage was isolated. In a specific example in accordance with this embodiment, the invention provides methods of preventing or treating an infection caused by a bacteria including, but not limited to, *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii*, comprising administering to a mammal in need thereof a composition comprising an isolated CHAP domain of a lysin, or a fragment, variant or derivative thereof that exhibits at least one biologic activity of the CHAP domain from which it was isolated (*e.g.*, lytic cell killing). In certain embodiments, the isolated CHAP domain comprises or consists of the amino acid sequence of SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758 or SEQ ID NO:759. In other embodiments, the invention provides methods of preventing and treating an infection caused by bacteria including, but not limited to, *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii*, comprising administering to a mammal in need thereof a composition comprising a tail tape measure protein or tail protein comprising or consisting of the amino acid sequence of SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, and/or SEQ ID NO:795, or a fragment, variant or derivative thereof, wherein the fragment, variant or derivative exhibits a biologic activity associated with the parent bacteriophage. In still other embodiments, the invention provides methods of preventing and

treating an infection caused by bacteria including, but not limited to, *E. faecalis*, *E. faecium*, *P. aeruginosa*, *S. aureus*, and/or *A. baumannii*, comprising administering to a mammal in need thereof a composition comprising bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, and/or SEQ ID NO:760. Combinations of the lysins (or fragments, variants or derivatives thereof as described above) and of tail tape measure proteins or tail proteins (or fragments, variants or derivatives thereof as described above), optionally with one or more bacteriophages of the invention or with other treatments, such as antibiotics, are also contemplated, as well as methods of treating and methods of preventing a bacterial infection using one or more of the combinations herein described.

[0117] As used herein, the term "in combination" refers to the use of more than one prophylactic and/or therapeutic agent. The use of the term "in combination" does not restrict the order in which prophylactic and/or therapeutic agents are administered to a subject with a disease or disorder. A first prophylactic or therapeutic agent can be administered prior to (e.g., 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 4 hours, 6 hours, 12 hours, 24 hours, 48 hours, 72 hours, 96 hours, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 8 weeks, or 12 weeks before), concomitantly with, or subsequent to (e.g., 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 4 hours, 6 hours, 12 hours, 24 hours, 48 hours, 72 hours, 96 hours, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 8 weeks, or 12 weeks after) the administration of a second prophylactic or therapeutic agent (different from the first prophylactic or therapeutic agent) to a subject with a disease or disorder.

6.3 DISINFECTANT AND ANTI-INFECTIVE USE

[0118] Bacterial pathogens most often infect at a mucous membrane site (*e.g.*, upper and lower respiratory, intestinal, urogenital and ocular). The mucous membranes themselves are often the reservoir, sometimes the only reservoir, for many pathogenic bacteria found in the environment (e.g. pneumococci, staphylococci and streptococci). There are very few anti-infectives that are designed to control the carrier state of pathogenic bacteria. However, studies have shown that by reducing or eliminating this reservoir in environments such as hospitals and nursing homes, the incidence of infections by these bacteria will be markedly reduced.

[0119] The bacteriophages and/or polypeptides of the present invention may be used in anti-infective compositions for controlling the growth of bacteria (*e.g.*, Gram-positive bacteria (*e.g.*,

E. faecalis, *E. faecium*, *S. aureus*), Gram-negative bacteria (*e.g.*, *P. aeruginosa*, *A. baumannii*) or bacteria not classified as either Gram-positive or Gram-negative), in order to prevent or reduce the incidence of serious infections. In addition to use in compositions for application to mucous membranes, a bacteriophage and/or polypeptide of the present incorporation may also be incorporated into formulations such as gels, creams, ointments, or sprays for controlling or preventing colonization of bacteria on body surfaces (*e.g.*, skin and mucus membranes) (*e.g.*, for sterilization of surgical fields or of the hands and exposed skin of healthcare workers and/or patients) and other solid surfaces (*e.g.*, appliances, countertops and, in particular, hospital equipment).

6.4 DIAGNOSTIC METHODS

[0120] The present invention also encompasses diagnostic methods for determining the causative agent in a bacterial infection. In certain embodiments, the diagnosis of the causative agent in a presentation of bacterial infection is performed by (i) culturing tissue, blood or fluid samples of a patient according to standard techniques, (ii) contacting the culture with one or more bacteriophages and/or polypeptides of the invention and (iii) monitoring cell growth and evidence of lysis after said contacting. Because the activity of bacteriophages and/or their isolated products (*e.g.*, polypeptides, or biologically active fragments, variants or derivatives thereof) tends to be species or strain specific, susceptibility, or lack of susceptibility, to one or more bacteriophages and/or polypeptides of the invention may be indicative of the species or strain of infective bacteria. For example, decreased growth of test cultures after contacting with a bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:1 or SEQ ID NO:2, or with an isolated polypeptide product thereof, may be indicative of the test sample comprising *E. faecalis* or *E. faecium*. Similarly, a bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:3, or an isolated polypeptide product thereof, may be used to identify infection by *P. aeruginosa*; a bacteriophage having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:760, or an isolated polypeptide product thereof, may be used to identify infection by *A. baumannii*, while that having a genome comprising or consisting of the nucleic acid sequence SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7, or an isolated polypeptide product thereof, may be used to identify infection by *S. aureus*.

6.5 AMINO ACID VARIANTS

[0121] Amino acid sequence variants of the polypeptides of the invention can be created such that they are substitutional, insertional or deletion variants. Deletion variants lack one or more residues of the native protein which are not essential for function (*e.g.*, antimicrobial or antibacterial activity). Insertional mutants typically involve the addition of material at a non-terminal point in the polypeptide. Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, such as stability against proteolytic cleavage, without the loss of other functions or properties. Substitutions of this kind preferably are conservative, that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine.

[0122] Once general areas of the gene are identified as encoding the particular lysin protein as described herein, point mutagenesis may be employed to identify with particularity which amino acid residues are important in the antibacterial activities. Thus, one of skill in the art will be able to generate single base changes in the DNA strand to result in an altered codon and a missense mutation.

[0123] Preferably, mutation of the amino acids of a protein creates an equivalent, or even an improved, second-generation molecule. For example, certain amino acids may be substituted for other amino acids in a protein structure without detectable loss of function (*e.g.*, antibacterial or antimicrobial activity). In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art. It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, interaction with a peptidoglycan within the outer coat of a gram-positive bacteria. Each amino

acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics; for example: isoleucine(+4.5); valine(+4.2); leucine(+3.8) ; phenylalanine(+2.8); cysteine/cystine(+2.5); methionine(+1.9); alanine(+1.8); glycine(-0.4); threonine(-0.7); serine(-0.8); tryptophan 0.9); tyrosine(-1.3); proline(-1.6); histidine(-3.2); glutamate(-3.5); glutamine(-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

[0124] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. Like hydrophobicity, values of hydrophilicity have been assigned to each amino acid: arginine (+3.0); lysine (+3.0); aspartate (+3.0 $\pm$ 1); glutamate (+3.0 $\pm$ 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 $\pm$ 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5) and tryptophan (-3.4). Equivalent molecules may be obtained by substitution of one amino acid for another where their hydrophilicity indices are within $\pm$ 2, preferably $\pm$ 1, or most preferably $\pm$ 5 of each other.In certain embodiments, the invention encompasses isolated peptides that comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more amino acid modifications (*e.g.*, insertion, substitution, deletion, etc.) relative to an amino acid sequence disclosed herein. In preferred embodiments, the mutation(s) are made such that biological activity of the particular polypeptide is retained. For example, the present invention encompasses polypeptides isolated from bacteriophage F1245/05, F168/08, F170/08, F770/05, F197/08, F86/06, F87s/06 and/or F91a/06, which are mutated to comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more amino acid modifications relative to an amino acid sequence listed herein, and which exhibit antibacterial activity against one or more species or strains of Gram-positive or Gram-negative bacterium, *e.g.*, *A. baumannii*, *E. faecalis*, *E. faecium*, *P. aeruginosa* and/or *S. aureus*. In specific embodiments, the polypeptides of the invention derived from F168/08 or F/170/08 exhibit antibacterial or antimicrobial activity, *e.g.*, lytic killing activity, against at least *E. faecalis* and/or *E. faecium*; those derived from F770/05 against at least *P. aeruginosa*; those derived from F197/08, F86/06, F87s/06 or F91a/06 against at least *S. aureus*; and those derived from F1245/05 against at least *A. baumannii*.

6.6 POLYNUCLEOTIDES ENCODING POLYPEPTIDES OF THE INVENTION

[0125] The invention provides polynucleotides comprising a nucleotide sequence encoding a polypeptide of the invention. The invention also encompasses polynucleotides that hybridize under high stringency, intermediate or lower stringency hybridization conditions, *e.g.*, as defined *supra*, to polynucleotides that encode a polypeptide of the invention and that encode modified polypeptides that have antibiotic and/or other biological activity.

[0126] The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, a polynucleotide encoding a polypeptide of the invention may be generated from nucleic acid from a suitable source (*e.g.*, bacteriophage F1245/05, F168/08, F170/08, F770/05, F197/08, F197/08, F86/06, F87s/06 or F91a/06). Nucleotide sequences may be isolated from phage genomes by routine methods known in the art (see, *e.g.*, Carlson, "Working with bacteriophages: common techniques and methodological approaches," *In,* Kutter and Sulakvelidze (Eds) Bacteriophages: Biology and Applications, 5th ed. CRC Press (2005)). If a source containing a nucleic acid encoding a particular polypeptide is not available, but the amino acid sequence of the polypeptide of the invention is known, a nucleic acid encoding the polypeptide may be chemically synthesized and cloned into replicable cloning vectors using any method well known in the art.

[0127] Once the nucleotide sequence of the polypeptide of the invention is determined, the nucleotide sequence of the polypeptide may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, *e.g.*, recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel *et al.*, eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY), to generate polypeptides having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

[0128] In yet another embodiment of the invention, the following nucleotide sequences are provided: the nucleotide sequence from nucleotide 1 to nucleotide 85 of SEQ ID NO:760; the nucleotide sequence from nucleotide 87 to nucleotide 584 of SEQ ID NO:760; the nucleotide sequence from nucleotide 594 to nucleotide 767 of SEQ ID NO:760; the nucleotide sequence

from nucleotide 724 to nucleotide 1035 of SEQ ID NO:760; the nucleotide sequence from nucleotide 1005 to nucleotide 1823 of SEQ ID NO:760; the nucleotide sequence from nucleotide 1816 to nucleotide 2130 of SEQ ID NO:760; the nucleotide sequence from nucleotide 2132 to nucleotide 2383 of SEQ ID NO:760; the nucleotide sequence from nucleotide 2383 to nucleotide 3690 of SEQ ID NO:760; the nucleotide sequence from nucleotide 3687 to 4469 of SEQ ID NO:760; the nucleotide sequence from nucleotide 4466 to nucleotide 5458 of SEQ ID NO:760; the nucleotide sequence from nucleotide 5632 to nucleotide 7956 of SEQ ID NO:760; the nucleotide sequence from nucleotide 8010 to nucleotide 8912 of SEQ ID NO:760; the nucleotide sequence from nucleotide 8915 to nucleotide 9262 of SEQ ID NO:760; he nucleotide sequence from nucleotide 9252 to nucleotide 10223 of SEQ ID NO:760; he nucleotide sequence from nucleotide 10213 to nucleotide 10782 of SEQ ID NO:760; the nucleotide sequence from nucleotide 10769 to nucleotide 11218 of SEQ ID NO:760; the nucleotide sequence from nucleotide 11202 to nucleotide 11420 of SEQ ID NO:760; the nucleotide sequence from nucleotide 11413 to nucleotide 12342 of SEQ ID NO:760; the nucleotide sequence from nucleotide 12339 to nucleotide 12515 of SEQ ID NO:760; the nucleotide sequence from nucleotide 12512 to nucleotide 13165 of SEQ ID NO:760; the nucleotide sequence from nucleotide 13170 to nucleotide 15599 of SEQ ID NO:760; the nucleotide sequence from nucleotide 15609 to nucleotide 15872 of SEQ ID NO:760; the nucleotide sequence from nucleotide 15979 to nucleotide 16173 of SEQ ID NO:760; the nucleotide sequence from nucleotide 16175 to nucleotide 16482 of SEQ ID NO:760; the nucleotide sequence from nucleotide 16494 to nucleotide 18059 of SEQ ID NO:760; the nucleotide sequence from nucleotide 18072 to nucleotide 18815 of SEQ ID NO:760; the nucleotide sequence from nucleotide 18857 to nucleotide 19879 of SEQ ID NO:760; the nucleotide sequence from nucleotide 19930 to nucleotide 20178 of SEQ ID NO:760; the nucleotide sequence from nucleotide 20180 to nucleotide 20545 of SEQ ID NO:760; the nucleotide sequence from nucleotide 20646 to nucleotide 21203 of SEQ ID NO:760; the nucleotide sequence from nucleotide 21212 to nucleotide 23506 of SEQ ID NO:760; the nucleotide sequence from nucleotide 23506 to nucleotide 24186 of SEQ ID NO:760; the nucleotide sequence from nucleotide 24201 to nucleotide 27068 of SEQ ID NO:760; the nucleotide sequence from nucleotide 27084 to nucleotide 30212 of SEQ ID NO:760; the nucleotide sequence from nucleotide 30214 to nucleotide 32505 of SEQ ID NO:760; the nucleotide sequence from

nucleotide 32515 to nucleotide 32880 of SEQ ID NO:760; the nucleotide sequence from nucleotide 32873 to nucleotide 33460 of SEQ ID NO:760; the nucleotide sequence from nucleotide 33460 to nucleotide 33816 of SEQ ID NO:760; the nucleotide sequence from nucleotide 33825 to nucleotide 35777 of SEQ ID NO:760; the nucleotide sequence from nucleotide 35774 to nucleotide 35872 of SEQ ID NO:760; the nucleotide sequence from nucleotide 35869 to nucleotide 36027 of SEQ ID NO:760; the nucleotide sequence from nucleotide 36038 to nucleotide 36193 of SEQ ID NO:760; the nucleotide sequence from nucleotide 36916 to nucleotide 36788 of SEQ ID NO:760; the nucleotide sequence from nucleotide 37209 to nucleotide 37427 of SEQ ID NO:760; the nucleotide sequence from nucleotide 37868 to nucleotide 38386 of SEQ ID NO:760; the nucleotide sequence from nucleotide 38383 to nucleotide 38586 of SEQ ID NO:760; the nucleotide sequence from nucleotide 38912 to nucleotide 39406 of SEQ ID NO:760; the nucleotide sequence from nucleotide 39406 to nucleotide 39915 of SEQ ID NO:760; the nucleotide sequence from nucleotide 39917 to nucleotide 40021 of SEQ ID NO:760; the nucleotide sequence from nucleotide 40018 to nucleotide 40101 of SEQ ID NO:760; the nucleotide sequence from nucleotide 40101 to nucleotide 40670 of SEQ ID NO:760; the nucleotide sequence from nucleotide 40720 to nucleotide 41838 of SEQ ID NO:760; the nucleotide sequence from nucleotide 41822 to nucleotide 42127 of SEQ ID NO:760; the nucleotide sequence from nucleotide 42105 to nucleotide 42308 of SEQ ID NO:760; the nucleotide sequence from nucleotide 42382 to nucleotide 42912 of SEQ ID NO:760; and the nucleotide sequence from nucleotide 42896 to nucleotide 43015 of SEQ ID NO:760.

6.7 RECOMBINANT EXPRESSION OF MOLECULES OF THE INVENTION

[0129] Once a nucleic acid sequence encoding a molecule of the invention (*e.g.*, a polypeptide) has been obtained, the vector for the production of the molecules may be produced by recombinant DNA technology using techniques well known in the art. Methods which are well known to those skilled in the art can be used to construct expression vectors containing the coding sequences for the molecules of the invention and appropriate transcriptional and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. (*See*, for example, the techniques described in Sambrook *et al.*, 1990, Molecular Cloning, A Laboratory Manual, 2d

Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel *et al.* eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY).

[0130] The present invention provides expression vectors encoding the polypeptides of the invention. An expression vector comprising the nucleotide sequence of a molecule identified by the methods of the invention can be transferred to a host cell by conventional techniques (*e.g.*, electroporation, liposomal transfection, and calcium phosphate precipitation) and the transfected cells are then cultured by conventional techniques to produce the molecules of the invention. In preferred embodiments, the host cell is other than the species of the parent bacteria from which the bacteriophage comprising the sequence was derived. In specific embodiments, the expression of the molecules of the invention is regulated by a constitutive, an inducible or a tissue, specific promoter. In specific embodiments the expression vector is pQE-30 (Qiagen) or pET-29(a) (Novagen).

[0131] The host cells used to express the molecules identified by the methods of the invention may be either bacterial cells (non susceptible to the bacteriophage protein or fragment thereof of the invention) such as *Escherichia coli.* A variety of host-expression vector systems may be utilized to express the molecules identified by the methods of the invention. Such host-expression systems represent vehicles by which the coding sequences of the molecules of the invention may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express the molecules of the invention *in situ.* These include, but are not limited to, microorganisms such as bacteria that are not susceptible to the bacteriophage protein or fragment thereof of the invention (*e.g.*, *E. coli* and *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing coding sequences for the molecules identified by the methods of the invention; yeast (*e.g.*, *Saccharomyces Pichia*) transformed with recombinant yeast expression vectors containing sequences encoding the molecules identified by the methods of the invention; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing the sequences encoding the molecules identified by the methods of the invention; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus (CaMV) and tobacco mosaic virus (TMV) or transformed with recombinant plasmid expression vectors (*e.g.*, Ti plasmid) containing sequences encoding the molecules identified by the methods of the invention; or mammalian cell systems (*e.g.*, COS,

CHO, BHK, 293, 293T, 3T3 cells, lymphotic cells (*see* U.S. 5,807,715), Per C.6 cells (human retinal cells developed by Crucell) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (*e.g.*, metallothionein promoter) or from mammalian viruses (*e.g.*, the adenovirus late promoter; the vaccinia virus 7.5K promoter).

[0132] In bacterial systems not susceptible to the bacteriophage protein or fragment of the invention, a number of expression vectors may be advantageously selected depending upon the use intended for the molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of a polypeptide, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther *et al.*, 1983, *EMBO J.* 2:1791), in which the protein sequence may be ligated individually into the vector in frame with the *lac Z* coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, 1985, *Nucleic Acids Res.* 13:3101-3109; Van Heeke & Schuster, 1989, *J. Biol. Chem.* 24:5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to a matrix glutathione-agarose beads followed by elution in the presence of free gluta-thione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

[0133] In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The polypeptide coding sequence may be cloned individually into non-essential regions (*e.g.*, the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (*e.g.*, the polyhedrin promoter).

[0134] Once a molecule of the invention (*i.e.*, polypeptides) has been recombinantly expressed, it may be purified by any method known in the art for purification of polypeptides, for example, by chromatography (*e.g.*, ion exchange, affinity, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of polypeptides or antibodies.

[0135] Certain modifications and improvements will occur to those skilled in the art upon a reading of the foregoing description. It should be understood that all such modifications and

improvements have been deleted herein for the sake of conciseness and readability but are properly within the scope of the following claims.

7. EXAMPLES

[0136] It is understood that the following examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggestive to persons skilled in the art and are to be included within the spirit and purview of this application and the scope of the appended claims.

[0137] Unless otherwise indicated, the bacteriophages of the invention were isolated, processed and analyzed according to the following methods.

7.1 METHODS

7.1.1 PURIFICATION OF PHAGE.

[0138] Stock preparations of bacteriophage isolated from clinical samples were prepared according to protocols described in Carlson, "Working with bacteriophages: common techniques and methodological approaches," *In,* Kutter and Sulakvelidze (Eds) Bacteriophages: Biology and Applications, 5th ed. CRC Press (2005) ("Carlson").

[0139] The bacteriophage stock preparations were concentrated by precipitation with PEG according to the protocol described Carlson and Yamamoto et al., 2004, *PNAS* 101:6415-6420. Briefly, the stock preparation was incubated in 1 M NaCl for one hour at 4°C with agitation. Next, PEG 8000 (AppliChem, Cheshire, MA) was gradually added to a final concentration of 10% (w/v). The composition was then incubated overnight at 4° C. After the incubation period, the composition was centrifuged at 10000 x g for 30 minutes at 4° C. The sediment was then re-suspended in SM buffer (0.05 M Tris-HCL at pH 7.4, 0.1 M NaCl, 10 mM $MgSO_4$) with gelatin at 1% w/v and centrifuged again at 1000 rpm at 4°C for 10 minutes. The supernatant containing the suspended phage was saved for further purification. The supernatant was purified using a CsCl gradient according to the methods in Carlson.

[0140] CsCl was removed from the purified and concentrated phage stock by dialysis. A dialysis membrane, Cellu.Sep H1 High Grade Regenerated Cellulose Tubular Membrane (Cellu.Sep, River Street, USA), was prepared according to the manufacturers' instructions. The

dialysis consisted of a first incubation of 30 minutes in 100 mM Tris-HCl and 3 M NaCl (pH 7.4) at 4°C. This was followed by a second incubation of 30 minutes in 100 mM Tris-HCl and 0.3 M NaCl (pH 7.4) at 4°C. After dialysis, the suspended phage was removed from the interior of the dialysis bag and stored at 4°C.

7.1.2 EXTRACTION OF PHAGE DNA

[0141] To 5 ml of the purified and concentrated bacteriophage samples was added 20 mM EDTA at pH 8.0, SDS at 0.5% (p/v) and Proteinase K at a final concentration of 40 µg/ml. The mixture was incubated at 56° C for one hour. Successive extractions in phenol:chloroform:alcohol at a proportions of 25:24:1, were performed until the interface between the aqueous and organic phases was clear. The aqueous phase was then treated with an equal volume of chloroform and centrifuged at 13,0000 x g for 10 minutes at 4°C. The aqueous phase was once again removed, and the DNA was precipitated by adding two volumes of absolute ethanol and incubating for thirty minutes at 20°C. The samples were then centrifuged at 11,000 x g for 30 minutes at 4°C. The pellet was washed with 70% ethanol at room temperature and resuspended in 50 µl of ultra-pure water (Gibco, California). DNA concentration was determined by measuring the absorbance at 260 nm in a ND-1000 Spectrophotometer. Integrity of the isolated phage DNA was analyzed by electrophoresis on a 1% agarose gel.

7.1.3 ANALYSIS OF BACTERIOPHAGE GENOMES

[0142] Sequencing of the bacteriophage genome allowed identification of potential open reading frames (ORFs) within the genome. The putative ORFs of the bacteriophages were used to search the NCBI nucleotide collection database for homologous DNA sequences using the BLASTN program (see, *e.g.*, Zhang et al., 2000, *J. Comput. Biol.* 7:203-214).

7.2 EXAMPLE 1: Bacteriophage F168/08

[0143] Comparison of the putative ORFs of the bacteriophage F168/08 genome with the sequences in the NCBI nucleotide database revealed that only small portions of the genome (≤ 1%) exhibited homology with known sequences. The F168/08 ORFs, their encoded amino acid sequences and known homologous proteins are provided in FIG. 2. Prediction of *orfs* was performed by integrating the results obtained with GeneMark.hmm and MetaGeneAnnotator programs (Besemer, J. and Borodovsky, M. 1999. Nucleic Acids Res., 27: 3911-3920; Noguchi,

H. et al., 2008. DNA Res., 15: 387-396). Protein homology searches were carried out with BLASTP program (Alschul, S.F. et al., 1997. Nucleic Acids Res., 25: 3389-33402) using the NCBI non-redundant protein sequences database. Protein conserved domains were predicted using NCBI specialized BLAST (Marchler-Bauer, A. et al., 2007. Nucleic Acids Res. 35: 237-240). *orfs* whose products presented homology with the same protein(s) are indicated with the same number added of a lowercase letter, in FIG. 2. Identification of putative transfer RNA genes (tRNA) was carried out using the tRNAscan-SE progam (Lowe, T.M. et al., 1997. Nucleic Acids Res., 25: 955-964).

[0144] FIGS. 3A-B provide the results of spot tests that assessed the activity of the bacteriophage F168/08 against 105 *Enterococcus faecalis* (A) and 56 *Enterococcus faecium* (B) strains isolated from clinical samples. Each spot consisted of 5 µl of bacteriophage suspension with the indicated titers, prepared from a CsCl purified lysate. Sensitivity to the phage is represented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

7.3 EXAMPLE 2: Bacteriophage F170/08

[0145] Comparison of the putative ORFs of the bacteriophage F170/08 genome with the sequences in the NCBI nucleotide database revealed that about 94% of its genome was highly similar to that of *Enterococcus* phage ΦEF24C, with individual ORF identities ranging from 80 to 100%. The F170/08 ORFs, their encoded amino acid sequences and known homologous proteins are provided in FIG. 5. Prediction of *orfs* was performed by integrating the results obtained with GeneMark.hmm and MetaGeneAnnotator programs (Besemer, J. and Borodovsky, M. 1999. Nucleic Acids Res., 27: 3911-3920; Noguchi, H. et al., 2008. DNA Res., 15: 387-396). Protein homology searches were carried out with BLASTP program (Alschul, S.F. et al., 1997. Nucleic Acids Res., 25: 3389-33402) using the NCBI non-redundant protein sequences database. Protein conserved domains were predicted using NCBI specialized BLAST (Marchler-Bauer, A. et al., 2007. Nucleic Acids Res. 35: 237-240). *orfs* whose products presented homology with the same protein(s) are indicated with the same number added of a lowercase letter, in FIG. 5. Identification of putative transfer RNA genes (tRNA) was carried out using the tRNAscan-SE progam (Lowe, T.M. et al., 1997. Nucleic Acids Res., 25: 955-964).

[0146] FIGS. 6A-B provide the results of spot tests that assessed the activity of the bacteriophage F170/08 against 105 *Enterococcus faecalis* (A) and 56 *Enterococcus faecium* (B)

strains isolated from clinical samples. Each spot consisted of 5 µl of bacteriophage suspension with the indicated titers, prepared from a CsCl purified lysate. Sensitivity to the phage is represented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

7.4 EXAMPLE 3: Bacteriophage F770/05

[0147] Comparison of the putative ORFs of the bacteriophage F770/05 genome with the sequences in the NCBI nucleotide database revealed that only small portions of the genome (≤ 1%) exhibited homology with known sequences. The F170/05 ORFs, their encoded amino acid sequences and known homologous proteins are provided in FIG. 8. Prediction of *orfs* was performed by integrating the results obtained with GeneMark.hmm and MetaGeneAnnotator programs (Besemer, J. and Borodovsky, M. 1999. Nucleic Acids Res., 27: 3911-3920; Noguchi, H. et al., 2008. DNA Res., 15: 387-396). Protein homology searches were carried out with BLASTP program (Alschul, S.F. et al., 1997. Nucleic Acids Res., 25: 3389-33402) using the NCBI non-redundant protein sequences database. Protein conserved domains were predicted using NCBI specialized BLAST (Marchler-Bauer, A. et al., 2007. Nucleic Acids Res. 35: 237-240).

[0148] FIG. 9 provides the results of spot tests that assessed the activity of the bacteriophage F170/05 against 100 *Pseudomonas aeruginosa* strains isolated from clinical samples. Each spot consisted of 5 µl of bacteriophage suspension with the indicated titers, prepared from a CsCl purified lysate. Sensitivity to the phage is represented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

7.5 EXAMPLE 4: Bacteriophage F197/08

[0149] Comparison of the putative ORFs of the bacteriophage F197/08 genome with the sequences in the NCBI nucleotide database revealed that the genome was highly homologous with multiple staphylococcal phage genomes. In particular, about 90% of the F197/08 genome is highly similar to that of *Staphylococcus* bacteriophage phiSauS-IPLA35, with individual ORF identities ranging from 80 to 98%. The F197/08 ORFs, their encoded amino acid sequences and known homologous proteins are provided in FIG. 11. Prediction of *orfs* was performed by integrating the results obtained with GeneMark.hmm and MetaGeneAnnotator programs (Besemer, J. and Borodovsky, M. 1999. Nucleic Acids Res., 27: 3911-3920; Noguchi, H. et al.,

2008. DNA Res., 15: 387-396). Protein homology searches were carried out with BLASTP program (Alschul, S.F. et al., 1997. Nucleic Acids Res., 25: 3389-33402) using the NCBI non-redundant protein sequences database. Protein conserved domains were predicted using NCBI specialized BLAST (Marchler-Bauer, A. et al., 2007. Nucleic Acids Res. 35: 237-240). *orfs* whose products presented homology with the same protein(s) are indicated with the same number added of a lowercase letter, in FIG. 11.

[0150] FIG. 12 provides the results of spot tests that assessed the activity of the bacteriophage F197/08 against 100 *Staphylococcus aureus* strains isolated from clinical samples. Each spot consisted of 5 µl of bacteriophage suspension with the indicated titers, prepared from a CsCl purified lysate. Sensitivity to the phage is represented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

7.6 EXAMPLE 5: Bacteriophage F86/06

[0151] Comparison of the putative ORFs of the bacteriophage F86/06 genome with the sequences in the NCBI nucleotide database revealed that the genome was highly homologous with multiple staphylococcal phage genomes. In particular, about 80% of the F86/06 genome is highly similar to that of *Staphylococcus* bacteriophage tp310-1, with individual ORF identities ranging from 85 to 100%. The F86/06 ORFs, their encoded amino acid sequences and known homologous proteins are provided in FIG. 14. Prediction of *orfs* was performed by integrating the results obtained with GeneMark.hmm and MetaGeneAnnotator programs (Besemer, J. and Borodovsky, M. 1999. Nucleic Acids Res., 27: 3911-3920; Noguchi, H. et al., 2008. DNA Res., 15: 387-396). Protein homology searches were carried out with BLASTP program (Alschul, S.F. et al., 1997. Nucleic Acids Res., 25: 3389-33402) using the NCBI non-redundant protein sequences database. Protein conserved domains were predicted using NCBI specialized BLAST (Marchler-Bauer, A. et al., 2007. Nucleic Acids Res. 35: 237-240).

[0152] FIG. 15 provides the results of spot tests that assessed the activity of the bacteriophage F86/06 against 100 *Staphylococcus aureus* strains isolated from clinical samples. Each spot consisted of 5 µl of bacteriophage suspension with the indicated titers, prepared from a CsCl purified lysate. Sensitivity to the phage is represented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

7.7 EXAMPLE 6: Bacteriophage F87s/06

[0153] Comparison of the putative ORFs of the bacteriophage F87s/06 genome with the sequences in the NCBI nucleotide database revealed that the genome was highly homologous with multiple staphylococcal phage genomes. In particular, about 82% of the F87s/06 genome is highly similar to that of *Staphylococcus* bacteriophage ΦNM3, with individual ORF identities ranging from 90 to 100%. The F86/06 ORFs, their encoded amino acid sequences and known homologous proteins are provided in FIG. 17. Prediction of *orfs* was performed by integrating the results obtained with GeneMark.hmm and MetaGeneAnnotator programs (Besemer, J. and Borodovsky, M. 1999. Nucleic Acids Res., 27: 3911-3920; Noguchi, H. et al., 2008. DNA Res., 15: 387-396). Protein homology searches were carried out with BLASTP program (Alschul, S.F. et al., 1997. Nucleic Acids Res., 25: 3389-33402) using the NCBI non-redundant protein sequences database. Protein conserved domains were predicted using NCBI specialized BLAST (Marchler-Bauer, A. et al., 2007. Nucleic Acids Res. 35: 237-240). *orfs* whose products presented homology with the same protein(s) are indicated with the same number added of a lowercase letter, in FIG. 17.

[0154] FIG. 18 provides the results of spot tests that assessed the activity of the bacteriophage F87s/06 against 100 *Staphylococcus aureus* strains isolated from clinical samples. Each spot consisted of 5 µl of bacteriophage suspension with the indicated titers, prepared from a CsCl purified lysate. Sensitivity to the phage is represented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

7.8 EXAMPLE 7: Bacteriophage F91a/06

[0155] Comparison of the putative ORFs of the bacteriophage F91a/06 genome with the sequences in the NCBI nucleotide database revealed that the genome was highly homologous with multiple staphylococcal phage genomes. In particular, about 82% of the F91a/06 genome is highly similar to that of *Staphylococcus* bacteriophage ΦNM3, with individual ORF identities ranging from 86 to 99%. The F91a/06 ORFs, their encoded amino acid sequences and known homologous proteins are provided in FIG. 20. Prediction of *orfs* was performed by integrating the results obtained with GeneMark.hmm and MetaGeneAnnotator programs (Besemer, J. and Borodovsky, M. 1999. Nucleic Acids Res., 27: 3911-3920; Noguchi, H. et al., 2008. DNA Res., 15: 387-396). Protein homology searches were carried out with BLASTP program (Alschul, S.F. et al., 1997. Nucleic Acids Res., 25: 3389-33402) using the NCBI non-redundant protein

sequences database. Protein conserved domains were predicted using NCBI specialized BLAST (Marchler-Bauer, A. et al., 2007. Nucleic Acids Res. 35: 237-240). *orfs* whose products presented homology with the same protein(s) are indicated with the same number added of a lowercase letter, in FIG. 20.

[0156] FIG. 21 provides the results of spot tests that assessed the activity of the bacteriophage F91a/06 against 100 *Staphylococcus aureus* strains isolated from clinical samples. Each spot consisted of 5 µl of bacteriophage suspension with the indicated titers, prepared from a CsCl purified lysate. Sensitivity to the phage is represented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

7.9 EXAMPLE 8: Bacteriophage F1245/05

[0157] F1245/05 ORFs, their encoded amino acid sequences and known homologous proteins are provided in FIGS. 23A-I. Prediction of *orfs* was performed by integrating the results obtained with GeneMark.hmm and MetaGeneAnnotator programs (Besemer, J. and Borodovsky, M. 1999. Nucleic Acids Res., 27: 3911-3920; Noguchi, H. et al., 2008. DNA Res., 15: 387-396). Protein homology searches were carried out with BLASTP program (Alschul, S.F. et al., 1997. Nucleic Acids Res., 25: 3389-33402) using the NCBI non-redundant protein sequences database. Protein conserved domains were predicted using NCBI specialized BLAST (Marchler-Bauer, A. et al., 2007. Nucleic Acids Res. 35: 237-240). Protein function was predicted based on genome localization of the corresponding gene and on the presence of putative transmembrane domains of the encoded product (TMHMM server v. 2.0; Krogh, A. et al., 2001. J. Mol. Biol., 305: 567-580.

[0158] FIGS. 24 A-E provides the results of spot tests that assessed the activity of the bacteriophage F1245/05 against 100 *Acinetobacter baumanni* strains isolated from clinical samples. Each spot consisted of 5 µl of bacteriophage suspension with the indicated titers, prepared from a CsCl purified lysate. Sensitivity to the phage is represented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

WHAT IS CLAIMED IS:

1. A purified bacteriophage having a genome which comprises at least 99% sequence identity to the nucleotide sequence of SEQ ID NO:760, and having antibacterial activity against *Acinetobacter baumannii*.

2. A pharmaceutical composition comprising the bacteriophage of claim 1 and a pharmaceutically acceptable carrier.

3. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:760.

4. The pharmaceutical composition of claim 2 or 3, further comprising one or more additional bacteriophages effective against *Acinetobacter baumannii*.

5. Use of a therapeutically effective amount of the pharmaceutical composition of any one of claims 2-4 for treating or reducing the incidence of an *Acinetobacter baumannii* bacterial infection in a subject in need thereof.

6. The use of claim 5, wherein the infection is a nosocomial infection.

7. The use of claim 5, wherein the composition is for topical administration.

8. The use of claim 5, wherein the subject is a mammal.

9. The use of claim 8, wherein the mammal is a human.

10. The use of claim 5, wherein the infection is an infection of the skin, lungs, urinary tract, or kidneys.

11. The use of claim 10, wherein said infection of the skin is an infection associated with a burn injury or a diabetic foot ulcer.

12. A method for diagnosing the causative agent of a bacterial infection comprising
    (i) culturing a sample from a patient;
    (ii) contacting the culture of step (i) with the bacteriophage of claim 1; and

(iii) monitoring for evidence of growth or lysis of the culture;

wherein evidence of lysis of the culture indicates that the culture comprises a species or strain of *Acinetobacter baumannii* bacteria susceptible to the bacteriophage used in step (ii).

13. The method of claim 12, wherein the sample is a sample of blood, urine, sputum, damaged skin, fluid, tissue biopsy, or swab collected from said patient.

14. A method for reducing or inhibiting colonization or growth of *Acinetobacter baumannii* on a non-biological solid surface comprising contacting said surface with the bacteriophage of claim 1.

15. The method of claim 14, wherein said surface is the surface of a hospital apparatus or a piece of hospital equipment.

16. The method of claim 15, wherein said apparatus or equipment is a surgical apparatus or piece of surgical equipment.

17. Use of the bacteriophage of claim 1 for reducing or inhibiting colonization of *Acinetobacter baumannii* on a biological surface contacted therewith.

18. Use of the bacteriophage of claim 1 for the preparation of a medicament for reducing or inhibiting colonization of *Acinetobacter baumannii* on a biological surface contacted therewith.

19. The bacteriophage of claim 1 for use in reducing or inhibiting colonization of *Acinetobacter baumannii* on a biological surface contacted therewith.

20. The use of any one of claims 17-19, wherein said surface is the skin, damaged skin, or a mucus membrane of a mammal.

21. The use of claim 20, wherein said mammal is a human.

22. The pharmaceutical composition of any one of claims 2-4 for use in treating or reducing the incidence of an *Acinetobacter baumannii* bacterial infection in a subject in need thereof.

23. The pharmaceutical composition of claim 22, wherein the infection is a nosocomial infection.

24. The pharmaceutical composition of claim 22, wherein the composition is suitable for topical administration.

25. The pharmaceutical composition of claim 22, wherein the subject is a mammal.

26. The pharmaceutical composition of claim 25, wherein the mammal is a human.

27. The pharmaceutical composition of claim 22, wherein the infection is an infection of the skin, lungs, urinary tract, or kidneys.

28. The pharmaceutical composition of claim 27, wherein said infection of the skin is an infection associated with a burn injury or a diabetic foot ulcer.

29. The use of claim 10 or the pharmaceutical composition for use according to claim 27, wherein the infection is an infection of the skin and said pharmaceutical composition is for topical administration.

30. The use of claim 11 or the pharmaceutical composition for use according to claim 28, wherein said pharmaceutical composition is for topical administration.

31. The use of claim 10 or the pharmaceutical composition for use according to claim 27, wherein the infection is an infection of the lungs.

32. The use or pharmaceutical composition of claim 31, wherein said pharmaceutical composition is for administration by inhalation.

33. The use or pharmaceutical composition of claim 32, wherein administration by inhalation uses a pump, a spray or a nebulizer.

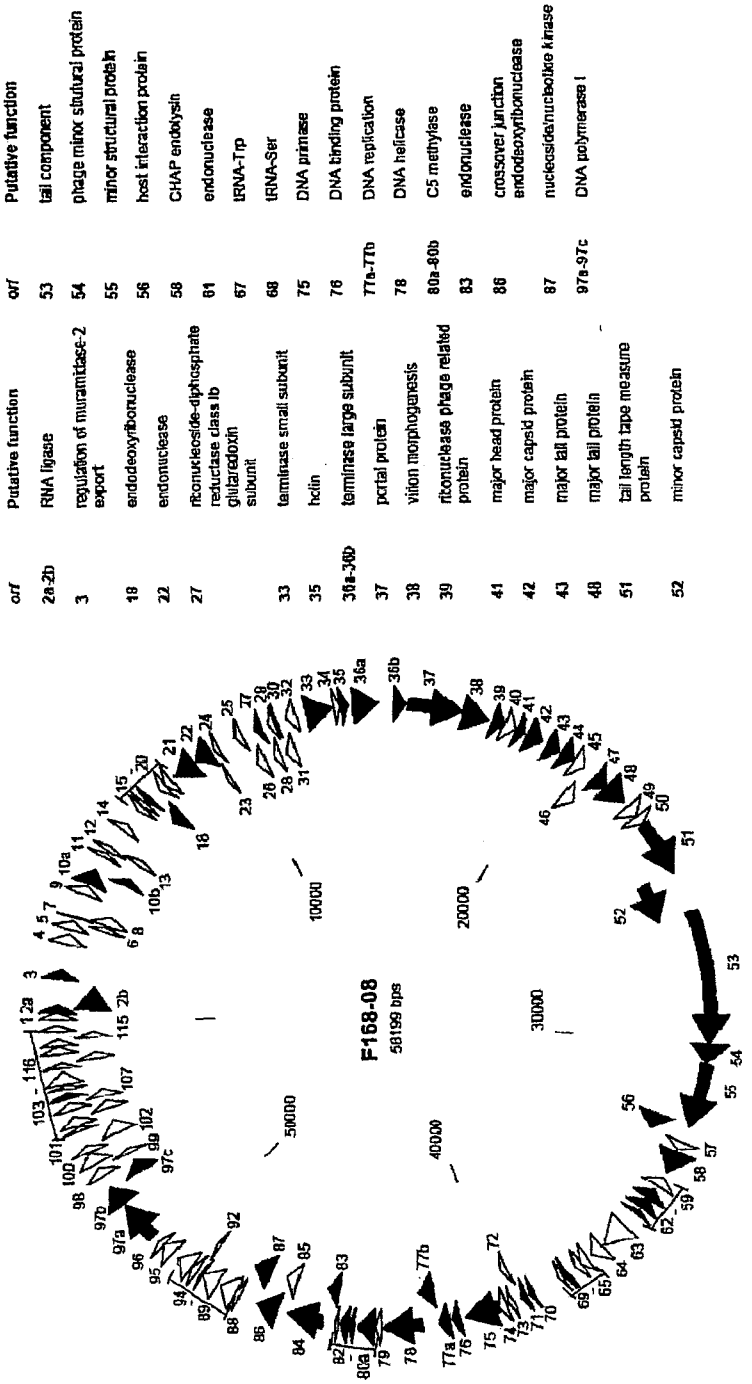
34. The use or pharmaceutical composition of claim 32 or 33, wherein said pharmaceutical composition for administration by inhalation comprises a dry powder inhaler or an aerosol spray.

35. The use of claim 10 or the pharmaceutical composition for use according to claim 27, wherein the infection is an infection of the urinary tract or kidneys.

36. The use or pharmaceutical composition of claim 35, wherein the pharmaceutical composition is for administration by a catheter.

37. The use of claim 5 or the pharmaceutical composition for use according to claim 24, wherein said pharmaceutical composition further comprises an antibiotic for treating infection by *Acinetobacter baumannii*.

38. The use of claim 5 or the pharmaceutical composition for use according to claim 22, wherein said pharmaceutical composition further comprises one or more additional bacteriophage known to have antibacterial activity against *Acinetobacter baumannii*.



orf	Putative function
2a-2b	RNA ligase
3	regulation of muramidase-2 export
18	endodeoxyribonuclease
22	endonuclease
27	ribonucleoside-diphosphate reductase class Ib glutaredoxin subunit
33	terminase small subunit
35	holin
36a-36b	terminase large subunit
37	portal protein
38	virion morphogenesis
39	ribonuclease phage related protein
41	major head protein
42	major capsid protein
43	major tail protein
48	major tail protein
51	tail length tape measure protein
52	minor capsid protein
53	tail component
54	phage minor structural protein
55	minor structural protein
56	host interaction protein
58	CHAP endolysin
61	endonuclease
67	tRNA-Trp
68	tRNA-Ser
75	DNA primase
76	DNA binding protein
77a-77b	DNA replication
78	DNA helicase
80a-80b	C5 methylase
83	endonuclease
86	crossover junction endodeoxyribonuclease
87	nucleoside/nucleotide kinase
97a-97c	DNA polymerase I

FIG. 1

orf	Start position	Stop position	Product aminoacidic sequence	Size (aa)	Homologous/similar proteins				Conserved Domains		
					Name[organism]	Acc No	E value and identity	Predicted function	Name	Acc No	E value
1	<1	207	WTSFFHNIVGYDEPLSKEVLTAY HLKEITDLNELPEHHKKVFETLS AIEYSTVEQALKTFKTNYVEGI (SEQ ID NO: 8)	68	**No significant similarity found.**						
2a	209	481	MEFLKYPSLVNHYAIGKSKRLVN RFDNILWYASEKIHGANASYALS ATGEEYFAKRSGIISKDDKQFSM LPECVTSDIREGTKKAFRILS (SEQ ID NO: 9)	90	RnlB 2nd RNA ligase [Enterobacteria phage RB43]	YP_239225.1	0,010 (30/72)	RNA ligase	RNA_ligase	pfam09414	1e-06
2b	318	1094	MEPTLLMPYQQLGKSISQSVVE LFLKTINNFQCFQNVLPQTFEKV PKKLFEYYPKAESIHVFGEFFGK GVQVMDYDLVKEGKKAFRVFDV IAKYDDGSMAVCGINTWKHLFE QDSIVPYYTLGKTLKEFLETPPS EESALGGYSEGVVLKPLQGYPI NSTQDFLGVKYKTEKYLEVRHK PSEQRKKPPKLNNEQVEALNEL GKYITKQRVLNVCSHGDFELIQN NIGKIMLAVKQDAANEFIKEVGS SFTEKRACRSL (SEQ ID NO: 10)	258	Hypothetical protein KAOT1_13772 [Kordia algicida OT-1]	ZP_02160357.1	6e-05 (66/245)				
					RnlB RNA ligase 2 [Enterobacteria phage RB69]	NP_861881.1	0,004 (61/229)				
3	1220	1525	MDFNTLIEQVQEWSANKGLDKA APEKQFLKVIEEVGEVAAAMAR NDREELVDGLGDTFVTLILCQQ LGVVPHEALDTAYGVISKRTGK MVDGVFVKSEDL (SEQ ID NO: 11)	101	ArpR [Enterococcus hirae]	CAA90708.1	4e-22 (55/99)	regulation of muramidase-2 export	HisI, phosphoribosyl-ATP pyrophosphoh-ydrolase	COG0140	7e-04
					gp45 [Listeria phage P35]	YP_001468829.1	2e-20 (46/92)				
4	2295	2618	MMKLIELDNGRKQVFYNNVLMQ YERRGSDVYGNPLYRVYPINFS FKRLKSVYRNYEKGGWEESYYL IQSYNILADMQNIASEVNAKNTF PEFDQTLLKDYREVSAYV (SEQ ID NO: 12)	107	**No significant similarity found.**				**No putative conserved domains have been detected**		

FIG. 2A

5	2719	2970	MALTMFEKESLQKENARLKREL ATLKASQKLGGGLNEKELQKAL NSCQRIFKTLNRGKRSLVLSKSA MVASVEYSGSGRSKNL (SEQ ID NO: 13)	83	**No significant similarity found.**				**No putative conserved domains have been detected**
6	2948	3106	VVAQKTYKDCSKTAIREAEKSA WEIMSLENDFRNIHHFLKHGTM KAEDKDNA (SEQ ID NO: 14)	52	**No significant similarity found.**				
7	3099	3167	MLNIIVTVISTAAVFKGARNGE (SEQ ID NO: 15)	22	**No significant similarity found.**				**No putative conserved domains have been detected**
8	3157	3450	MVNKKLSDRLTKSIKFSRKKAKK RFIIARVTEEQAYTLRLLKAISKE DEAVCKATNKALLEYGYEEAGG HSYEKAREKFSSLPDVKKWHTN RRTRKR (SEQ ID NO: 16)	97	**No significant similarity found.**				**No putative conserved domains have been detected**
9	3829	4062	MTKNHYKLYVDMKEGTHDYVSA TVYSMFDEKVLWLPDIKKPENV ADYTDEWKNGLYSYYEKLAISEL NDYNATFSHL (SEQ ID NO: 17)	77	**No significant similarity found.**				**No putative conserved domains have been detected**
10a	4153	4611	MTEFANMNKEEVLELLNDWFGV SDYVTVMAELEKMKQVTFTGST DIPLLGGNNDLIGLPQFFKGNEV EPEFPTYEELLEELEKDTWNLEA EDNTYNYSGFLERDMDFKTIHA ENSDTTIAFFAIHTGGRHKSGLL KSNPIYFLKLTTIFKSS (SEQ ID NO: 18)	153	Hypothetical protein EFP_gp144 [Enterococcus phage phiEF24C]	YP_0015042 53.1	3e-56 (116/142)		**No putative conserved domains have been detected**
10b	4572	4850	LFFETYYDFQEFLGNYFYGQGY YAFKHDNKEYTISLDISATSEYV RIYISDENNEELQQSYEQETFMD LDREGVEAYLKDEGIEFTDLKHA L (SEQ ID NO: 19)	92			2e-34 (73/92)		**No putative conserved domains have been detected**
11	5060	5206	MENNKAYERLLKEVELLQNDLM DIEDYSEEVYQAFQKVIDELEYIQ AS (SEQ ID NO: 20)	48	**No significant similarity found.**				
12	5297	5455	MTKQFKNIIATLTILVIALAAASGI ATIKAVENANDKAILAERVEALEK	52	**No significant similarity found.**				

FIG. 2B

			TFR (SEQ ID NO: 21)								
13	5400	5588	MIKLSLPNVWKLWKKLSDKQEY DIAVKSNVIGAYLINHEEEAQKEY TEAYKAHKPTLLKKLP (SEQ ID NO: 22)	62	**No significant similarity found.**				**No putative conserved domains have been detected**		
14	6024	6221	VRGFSEGYLKGVSGRNLKANLE RQVESFVVDLFFIKGNEKPLRNA VAAGLWERWLERLSDSFQID (SEQ ID NO: 23)	65	**No significant similarity found.**						
15	6889	6710	MVPNPSYNLINACVNTPLERGK ASRAADKRRPLYLWNLFLKGSK EEPSGKVALKLSDVY (SEQ ID NO: 24)	59	**No significant similarity found.**						
16	7021	6893	LTWPLFLWYTIRNDKKGVLKAM LERIKGMLRKIRLANGLATA (SEQ ID NO: 25)	42	**No significant similarity found.**						
17	7232	7038	MVAGIQKISLSKGKPVKGVNIKT GEEITFQTVSEVISYGFDKSHVA SCARGESKTHKGFIWKYV (SEQ ID NO: 26)	65	Hypothetical protein [Stx2-converting phage 86]	YP_794120.1	1e-04 (19/51)		**No putative conserved domains have been detected**		
18	7530	7168	MVEWRDIEGYEGLYMVSDQGDI FNCSRNSLMKLRKDRKGYLLVG LTKKGNQKTYRVHRIVANAFINNI FKKPQINHLNEVKHDNRVDNLE WVTNKENSNYGSRNTKNKFKQ RKACKRSKY (SEQ ID NO: 27)	120	putative endodeoxyribonuclease [Lactobacillus phage phiAT3]	YP_025078.1	3e-18 (49/111)	endodeoxyribo-nuclease	NUMOD4 motif	pfam07463	2e-07
19	7810	7601	MNWKAFRLVSLYYLLALVIAFGLI VVITLVFGASVTIAIGRILGNLIILK VIWDMLHKEYEEAKEDLEK (SEQ ID NO: 28)	69	**No significant similarity found.**				**No putative conserved domains have been detected**		
20	8042	7812	LSEKLTKRIILAAVIIAYLITVGIIFG ILWLVSLITGWEQLFFYLGVLFLI DLLWETTKYAFIRYNKDKHKTLE EL (SEQ ID NO: 29)	76	**No significant similarity found.**				**No putative conserved domains have been detected**		

FIG. 2C

21	8857	8159	MLFKKDENKLIKELKQEIELLTGR KAVYQLALDRLEMANEELQKEV DFLKIREAGFEERLKVASEKEVE AIEMANESAEESLLRQEAYDRL GKKFEEVCQKLTVEEEQNKRW EQEMGRLQEEYNGLKREYREL QKAIPSKPQLTATIKVDTKEIQEM LDNALQEIKEGYSPRLQEEPEYT YWIKSEGSSEKHFVSDSPQQLL RKANVFYMPYKAGILTLSESLIE MVTRKKA (SEQ ID NO: 30)	232	hypothetical protein [Trichomonas vaginalis G3]	XP_0013256 48.1	0,020 (38/120)		**No putative conserved domains have been detected**		
22	9436	8933	LEGEWKVVNGFSNYSITKTGKV VNNLTGKILKPFINDRGYAEIGLG DGNIKRLHRVLLSTYNPIEGWEE LTVNHMDGNKLNNNLDNLEWLT HEDNLKHYYDNNKRILVFDDAT GEVLEEVTRMEKASTKYGVPKG VIQELCDLYHEGIYAHENGYGFC RMEDFGLDG (SEQ ID NO: 31)	167	putative endonuclease [Staphylococcus phage K]	YP_024518.1	2e-13 (40/94)	endonuclease	NUMOD4 motif	pfam07463	0.009
23	9539	9426	VLKNKVYAGHVWSYTGREFEK GSPLASKKPIKKVFGG (SEQ ID NO: 32)	37	**No significant similarity found.**						
24	9693	9526	MLIEEDLGGFLVKLIKEVKSVDV ETGLETVYRSAYAASKDLGKYS TSVRNACAKK (SEQ ID NO: 33)	55	**No significant similarity found.**						
25	10452	10237	MKLIDATVVLNYIEKTKNELNTTS PANNSKFGKGWDAGFIRGIESIK GLVKDIIIEDEIPLANPSDMIPKK (SEQ ID NO: 34)	71	**No significant similarity found.**				**No putative conserved domains have been detected**		
26	10772	10449	LEYPEDDYDEGYQDAVETCMD EIKAALSVAKEEDSPEPIKLAVD GNIVAESFTGSSVTPINTLPNNY TKDVLEALLEASEDFYDASEIQA LLKGAIQAIPKGKGVIL (SEQ ID NO: 35)	107	**No significant similarity found.**				**No putative conserved domains have been detected**		

FIG. 2D

27	11087	10821	MGMNRIKVYTKDACAACKMTKR VLTEAGVSFDEVFVDVRNDTET VEMLRLVGFRSFPVVMLDEDFD TAISGFHPPRLKVFIETVKEEA (SEQ ID NO: 36)	88	ribonucleoside-diphosphate reductase class Ib glutaredoxin subunit [Pediococcus pentosaceus ATCC 25745]	YP_804960.1	1e-9 (33/76)	ribonucleoside -diphosphate reductase class Ib glutaredoxin subunit	NrdH	cd02976	3e-12
28	11287	11078	VLYGKKEDLNEEIYSLEREIEDLE GQVYDLENELGSSEETVEELTE EVDTLSERVEELEEIIESMEEWE (SEQ ID NO: 37)	69	**No significant similarity found.**				**No putative conserved domains have been detected**		
29	11465	11244	MSKLPFEKELKEACSKPTLTQR ETALIELVGKLQNALVDSNWDKL IAEQELEYAEERLTSVVWEKRRL ERGDL (SEQ ID NO: 38)	73	**No significant similarity found.**				**No putative conserved domains have been detected**		
30	11520	11467	MQEITVEEFKQEEIGEF (SEQ ID NO: 39)	17	**No significant similarity found.**				**No putative conserved domains have been detected**		
31	11795	11520	MEGIELDNYYNFLEIGYLEGDQA NVETTVYNLTGMLSAKVSDVTE SEFEAAVEEVTEAIDNLTNSLEV LSELFTEAKQYLAKEDKKWEDN V (SEQ ID NO: 40)	91	**No significant similarity found.**				**No putative conserved domains have been detected**		
32	12106	11795	MRAIKMYSIKSYQQYLEKLGTVR KAAADFELNNSFSKKAHELIANQ YAEDIEKLSQKVQEYHELIENIVS DEAEEDEKQLMEYLGTIRKQQKI TEELESGGKE (SEQ ID NO: 41)	103	**No significant similarity found.**				**No putative conserved domains have been detected**		
33	12390	13157	MVRIGNRELEERQRKYLTTSKE PDEYEGVDLTTLKPKMKRFARH YMQTMNIAESCRSVGYNESSGY RVLKREDVKAYLQWLVSENADA AIMSPTQVLEELTNIALRNSSDY TVTVKGDVVEKPIDTSVQLSALN SLAKFHDLLAPDVKVEQSLNIVV DIADDVPNEAEEVEEEEFVEGD FTEVEEEDSDVSYDFLSGFLRK EIPMPFEESNLEVIVNDLIKDVNT HANQIASIQSDLNRMTTDISSVR	255	bacteriophage terminase small subunit [Staphylococcus aureus]	AAP55238.1	1e-07 (42/168)	terminase small subunit	Terminase_ 2	pfam03592	2e-10

FIG. 2E

			DLLIKKH (SEQ ID NO: 42)								
34	13204	13380	MLKLLTEERRRQTESYLADEAS DRKNKEFSQKQMWAVATALVT GVGSALVTIVKLIMS (SEQ ID NO: 43)	58	**No significant similarity found.**				**No putative conserved domains have been detected**		
35	13399	13647	MDVVISIAVVLGGVTTGLVNLVK SMDVVSPKYLPLVSLAIGMVFGL AMSPLLGITLYVGAISGLVAGLS AMGFYELTKTPAE (SEQ ID NO: 44)	82	hypothetical protein BL01378 [Bacillus licheniformis ATCC 14580]	YP_081408.1	0,001 (30/79)		**No putative conserved domains have been detected**		
					holin [Bacteriophage PL-1]	BAA96748.1	0,15 (23/81)	holin			
36a	13753	14514	MKPIYHTCTTSLKDNIEQWYFYG GAGSGKSKFVVQNAILKGLSER RKFLVLRKVDNTIRDSIFQEFLVC LEEWNLLDFCEVKASYMTIKLPN KTEYIFKGLEDPERIKSIQGLTDII MEEATEFTREDYDQLQTRLRHP TARHQQVFVMYNPASKDNWWY QYFHNPATKRPKGSKVICTTYK DNRFLPKAYLDHLQDLKNTNPV YYEIYALGKFASLGKRIYTNWKID SEFKPNQLVKQGYEPRFGLDFG LSM (SEQ ID NO: 45)	253	phage terminase, large subunit, pbsx family [Clostridium perfringensC str. JGS1495]	ZP_0286535 7.1	9e-55 (118/234)	terminase large subunit	Terminase_ 3	pfam04466	1e-34
					terminase large subunit [Lactobacillus prophage Lj928]	AAK27930.1	1e-53 (108/235)				
36b	14906	15295	MIAPEIFDVIKRKKLTNQLIYADS ANLETIEQIKRLGARKIKPVKKGR NTVLHGIQYLQGYTIYVHPRCVH TIKELENYEWKPAKGSDDYENK PKQNGFDHCMDALRYAVNDLIP RNRIRTINKSVLGL (SEQ ID NO: 46)	129	PBSX family phage terminase large subunit [Clostridium novyiNT]	YP_879274.1	1e-22 (49/106)		Terminase_ 3	pfam04466	5e-06
					ORF009 [Staphylococcus phage 53]	YP_239642.1	6e-19 (47/121)				
					phage terminase, large subunit, pbsx family [Clostridium perfringensC str. JGS1495]	ZP_0286535 7.1	3e-17 (47/117)				

FIG. 2F

				terminase large subunit [Lactobacillus prophage Lj928]	AAK27930.1	2e-17 (44/112)				
37	15354	16889	MAIPNGQINAGDIITTNIRRKHFIR RNYDIRELVTLAEMHSRSSSAY GVLYDYYKGNHIAIQSRTFDDTN KPNSKIVHNFPKLLVDTSTAYLA GEPITESGDEKTIKAMQPVMKE NYVTDVNSEEIKLSGIFGHCFEIH WIDRNNKHRFKAVSPMNCLIAY SADLDEEPLAAIYYNTVISDITGH VIRTYEIYTEDKILKFSTDDERDV YKEIPEVLDIRGYEEHPNLLKKFP VLEIIANEERLGDFEAQLSLIDAY NLAVSDSVNDIAYWNDAYLWLQ GFDLSADSDSISNMKNDRVIVTD DTGNVKFITKDVNDKHIENIKNR AKLDIFSLSQTPDLVSKDFTAAS GQALKAATQPLENKSAVKESKF RKVLAKRYELICSYLELMSKEKD LKPNEVTPVFVRNLPQSYAELA DMAVKLRDMLPDETIINQFPWIT DARLEVEKADEQRQIKRADIALQ NFKQTSAVQGASTAAANKLDKN PANTSTITTTDPVAAKEQEKAIQ KKPKTD (SEQ ID NO: 47)	511	hypothetical protein ANACOL_00534 [Anaerotruncus colihominis DSM 17241]	ZP_02441264.1	6e-49 (151/473)				
							portal protein			
				portal protein [Streptococcus phage 10270.2]	YP_598434.1	9e-38 (118/423)				
								Phage protein Gp6		
									pfam05133	1e-49
38	16901	17656	MARKKDKEKRQQEIEDALVALM TAQNHKYHRFTDRFTVLLDGFV NELIVNLADPKLDAFAILQVSQYE AIRKLQAALIDYQEEFREMLLES MSDTLEETLGQLFPNKAIPSATD NAYIEQVIAEAYDYFEEIFLQLLV EIEAIAVGTIPSTEDIVTTIQKLRD RLSYTLRRHIEAQMSAVINLAVIE ASKQYEIELWKWCIRPELTESGT CADCRELAEGGIGNEGLYTLAT MPLLPRHPHCVCILIPYVL (SEQ ID NO: 48)	251	Phage Mu protein F like protein [Lactobacillus casei ATCC 334]	YP_807132.1	3e-06 (33/135)	virion morphogenesis	No putative conserved domains have been detected

FIG. 2G

39	17767	18102	MNPEEQGQGQQVDLTPEVIVGA IESNPELAQAIQPHVLTKDAVSS FLKTDEGLGVVAPMIDQSVSKGI NAWKEKNLENIVQERLAELNPA ETPEQKQLKQMQAQMAAIQKR (SEQ ID NO: 49)	111	putative ribonuclease phage related protein [Bacillus licheniformis ATCC 14580]	YP_078653.1	2e-08 (26/73)	ribonuclease	**No putative conserved domains have been detected**		
40	18107	18436	MLEMRGVAQEALAKAGLPASLA GYVLSDNPEAVKHKVSELDIEIQ NIVSGLVDQKVAGIAAKAAPTNS DDMSSIGGSKTVERLTDLTVEEA TELARTNPAKYRQLVQRG (SEQ ID NO: 50)	109	**No significant similarity found.**				**No putative conserved domains have been detected**		
41	18485	18748	MAHEVTKIADLINPEVIGAFLHQK MLDNLVLAPFAEIDRTLQGRPG DTLTLPQWNFIGLAEDLAEGEEL QSVKLTAEDRKATVKKGC (SEQ ID NO: 51)	87	putative major head protein, phage associated [Streptococcus phage 370.1]	NP_268925.1	4e-13 (36/85)	major head protein	**No putative conserved domains have been detected**		
42	18825	19292	MAIAGKIDNDLFAAMRALTPSDV EITDSYEWVLDAQVAFGEEFDE ETYLFISPKRRATILKSKDFVHIQ QGVSVIKGHLGEIYGMNIVVSNK IGENEAFVLKRGALTLLMKRDYM VEEVREGMKRQTNITADQHYVA FVKDAKRAIFINKVAAGK (SEQ ID NO: 52)	155	ORF015 [Staphylococcus phage EW]	YP_240157.1	1e-15 (55/161)		**No putative conserved domains have been detected**		
					putative phage major capsid protein [Staphylococcus phage PH15]	YP_950669.1	3e-15 (59/160)	major capsid protein			
43	19447	19884	MAKTYNIYQDEVKVQEGVAELT KTITGLTPNTSYKFEVTAVEEGV ESAKSTAVTAKTNPRKVATVTAS QKTMSLASDGSKALTFTVAPED ATNKELEITNSNPEFATYADGTV TAVVAGTTTITATAKDGSGATAN CVVTVQAPA (SEQ ID NO: 53)	145	hypothetical protein ABC1334 [Bacillus clausii KSM-K16]	YP_174833.1	8e-18 (64/144)	major tail protein	Fibronectin type 3 domain	cd00063	0,010
					major tail protein [Staphylococcus phage phiSLT]	NP_075510.1	5e-11 (51/148)				
44	19945	20349	MELIENTELFKSFEDVTLPPETE AIDITDLKLMLGYGNSTIRDNVLK VLKKRARQHICLFINKEVTDFPM ELDYIADELTASRMSQLNSEGLK TESTDITRYDYKDDIYANWYGIL NRWLEQQGEYRNKAFFML (SEQ ID NO: 54)	134	hypothetical protein ul36_44 [Lactococcus phage ul36]	NP_663678.1	0,007 (22/70)		**No putative conserved domains have been detected**		

FIG. 2H

45	20365	20742	MRYNDIVDLIQFNDWEDPDDDY GTISYKTRGTIVVKDLPVSVGSL RVQGKLLQNQDQQWEKRYLIQ HKVFELKNLRVDAVRRHSTGEIL NVYWDNTTGTDQTVSYKVEYR DIRRDKEDGVIWQGS (SEQ ID NO: 55)	125	**No significant similarity found.**				**No putative conserved domains have been detected**		
46	20727	21107	MAGFLEITKRIDFAGLEREFVNE VKGVVEKNSAQMATAVRLNIVR RGNIDTGTYYDGIKSKTEVEGKG KSVTGIVESDVSGNPYGHRGYA VYLEEGTYRHQAFPNFTDALEE YSDILVEQLSRIKV (SEQ ID NO: 56)	126	**No significant similarity found.**				**No putative conserved domains have been detected**		
47	21120	21551	MSNRPPFRARSSSVALQRAIVK EIRAQGINVWDGTNKFPEYPFIKI GEELTSGRTISKDAIGKMHNLTL HIWSDYDSSFEVKSLTDFLVDLLI NSPLNLEDGFCIGEKSLDHVRYT EAANGTYKNERAYLFLDFEVIDS TIEP (SEQ ID NO: 57)	143	gene transfer agent (GTA) orfg8 [Rhodopseudomonas palustris BisA53]	YP_7808040.1	0,008 (28/98)		**No putative conserved domains have been detected**		
48	21577	22266	MEACKSSYIRGTAVLIEVQNDLG EWIKVAAQRGGTLNRTAATLDV SNKEGFGWDDAEAGNKSWSID CDGLFVEDNAGFQALNAAWVN GDCVRVRVKFPSGLTYVGQAIL TDFPYEFGYEDAVTYSLTFQGK GALEEQQVAPTILPKKVEFTNET KEVKVGETLQATIKFTPENVSDQ SVTYTALTPALATIDESGLITGVK EGTASFNVRSNVNTAVSALIDIE VKPAG (SEQ ID NO: 58)	229	hypothetical protein PTH_2181 [Pelotomaculum thermopropionicum SI]	YP_0012127 31.1	2e-16 (47/131)	major tail protein	PhageMaj_Tail, phage major tail protein, TP901-1	pfam10132	2e-20
					phage related protein [Bacillus licheniformis ATCC 14580]	YP_078735.1	2e-05 (31/85)				
49	22411	22776	MIIRFQGKDLNLRLTYKSIHFLEL AFDQDYASFIAEQTPFNQSLYIF WAMLQNESDYEGVSVLDVAELL QDSLDSYEFTLEEYFEKVNSSY ASSILVKQLFKKQHWLVTQRRR KTRTSFRS (SEQ ID NO: 59)	121	**No significant similarity found.**				**No putative conserved domains have been detected**		

FIG. 2I

50	22791	23087	MVLCSDLGIPSSDFWTSTPYEF NGMLRGAYQRQSREASLFLSLV QSKKPVKLEKYQGFELVNETNK PKTTRDMAETMDELDRAAFKEE ELSNLFDYFD (SEQ ID NO: 60)	98	No significant similarity found.					No putative conserved domains have been detected
51	23100	24734	MADKEMRIKVRVDNSDYASKMK DMEGTQSRLGKSTEQTTGIFGK FFNKLNGGASLANSSMLGLGKS FLSTSVGFGTLTAAATPMAAAV MGAAEATKVAGRFAMDSIKDYA NFEGTLKQVQIIAGGTQADMDM LGDTAIEIGGKTSKGAQEVAEAM VDFAKLGFTAKETSEAMKGIVYA AEASGSGVQETAGIVATALNNW NLKATEAEHVADVLAKTANETAA DMQDMGYVLQYAGSSASLAGA SLEDLSAMAGIMADNGIKGSKA GTSLRTAFTNLINPTDGAAAAME SLGVQFKDAEGKARPTMDVIYD LQDAVKGMDDIQIQELSTILFGK PGAAGMSFVLKSTKEQVQDLSK ALVDSTGTAAKQAAAMRETMAG QLDQLGDSVDAIKLKIGRAFTDM FALDAVKGFNKALDGVDEGLSN FGKGFKRTSDLLETSNGLISGTK DANKFVEAVRDAGTNLTNIPFQE SLAQSQVWGIGISKRAYETNEV MYQLNKSIQEFSFLPDDWEGKVW GQASTILKDSVGQMELKLASAA AKGKHGGRS (SEQ ID NO: 61)	544	tail length tape measure protein [Staphylococcus phage phi2958PVL]	YP_0022680 17.1	4e-56 (131/349)	tail length tape measure protein	No putative conserved domains have been detected

FIG. 2J

52	24718	26004	MGGEADISGIMNQTIQENLPALQ TALDEQVAVFGTANQSRLDALQ TFFTNEKTLTDEQKSIMIQGELT HGQQLSDTIQTNNNKILELYQSM GQQDYAQRQETGAAINALQQQ NSEILQNIATTESSSIVETLRAQA SSTGTITQQMANDSIAAANQQY SETVAAASKQYVETVSSINHMS DESIAAAGTTRDELIEKARQQMV GTVDHAKTQKEQTVGEIQKIADK SEEVDGTHIQINADADTTSAMEE LGQLAARINDVFRAFGETAGKIQ GGIDGFESKLKQADNWIAGKVG GIFKARGGLTSGVGYGIGGGNA QYSPMATAVGVGTQLGQGGIN QGVIHNERGREVTMPIQNATYM RPFAAAVANELQAMGGGLGGG GVQEVIVPLYINDREFARATNKA MTEEQQRVKRIANRAVGKKVKE TFK (SEQ ID NO: 62)	428	minor capsid protein [Enterococcus phage F4]	ABs50440.1	7e-80 (151/173)	minor capsid protein	No putative conserved domains have been detected		
53	26001	29993	MTCSNKPNYTPFKLQGLAPTKQ WGLGRSASYERFNPNEFHALED EVKITFPVDFRGKVKGNSNPNP SRGFSHASQIYRENVLRGSQFL SKPSLLFNGAVYNEKTVYNGAM VASTQEVNQGLMFYWEDFINPD PRIKEGDMVTFSVDVRSTGEDIP TGAVAFKGTSNFEEYYKVLEQPI TKEFTRISFTTRFLSKDWEWDE AFGMFWGAENVPVTDYPMFQY DKDKLVGFIQAQESVQLEFSRP MVSTIGKTAYIESGDDMFSNNK WDWSKAVSKGRLNEFDGKYNT NGIKQDWAMPEFIPIFKGSERIH FYKKTTLTETTDAGHGYGKILFY SAANEDSYMNVYKKFPHEAGVY GGYAAEVEVPIGATHYRVHITSE RGSATTEAYVQSSANDWSEFS QEWYDGLSGKLDGKTARAETFY RKEMVEMEFELHFAEAVQKALP NIFKDLTTDAEKQQRLRDIAYQF DSTMIARGRGQGGNNLADWIFYR WAPDGSIEEQTMKQFRGEGLTS VTHPSSYQEWNPQGRIVTSLRS	1330	phage putative tail component [Bacillus cereus subsp. cytotoxis NVH 391-98]	YP_0013758 14.1	2e-20 (131/533)	tail component	Siphovirus tail component protein	pfam05709	2e-15

FIG. 2K

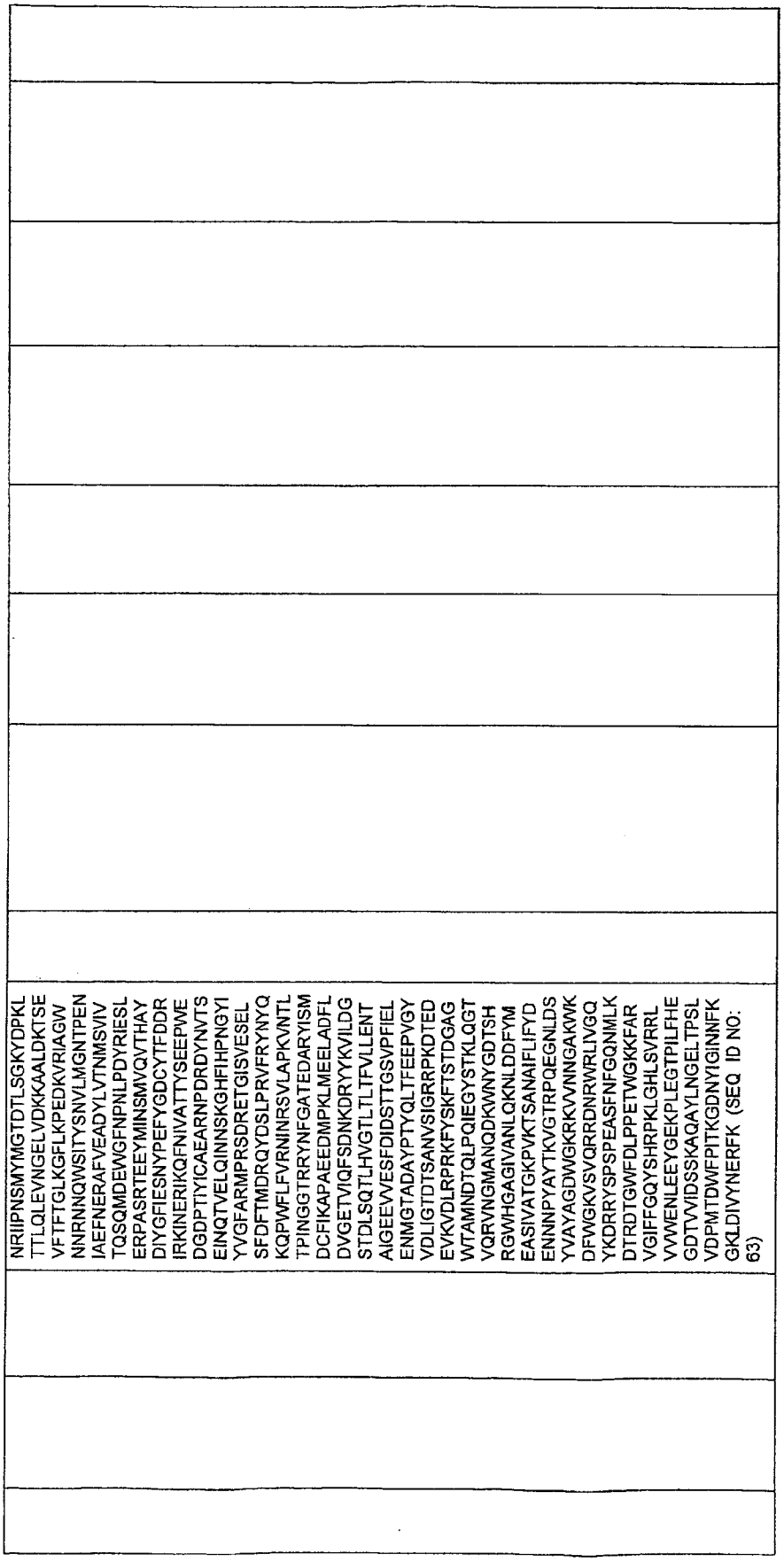

NRIIPNSMYMGTDTLSGKYDPKL
TTLQLEVNGELVDKKAALDKTSE
VFTFTGLKGFLKPEDKVRIAGW
NNRNNQWSITYSNVLMGNTPEN
IAEFNERAFVEADYLVTNMSVIV
TQSQMDEWGFNPNLPDYRIESL
ERPASRTEEYMINSMVQVTHAY
DIYGFIESNYPEFYGDCYTFDDR
IRKINERIKQFNIVATTYSEEPWE
DGDPTIYICAEARNPDRDYNVTS
EINQTVELQINNSKGHFIHPNGYI
YVGFARMPRSDRETGISVESEL
SFDFTMDRQYDSLPRVFRYNYQ
KQPWFLFVRNINRSVLAPKVNTL
TPINGGTRRYNFGATEDARYISM
DCFIKAPAEEDMPKLMEELADFL
DVGETVIQFSDNKDRYYKVILDG
STDLSQTLHVGTLTLTFVLLENT
AIGEEVVESFDIDSTTGSVPFIEL
ENMGTADAYPTYQLTFEEPVGY
VDLIGTDTSANVSIGRRPKDTED
EVKVDLRPRKFYSKFTSTDGAG
WTAMNDTQLPQIEGYSTKLQGT
VQRVNGMANQDKWNYGDTSH
RGWHGAGIVANLQKNLDDFYM
EASIVATGKPVKTSANAIFLIFYD
ENNNPYAYTKVGTRPQEGNLDS
YVAYAGDWGKRKVVNNGAKWK
DFWGKVSVQRRDNRWRLIVGQ
YKDRRYSPSPEASFNFGQNMLK
DTRDTGWFDLPPETWGKKFAR
VGIFFGQYSHRPKLGHLSVRRL
VVWENLEEYGEKPLEGTPILFHE
GDTVIDSSKAQAYLNGELTPSL
VDPMTDWFPITKGDNYIGINNFK
GKLDIVYNERFK (SEQ ID NO:
63)

FIG. 2L

54	30006	30602	MITVLNANGQTVAHFVNNVSEG VPYFEPTLTENETLVSTFSFSVP LDCDESQYLKGLNKVLVKDKDG DLRQFNIIHTEEVFQEVDSRILVE CEDFSISEMNDTVIYPFNGHNLG DTLTKAVKGTGWGIEYSADTWQ EGEEPFILAEYTNMREVFGNIQK TYDVDFKFTAERTAFNQTKRIVK VYKKQRSSNRPLLHL (SEQ ID NO: 64)	198	phage minor structural protein [Paenibacillus larvae subsp. larvae BRL-230010]	ZP_02240714.1	3e-08 (49/192)	phage minor structural protein	No putative conserved domains have been detected		
55	30631	32562	VQYNTIKTAILPYYTGVDGKVWT LKGMVPVNPIEGITKDKESPLVV HNQAHADYDEPFFFKAMPFKAS STNPEQVYRQGVEELLKHIAPIY TYTVNVILLNRVQGWEGETLAL GDTVWMKERVGSREIGLEARVI EYIYHEDDPSLDEVTFTNFREID TYDTSDIAGIRDALNDLKDQVDS NTVIIETTREQISKLEEGQSGIIED LGNKNSISGDTPKPNPIDGDTW FSTRVNEAGQTIHEIKVWDGVE KVWKLSMDTSKAFEAEDTAKAA QKDAEESLDKANQAVADADTAK TAAQEALDRYNNLMISGRNLAL NSQKITVPDVVAGTTTRRKTIPL SIPTKLGTEYKLKFKYKLTEGTLP EGITVGYNVPKLAWASNIVTIPT EGKDEGELFAELTTNATEGDVLL IYQGVRSAVKNDDNFDFTEVYL VEGDKIGDWQPAPEDAIASITNI NGEITSLVTKTDGLETSYSQISQ TVDEIQFTVGDKADKSQITQLQD QINLRVEKDDVINQINVSTEGIIID GAKVQITGKTYIEDAVITDAMISG LSATKLTAGVIDASKINVTNIDAS QIKAGTIQGIDIIGSKITNPFEIGS EGYTLAGQTVMERAQVKIDYSV SETGQKRLVNTSCKRYSKSAT (SEQ ID NO: 65)	643	phage minor structural protein [Paenibacillus larvae subsp. Larvae BRL-230010]	ZP_02329034.1	3e-10 (63/225)	minor structural protein	Gp58-like protein	pfam07902	2e-11
					hypothetical protein P9_gp44 [Streptococcus phage P9]	YP_00146924.1	2e-07 (59/217)				
					hypothetical protein PEPMIC_00050 [Peptostreptococcus micros ATCC 33270]	ZP_02093315.1	4e-25 (71/155)				

FIG. 2M

56	32483	33034	LTTAFQKLVKKGWSILHARGIQN QLLNLDGTINSFSSLASDGLSIQ DSLGNSGYLSAELLMQFSNTGK KIYPGNSWVTNTDRIVPSLTMNK CAIGWLFLWQPYDTTGGKPYT WDYTYYLVPKAHANFNSGKGIN MRLQGAGKGGGADDTVYKYVY VSNDSITGTVNNGTGNGAKWVL TGVFSV (SEQ ID NO: 66)	183	tail host interaction protein [Lactobacillus casei ATCC 334]	ABD83364.1	3e-08 (37/132)	host interaction protein	**No putative conserved domains have been detected**		
					putative host interaction protein [Lactobacillus phage A2]	NP_680496.1	4e-05 (37/129)				
57	33048	33335	LRVWIEDKVGLLTGYSTEPLEGY KCVNIDPSESLEMLGGMLDFHN YYYDGEKVYRDTNNDFQKFLEE EANKPPEPSKEEMEERLAKLEA LLADLL (SEQ ID NO: 67)	95	**No significant similarity found.**				**No putative conserved domains have been detected**		
58	33383	34096	MVKLNDVLSYVNGLVGKGVDAD GWYGTQCMDLTVDVMQRFFG WRPYGNAIALVDQPIPAGFQRIR TTSSTQIKAGDVMIWGLGYYAQ YGHTGIATEDGRADGTFVSVDQ NWINPSLEVGSPAAAIHHNMDG VWGVIRPPYEAESKPKPPAPKP DKPNLGQFKGDDDIMFIYYKKTK QGSTEQWFVIGGKRIYLPTMTY VNEANDLIKRYGGNTNVTTYNY DNFGLAMMEKAYPQVKL (SEQ ID NO: 68)	237	amidase [Staphylococcus phage CNPH82]	YP_950623.1	4e-17 (49/134)	CHAP endolysin	CHAP domain	pfam05257	3e-10
59	34550	34248	LDVPHVYLRDTKDCSKITIGNLP TEPFEVTVSAYREPSDITVGMIP VSFIEGDFDKYYEDFASDITKRL KDMAKLKEDSHKQAVDSINKEK VAEVVMFFE (SEQ ID NO: 69)	100	**No significant similarity found.**				**No putative conserved domains have been detected**		
60	35006	34647	MAWIRTKENKLYKDADGNKVDT KDWKNAPLSMWNTTTFMEYVA YLNQQKFGKVPINASLQTLRAIM KKDIERFGAEALKIFLEMAIKDYH GNSRYPTLSYSQARLLYMERFM SVALEKS (SEQ ID NO: 70)	119	hypothetical protein Plarl_22418 [Paenibacillus larvae subsp. larvae BRL-230010]	ZP_02330367.1	1e-05 (28/98)		**No putative conserved domains have been detected**		

FIG. 2N

61	35349	35008	MSIELSQKRFLPNNFNLPCINHK DENPKNNKVSNLEWCTHKYNS NYGTAIERKTKKISKPVRATNIKS GDVIEFSSMKAAHRAGFDESTIA QCCRGVYIQHNGYVWEFIEEGI (SEQ ID NO: 71)	113	prophage LambdaSa2, HNH endonuclease family protein [Lactobacillus rhamnosus HN001]	ZP_03212345.1	6e-15 (49/112)	endonuclease	No putative conserved domains have been detected		
62	35591	35424	MCYDGFIKDLRRGFIMEVWKPV VGFESHYEVSSLGRIRSLDREVY SEKRLIYEIS (SEQ ID NO: 72)	55	gp33 [Mycobacterium phage Ramsey]	YP_00224182 0.1	2e-04 (24/38)		NUMOD4 motif	pfam07483	2e-04
63	36058	36882	MAKGLEAIAQAAQAQSKGSGEQ SKKTYLKKGQSIRARIPEDILENL HVNQVVSVFEPQVLPTLSYHAE GRTDVRDLYHEATEIMLADHRA KVESGEIERGSQADKDSYKAARI LTPKPLILFGVIPLADFTQGTKKT NTYPAGEPILLETNLGRDNANID ALTNFLSKETNAKKFPKKAFEIT CEAANRYTFTPLDDEDLTPEELE VFKATEGATVPEEDFENAIFEST VERQIEDLKKIGFDTTRLPNLPTA APSPSQGADEAGTVDPSGIDF (SEQ ID NO: 73)	274	No significant similarity found.				No putative conserved domains have been detected		
64	36934	37365	MKKDNPQVNPIKFTEEDYFRLL QTVVMTNTFIGSLSAGYQGKER LEKITKIAENMFVLNRLMESAES NGEDWGDEMLLDSLYSDSEVLV TKYKHLLSEAQLESINNSIKNFAE SAEKARKEAYEEKVAQAEVIDFK KGQEEAR (SEQ ID NO: 74)	143	No significant similarity found.				No putative conserved domains have been detected		
65	37489	37749	MLKEAVSESLWNAAYEILHTTM ATADKVIALVTVYNASNLEESTY AYEAIQDSVNKAICGGAVEDVK WKQFVGSLDSDYKEFFEKV (SEQ ID NO: 75)	86	No significant similarity found.				No putative conserved domains have been detected		
66	37751	37951	MDYSKFKIGDTVMYQGQLCGA GTVINGNTYTVVQLTSKPRYAFII DEHGNKKLIQMGFNFAKIKEA (SEQ ID NO: 76)	66	No significant similarity found.						

FIG. 2O

67	38192	38261	GCGUUGUAAGUGUAACGGCU GCACAAUGGUCUCCAAAACCA UUAGAGAAGGUUCGACUCCUU CACAGCGUG (SEQ ID NO: 77)					tRNA1-Trp			
68	38266	38351	CGGGGAGUAUCAUAAUUGGAA AAGCUUCGGUCUUGAAAACCG AUAGGCGUGUAAAAGCGUUU GGGGGUUCGAGUCCCUCCUC CUCGG (SEQ ID NO: 78)					tRNA2-Ser			
69	38381	38506	MNVESRNSEKAWNRAIVKAEQE AAKKKMERLAKMRAKSKRK (SEQ ID NO: 79)	41	**No significant similarity found.**						
70	39337	39462	MKDTVTISKSEYERLLKAEAFLE ALEEAGVDNWEGYAMAFF (SEQ ID NO: 80)	41	gp21.6 [Bacillus phage SPO1]	ACI91017.1	0,0019 (18/36)		**No putative conserved domains have been detected**		
71	39531	39731	MILRIGFFWRSNSESLHCKSIEYI DMFQCGEEGYYKVVFKINEYTY EEHLPDSAYTAITLINKEEE (SEQ ID NO: 81)	66	hypothetical protein EFP_gp156 [Enterococcus phage phiEF24C]	YP_0015042 65.1	9e-10 (30/59)		**No putative conserved domains have been detected**		
72	39731	39943	MNLGQLLDTVEYGTRVRLVYYK STYNSDEYITTFVMSDTLEYTKA YELVEPHIEKRSNYNLCYSRWKI MC (SEQ ID NO: 82)	70	**No significant similarity found.**				**No putative conserved domains have been detected**		
73	39966	40100	VETMYTVIYKNAVESEPALEGGS FLTDAPKTDGLKLMTFGTRVF (SEQ ID NO: 83)	44	**No significant similarity found.**				**No putative conserved domains have been detected**		
74	40168	40386	VWNQWTLYWTDRETGEEGNFK IPRPNALFIGMPIDIDEYRYTVTA VSTPTKEVWTERIPFDFGTKPP WEHNN (SEQ ID NO: 84)	72	**No significant similarity found.**						

FIG. 2P

75	40409	41353	MLDTIHLTKDIQIHIDIQEYLERFE VWNRAKWTEDRLIAASPFRDDNH PSFFVNYNNDWAGTWGDSGTG DSGNFIQLVAELHETDYETALEM LKEEFWKPYEAPAISVKLSVKK EKSIFDIPTHNTSKYLLGRGISKD TQKLYRTSEDESKVCLPYINGM GLATALKYRRTDNKDFFYEAGN NHLKNMLFGYHVIYEKLPNTLVI CEAEIDAMTAYEMGFVGISLGAA NLIERQVDLIKKVDVKNIIIGTDND EKGNLAAKSIDDAFWKTHKLFR YDMPSGYDLNLYWQEFHKAPPL KKISEPKLLRRKLWYIQ (SEQ ID NO: 85)	314	DNA primase [Bacillus weihenstephanensis KBAB4]	YP_0016427 82.1	6e-39 (106/314)	DNA primase	TOPRIM primass	cd01029	1e-06
76	41524	41757	VAEFLGRTPESVKAKYYELRKQ GLLEYPSSINKKWTEEERQYYL DNYGKISNKEMARKLGVKTSQLI QLKWYHTHKK (SEQ ID NO: 86)	77	DNA-binding protein, putative [Listeria welshimeri serovar 6b str. SLCC5334]	YP_8494401. 1	0.044 (23/59)	DNA binding protein	No putative conserved domains have been detected			
77a	41833	42144	MRKQTLLEKLKQVTGKTEKELN PTLSHIHIQLCGGSGTGGKFGAA KVPYDYSDNFLFNSPARDTQKD VYKQLEVYVESFKRDFQKDGNI NQDERPIKKYLSME (SEQ ID NO: 87)	103	DNA replication protein [Paenibacillus larvae subsp. larvae BRL-230010]	ZP_0232877 5.1	1e-06 (27/78)	DNA replication protein	No putative conserved domains have been detected			
77b	42142	42611	VKIKVMEKTSTAAALLNEYMFMS WQASVILKTNMKQPPAYFLDVN SFQTLYNKFTRNGIAKDIAEKTS REYYEMMELAETAPLVVFDEIG NRSATEAFRADLHDIINKRMVNK LPSIFTSNHPIEYLEQVFDERLAD RVRERTIMVYNFKGESHRGL (SEQ ID NO: 88)	156	DNA replication protein [Bacillus weihenstephanensis KBAB4]	YP_0016427 86.1	7e-34 (73/150)		PRK08116, hypothetical protein	PRK08116	9e-09
					DNA replication protein [Paenibacillus larvae subsp. larvae BRL-230010]	ZP_0232877 5.1	2e-27 (65/148)					

FIG. 2Q

78	42623	43756	MASITAEMLLSKVINENDVQALN RHGVSEDLFQSPIHKDAYNFIIKF SRENEGNAPSYQTLLQKVPELD YQSSTEESFTSLTKSLKNSRLQV DTAAFINKDLGEFWENSVKSDD PTEFINQTIAALEQIKAEHNVGGA SGRRLEKASEWYLEEFYKRKEG LSVKFWDSHFESLTELIGGGYQ SGNVYTWYGRSGRGKSTITLVE AIEAAVQGANVLMWVLEMPKYE FASRAISFISARDEVKKSRINGSD YLAGFNIANLTQATFDTAEEEQD FVDFINSLNDKLEGSITIRAVDDE DFMNRSLKQLERDIVENGADVV VIDPFYYLHYEKNTSKTAGGDAS QTSKALRLLAGRTKTVIHAITQAE EDSNEKRRRRA (SEQ ID NO: 89)	377	replicative DNA helicase [Enterococcus phage F4]	ABS50442.1	3e-139 (234/301)	DNA helicase	DnaB-like helicase C terminal domain	pfam03796	1e-04
79	43794	43988	MSLLEDAAYVLAFDSCDSRFAV EVVKGRSGNEGKQVEGIFLPVIG YVEESSDEAVTDVFEGIEF (SEQ ID NO: 90)	64	**No significant similarity found.**				**No putative conserved domains have been detected**		
80a	44001	44498	MIIWSLFDSGNGCYSQVFSEKE GVENYSIGMDKEKGTSKNHLNL DLADMSGYFGESNMIKSLENLP KPDVIIASPPCESWSVASAMAG GNACWNHLKGDPFTIRTSKEYE SVQFNHENSFYNRMNGELTVFN LIKIIKHFQPKIYIIENPAFGKIWEY IDKVLGF (SEQ ID NO: 91)	165	putative C5 methylase (MAV1virus-like) [Haemophilus somnus 2336]	YP_0017840 27.1	2e-43 (80/170)	C5 methylase	Cyt_C5 DNA methylase	cd00315	4e-05
80b	44540	44721	FEIKKPTKFKSNINLNLKSENVKA GTEFRKASRIGGSYNVRSNIPLT LIDEIYKRIEEEL (SEQ ID NO: 92)	60			3e-05 (29/60)		**No putative conserved domains have been detected**		
81	44722	44946	MSFYLSQMNNLKEKIRYEKTSV KLIRESIERIGKPTGEYSLGYTDA LKMELLIHQKMLEDAQKELLDLE KERNK (SEQ ID NO: 93)	74	**No significant similarity found.**				**No putative conserved domains have been detected**		
82	45019	45123	MTATKELWKPLVFKGIHSDIYEV SSEGLVKKQVD (SEQ ID NO:	34	**No significant similarity found.**						

FIG. 2R

		94)								
83	45116	45472	LTDKLLKPQDSGYLHVRIPLEGK YYNARIHRIVAETFCERPAGCNV VNHINGDKKDNRASNLEWTQR DNVIHSIKLREEESKHLSMIEKM DMLLEKLIPSPEAKYNFMEEYVE WLKG (SEQ ID NO: 95)	118	DNA endonuclease I-HmuI [Salmonella enterica subsp. Enterica serovar Schwarzengrund str. SL480	ZP_02686476.1	7e-10 (32/74)	endonuclease	No putative conserved domains have been detected	
84	45457	46485	MAKGLTAINKAAGKTLVDTIAED FKRQLNKWGETGYTYDSEVHH QLMRDYLKIVDRNPFEDFPENV PVFRSSGTGKCLREQTLFAIDKI EGSDRKDPPKMQAHQSRWVQI GTKVGDMIQEQVLMMEKNYRR FTGEDCHFRFERTEEGFPHFEE FSTTFKKYKSGRMEFITGGSMD GIMIWTDPSSGEEFRVGLEVKS KQTTPAATSAFSMRQPNSKHV WQVKNYAMLKDLDLYLIVYVNC AHKSWEMAEEDYAKNPDLQVF GVNITEQDKKDVRNRFFTAIEHA HAGTLPPLELSGFTFSDYKYALA NSLTYKELEELEKKAVSKFDQKA LEEIKKIRGDVK (SEQ ID NO: 96)	342	hypothetical protein BAT_0151 [Bacillus pumilus ATCC 7061]	ZP_03054125.1	6e-50 (116/323)		No putative conserved domains have been detected	
85	46485	46814	MNESIYEGIPEDILQEKFYGVFIK FRCDNRTKPLAMHISELSKEML DATYLQREAGESNIILKDVNTGL EMAFDLTDIVVYSTKEIALGDTE AYYSFAEHMADMMLGDD (SEQ ID NO: 97)	109	No significant similarity found.				No putative conserved domains have been detected	
86	46807	47385	MIKIRFISFDVSSVSTGVAVIDRE PSGYLTLVHTDIISTNPKHNVGR RLKNFAEAVQILLETFRPDYVVK EQTIARMATQHILLKFAGVLEMIA SNEGFPKIYEYSPTTVKKVVGG HGRATKEAVLMGTTEYINWNEPI DLVIDDISDAVAICLTHIGKEFVLV PLGEVEKAKEEAMIVEAEASKYL EEATE (SEQ ID NO: 98)	192	crossover junction endodeoxyribonuclease RuvC [Bacillus weihenstephanensis KBAB4]	YP_00164276 69.1	4e-17 (58/159)	crossover junction endodeoxy-ribonuclease	RuvC_resolvase	cd00529	3e-14

FIG. 2S

87	47382	47951	MKQQLRIAITGTSRSGKDTFAQA IQKKLVEMGFAEAMPIAFADPLK QLYKRYFFYMEDKEKPRDAYVTI GNAMREVNENVWINNLLIQAAK DWDEGFSTLVTDVRFENEAKTLI NDYGFILVKVDADPLIRLVRAEAL GETLDLNNKGDIEVGMIEPHLTFI NNGESDLMQMDKYAEIIINMAQE VANG (SEQ ID NO: 99)	189	hypothetical protein SERP1509 [Staphylococcus epidermidis RP62A]	YP_189074.1	7e-12 (53/180)	Nucleoside / nucleotide kinase	Nucleoside / nucleotide kinase	cd02019	0,010
88	47944	48096	MANLLISEKSYYEKLVEAETANE FRMVLIRLINRVVMKVKVPLEVR ELFL (SEQ ID NO: 100)	50	**No significant similarity found.**						
89	48110	48601	MYYERFGDVALPDSLANILSTYY MQDDTRGDLEGTNKFARCSKM EYSFASDKKEKRIRTEDLYKESP INLEVLEGNGYSRNNIASSLDME RAALRTDLLKAMAKADLTEMEK KVLELNLIYDYTMREIEVLPEMP SRSTLSRHLTSARKKDYATNLKY FQKGA (SEQ ID NO: 101)	163	**No significant similarity found.**				**No putative conserved domains have been detected**		
90	48676	49161	MPRTNNKISRKKALEVYLEGSN PLAAISELIEEHTWTVGFDMESA TFYKERTSNPYDTCKNPRCKLC KQIREHAERIPAYSLGKTLAKPF EELSLGHFGKLAANDVAKSDMP KLLKVSMKDINNHIEMLVEKNWI RQFHQPSKRLRVIRTSYPTAFR DWCL (SEQ ID NO: 102)	161	**No significant similarity found.**				**No putative conserved domains have been detected**		
91	49163	49240	MRQFKKRMYEGKKQRIAEAKKG EWA (SEQ ID NO: 103)	25	**No significant similarity found.**				**No putative conserved domains have been detected**		
92	49240	49350	MKQYIKIGAAILILLIGVAVWLIEFI LPFVLLKWAL (SEQ ID NO: 104)	36	**No significant similarity found.**						
93	49369	49563	MGLLERITYSLFIALVVVLAVGAF FVGVYWLAVWTSGLGGLGTFV AVGIVMFVFTALAVFLGFD (SEQ ID NO: 105)	64	**No significant similarity found.**				**No putative conserved domains have been detected**		

FIG. 2T

94	49577	50008	MKLKDLLEVVDPMQDISLEIAEL TAPEGIYAKDIQKLRPMAVEMEV VDVHTAWYSGEDSIETTLGVVV TGGVKVMRKLFEENFTIDEMSE MWYGWDNEGLLYGWENGEAG EVYNILEENGYNMDSIKIMYGAF VTLGELVGAI (SEQ ID NO: 106)	143	**No significant similarity found.**						**No putative conserved domains have been detected**
95	50225	50602	MSLGMFDKELLAALAALRWVVE DPEIKERHDEILNTAYMENAYEK GDSFPDEKFVEWDFINALTTFEI EAAARGLITDDEAYDEEDDMDW ASDTYSCGCCTCCGCTCDYYM WEDDGSFDEDDLED (SEQ ID NO: 107)	125	**No significant similarity found.**						**No putative conserved domains have been detected**
96	50606	50791	MANYYVLKRLDDGSGKLHQVKC YKSLDKAIKYAKEMSTFKKTYQV AGQFDMNRLANTGRLI (SEQ ID NO: 108)	61	**No significant similarity found.**						
97a	50988	52235	MKNSAKDKERLKLVKEYLEEGK VSREEDKLNKNFSKAEALRIYQK VQEMEREAKFDEIRKKEWKKFPI INNIVELASWIDNALECDNEYLA MDFETVGDNGGTDMYREEISGF SLTYRYKGEIINGYVPMRHREED GSPSHLNIANVKWAEEGIKRVFE SDKATVWHNATFDMGLAKASLG IAPRTPVHDTLILMHLLDEDLPSY QLKVLATRFLNIPSDTFEEMFGK NAKFADIAVEIARWYAGKDTYVG FLLFEWQLNILNKPSFAKIKKVYE RIERPCIMATFEMESEGFHINME EVEVQRKESEAELEEISARLQAR FGDVNFSSPSQLLKLLYVDNDW SKYVTPDHKSILRGHVGYNEHGI SNNKLFALMPNGSVILDPVVNAE GKVVPKNDRNKLQANAKAMKK DCQSC (SEQ ID NO: 109)	415	DNA polymerase I [Enterococcus phage F4]	ABS50441.1	2e-174 (294/299)	DNA polymerase	DNA_polA_I Ecoli_like_exo	cd06139	3e-27
					DNA polymerase I [Pelotomaculum thermopropionicum SI]	YP_0012127 08.1	1e-28 (90/255)				
					DNA polymerase I - 3'-5' exonuclease and polymerase domains [Bacillus pumilus ATCC 7061]	ZP_0305429 7.1	3e-28 (108/339)				

FIG. 2U

97b	52279	52881	LTAFVNKIDTFIAPDGKLHGQFN QFGTVTGRFSASNPNLQQQPKK ARKMFEAPEGSLILGADFSQQE PRLLAHSSGCQELINIYNEGRDL YSEMASAIFNKPIEECLDGSIYRK NTKMIVLAIMYGMGAYSLADILRI DAQEAQKMIDDFFVVYPEVEAW IEGNKKTVVKQRYVETLFGMRR RFKHENFDILKKELELLR (SEQ ID NO: 110)	200	DNA polymerase I [Pelotomaculum thermopropionicum SI]	YP_0012127 08.1	5e-43 (85/184)		DNA_pol_A	pfam00476	1e-37
					DNA polymerase I - 3'-5' exonuclease and polymerase domains [Bacillus pumilus ATCC 7061]	ZP_0305429 7.1	8e-40 (87/185)				
97c	52835	53227	MKTSTSLKKNWNSLDENDKKLR SAASRALRQATNALIQGGAASQ TKLVMNAARIRLKELSEARGEPN SFGFLAQVHDELLFKVPENVTQ QEVDAIEDVMINTVKLVVPSKTDI EIGKNWGKMTARKDWFK (SEQ ID NO: 111)	130	DNA polymerase I - 3'-5' exonuclease and polymerase domains [Bacillus pumilus ATCC 7061]	ZP_0305429 7.1	7e-14 (50/121)		DNA_pol_A	pfam00476	7e-10
					DNA polymerase I [Pelotomaculum thermopropionicum SI]	YP_0012127 08.1	3e-07 (37/100)				
98	53302	53583	MNSLYEQFKEGTLKEGQRFSVT GTIVLIDAEDPALPLKVDIDGEGI KWLKEGAIKYMEPAAEKLYEVSI GGRLLSYYGSDYEEGKWTCFFV EK (SEQ ID NO: 112)	93	**No significant similarity found.**				**No putative conserved domains have been detected**		
99	53543	53704	MKKGNGHAFLWRSREEPKDIFV QAFPMSFLEKHFPEVVEIAKESN KEEGGNAL (SEQ ID NO: 113)	53	**No significant similarity found.**						
100	53701	54093	MKRFAIITRIEECTPDEDLLELGK AYEIVNELVGGAHVYVDERHKR YFVDSHQYVEVAEGIFELTLGML LSKLDEDINTNLEISFEGRATKIV SENYYKDELKDYFDREVKWYSP DTVVDGLSILLEGGV (SEQ ID NO: 114)	130	**No significant similarity found.**				**No putative conserved domains have been detected**		
101	54096	54311	MEIKVEQPKEILLEVGWRYTSD WIVNSTTVSVEDNVYAYENACY KVLEELCESIDAKYIDICFVREAT	71	**No significant similarity found.**						

FIG. 2V

			ENA (SEQ ID NO: 115)						
102	54304	54765	MPKKYYLKAISMYILYAFIAAVIIG GTFLLVGAFVWVGKYVYGRFGD TVGTILFLSTAGLIALCTALYYEA RKEFRKDALRVRIQDPEDGINTQ SHKIVYMLPEDVIRQASTIVGIIPK DIQHIESEELRKKGSPCHHEVFT SGVWIYAYHRV (SEQ ID NO: 116)	153	**No significant similarity found.**				**No putative conserved domains have been detected**
103	54782	54901	MLREIWDLNYTFKTRGKLMEKLI DRGVGLDGEFLKYLVD (SEQ ID NO: 117)	39	**No significant similarity found.**				
104	54957	55235	MNYEEFKKEIESIDYLSVENRYD RVLVYSSLGDYPLVAVSILETGF VDYNWRGHVRARDIPVLTEAVE KFAETPYEERFPKKLLPTYWRKL C (SEQ ID NO: 118)	92	**No significant similarity found.**				**No putative conserved domains have been detected**
105	55180	55404	MRSVFQKNYYLLIGENYVSGITF TYPWLSADCEPEEPIEVTFNEAF PHLFTNRNKEQASKMLDAAKIK HTWEVV (SEQ ID NO: 119)	74	**No significant similarity found.**				
106	55448	55666	VLLTELALIFWEEGSVHEVIKRN GTLIIDDDDTLGRGIRNSDDILSY LNLEYPVKNGSSGGRHHEKHW GTHN (SEQ ID NO: 120)	72	**No significant similarity found.**				
107	55614	55907	MEVVEEGIMKSTGERITRDNIKE GMKVVCVKSIYESQGYFTVGKE YEVVMGNCGYLGIKDNGRDGFI WDCAIFNEDKFVFEILEEPSEKS FFKSFRK (SEQ ID NO: 121)	97	**No significant similarity found.**				**No putative conserved domains have been detected**
108	55795	56040	MAVMDLSGIVQSLMKTSLSSRF WKSLQKKASLKALESKIRELNNH QQELFQKRDRINKQAIQLGSKA RRLEEAKALIEKYI (SEQ ID NO: 122)	81	hypothetical protein EFP_gp188 [Enterococcus phage phiEF24C]	YP_0015042 97.1	0,003 (24/53)		**No putative conserved domains have been detected**

FIG. 2W

109	56135	56260	LWKALKKELSEQLSEDLTPADIT VLNIIPMDKKQSSLITGI (SEQ ID NO: 123)	41	**No significant similarity found.**	
110	56274	56684	MLTTDFIKAVEKIGLEVDNSYSS VLYVESHDGVVVSINKGCSETFT WCNGTDIHVGSLLELIPLVEEYA NTPIGEREKKVSEKPLESYPIEEL GEAISKILLNKHNPNAQVVISQE RIHFYEPKWSTPSEWALENL (SEQ ID NO: 124)	136	**No significant similarity found.**	**No putative conserved domains have been detected**
111	56763	56951	MEDLFKFACTLVLMTVLISGYVAI QLVIIAVAGTFLPTWAFVIVLGWL VYTNYRVLLKGGEY (SEQ ID NO: 125)	62	**No significant similarity found.**	**No putative conserved domains have been detected**
112	56951	57136	VNTVYQDTQDIYLKAFWICIDRA RNRAGVTWTYLQGGDTPRAING TANPSIKKDFAAYGQA (SEQ ID NO: 126)	61	**No significant similarity found.**	
113	57209	57421	MNILNGSEMSRLIYMVECQLAD VKCNLAFYQQDSISGSPGIIESLT EDLTELTRIKARLEVMLEQFEKL V (SEQ ID NO: 127)	70	**No significant similarity found.**	**No putative conserved domains have been detected**
114	57434	57649	MDLTAEELTFLACLVENNNEEV QDSINIYKSFDKDAAAKVLEKQL LESIRLASRLREESKKSMLIGGL SIC (SEQ ID NO: 128)	71	**No significant similarity found.**	**No putative conserved domains have been detected**
115	57643	57834	MLIKKEKKAYLFTIYGLHSYPSVI GVDSYSDSVAMERFYKIWRKHY PKHYKTHKEFTVKKFDI (SEQ ID NO: 129)	63	**No significant similarity found.**	
116	57897	58037	MIPEGTYLKDSSGLNHYFIEGHI VGVRTGVRGYQTVVWDKELDK NV (SEQ ID NO: 130)	46	**No significant similarity found.**	

FIG. 2X

Phage	Titer (pfu/ml)	Phage sensitivity (%) of EFS strains (n=105)					Total of infected strains (%)
		++++	+++	++	+	-	
F168/08	$6x10^{10}$	22	11	10	4	53	47
	$6x10^{9}$	19	14	8	3	56	44
	$6x10^{7}$	16	4	2	3	75	25
	$6x10^{5}$	15	1	0	0	84	16

FIG. 3A

Phage	Titer (pfu/ml)	Phage sensitivity (%) of EFM strains (n=56)					Total of infected strains (%)
		++++	+++	++	+	-	
F168/08	$6x10^{10}$	6	5	5	0	84	16
	$6x10^{9}$	4	6	4	2	84	16
	$6x10^{7}$	4	2	0	1	93	7
	$6x10^{5}$	2	3	0	0	95	5

FIG. 3B

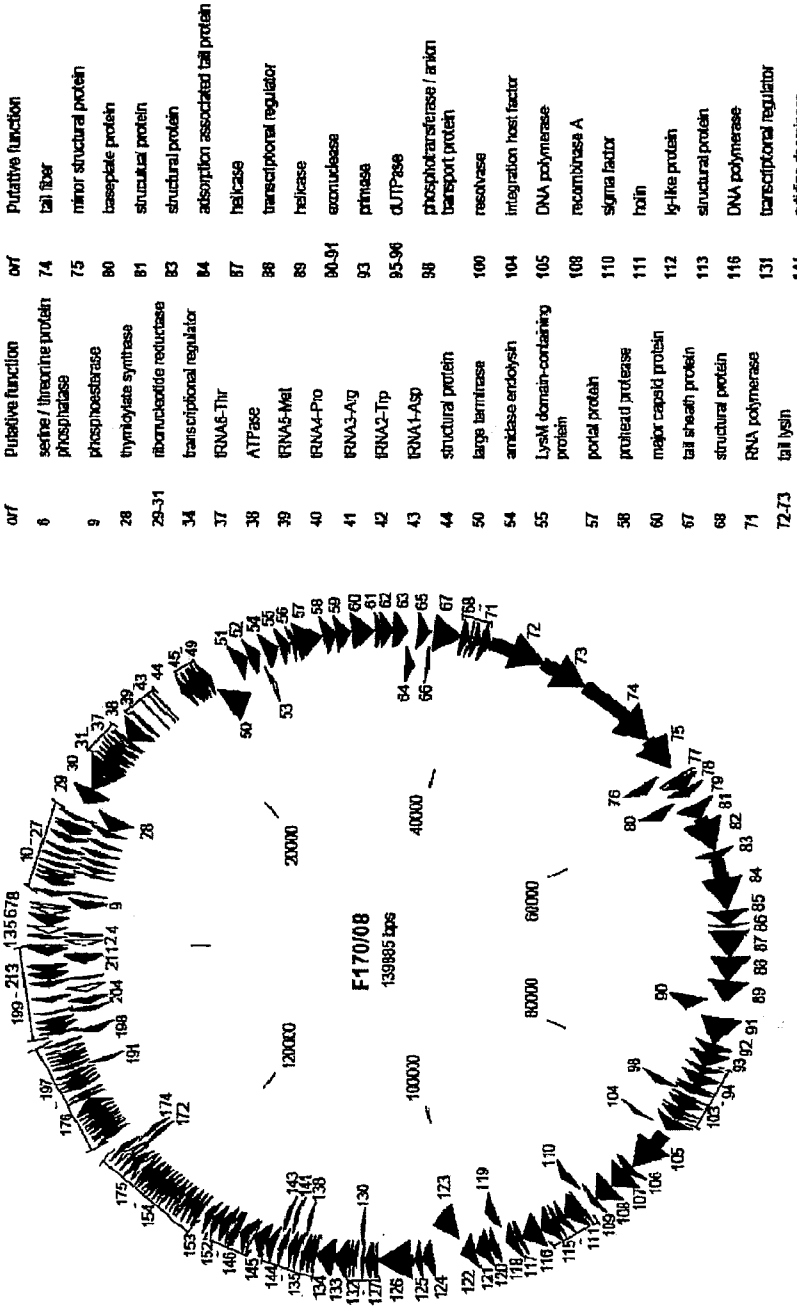

F170/08
139885 bps
20000
40000
60000
80000
100000
120000
orf Putative function
6 serine / threonine protein phosphatase
9 phosphoesterase
28 thymidylate synthase
29-31 ribonucleotide reductase
34 transcriptional regulator
37 tRNA6-Thr
38 ATPase
39 tRNA5-Met
40 tRNA4-Pro
41 tRNA3-Arg
42 tRNA2-Trp
43 tRNA1-Asp
44 structural protein
50 large terminase
54 amidase endolysin
55 LysM domain-containing protein
57 portal protein
58 prohead protease
60 major capsid protein
67 tail sheath protein
68 structural protein
71 RNA polymerase
72-73 tail lysin
74 tail fiber
75 minor structural protein
80 baseplate protein
81 structural protein
83 structural protein
84 adsorption associated tail protein
87 helicase
88 transcriptional regulator
89 helicase
90-91 exonuclease
93 primase
95-96 dUTPase
98 phosphotransferase / anion transport protein
100 resolvase
104 integration host factor
105 DNA polymerase
108 recombinase A
110 sigma factor
111 holin
112 Ig-like protein
113 structural protein
116 DNA polymerase
131 transcriptional regulator
144 cytidine deaminase

FIG. 4

orf	Start position	Stop position	Product aminoacidic sequence	Size (aa)	Homologous/similar proteins				Conserved Domains		
					Name[organism]	Acc No	E value and identity	Predicted function	Name	Acc No	E value
1	53	<3	MKKRLEELTPDELQQYA (SEQ ID NO: 131)	16	hypothetical protein EFP_gp173 [Enterococcus phage phiEF24C]	YP_001504282.1	3e-08 (17/17)		No putative conserved domains have been detected		
2	511	50	MEDKDYALALEEDTGVWKA CETFPTREEAVSAGKLALLS INEGKTYVDSLGMHVEDIFG ALPEKGATSFAVGQFNKAVI SVDVVGMLESVGEQLYSEY GEVAEDYYPTDEVSDEAIDE LHDIIANWLNKNLTQPPSFG SVDDVEKITLEGENK (SEQ ID NO: 132)	153	hypothetical protein EFP_gp174 [Enterococcus phage phiEF24C]	YP_001504283.1	6e-80 (147/153)		No putative conserved domains have been detected		
3	701	525	MNNLTAQDLLDELLELKDQ GHALEDYIVVGEPINPYDHY LEFDGWHLDSNTNMIILKG (SEQ ID NO: 133)	58	hypothetical protein EFP_gp175 [Enterococcus phage phiEF24C]	YP_001504284.1	3e-17 (52/58)		No putative conserved domains have been detected		
4	892	698	MNVLKQYIKEVHSVTPYTED WTKHDKGFLMVDLTVNCYG SLSRREHLFYVDEWEEAKK KGYYMA (SEQ ID NO: 134)	64	hypothetical protein EFP_gp176 [Enterococcus phage phiEF24C]	YP_001504285.1	4e-23 (54/65)		No putative conserved domains have been detected		
5	1326	889	VRDEKEVNYFIETLAEERKK KWNGYLTSLRDSVTLREIRT SYSVMTGAYIVFLYIYNYDL NKRTIVKATLDDWRMPYVD LGEFEYFRELGKMYDDKVR EALDLYVRQIGRSRPESKAL GIRRYKEVSRNNRTQTRKF KPRKGHVK (SEQ ID NO: 135)	145	hypothetical protein EFP_gp177 [Enterococcus phage phiEF24C]	YP_001504286.1	5e-76 (140/145)		No putative conserved domains have been detected		

FIG. 5A

6	2101	1418	MLLNKHWNSDEEDLILLGDY VDRGSKSAEVLGFVYKHILN GGTALLGNHDQMLLDFLTF PLIREADYEDLSEMYAMWM YNGGDKTISSLLDLDEHLQD AFTTRKMLLEKTNVVEVISLL EPYYEHGDTLCVHAGIPVYR QPDWKTATKDEMIWTRPLA LQKNKTDKTIVMGHTPTINL RKENSYDVFLGDRSIFIDGA CAYGGQLNAVVVDSKGSLL NTYKQESLSK (SEQ ID NO: 136)	228	putative serine/threonine protein phosphatase [Enterococcus phage phiEF24C]	YP_001504287.1	4e-131 (227/227)	serine / threonine protein phosphatase	Putative protein phosphatase	PHA02239	**No putative conserved domains have been detected**		1e-08
7	2634	2155	MTMHTENLLAVTIFLLIQMAV VAFIFTKGIVVDRLLSEYRD VVGIAFSILLFGNGAMLIIHQ VIAIFSIWFNNSFRESDVFLA QGYFIVLLLLYIALNVYGSTL FKNIRVNIKNYINYNARSKNY KLALVIVITFIVNTVLVLATYW LAEVVKGAIIH (SEQ ID NO: 137)	159	hypothetical protein EFP_gp179 [Enterococcus phage phiEF24C]	YP_001504288.1	1e-82 (158/159)					
8	2889	2638	MKPDYSSIIGKRFIPKKRYPR ILMKEVYPTRVFYDFPRVLP WEKAPDIPLRVKFVEFTFIH EGRVEKERYTYYSFFTHFE RSG (SEQ ID NO: 138)	83	hypothetical protein EFP_gp180 [Enterococcus phage phiEF24C]	YP_001504289.1	3e-39 (82/83)				**No putative conserved domains have been detected**	
9	3497	2886	MGREYVISDMHFFHRNICG EASFMDTRKQFKDVEEMNE YLINEWNTTVRPEDVVYHLG DFAMGAKVNSIANVLERLN GTIWLIKGNHDNSPLRKEIK RNTSLNDRVHWEDVGIILKR MHKVVHMTHYPLILGDRGN LINLHGHIHELARPEPNLLNV GVDSPELDNHKLGKPLLLED AIRLVNKKQVNFNKASRAYS IHGDLQ (SEQ ID NO: 139)	203	putative phosphoesterase [Enterococcus phage phiEF24C]	YP_001504290.1	5e-98 (176/180)	phospho-esterase	Phospho-esterase or phospho-hydrolase	COG4186	6e-17

FIG. 5B

10	3860	3510	LNYLYYVIILTMAHAVGDYAL QSDYIAKGKQTDLYLLIIHVNI WTYIIVATTLFLGTPVKLGLIV VCLWVPHFIMDYLKAQSAW FLKTVPNKKTQLIIDQTVHYL QLAVFVWFATH (SEQ ID NO: 140)	116	hypothetical protein EFP_gp182 [Enterococcus phage phiEF24C]	YP_001504291.1	4e-42 (84/116)		No putative conserved domains have been detected
11	3973	3857	MKLVTCPECGGNILEGAPN EYGFECDTCPYPYKEEDLI (SEQ ID NO: 141)	38	hypothetical protein EFP_gp183 [Enterococcus phage phiEF24C]	YP_001504292.1	9e-13 (35/38)		No putative conserved domains have been detected
12	4693	4280	MTYRMKCVITNPQEPFFTE GKEYRIAHNNTIGYFIKDDD GTTAESGKTRGELLNKLNE YWYSQFELIEIEPKQPINECT EIRKKFQQTLIQYNMDIGHL EGRLVGKPSNIISTQIAMLKV KREAVQELYDELFKEDS (SEQ ID NO: 142)	137	hypothetical protein EFP_gp186 [Enterococcus phage phiEF24C]	YP_001504295.1	7e-50 (98/137)		No putative conserved domains have been detected
13	5081	4695	MTVKIRCTLKTEHIFTEGKEY DVFYDDARGYFLRDDEGDII ESGATPELLLAELNNYWHS KFELLGAEPKKLTLYLGIDK GTGTNMAVGTSLQGVLEKV KELDIYFSSDSDFYANYKSQ YIIEEWETY (SEQ ID NO: 143)	128	hypothetical protein EFP_gp187 [Enterococcus phage phiEF24C]	YP_001504296.1	1e-64 (121/127)		No putative conserved domains have been detected
14	5358	5083	MTKLSSAWLVKFEYRAVKM RAFTSYDKAVTYYNEMVQNI DEQIEESYYETKTTYTDDHK PLLTQFIYWNEDRTFRNILG FVSIKEIELEEN (SEQ ID NO: 144)	91	No significant similarity found.				No putative conserved domains have been detected
15	5548	5321	MIRKQLLFELEVEVDEPMVG RNGYRTVMQTTRLYAYSLD DAYHAFRENHRYIIKSIKEVE EEINDEIKLSMVSEI (SEQ ID NO: 145)	75	hypothetical protein EFP_gp189 [Enterococcus phage phiEF24C]	YP_001504298.1	1e-27 (60/61)		No putative conserved domains have been detected
16	5811	5638	MRIRKHANKIIGWLFIFLAVL TIVKVIVLGKPLDGFDIVLYVL LQLLYGMEKLSNDE (SEQ ID NO: 146)	57	hypothetical protein EFP_gp190 [Enterococcus	YP_001504299.1	2e-23 (56/57)		No putative conserved domains have been detected

FIG. 5C

					phage phiEF24C]						
17	6145	5801	MNELDGISKLEADIIKTTQLL ETQQELKKNFIRNEKLSKRN YELSIDVLKLRNTLLDVMED LDNLMENVEGIKEDANKHS KVEKEMVKGWLERTGKLAN ETRKNIEEVLESYEN (SEQ ID NO: 147)	114	hypothetical protein EFP_gp191 [Enterococcus phage phiEF24C]	YP_001504300.1	7e-55 (111/114)		**No putative conserved domains have been detected**		
18	6399	6145	MVLTMNKPVRATSEQVVYR EEYANGWAVEVIHSLKGFG HIYVENKPYSVAIMKPAENF ADYSTVGTAEEVLKLIEEVV EYEEDM (SEQ ID NO: 148)	84	hypothetical protein EFP_gp192 [Enterococcus phage phiEF24C]	YP_001504301.1	1e-40 (82/84)		**No putative conserved domains have been detected**		
19	6634	6380	MTIIDYGSKPLNNCSKNELL DIIQSQLENEVKLIKLIERTTK EVEEEKEVPHYKNYISPEKR SYLEGMERVENIVRNFYGF NNE (SEQ ID NO: 149)	84	hypothetical protein EFP_gp193 [Enterococcus phage phiEF24C]	YP_001504302.1	2e-40 (84/84)		**No putative conserved domains have been detected**		
20	6980	6645	MNYRIVSYENSQEWLDAFN EFSGNSFKMNEAIHPDIYEPI KTAVLLFNHEVAEGEAIRLE KIDESEEDTCDHTYETYAVQ TGYSSIDIEQAGFCTKCGHD THKGYKEYTLK (SEQ ID NO: 150)	111	hypothetical protein EFP_gp194 [Enterococcus phage phiEF24C]	YP_001504303.1	2e-58 (108/111)		**No putative conserved domains have been detected**		
21	7392	6955	MNNEVEVPKQVKEFIDKQR EQLMDKLQIILEGQRYSCEY PKSEFSKWFFANTDTFIQAV ANTASLPKYYVVMPEKQKR DYGLLLRKDGKLAVSILPRN EPLSQDTLSKLKDYYLTEAEI KEIDERYWLFKKTREELSYE LQNCII (SEQ ID NO: 151)	145	hypothetical protein EFP_gp195 [Enterococcus phage phiEF24C]	YP_001504304.1	2e-76 (137/145)		Protein of unknown function (DUF1642)	pfam07852	3e-04
22	7869	7408	MGKQILKGWVTIDNSPGAE TNEPYLIKEKVKEIEYHHEH RALNMLICNALHALGAEDTT TEEEYDGGISSKYHLDNAEI QIFSAVERTSLEDITKNIVLK SMGVLDFEEGWYGWSSFTI EGFETNTFKLGGHDILNIVR QLEGKYVYITIDKV (SEQ ID NO: 152)	153	hypothetical protein EFP_gp196 [Enterococcus phage phiEF24C]	YP_001504305.1	3e-77 (138/153)		**No putative conserved domains have been detected**		

FIG. 5D

23	8089	7862	MELMIEGVSRGEFSKQFIKV SQTTEATVDIAVINRTVEVFR PDCVHEQTVTLTKENLDLLV TAIGYTKERMSNHG (SEQ ID NO: 153)	75	hypothetical protein EFP_gp198 [Enterococcus phage phiEF24C]	YP_001504307.1	3e-29 (62/72)		No putative conserved domains have been detected
24	8508	8077	MFYKIIELMAELTKEIKEIKDT LGCSMPIAEDRKVTRIAYLS EQLDDLNSLLLDIPVNYHET WLLDEPLTQNTPYEFHIEVM VLPYGEMGVDVKCYYEEVA SSISLGVDEFRTLPDTVDEL QERTFHNFHGLSREEAINK WSL (SEQ ID NO: 154)	143	hypothetical protein EFP_gp199 [Enterococcus phage phiEF24C]	YP_001504308.1	6e-78 (141/143)		No putative conserved domains have been detected
25	8741	8511	MSKELISCGACNEVFSEMD EVVRLTDDSMYHKDCVTLY STGYCAFLDDEYLGDTENG EGEPACFFLEEGEYIEEEE (SEQ ID NO: 155)	76	hypothetical protein EFP_gp200 [Enterococcus phage phiEF24C]	YP_001504309.1	7e-35 (73/76)		No putative conserved domains have been detected
26	9169	8738	MGLTKIETREWYNSDLDKL HKEGRDIYVKLKIGKRLTYG EYEREPNNGFQVINNEDTLP LILDNYEVYTETTTELTEKQL IVLVWLIHYLERTKLTIADSL HNLISGKANDATLQVWADL SSVEEAEVIRELVDYVIDKG GSL (SEQ ID NO: 156)	143	hypothetical protein EFP_gp201 [Enterococcus phage phiEF24C]	YP_001504310.1	5e-69 (140/143)		No putative conserved domains have been detected
27	9325	9173	MANKVSLENLLAMAVTAKE HEMSRHANKMRQLEKTEAN IKKRIKELSKEG (SEQ ID NO: 157)	50	hypothetical protein EFP_gp202 [Enterococcus phage phiEF24C]	YP_001504311.1	1e-18 (49/50)		No putative conserved domains have been detected

FIG. 5E

28	10272	9325	MDFDKIYKDLVMDIIKNGVT ELPEGTRAVYADGTPATTKF IEGVNFTITPDMGAPLLRSK HVGIKWALTELQWIWQEMS NEVSWLKERGVTIWDEWE QEDGTIGKAYGYALFNKERF IPVYSGDVELAKNRKAGSLI PKVVPKKGGWIAGTHQPYL KLNQVEAVIEQLKSTPNSRR IMTTLVWNVEDLYDMSLEPC VWTTHWTVVEGKLNLHVKA RSSDVCLGLPFNIIQYHALQ LVMANTVGLELGNLYWTSD NA (SEQ ID NO: 158)	315	putative thymidylate synthase [Enterococcus phage phiEF24C]	YP_001504312.1	0,0 (313/315)	thymidylate synthase	Thymidylate synthase and pyrimidine hydroxy-methylase	cd00351	3e-44
29	11375	10392	MNLQEKYEGINWNKIDDVID QATWKKLTEQFWLDTRVPV GNDVNDWAKLSDMEQDLIN KVFGGLTLLDTVQSESGVH SLLDDVRTQHEEAVLNNIAF MEAVHAKSYSTIFSTFNTPT EIDNIFEWATNKRLQYKANI INDIYRNGTPLQKKSASVLLE SFLFYSGFYTPLRYLGEAKM VNTAEIIKLIIRDESVHGTYIG YKYQLGFNQLPETEQKEME QWVIDLAFKLWENETQYTA ELYSEIGWTKDVNTFL (SEQ ID NO: 159)	327	putative ribonucleotide reductase [Enterococcus phage phiEF24C]	YP_001504317.1	0,0 (327/327)	ribonucleotide reductase	Ribonucleotide reductase, R2/beta subunit (RNRR2)	cd01049	3e-63
30	13538	11388	MNTYIELNNQLNIPNNGKIQL DKDKEAVRAFFLEHVNKNT VFFYSLEEKISYLIREGYIDK TVITDKYSMEFIKKLFKFIYS KKFRFDTFMGAYRFYKQYA MKTDDGERYLERYEDRVAF NALTMGDGDEELAMKIADE LINRRYQPATPTFLNAGRLR RGEYVSCFLIQVEDSMSSIG RTLNSALQLSKLGGGVGINL SNLRALGDPIKGIEGAGSGV VPVMKMLEDGFRYANQLG QRQGAGAVYLNVFHADIM (SEQ ID NO: 160)	718	putative ribonucleotide reductase [Enterococcus phage phiEF24C]	YP_001504318.1	0,0 (710/716)	ribonucleotide reductase	Ribonucleotide reductase, classI	cd01679	1e-132

FIG. 5F

31	13783	13541	MTKVTVYSKDMCGQCLFLK NMLNGKNIPFDEKNISHDEQ ALAYLKEKGVSSLPYVEADD GFSFNGVRPDLVKKLEKEL GV (SEQ ID NO: 161)	80	putative ribonucleotide reductase [Enterococcus phage phiEF24C]	YP_001504319.1	9e-40 (80/80)	ribonucleotide reductase	NrdH-redoxin (NrdH) family	cd02976	8e-12
32	14176	13910	LATRNKIGTYTNDEGNVVVQ MAGSKAELLELLSFLNAKYL LEVTDTPEEYQKVFNRLQV ETGKNYSVLLLDKVTNKSQE SEDFLGDKV (SEQ ID NO: 162)	89	hypothetical protein EFP_gp211 [Enterococcus phage phiEF24C]	YP_001504320.1	3e-41 (84/88)		**No putative conserved domains have been detected**		
33	14487	14182	MKTTDLQKKELLEKDLRSYK KLYELQKSIKEEIDELKSSIIS DMEELGESKISIDGGTFKLM PEYKRASADTKLLMNVYPN VWEKVKNVYTVNKYIKFTKD (SEQ ID NO: 163)	101	hypothetical protein EFP_gp212 [Enterococcus phage phiEF24C]	YP_001504321.1	2e-49 (100/101)		**No putative conserved domains have been detected**		
34	14808	14578	MEEKVPKPKVLKRVREARG ESLRELANMIGVHWSSISY WENGIKEPRVKNRVKLAKL YNIPVEILFEEDNGQELPL (SEQ ID NO: 164)	76	putative transcriptional regulator [Enterococcus phage phiEF24C]	YP_001504322.1	4e-34 (74/76)	transcriptional regulator	Helix-turn-helix XRE-family like proteins	cd00093	3e-06
35	15096	14872	MKKFYGIISTTTTRTEEYEKK LKNGKTEIRTREVTVPKEITV QSSQPDRLGARKELEAFAR KCNGKVTYIGAFA (SEQ ID NO: 165)	74	hypothetical protein EFP_gp214 [Enterococcus phage phiEF24C]	YP_001504323.1	6e-35 (74/74)		**No putative conserved domains have been detected**		
36	15491	15207	MILQILGERKYDCKDSTEEPI VKPFIELIDGVQFLLEQENAF SLLNSKHEEITRVPNSPYEY RTEKEGYKTFVNSVYVLND EGKTLRRLFERGL (SEQ ID NO: 166)	94	**No significant similarity found.**				**No putative conserved domains have been detected**		
37	15614	15543	GCUGAUUUAGUAUAAUGG CUAUUACUCCGGUUUGUA ACCCGGGAAUGGGAGUUC GACUCUCUCAAUCAGCA (SEQ ID NO: 167)					tRNA6-Thr			

FIG. 5G

38	16731	15640	MKVINYGSNYEIYANDLKTY DKLPAQTYKVRFNPMSGFS LAVTDDFKLKESKVYGDRLV KIEKVLHTFKTINRSLGVILS GDKGIGKSLFTQILSQRAIEE GMPVILITEAYPGIAEFIDSID QESLILFDEFEKVFNDRDGR ESQEKLLSLFDGLSQRKRIY ALTVNNLNRVNDFMLNRPG RFHYHLRFDYPDADEIRTYL QDKLDKAYYGEIDSVVKFSR RIKLNYDCLRAIALELSFGIS FGEAIADLNILN (SEQ ID NO: 168)	363	hypothetical protein EFP_gp215 [Enterococcus phage phiEF24C]	YP_001504324.1	0,0 (360/363)	ATPase	AAA+ (ATPases associated with a wide variety of cellular activities) superfamily	cd00009	3e-04
39	17175	17102	GGACGUUUAGCUCAGUUG GUcAGAGCAUUCGGCUCA UAACCGAACGGUCGCAGG UUCGAGACCUGCAAUGUC CA (SEQ ID NO: 169)					tRNA5-Met			
40	17307	17234	CGGAAAGUAGCUCAGCUU GGUAGAGUGCAGGCUUUG GGAGUCUGAUGUCGCAGG UUCAAGUCCUGUCUUUCC GA (SEQ ID NO: 170)					tRNA4-Pro			
41	18179	18106	GUAGGUGUAGCUCAAUCG GAUAGAGCAUCCGCCUUC UAAGCGGACGGUUGGGG GUUCGAUUCCCUCCAUCU ACG (SEQ ID NO: 171)					tRNA3-Arg			
42	18736	18665	AGUCGGUUAGUGUAACUG GUAACACGUUGGUCUCCA AAACCAAUAAUAGGGGUU CAAAUCCUCUACCGAUUG (SEQ ID NO: 172)					tRNA2-Trp			
43	19063	18991	GGCAGUAUAGGGCAGAGG UUGUCCCAACACGUUGUC AGCGUGGAACaCACGGGU UCGAGUCCCGUUACUGUC G (SEQ ID NO: 173)					tRNA1-Asp			

FIG. 5H

44	20880	20542	MNYPKREKVVEVSLTSGTY SVFPRRLGVTTNDAMSIVN GAMKGAELPMIPVHKLADR DSELTYVNAFQIQTATENVV DVPERITSLYTKPEDETPED EEIRLGTINNYFSLR (SEQ ID NO: 174)	112	structural protein [Enterococcus phage phiEF24C]	YP_001504328.1	4e-51 (109/112)	structural protein	**No putative conserved domains have been detected**		
45	21288	20944	MNDYQVNDLVLRLQRLEDK LQHGELTEKGIKQDNVELNS AVSELRDIVNSLDKRLAVHE EKYAHLTYQITKLEETIDALE GVNDKEFDHKRDIVENVFMI VLGAVVTYVFSMFK (SEQ ID NO: 175)	114	hypothetical protein EFP_gp220 [Enterococcus phage phiEF24C]	YP_001504329.1	9e-59 (114/114)		PHA02414, hypothetical protein	PHA02414	1e-39
46	21583	21323	MYETALVCVLLLQMFVYLM SYYVTRALQYKKLQAELSPL ASYKFTFVLYGISIGSLYLFF NGYYIPIVYTVGAIIGILVCLW FTSD (SEQ ID NO: 176)	86	hypothetical protein EFP_gp221 [Enterococcus phage phiEF24C]	YP_001504330.1	3e-41 (86/86)		**No putative conserved domains have been detected**		
47	21700	21969	MDNSKRIIKKIIFITISALVMVT LSKLFSKYVIVEQNAPFQALI GGASCALLSSILFDWYTNKK KKENVENQLKEAISDLQKIK AIIKR (SEQ ID NO: 177)	89	hypothetical protein EFP_gp001 [Enterococcus phage phiEF24C]	YP_001504110.1	5e-43 (89/89)		**No putative conserved domains have been detected**		
48	21990	22268	VSITNKDIKDKRRYIFSQSSK TTTIKRGDKRISSATRICAVC GRPLSKLVLRTGVPTVVVD HISCKISDIVRLNVCEDIRSC YAYSSKKGES (SEQ ID NO: 178)	92	hypothetical protein EFP_gp002 [Enterococcus phage phiEF24C]	YP_001504111.1	3e-44 (91/92)		**No putative conserved domains have been detected**		
49	22272	22700	MGMADRLKDNAKQKKLERT PEQQLRDTFNQASIKLINQF MANVTSGAIEVDDIADLTRL FQIYLQVNNINDGMQEGTG TLPALTSEHKDIISEKVSTEKI IKDGEEEELISLDELASLPDD QLEEVLVNRELQMNRENEA TF (SEQ ID NO: 179)	142	hypothetical protein EFP_gp003 [Enterococcus phage phiEF24C]	YP_001504112.1	2e-74 (140/140)		**No putative conserved domains have been detected**		

FIG. 5I

50	22700	24535	MTTKAQHIAKMAKEMYGTD KITTEQLAYITDMLTPSTYLL RNHSVRNHPITFIISGRDATK AQAHRPWQPKIINDQHRDK AIIKSRQLGLSEMGVGSMLQ FADTHSYDAVKCLYTFPTNE QMTKFVQTRLDPVLQNGYY STIVDQEVNSLKAKKIRNSFL YFRSSSKPGAVEGVDIDYLS MDEYDRVPALAEASALESM SSSPYKIVNRWSTPSAPDM GIHGLFKGSDQHWYLHKCE KCNYYNEMSYDAYTPEAP (SEQ ID NO: 180)	611	putative large terminase [Enterococcus phage phiEF24C]	YP_001504114.1	0,0 (494/494)	large terminase	Phage terminase large subunit (GpA)	pfam05876	1e-09
51	24635	25423	MVDNNVKISKSTIEGLINKSL SYEYVIKNNELLTNEYQHIVK AYGFDNFYDMYLYADSCDS KDMYLVKGGQKDLSKLKPV KRKVVRNGKTMTTTIYEDTG SSDNNNSNPLDKESKKKKE LEPVNAKELRKVSLGSDEEE KLDPKKIAKLLADTKKFGNN FDTQCTDYLILEQDSVTRGV VGFTREGSYLKMSFSMSDE AVEGMKMLAFSQLTLKAWK LGLGAKISTDNAPDVEELISL YGYKRNKTEYIVSMSSL (SEQ ID NO: 181)	262	hypothetical protein EFP_gp006 [Enterococcus phage phiEF24C]	YP_001504115.1	2e-148 (261/262)		**No putative conserved domains have been detected**		
52	25612	26244	MELIMNNKKLDELTNKVATD EDYDIFVEKMGNLVKDLYEN YQFLQQNPPEGDYTSGYFL GFQVIRAEYPVEYENLFRLA VDKNLNELEINKRFVEAVKD GKVLPLGEAVIDELQTGCSS ILQAQEVRVNIVFGTKEYMA KQEEERKERQAKLEEERER AMEVLKTKDDVLNTLRVTEA LANELTDEVAEKYDLMELVN SMREGLKAHNGN (SEQ ID NO: 182)	210	hypothetical protein EFP_gp007 [Enterococcus phage phiEF24C]	YP_001504116.1	6e-116 (209/210)		**No putative conserved domains have been detected**		

FIG. 5J

53	26234	26578	MEIKNSLGKALIKNLRLLKEK RDAMPDNLEYTSQVMIPVP YYLIKKGDNAVESFLMCAG MINRNKDLGLPISLEKGKQQ VKLNNGELTTIVECVATYSD KTDIDGVERFLVEHL (SEQ ID NO: 183)	114	hypothetical protein EFP_gp008 [Enterococcus phage phiEF24C]	YP_001504117.1	1e-59 (113/114)		No putative conserved domains have been detected	
54	26672	27541	MAGEVFSSLITSVNPNPMN AGSRNGITIDTIILHHNATTN KDVAMNTWLLGGGAGTSA HYECTPTEIIGCVGEQYSAF HAGGTGGIDVPKIANPNQR SIGIENVNSSGAPNWSVDP RTITNCARLVADICTRYGIPC DRQHVLGHNEVTATACPGG MDVDEVVRQAQQFMAGGS NNAVKPEPSKPTPSKPSNN KNKEGVATMYCLYERPINSK TGVLEWNGDAWTVMFCNG VNCRRVSHPDEMKVIEDIYR KNNG (SEQ ID NO: 184)	289	putative N-acetylmuramoyl-L-alanine amidase [Enterococcus phage phiEF24C]	YP_001504118.1	3e-169 (288/289)	amidase endolysin	Amidase_2, N-acetylmuramoyl-L-alanine amidase	pfam01510,	3e-10
55	27708	28346	LKKTSILGLSLLSLGLVVGLG TEAKAEEVTENGKTYWKVE SGDTLSEIGAKYNLDFTNIH KVNKGVVADPNVIFVGDKFL LPLDENGKLVEQVNTTEPDI EVQYNAPVTPEQPVVEQE VVEQPVVVAETPAPVVEAP ADSSSAKEWIAQRESSGSY DATNGQYIGRYQLSASYLN GDYSPANQERVADEYVAGR YGSWENAKSFWLANGWY (SEQ ID NO: 185)	212	peptidoglycan-binding LysM [Enterococcus phage phiEF24C]	YP_001504119.1	2e-92 (206/212)	LysM domain-containing protein	LysM, lysin domain	cd00118	7e-05

FIG. 5K

56	28488	28832	MGYIQDETWQMVKKVAKKN GFVGDWLIIHSYYEYGGNH VQIHTTINGESYRILRLLDSR EILLLDRKGNPVIYDYEIVND GQKSFFYNDMEEKEIEIPNG RCLNDKTRVKIYV (SEQ ID NO: 186)	114	hypothetical protein EFP_gp011 [Enterococcus phage phiEF24C]	YP_001504120.1	2e-60 (113/114)			No putative conserved domains have been detected		
57	28847	30568	LPKVLDKALGIEKSSIEETR NMENYKMHLREIDTNVVNN EPYSMESIEKGMNGKTTAY MQPIIGEMSVNPGYKTKPSI RNSQDLHKTLKKFGNNIILN AIINTRSNQVSMYCKPARNS ETGVGYEIRLKDIEAEPTSH DIANIKRIESFLENTAQFRDP NRDNFTTFCKKLVRATYMY DQVNFEKVFDKDGNFIKFDT VDPTTIFLATNGEGKLIKNGE RFVQVIDNRIVAKFNERELA FAVRNPRADIEVGQYG (SEQ ID NO: 187)	573	putative portal protein [Enterococcus phage phiEF24C]	YP_001504121.1	0.0 (571/573)	portal protein	Phage portal protein	pfam04860	1e-05
58	30679	31470	LSEVREKYSIFVPLDIENSIQ KSESVNDGEWVVQGYATTP DLDLQGDIILPQGIDISYFIEN GWNYEHKNDAEFIIGAPTS NCYVDVDKGLFVEAKLLKD NKYAQSMWKLANTIQKSGIS RQLGFSIEGAVVSRNAQDN RIIEGVKIHNVALTTHPANPR ATWETLVKSWTTGYGTAPD AQVDAGALRREMFKEDISN LTYAVRTIAGLYSKKPAEKE FILREVAKDIEVDTSENELSK FMLQLSRGISLKEAT (SEQ ID NO: 188)	263	putative prohead protease [Enterococcus phage phiEF24C]	YP_001504123.1	9e-152 (260/283)	prohead protease	Peptidase_ U35	pfam04586	3e-07

FIG. 5L

59	31477	32430	VAKTLNDIIEDFDAQLNEKVK PTTDEEITKSVEEPTEPEKV EEGAEVEQEEKPNESEETA GNDGEESGVTETVEAEQEE PETVEEVVVEEPVEESAETV EKSDKTKENKDEEEEEDEE DEDKKKEKDKKDKDKKDKE DKEDIEKSTEVEQVIKSSEIL GAMEAIFKNMLGLSEKLDEI HREFKEAKEAKEAKEKDEA ESVEKSLLDNPEIKTGKEDS EGKAVGFVNKSVAVEEEVA TEEPTVDVVVDGEQDTAEP (SEQ ID NO: 189)	317	hypothetical protein EFP_gp015 [Enterococcus phage phiEF24C]	YP_001504124.1	1e-116 (290/317)		No putative conserved domains have been detected
60	32571	33971	MTEKKNTERQLTSVQEEVIK GFTTGYGITPESQTDAAALR REFLDDQITMLTVADGDLS FYRDITKRPATSTVAKYDVY LAHGRVGHTRFTREIGVAPI SDPNLRQKTVNMKYVSDTK NMSIATGLVNNIEDPMRILTD DAISVVAKTIEWASFYGDSD LSENPDAGSGLEFDGLAKLI DKHNVLDAKGASLTEALLN QASVLVGKGYGTPTDAYMP IGVQADFVNQQLDRQVQVIS DNGQNATMGFNVKGFNSA (SEQ ID NO: 190)	466	putative major capsid protein [Enterococcus phage phiEF24C]	YP_001504125.1	0,0 (462/464)	major capsid protein	No putative conserved domains have been detected
61	34070	34333	MLKSEILINKTVTTAFGEVTF DHNGETTDLTVEQQEHLGT KVPYIQYIPDAPKAKEKEAT AEKADEAPKKAKKAPAKKTT KSKKEED (SEQ ID NO: 191)	87	hypothetical protein EFP_gp017 [Enterococcus phage phiEF24C]	YP_001504126.1	2e-41 (87/87)		No putative conserved domains have been detected

FIG. 5M

62	34346	35245	MYPDYGYEEQGDNTYQYQ PYAHGNPKHIDLDKIDDIQP ADYGWTPATLKQYMFGVEV VNPETGEPLGDTFYEHIIDS AIAKAEKRLDIAIMPRLIRGE HHDYHQSDFNSYMYTHVFK RPIIQAEKLQLEVNGRGLYR YPSNWWKYYALAGHIQMYP TSLMQTGTQFGYEMTFSGY PQLAGMPPSGGQVDAPQMI HIDYVAGMLPRKNRGYNED WECPADLEQLVIKYALKEIF QQWGRLIIGAGIASKSLTVD GI (SEQ ID NO: 192)	299	hypothetical protein EFP_gp018 [Enterococcus phage phiEF24C]	YP_001504127.1	4e-176 (299/299)		No putative conserved domains have been detected
63	35262	36131	MGEKPIRFGGAGETGNPNK QLNTSRVEFETKGMASFIEN RGIDVLWERAWLCTCRNPM TLSPKSDCPICRGRGIAYQP AVKLRMAIQSQEKGISNQDL GLLDTGTAIGTTELDSKITFR DRITVPEVKIYQSFIFNVNKR RVANGLFLSYDVNSIEDIYG KDGRILVDGVDFRMDYDTN TIYPNESLIDTNISINMSVTLR YIVIDLLKESRYQYTTFGVKQ TQFESLPKKLLLKREDVFIDS EPFSLDIDTASR (SEQ ID NO: 193)	289	hypothetical protein EFP_gp019 [Enterococcus phage phiEF24C]	YP_001504128.1	4e-167 (288/289)		No putative conserved domains have been detected
64	36124	36747	MARKGQRPYLFTDSKAILG NLTRAVVDEVLSDAQDVAL RNGSSVQRMPSYLIVTESR MAKNGVIDLKPFFARSNKKK YNKKGEWYLYIPISMKTRNM SRRLYDELRAVPVGTKPVT VKMDYLYDRRKQSPSVSSI NYKPKSTNVTVIPQSWGKG TRNTYVAFRTVNANSPANS WIINRRNVNDDDMSKTMLR NIDRLMKWKLKNLGG (SEQ ID NO: 194)	207	hypothetical protein EFP_gp020 [Enterococcus phage phiEF24C]	YP_001504129.1	5e-116 (207/207)		No putative conserved domains have been detected

FIG. 5N

65	36751	37596	MIPSLDTYLYKEFEERLRIILS ECYIIDEALKGMDKEALESF KNTYCSIDGKPPKREVEMS YSFPQEHLDSFARFVVTLGS SEEDSKSIGGIQGGYEYRE GNVISEEATIIREGDKLIINTS KPVADYLNSSDISFAESDHF RIEDNKPVFDFSYNEELEGI SINVSYISKVSDDDVAGVYK GYQSNDNVSIIGISSNIDTAR CLDAIARIILITMRDSLDEKTG YMLQTLHFGDMQVVIESGE TLVFGRPCTVN (SEQ ID NO: 195)	281	hypothetical protein EFP_gp021 [Enterococcus phage phiEF24C]	YP_001504130.1	3e-161 (281/281)		**No putative conserved domains have been detected**
66	37596	37829	VAKETEKVVKKEVKKEQPK KPKGYVHVDTFLDYAKVLY GLNKYQVAGFRALMAGREY QHEDADFVPFLEKYIGKEVK (SEQ ID NO: 196)	77	hypothetical protein EFP_gp022 [Enterococcus phage phiEF24C]	YP_001504131.1	1e-35 (76/77)		**No putative conserved domains have been detected**
67	37833	39542	MAVEQFPRKKVSRPHTEITV DTSGIGGASSSSDKTLMLV GSAKGGKPDTVYRFRNYQ QAKQVLRSGDLLDAIELAW NASDVNTASAGDILAVRVED AKNATLTKGGLTFASTIYGV DANEIQVALEDNNLTHTKRL TVAFSKDGYKKVFDNLGKIF SIQYKGSEAQANFTIAQDKIS KKATTLTLNVGAEPESTTEV MKYELGQGVYSETNVLVSAI NSLPDWEAKFFPIGDKNLPT DALEAVTKVDVKTEAVFV (SEQ ID NO: 197)	569	putative tail sheath protein [Enterococcus phage phiEF24C]	YP_001504132.1	0,0 (566/569)	tail sheath protein	**No putative conserved domains have been detected**
68	39603	40025	MASVGNQTVHTGNTVYLMI GNKIIGRAQSASGERQYGT QGIYEIGSIMPQEHVYLKYE GTITLERMRMKKEDLASLGI TALGEDILQRDIIDIVMMDNL TKEIVVAYRGCSAISYSESFT ANEVTSESTQFTYLTSAKVK (SEQ ID NO: 198)	140	structural protein [Enterococcus phage phiEF24C]	YP_001504133.1	5e-76 (140/140)	structural protein	**No putative conserved domains have been detected**

FIG. 5O

69	40117	40263	VKYPYLVELYAKHVIRDSGYI ENVPPVIYEDVVKRVEEIKR EENLTID (SEQ ID NO: 199)	48	hypothetical protein EFP_gp026 [Enterococcus phage phiEF24C]	YP_001504135.1	7e-18 (47/48)		No putative conserved domains have been detected		
70	40399	40872	MTENNEKVFTPTPNLSREQ LIEKLQRGENLTDEEVNILKY YNDAEERKQLDRIIPGVNDV FSKHYNLKEYGLEFDIKIKAP NIIENGKIQARREAYLEGMG MAVSNFIFQSYQMLATIRVC GVEVPEVLADDEKIYNLYVL GVIAKDYGEWLNSFRY (SEQ ID NO: 200)	157	hypothetical protein EFP_gp027 [Enterococcus phage phiEF24C]	YP_001504136.1	9e-87 (157/157)		No putative conserved domains have been detected		
71	40940	41515	MKKFKVLPSDPAWQNLTSD QVEWILYNMERDIEEQERLA KGMQLESEFQDYDDSWYD KPHDEFSPIREGDDEEEIAR KLSEITSEEDMAKLKARWEA SQEVDAIRAEGGTTEEDTIN ELIANNVKKAMEEARRIEKH GGNKWQEKSSIELEEERKN LEFNSQLKQGDIQEAIDLFN KDVEPTSLDDEFQI (SEQ ID NO: 201)	191	putative RNA polymerase [Enterococcus phage phiEF24C]	YP_001504137.1	6e-105 (190/191)	RNA polymerase	RPO41, Mitochondrial DNA-directed RNA polymerase	COG5108	0,010
72	41560	45216	MSNNYRFYVEAMTGDAVAK LNEIDKLMDKIDSKSAKGTQ NFFHTSQKDIDKAVEEMQKL IKAKKELDRAFDNQKINAES MGDMTAYKRAVSDAEELTR RFNKTQKEFQNHARMQAN PNYINASTLRQQKAFRDELT EQERAIRNISRAQQELNRVN SRVNHRANQASATGRMTY NQSESMKRDLRRTGVFESL GSENKSRQQELRERYKQR QEELAETRSNTNLDRQVRK NRETSIQAEIKEIEKEIEARK RLAD (SEQ ID NO: 202)	1218	putative tail lysin [Enterococcus phage phiEF24C]	YP_001504138.1	0,0 (1201/1218)	tail lysin	SLT domain proteins	COG3953	1e-08

FIG. 5P

73	45255	48440	MSVELRYPRFDLTFFTETDN YHIVYDAKDGLTGRNNNNG ETEKVSNNFMAESVISLTTK NALEDDSAVFSFVLAGDVY WDRVLNANDAVILKIDPDTS STKKSDNPVLLVGLISEVRL EGDYGENSKMYRITGQSFA KALMQFDLGVIQEVSVVLTD LGWLPDDAQEGIKMSGSSA SQIAESLMKRFLQYMKFNFN GQGIDKFLEWELDSWTEAE RLIDSTPYINYEGSLKQLIDD VTAKPFNELYFDATPEGKC (SEQ ID NO: 203)	1061	putative tail lysin [Enterococcus phage phiEF24C]	YP_001504139.1	0,0 (1058/1061)	tail lysin	NlpC/P60 family (function unknown, found in several lipoproteins)	pfam00877	8e-06
74	48534	54002	LVKRRFQAGLGSEIKRVYKE GQQINTLLAQVIQVNYKYN TVDLLALQHKEVFQNSYAN EGRFSARLPMEFGGRNIVG QPYGQVNPIAVGTVVLVGFI NSDKDMPIVISVYNNNDVSK QLSRTQFSNSDPKDLELIGD MHQKFSLYPSLTYDSVDGE GGRVVTFSGKSFIAFDTKEV ANSSTTDAGYGTKYEDLET SYYNNGDLIEPMKGRAPNV LFKHQGVLDDDGKPDLHDL LIHINPDGTYRTSMMNKEED W (SEQ ID NO: 204)	1822	putative tail fiber [Enterococcus phage phiEF24C]	YP_001504140.1	0,0 (1820/1822)	tail fiber	No putative conserved domains have been detected		
75	54102	56513	MALNGTKYTAFARHRLVLE WRANQNIAGNYSTISVWLYL QSMDKWGRLDAPAIGDAKV TVDGTTQTEKASSMLNAFQ KKLLLAKEWRVNHNNDGSK RITIGGSYFVNVTFTDNGVP TYYGTITIPNFSVDLNRIPRR SSLNPVPTLNLPGNLPITINR QSSTFKHNLTAWVANRDNP TLNNDDHWTYLTNLNDVGT SGAFSFTVANNKTIFTALNN RTSWQGKVKLWTIGLDDVV SQERTYKIVPPMNAQASGG K (SEQ ID NO: 205)	803	putative minor structural protein [Enterococcus phage phiEF24C]	YP_001504141.1	0,0 (769/810)	minor structural protein	No putative conserved domains have been detected		

FIG. 5Q

76	56507	57232	MVEETQKIFVTLDDKDFVSN WGTSLNSDEPVYEVDLPMD SPFFSHYYSNCFQYVDGEL VLSEEKLLKVELLAVASKFK RDCEETYILQKVPYTISGTTY LFDVISDDEFINKITLLDNKIQ DYVGITAYATSDGSQLILKF DKSQYTTMTRYIKKVVESRE NKLNNKLLPMIENAKSVEEA KEISWSSVPDELLPEQESNE PQDEQSIDSLIKENKELRQK VEFNELALMDAINMFSEMN K (SEQ ID NO: 206)	241	hypothetical protein EFP_gp033 [Enterococcus phage phiEF24C]	YP_001504142.1	4e-134 (237/241)		**No putative conserved domains have been detected**
77	57264	57410	MYPYLSMLYASYVIKDPENY PLEKVPALIREDVEKIVEEMA KKNEKQG (SEQ ID NO: 207)	48	hypothetical protein EFP_gp034 [Enterococcus phage phiEF24C]	YP_001504143.1	9e-19 (48/48)		**No putative conserved domains have been detected**
78	57547	58236	MGQSDGMGGTLKRIAIQVG NDPNKGWYRFQVNPTQYK YNKPHRVTIFKTKSNIITEDF GKDIETIQFSGTTGFRVDSR GKNGADRLKELEEIIDNYAK QGGNGNRSSVEMKFYNFT DDKYFVVHLAPEGLSIERSA EQPLLFNYTLSLVVLREAGQ PSERAQVSPQIGNVSPSIGR TYNAQQDTRTPAQILHDEY RRSVMPNTAVNPAVTSGAY NYGVNELKKIIGYGG (SEQ ID NO: 208)	229	hypothetical protein EFP_gp035 [Enterococcus phage phiEF24C]	YP_001504144.1	3e-130 (226/229)		**No putative conserved domains have been detected**
79	58240	58776	MEKVEQSADLLRFFRYLNV DINGEVVANVIDDQPNFISR FYTPHTRVNKISSTLLDIVRD NDIGETNKALSKDSLTYKFL KSGLKLSSPRIYELAQIVVLE SFALIYAIEEEPEMFKMINES DVKQTRENVKYLIDCLGGAK DYTDIVMDLQSMDVALGYIQ EQVPLIQGGLPVNGTI (SEQ ID NO: 209)	178	hypothetical protein EFP_gp036 [Enterococcus phage phiEF24C]	YP_001504145.1	6e-99 (178/178)		**No putative conserved domains have been detected**

FIG. 5R

80	58763	59467	MARYKKHLIVYGDTMQSIAQ KETGSVDNWVKIAEYNDLV YPYIVDTMQEKMSNLEHLAT LGDTLFIPDEGNLLDINTSSL NQRDMDFLLGLALGKDLDM TSDTDYYENHGTSDEVFAIT HNGHGDLKIASGADNIKQAT ISRLMTAKGSLMLHPEYGSD LHLMFGKTTIEQMKIISIEVC DTVLKDTRVAECVLVNHYIE EDRYVGNYRATLQSTREQF EFVVQNDNSGALIIV (SEQ ID NO: 210)	234	putative baseplate [Enterococcus phage phiEF24C]	YP_001504146.1	8e-135 (233/234)	baseplate protein	No putative conserved domains have been detected			
81	59483	60535	MRLKKISEILGRLIDVTMINT HEINDFSVGSTIRSIYEAVSM ELEQYYILGRENILWGIEQG VLNAFDFRKREAKRAYGMV TLEFHTVTQTPVYVPTGTTF DSSLSGAPSTLTFQTMQDYI IPEGVITAKVEVYCTTVGTK GNIPKGRINRVINNISNLKTV YNEFDFLTGTDEESIESVKK RFHAFVESRGRATIKALDYG TRQVEEVAGVYIKEEVGYV RIYAHDLNGDLKQETLDKIK VAIEDYRPAGIKLD (SEQ ID NO: 211)	18	putative strucutual protein [Enterococcus phage phiEF24C]	YP_001504147.1	0,0 (348/350)	strucutual protein	XkdT, uncharacterized homolog of phage Mu protein gp47	COG3299	2e-05
82	60553	62970	VSNFYKNIHPLLRRGKKPNK YDDTNFAVLNALNYELTQAE QETIASKIHSSLETATGEYLD TWGDWFGVYRKDDWNDEY YRKRIIRELLLKRATIPAIIDAL LDFLNDNDAVIQIYEPWRNIF YTNKSKLNGDDHLMGYYYR FAIIDISIDRPFPPEIVEIIKAFK PAGVLFYLRLDTSLNKNKTT VESPYVYLDVTNKTELEFLN GLYYDLRGNINLSDQRTQV VESNIFHTNNSMLNGEDVLA GAFDHGRGYI (SEQ ID NO: 212)	805	hypothetical protein EFP_gp039 [Enterococcus phage phiEF24C]	YP_001504148.1	2e-132 (228/305)		No putative conserved domains have been detected		

FIG. 5S

83	63076	63621	VAIATNNSRVYASLQLKNKQ DSMYLAIGKTTPWTNEDAP PAPDPNTTTLTEVIGYKKVA RVSLCREYLPSDDSKYPVV SYGSRKFTLIPDEDGYKEQA WMVYVEAEITGDELPTGTF RQVGIHTDLVSKASSEKKAL LPTDVTDAGILQFFENRQQQ NRTSDVILKEKFIITMENKKS VKQ (SEQ ID NO: 213)	181	structural protein [Enterococcus phage phiEF24C]	YP_001504149.1	1e-101 (179/181)	structural protein	No putative conserved domains have been detected
84	63636	67100	MAKNITNDDLGKEPYNNRY YQGKRFSGLLFKPDKPLQQ AELNELQSIIQGDLGNVAESI FSDGDIQTGMEYVLQDKKL TIKKGKVFLGGKMRNFDEQ SIDITGEGTEYVGVKLVQKVI TAEDDPSLLDQTSGVPSHF SEGADRLDEDVVLAVNDDS ASNIYHFVNGELYINPDTPE MDKINKILAERTYDESGSYR VRGFDMYTEVHPTDPNNKI QLVVDSGRAYVLGFKVDKP TTTRIDIEKSRELETINNEGF (SEQ ID NO: 214)	1154	putative adsorption associated tail protein [Enterococcus phage phiEF24C]	YP_001504150.1	0,0 (1152/1154)	adsorption associated tail protein	No putative conserved domains have been detected
85	67198	68151	MGKFKDLTGQTFGKWTVVD IDETKDRIHWWCECECGKE QSIRASSLTSGNSKGCREC TRNNLMGKTFGRLAVIKDS GERAKNGNILWECVCDCGK KRLVLGANLLNGQTKSCGC YSTDILKKVSTKHGLSKVNG KKTKLFMTWDAMRQRCTN SNHASYKDYGGRGITVCPE WLNNFKSFYDWSMDNGFS NDLSIDRIDNDKGYSPDNCR WVDAKTQIRNRRNTVTYNW KGSEYTLAELGELTGINKMTI KSRLNR (SEQ ID NO: 215)	317	conserved hypothetical protein [Bacillus cereus G9241]	ZP_00241204.1	3e-37 (82/195)		No putative conserved domains have been detected
					hypothetical protein 39-O_gp07 [Clostridium phage 39-O]	YP_002265415.1	1e-35 (84/209)		
86	68231	68437	LPETHRQTSSGALIFKPTIAE QEHKNAMESIKQERTELEK ELANVKAIKDELSKELADIKQ LKDELSK (SEQ ID NO: 216)	68	hypothetical protein EFP_gp042 [Enterococcus phage phiEF24C]	YP_001504151.1	6e-30 (67/68)		No putative conserved domains have been detected

FIG. 5T

87	68692	70464	MRLVVDIMHTQIRYEDSENY LRPEIHKVMHSELGVKADG YQFSPAYKAGYWDGIIDFFD KENDTFPTGLLPHVETILGN LQSTLSKSGYIFQFEIIDDRP DEFMSVEDMDKEIVLNGDN NDKITLRDYQYESVEQVIKN RIGIVNVSTGGGKTEIASGLI QQITPYLESGERIAFFTNSS SIFSQSIDRIEKRLGIKVGAF GAGKKDIQQVTFVMIPTIVS AISADPEAKLKLTAKERMYK KIAKDIAPKFERGF (SEQ ID NO: 217)	590	putative helicase [Enterococcus phage phiEF24C]	YP_001504152.1	0,0 (588/590)	helicase	HELICc, helicase superfamily c-terminal domain	cd00079	2e-11
88	70492	72120	LQSPCLNIELKEKFKLNKGIT DFLERVADKSQRWGETVAS PIRKTDMAKETGKNPRTITTR YINQLEELGLIKTETKRGMN GGTLVVFNTDMLNFEPKEN PITSDTKQAKEIREQVFPKA PTKVPKRRYRTKAEIAEARIL SEKLKKREDILNDKIEFNVVT RSFFDSFDEPEVYFKGYLIS RMYNAYVTIIPYEKYNRLKN LDEKKAKQQLRAYESSYNY DVLPRRFVGTPQYKKFVEL AKYCEENNINPLVYLT (SEQ ID NO: 218)	542	putative transcriptional regulator [Enterococcus phage phiEF24C]	YP_001504153.1	0,0 (539/542)	transcriptional regulator	HTH_CRP, helix_turn _helix, cAMP regulatory protein C-terminus	cd00092	0,003
89	72153	73625	MSQIQKQVIYRALSEPFFAK EILSKIPMDEFKDSGYEMIVS TINLYYRTHDESLEEQSILTL VEDKMLKQNKSLEAQNKVF EVVSDLYELENEDVDSEVIS ENIQNYVRKVLTREAIMKSV TNEGTLGSDSNIQQLMDDL RDILTIETAGNNSELLDFFDD VDKKMELLANLQQNKYPTG FTAIDAISDGGLARGEVGMV VAPTGGGKTTWAVNQARN YVVRGLNVLYVPLEEKVDR MIVRFEQLLSQQSKKNIL (SEQ ID NO: 219)	490	putative helicase [Enterococcus phage phiEF24C]	YP_001504154.1	0,0 (490/490)	helicase	DnaB_C, DnaB helicase C terminal domain	cd00984	6e-13

FIG. 5U

90	73625	74680	MKHIINFSDFHMHFFKDFSK PDPEYGTDRAKEQITILDNL MNYARNKNGDVLFNGDMF HKRVSIDVRIFNMLFQVISSY PDVDVIMVSGNHDKVTNSL YSDSALAPFSALPNVTVCST LNKIVKDDYTLYAVSYGEEV EEMKAWIKEQADNLDHETV NILSAHIGVDGSSTGKYSHT LGGAFKVADLYPDKFDIVTL GHYHKRQFLGNLSNVFYVG NTLQTSFADEGQEKGFYDIT IEGKKWEQKFIKTDYTPFE (SEQ ID NO: 220)	351	putative exonuclease [Enterococcus phage phiEF24C]	YP_001504155.1	0,0 (349/351)	exonuclease	Metallophos, calcineurin-like phospho-esterase	pfam00149	8e-04
91	74796	76688	MLKFKRVSAENYMSIGSVSI DLDNQGLVLIEGINDTNETF QSNGSGKSTLLSTVTYALY GATPSGLKADAVINKQAKKN MSVILEFEKDGVPYRIERYR KHSKHKNTTRFFQGTNDITQ KSVADTDKKIQDVFGIDYLT YANSIMYGQGNVEIFATATD KGKKQILENLADIGVYRYAQ DVAKERAQKALALAEELNR QYIAKVYEKDGLTQSYNSAL QQYENTEKLIQQKESELANA ELVIKQSEKNLSEGRAL (SEQ ID NO: 221)	630	putative exonuclease [Enterococcus phage phiEF24C]	YP_001504156.1	0,0 (6207630)	exonuclease	ABC_sbcCD, SbcCD and other Mre11/Rad50 (MR) complexes	cd03279	8e-09
92	76697	77362	MKIYTLSRELNEGTIFVPTSS SNEGKLFSFPLGTLFDWYP CCPRYEYQYSTSRKKLYLR LLDSDKTLVARYGVGDNKK RVISKIACFNENEWYNEEVA NENAELFNFAEQYDIVTPLK DDYTLKEVDDSISKVLDILDL LYTNQKVKVEEELINKVDTL QLSKPDSDELKQAYKDISEY MRLDREEKATYVLSRSLDSL NSVYEKFGNVYTMLNIMRK VVA (SEQ ID NO: 222)	221	hypothetical protein EFP_gp048 [Enterococcus phage phiEF24C]	YP_001504157.1	4e-123 (219/221)		**No putative conserved domains have been detected**		

FIG. 5V

93	77363	78421	MFTDLLSNELGSPKYAVRD YRYNCPFCDYDTKYKFYVR VEEGHPKNNLWHCFKCGS SGNPVSFVMKYYNVSFKEA LEILEEYGYRFNNKNYVPKS DKLTDEEYLLLLLGSLGKPK EETKQAKKELVAPPLPDGFK LLSQNLREPEAYPFLLYCNK RGFTLNDIYIHNIGYVKDSW VPLENGKSVRLKDHLVFLTH GKDGKYQYWNTRAIGQSFI KSLNAPSKEGEHSKKDTIFN INRASQTPQIVTEGVPDALT (SEQ ID NO: 223)	352	putative primase [Enterococcus phage phiEF24C]	YP_001504158.1	0,0 (350/352)	primase	CHC2 zinc finger	pfam01807	9e-10		
94	78438	79070	MRYTLEDLHAGMKLRCTDS KNYSFWTTNKIYEVTKKESG SLCIFDDYGIESLDEDILVRL NGNTGNAEFEVVSKVMKDA DYTEEDLEEGMLLHCKDGM SFPWMATGQTYEIYKGEKG ILFTKSGDGNQYCAKEIVAR LNGSASGSFELLERPHKTEL EKKVEARIKELKEKKLCLFY KQQQIKEENEISIEISKLSEA LKAIDVLREFE (SEQ ID NO: 224)	210	hypothetical protein EFP_gp050 [Enterococcus phage phiEF24C]	YP_001504159.1	2e-90 (165/210)	No putative conserved domains have been detected					
95	79096	79980	MGRVSVYFLNSRNIMDEDE TKRTYHGTFNSMKEAEQSV RDWWKANDFKCGTLRIIEG TEDGIVRWDYGNHTGFYLF VPEGAVVKYTIREGAKKPKR GRENDVAHDLFTADDGVVI PGRLGSNVISTGIKTSFDPK QYGLFINPRGGMMKYPITLG NTQGVVEGEYRGEVGLPLK NTFSLQLDARAVSKNVLTIN EEGKLINIPVTVARSMYPSF NALYEKQLEKLSEELQLVYG GEVRISNADEYVVAGTLFIP K (SEQ ID NO: 225)	294	hypothetical protein EFP_gp051 [Enterococcus phage phiEF24C]	YP_001504160.1	2e-171 (294/294	dUTPase	dUTPase [nucleotide transport and metabolism]	COG0756	2e-05		
96	79983	80213	MLIPEFKPPLLYVMGSFSVM LEKHQCSVTFYLREPYLGTS YDKIVKLIKMTYPNYSLTYVG MADNKYKFTLKNKED (SEQ	76	putative dUTPase [Enterococcus phage phiEF24C]	YP_001504161.1	6e-37 (76/76)	dUTPase	No putative conserved domains have been detected			

FIG. 5W

			ID NO: 226)								
97	80215	80523	MYTKKEEVVTVKHLVDKEQI RVGDIVGYKKTIRGFDAKRV KDTLSVTNQIGVVSRVCDEY ITVHDFFDKCSREIWAKTFE NLEVRKIEDGNSLLRRYENE FR (SEQ ID NO: 227)	102	hypothetical protein EFP_gp053 [Enterococcus phage phiEF24C]	YP_001504162.1	4e-52 (102/102)		**No putative conserved domains have been detected**		
98	80510	80821	MNFVDYFNQMQNLVIEEKT DEYVLLEKEHGQKYVTYQE LEGALSTVARNTAFMVENY NLMQDINLKIVLKKLKDSGTI TEELEKEILKEFKNIESLMED ETYE (SEQ ID NO: 228)	103	putative phosphotransferase/anion transport protein [Enterococcus phage phiEF24C]	YP_001504163.1	1e-50 (102/103)	phospho-transferase / anion transport protein	**No putative conserved domains have been detected**		
99	80814	81185	MSKESKRNKRIGELSEADM RVWAEWLATGQVHDKNHQ KQLERLSKRSVSLSDVTTIV EFMGKRNDGYISSLIEQQAV FDNLLTKLGVTEENRLEAKA EYEKELSLIQEKIQKELESIK ENKEK (SEQ ID NO: 229)	123	hypothetical protein EFP_gp055 [Enterococcus phage phiEF24C]	YP_001504164.1	1e-63 (123/123)		**No putative conserved domains have been detected**		
100	81205	81873	MTDYSAVGKKSRNKGGRFE RQMAKELTEWWGYEFNRV PASGGLHWASSNNVAGDIV VPSDANFPFVIECKNREYW TIENLFLNNKEIKNWWAQVV GDAKETKNIPLLIFTRNRAKN FVTMAYNEKLVNEIEKRGYP LMVSNITYVDDYKDTHCYKT FTTVLDAITSFKPYGSKDKD YFLFYFPSDYNWEDSLVYE TTIMDDAKQMDAEDSLDAL VNSYLGGE (SEQ ID NO: 230)	222	putative resolvase [Enterococcus phage phiEF24C]	YP_001504165.1	2e-127 (221/222)	resolvase	COG1591, holliday junction resolvase - archaeal type	COG1591	0,002
101	81875	82174	MAKTYQEALATVQSYLESD SVMKETSSISVSFSANWTG EREDYVIDTLTYDIDLRVFSL ETAHVVAIGKKLPQDSNEHA ELLKRLKKEFKQASKKLRED (SEQ ID NO: 231)	99	hypothetical protein EFP_gp057 [Enterococcus phage phiEF24C]	YP_001504166.1	2e-48 (95/95)		**No putative conserved domains have been detected**		

FIG. 5X

102	82180	82659	MIDNVNSPSHYTQGEIEVIE VIEYITAKYPAEIRYHLGNVIK YICRAPFKGKLQEDLNKSS WYLKRAQLVLTWSPSSYTG KCKKKFLENFLFKNSHIRDAQ LIEIPEEPIIEKFLFQTAQSYN KEQQNYIISALMELNSSSGD VKTVLENTENYLKFITT (SEQ ID NO: 232)	159	hypothetical protein EFP_gp058 [Enterococcus phage phiEF24C]	YP_001504167.1	1e-87 (158/159)			**No putative conserved domains have been detected**	
103	82752	83546	MTKAPRVKRLNIYNTDRYFN INLMKKEDIAKKIKVNRLNEE EIEREMDELASNPLKTPIGY MDRTNEKSYILYQEKYTND RLIQKLFKHAGSVSYYTDTIV PYYIIEQISKNLTSEVIYPTKN SYENREIENVQLAFTACPVTI DCPVVLPDVSPYDVLFALHP LKTNVDKIQISFPCLTEEEFD TRHEEYYHKVGSHYEVKSE YKYKFFKYVQTSLSIWAMNI WLVCDSDEDYNKIDRYIQKE KIKRNANRERA (SEQ ID NO: 233)	264	hypothetical protein EFP_gp059 [Enterococcus phage phiEF24C]	YP_001504168.1	7e-153 (264/264)			**No putative conserved domains have been detected**	
104	83539	83850	MSKDKTINRTDIARTISHHTG YRMKDILKILEVEDEVVAQA VSQGISVKNHKLWKLNIKKK PEKVAWDGINSKSFIQPEKY VVKFVPLSKLKESIDTYNKE SK (SEQ ID NO: 234)	103	putative integration host factor [Enterococcus phage phiEF24C]	YP_001504169.1	2e-52 (102/103)	integration host factor	HU_IHF, integration host factor (IHF) and HU members of the DNABII protein family	cd00591	3e-04

FIG. 5Y

105	83940	87011	LKILFLQEYIRENHVHNGKN GQTVDFKRTEMGKKLTGLL NTIGLTGRDYAVDYVYDMIP EVQKVNPRTGKPIKYKTPTL RQRKEPEERLLRRLMKYKP DIIIPMGEMGCKNLLGSTSIT KNRGVPTKKTITNENILRTA DEQGLEVDEVVDSFETWVL PMFSMEYWTANPNIENFIM ADIDTLGKFVQEGEQAFIPK KVDYEFVDNIERVRQIFGFL DKTKPVTAWDLETNSLRGD LLGAKPLVMSMSWLEGQGV (SEQ ID NO: 235)	1023	putative DNA polymerase [Enterococcus phage phiEF24C]	YP_001504170.1	0,0 (1021/1023)	DNA polymerase	DNA polymerase family A, 5'-3' polymerase domain	cd06444	2e-86
106	87114	87656	VLNLRVDDLEFKTIKIIDDNG EVVTHDLQTELQVNEFNVR TAFLEQPAKYTYWTSILERL RMYQENYELKAEKKKAELY EPSRVALINQGVAKPTKDQI EAQIMLDEDYYKLRQSIVNL SFNVRQLQYIVKAFEQRKD MLIQYGADLRREYEYSQKV SMPDPMKNKVNNGFSDFQ WNLEQ (SEQ ID NO: 236)	180	hypothetical protein EFP_gp062 [Enterococcus phage phiEF24C]	YP_001504171.1	3e-100 (179/180)		**No putative conserved domains have been detected**		
107	87712	89001	MNFQEQLQQQLKQQNIGER EAVDYPSNHLKHKELYFPKA ENGQPSTLYVRVLPPAVPG ENYNVSAREAFLTTRNRNG KDLKSNFIFSEHPNAEDILEQ AMIRWNAENRVPNPYSRNT KPRQRYYVNVVQLIINQQTG EVNYETDSNGQLMVRLLKL PQTACMAINESLSNPMLRP QFSPDVPEEVAQYSFISSAD AFPISITKPPRSNKPTSYNV QVISNRSLGALPQGWENLL EDLKYQATPSVEYNREFIEY F (SEQ ID NO: 237)	429	hypothetical protein EFP_gp063 [Enterococcus phage phiEF24C]	YP_001504172.1	0,0 (428/429)		**No putative conserved domains have been detected**		

FIG. 5Z

108	89086	90333	LARKRKSEEIDFGTIDLTKEV GLTTFTDTKFSNVSDRLPTM IPQLDYILGGGLPFGRMVEV FGKNSSGKSTLAVHLTKVA QMLDVPTVWIDVEGTADPE RLAELGVDFSAGGVFMVEP KQNKDGSKDTITVERVAEEL QRLLPVFSKLGKPVLIIWDS VAQTASEKELEKGVGNQQP GIKAKAMAQFAQIIAPLMTN SKALFIAINQARDELGSMFG GVDSPGGHALHHWASLRLE VVKASQIKNKELNAFGAEE (SEQ ID NO: 238)	415	putative recombinase A [Enterococcus phage phiEF24C]	YP_001504173.1	0,0 (414/415)	recombinase A	RecA	cd00983	1e-36
109	90387	90773	LRKGLAPNPFFEILEKHQDS SKRTMTMNSSGTPSSLQPI RDMFLKAMREGKRVLIENS DLSSANSVVIEIEYVGNRWC LGYQRVLFYGMELKIPHTIH FCDVYGAYGHDAQKVKRQ VKVVFEGDNPFE (SEQ ID NO: 239)	128	hypothetical protein EFP_gp065 [Enterococcus phage phiEF24C]	YP_001504174.1	1e-70 (125/128)		No putative conserved domains have been detected		
110	90766	91380	LSRDVQKEEKEIRNGNRFIT ETHGKGVFPRDVDRLYHKY SNLRYKVYNTHKDSFNSEA SRKELKSYIDEQFIKLTKEYD INGEVDFPGYIKKALNLRVR HSYVKGRFRDTARERLGTQ DNEVELLLGIDDSSQADIED AELIESLLSKANFSEIELAVF QQLIQGTVRDARIITELSENY GVSKKAVKDAIKNVREFVLI NLTD (SEQ ID NO: 240)	204	putative sigma factor [Enterococcus phage phiEF24C]	YP_001504175.1	1e-112 (202/204)	sigma factor	No putative conserved domains have been detected		

FIG. 5AA

111	91441	91716	VEQNNTGKYAPFIRLIVMGIS FVATGLTTIFGWEPLPFTDE QMNQGLMLVLSVGLAIYNW YKNNAVTSYGKAKEEAGKE VVGTRQDFKNRD (SEQ ID NO: 241)	91	putative holin [Enterococcus phage phiEF24C]	YP_001504176.1	2e-46 (90/91)	holin	Phage_holin	pfam04688	6e-04
112	91764	92726	MKIDEISKLELPNLFGKFLVV ETISDGYTGTVSGHYNYEID QKSEETYIYPVFWNDKLNKF IRSDELVVYTNKNKVYYVCK TTIDPYNHAVVDELTVEEGM DKDKRTLQAFKLFVNDLFSF GSYNIFLTGNLSLENNPDIVL VSSVSLDKQTAKMYTERTL ELTATVLPEGATNKKVIFSV DKPELLGLTVSDNKATVTSK DKAGTAIVTVTTEDGEHTDK CTVQIEEYIKVTGINVSGESA LEKGKTYKFTASI (SEQ ID NO: 242)	320	putative Ig-like protein [Enterococcus phage phiEF24C]	YP_001504177.1	0,0 (319/320)	Ig-like protein	PHA02283, hypothetical protein	PHA02283	9e-12
113	92747	93190	MAKEILNIEDLLKPETLEVAI DGKYLIVPTLSDGFTGTVAG GYAYAVTKKGTDYTVNELIY NQKDNTFKPSDEPIIITDDNE IFFITRTLEDPYNYPVVATEK LKTKDVKEKQVLQAFLAFAD DRFKLGVYNVFLADEPFVY GDKTE (SEQ ID NO: 243)	147	structural protein [Enterococcus phage phiEF24C]	YP_001504178.1	8e-78 (147/147)	structural protein	PHA02283, hypothetical protein	PHA02283	4e-19
114	93297	93593	MNDNKEKCVKQEIRDTYKG YDILLDEENGFFYVSVLDPD GKEIISGFVEADKPIEEYYKE LLGKCDQDISFKDLLGFLNG RRDTERTDIRFLKRDSGV (SEQ ID NO: 244)	98	hypothetical protein EFP_gp070 [Enterococcus phage phiEF24C]	YP_001504179.1	1e-41 (86/94)		**No putative conserved domains have been detected**		

FIG. 5AB

115	93598	94551	MTKIKLITKKNTQGYVMNTL LRRFYKNNVDVEFLNKFNLP DIHNHIGEYDAVIIVGFPFFE SQRGALDTALSSMDNPFSK VYHLATFGDTYRNEGSFRS FVDEVISPVGHFVELIIDLTK FTNTGTKEDEQNVVALAKE ALVFAKDIIEETDNYNRYEVT DRTISWVLLVDLLGENLYKV TEPSKELDTILKEQEVLVDAL NINMQDYVLRTIGKMSANVI NGTVVCFGYAEQHVNEVAH KLINFYKSHNYQKVI (SEQ ID NO: 245)	317	hypothetical protein EFP_gp071 [Enterococcus phage phiEF24C]	YP_001504180.1	0,0 (315/317)		**No putative conserved domains have been detected**
116	94605	95888	LKNNEPLEKLLDKLDEPRIL QTIIIGSLQRSFNRVHVGKFN KLAQEFDLDKENLYSLKALV KEIEEDKELHELYEASMAGK ITLEAVRKVLLQDDKSSFDV LSSYVVENQAVLARNREFG KLQREGAYLDHLISGLKTYL LAELKDMSSLKYINKNLKAP KVSSDRELILCLSDWHIGAF VNNIDTGGYNFEIFKERLEK LLEEVFQVAMEQDIKKIHVY HIGDIIEHINMRNVNQAFEAE FPATEQIAKGIRVL (SEQ ID NO: 246)	427	hypothetical protein EFP_gp072 [Enterococcus phage phiEF24C]	YP_001504181.1	0,0 (425/427)	DNA polymerase	**No putative conserved domains have been detected**
					putative DNA polymerase [Lactococcus phage Q54]	YP_762586.1	3e-16 (71/255)		
117	95900	96274	MGGNLVYILLAIAYVGEGITA FTNTKRKERYMIEEGEAPLP RSSYVFLGINYLLRIAIAISLIF IIPTSLQLNVTGIALFTLMVFV VPFIARIIEVMRTAIVRYVQK QYIKQLEERKGKRETN (SEQ ID NO: 247)	124	hypothetical protein EFP_gp073 [Enterococcus phage phiEF24C]	YP_001504182.1	3e-62 (123/124)		**No putative conserved domains have been detected**

FIG. 5AC

118	96313	96933	MNFTEVISPNGETSLIDVNN PPTLIRRGVLSIKTKVNNEVK ETPVYIVELAEELTGTDVVS VYKVKEIGDSIQKDYIEEKVT PRFKSTTYLGELAQKIKGRSI KEQRRVETKPPLFLAPVVN GIDTFTGIEGKGFYEREEDR HILLPDGKPGIAYGDNTGVFI GLSSIKWDKAYVDVESITKG YLSQKQIWFNLDGQRPQFR SETL (SEQ ID NO: 248)	206	hypothetical protein EFP_gp074 [Enterococcus phage phiEF24C]	YP_001504183.1	2e-114 (206/206)		No putative conserved domains have been detected
119	96933	97673	MTDKQFYEADIQELILNKQRI FGDIGKSAIVFEKAIMQGNTI CDCLVFTEKRGLIGIEIKTER DSTKRLNKQLSDYEKVCDY VYVLCHDSHVPKVEQILTRH NHKHVGILAYTEFMGEAML GEYKQPSRSPKKSAYHMLN ILWKEDLIRMLGTFRRYGDR LEANGAKVMKTNSRSGGVS GLYVKSTTARRMTKPELINN LINRVGGTEEATRVFCDVFI HNRNHPEKAIKLRHFKAKEN RGDLDGV (SEQ ID NO: 249)	246	hypothetical protein EFP_gp075 [Enterococcus phage phiEF24C]	YP_001504184.1	3e-143 (244/246)		No putative conserved domains have been detected
120	97663	98169	MGFKGAKYGSWNTVVGKN YVGTGGRTSGSNTKRLSTK GYYQVGFVKEYQNLTEKDI MLKLEYGKDLVSSYTGVPA DMIKLRKKKEEQTLASLDTV YYVSIGKEPVGKLSIRAQRR FREVGLTFIYLEKNYVQRKL RGGNVRSVGYTNATKSQKR KADRRKSNKSKTTR (SEQ ID NO: 250)	168	hypothetical protein EFP_gp076 [Enterococcus phage phiEF24C]	YP_001504185.1	2e-90 (168/168)		No putative conserved domains have been detected

FIG. 5AD

121	98183	99040	MLKKGKEVTLRKFYNIITDKE SVLLGARYTSSIMTTDIPITT TFEDVEVDLKKETVAGTISF RPVGERQINALSLLKEASTA YGGYGEFLDDTIEKPLINSD FAVDVSLADSAFSNLQEIPF NLYMSSPKVFYTEVSIRGRK HMQYVLEDESSSGVTSTLA LVFRKKLYDGETLLGVHTYT EALARVEGIKVLQFIANGSVL EQVIGAVSVLGGSTGTTLFP MFDDMVMQFVMIESVPWV HISCDTGAIAFKEED (SEQ ID NO: 251)	285	hypothetical protein EFP_gp078 [Enterococcus phage phiEF24C]	YP_001504187.1	2e-163 (285/285)		**No putative conserved domains have been detected**
122	99144	99989	MDYKEKVYVGALTWLGTLG ERRYLGQMRDVLAVYELGS RYAGYYTENSDYDYMVVYM PSPHDLMYPTTIYKQETKID GNKVEVKYMSIMEYVYRIEN GDLEALQMLNATSSQSFFG EPIEGIDNKRTRLVTYMKEL EYRRETFTYLAPEKLFRGVN GRIKATKARMDKAIENDDME VAVKCAILIRYFMDLLVVLAD GESIREGLTFSPIIANIIREFR EDCESAQAKTLINTAQVLLE ADREEILNSIKDHGLS (SEQ ID NO: 252)	281	hypothetical protein EFP_gp079 [Enterococcus phage phiEF24C]	YP_001504188.1	7e-156 (269/281)		**No putative conserved domains have been detected**
123	99982	101610	MTKLEQNKEILDIFNRKGKV TDKVEESAKIMLELDHDYDF GTGDIAYTERGTDKKGRFYL ESRLFIHKLMPYGFILNAVVS KVHYGDQEETLEREVSRVY ELEYNLRDKVAVLIKNGKPL NFSENNISNMFSGHVAQNIL EQLDTMSGSDMYVSVYKRV SRVKDEQIGKVSRFFDRLM KYNKIELIYKSGVPEGFALAY AYRVVVVGEGKVRNKWYE PVKSVDYLDKEQTNPAKHL GIPKSIFKIICEGGLEWTF (SEQ ID NO: 253)	542	hypothetical protein EFP_gp080 [Enterococcus phage phiEF24C]	YP_001504189.1	0,0 (522/542)		**No putative conserved domains have been detected**

FIG. 5AE

124	101929	102618	MAKKEVNNSSVLLNLYNNK LLVSKVDEALDEGKPYDFIIA FCKEKFDFEINKPALSRYKE KRRESLETGVDLESLLDKRR KSGKIIDIKSKEVTPLPNETY DNTFGQVEQIYNDVEVLDTII QKGFNSLKEVDYVEAPLAM KAIEVKAKITANQFQGLSLT GLRELRLRQSAKEQAMTEII LQFIPEEQHEEVFNAIESAE KEFYENLDLTEEDQRITKAL QASGMDII (SEQ ID NO: 254)	229	hypothetical protein EFP_gp081 [Enterococcus phage phiEF24C]	YP_001504190.1	3e-128 (229/229)		**No putative conserved domains have been detected**
125	102629	103096	MVENLREVNYKTLTLEESLH ALLEGKTLIVKGLEQRRKLD VLVRIFSEGVVPVTQISYDTT PADGYWRTGYWQIYDLPIN ALSTYPCFIYDDLNTDELPK FMIGDTVYYTSKEDSIKDSAI VISVYKDDANNKWYYKLSR DNEIYAESEIRRDRL (SEQ ID NO: 255)	155	hypothetical protein EFP_gp082 [Enterococcus phage phiEF24C]	YP_001504191.1	6e-84 (153/155)		**No putative conserved domains have been detected**
126	103197	105476	MANILDTLKWLDKGDKVTIE FDKERSKYAKLTLHDSSAKT NIVRNIVFYDLDKGVYAYTG EYTPVWDNLLDDMRKTQGA EPEIKTTKVNQLATYEDALK FIETNGTFYIIGEEVIVKVKDA KELALMLMYFRDAMEELRG EYDPKKHHVDMTIELSKDVL KKMAVPRHELDLSLGGLMR AVSHNVGEDLFETLGFDYM KQAWEVLVNCLSLDTIHEVP FRVLDELEKVTDSMSTTDHI VTLYAGRELKKFYSEEE (SEQ ID NO: 256)	759	hypothetical protein EFP_gp083 [Enterococcus phage phiEF24C]	YP_001504192.1	0,0 (746/759)		**No putative conserved domains have been detected**
127	105536	105742	LILFIFSIITMLSMFLLYLFGM ASVALIELGLLMGSQNDITK GAHSLLFTGVTLTVVTEITK QCLLLF (SEQ ID NO: 257)	69	hypothetical protein EFP_gp084 [Enterococcus phage phiEF24C]	YP_001504193.1	9e-26 (61/68)		**No putative conserved domains have been detected**

FIG. 5AF

128	105816	106268	MYDSYGYLDWASWLFSIVI GSAVAAFFTLAVVGITFDVA PSHGVTKSHELHPIYENSKV VVEAKKEQFEINVDGGLVAI DAEGTTILSTKGEIKPKIVFT ENYINNNWWTRFLGIAGKV KDTSSVLYLDSGTLVYNKPE KNSSAPDLKIK (SEQ ID NO: 258)	150	hypothetical protein EFP_gp085 [Enterococcus phage phiEF24C]	YP_001504194.1	3e-78 (144/150)		**No putative conserved domains have been detected**		
129	106343	106513	MSYTKRALEARGYDFDTMS MLEKMNALLELLEEPEFQE QMRKEYEEFSKECATNGE (SEQ ID NO: 259)	56	hypothetical protein EFP_gp087 [Enterococcus phage phiEF24C]	YP_001504196.1	5e-24 (56/56)		**No putative conserved domains have been detected**		
130	106503	106775	MENEKLESYFMKEIAPILDEI EMSEELIKGMENNNPSDMIT VSFSKEEVDILLAMLDLELP RLDSGSELFSPNLVREAKLQ LIKNKLTSK (SEQ ID NO: 260)	90	hypothetical protein EFP_gp088 [Enterococcus phage phiEF24C]	YP_001504197.1	2e-42 (90/90)		**No putative conserved domains have been detected**		
131	106883	107134	MNEQKKVYAKLTEDEAVFA CELGDKIKQIRESQELSRLE LAKRAKVDHSTLILIEQGKRL PTLRIMMKLSKALHRELAISF TD (SEQ ID NO: 261)	83	putative transcriptional regulator [Enterococcus phage phiEF24C]	YP_001504198.1	4e-40 (83/83)	transcriptional regulator	Helix-turn-helix XRE-family like proteins	cd00093	7e-06
132	107146	107433	MRGSLDYYNYLYQTIENRPT EELDVLYDGLYKKAGDLFAI DNFQGVKEGRLILKILKAIRE EINSRIDEEIDLYLYNIYDSIS DEDKRVNWLYEV (SEQ ID NO: 262)	95	hypothetical protein EFP_gp090 [Enterococcus phage phiEF24C]	YP_001504199.1	8e-46 (94/95)		**No putative conserved domains have been detected**		

FIG. 5AG

133	107436	108224	MFSVVKADSYVKSDIEMYEF KNVKSLALTKKEKELWSGKI AKYVNEFIVNAYGDYHGNKI PEINVVINGKLKKVLGSFVQ FTNTNIHYIEISGRFVKEVILL QETPLAQRALDILMDVARHE AIHYTLCYLNSLSGGDLPTF NYHDGGEDFEKDLCLTGTS PSGATKEEYIYSSFTLGAIRC RHHSTCPECGLETYMYTRG RYYCYNGCVGDNGRKIIFRP QGDIAIYIDEPKSKAKPKVEE ALKDYKGALKLPY (SEQ ID NO: 263)	262	hypothetical protein EFP_gp091 [Enterococcus phage phiEF24C]	YP_001504200.1	1e-148 (255/262)		**No putative conserved domains have been detected**
134	108306	109379	MAYVTNIDVVADGLDLYNG NYVVERGQVVTFKLHVATW NNEPTPENAYAIIRNNGVDY KSKVDEFGNAEVTFPVNGR PDQVTTSIFALTSGYEGDMP RVMSAIFSDETEIKQTVMNV TASINGEPVSREGVFLERDQ VVTVDVKATLSTGKFWEGA QVGVYNNNTEYLGDLDADG YGSVTFQVKGKQGMDTSAI YVFVKDHEREATLTVPVKFT NTTVTTETSTEESSTVDTTT GTEESSTTDTTTVESSTTDS T (SEQ ID NO: 264)	357	hypothetical protein EFP_gp092 [Enterococcus phage phiEF24C]	YP_001504201.1	0,0 (355/357)		**No putative conserved domains have been detected**
135	109504	109806	MSQVSKHGEKRVRERVGV NKSSVDRQFELALERGYRQ KELTGRLKKWVVSRVFNSK YPQTCILYNGKCFIVSSEGT LVTVLNIPSNLLKDFAKLSKK RGK (SEQ ID NO: 265)	100	hypothetical protein EFP_gp093 [Enterococcus phage phiEF24C]	YP_001504202.1	3e-51 (100/100)		**No putative conserved domains have been detected**
136	109808	110110	MDIMDIEFLEEHKQLVKEHV EQELKLMHPLKKLQVMTDW LGDTEDKLSQGDLDYFNDL TETELIEAMDASEIVESYSDV LLDFIDYYNIDLTGLEEQLGV (SEQ ID NO: 266)	100	hypothetical protein EFP_gp094 [Enterococcus phage phiEF24C]	YP_001504203.1	1e-48 (99/100)		**No putative conserved domains have been detected**

FIG. 5AH

137	110113	110406	MDKAEKVDNIVRQVTGAIIK TTAKVAFIVFVLTFAGILVGY YSYSFLTNAGWFALPMILSV DLLYVAVLLGGLAFIFAEVYK VVLEVKKIVKRGGQL (SEQ ID NO: 267)	97	hypothetical protein EFP_gp095 [Enterococcus phage phiEF24C]	YP_001504204.1	8e-46 (94/97)		**No putative conserved domains have been detected**
138	110403	110582	MSNKTLEQRVIDANKEINDK LNESSIIRKQIEELEEQEAILL SDVEDLLDYLENIGVDL (SEQ ID NO: 268)	59	hypothetical protein EFP_gp096 [Enterococcus phage phiEF24C]	YP_001504205.1	2e-23 (59/59)		**No putative conserved domains have been detected**
139	110595	110960	MNKKVEEMTMEEKDKALIA MGLIDVTQEADWVVLATCE ECREEYEGEEYEEGDCAEC EHCGGEYFMIETALEGTRC GRCDDYFDMWDDYFEFEN EGNPYKDKHICEHCYEELVS MGMEEKF (SEQ ID NO: 269)	121	hypothetical protein EFP_gp097 [Enterococcus phage phiEF24C]	YP_001504206.1	2e-40 (102/120)		**No putative conserved domains have been detected**
140	110987	111364	MNELEELKNTLIRQKLSMLE SYEMREASFWIMFNGILRTI MSVAVVAFVSYAKHVRPDN VATWFLALIWVIFLAEGAKG AYDAIAFGIHRKKFAKHIKNM RGIITITQLLIEEDEEKLNGGK LDE (SEQ ID NO: 270)	125	hypothetical protein EFP_gp098 [Enterococcus phage phiEF24C]	YP_001504207.1	4e-62 (114/125)		**No putative conserved domains have been detected**
141	111357	111587	MSKDEKLVEWFVVALMVIV WLLITFSILYTIVSLPFMVHE GDWLGIVRNVLLDIVVLVIGV VATWLQLRFKKGMEE (SEQ ID NO: 271)	76	hypothetical protein EFP_gp099 [Enterococcus phage phiEF24C]	YP_001504208.1	5e-34 (76/76)		**No putative conserved domains have been detected**

FIG. 5AI

142	111591	111965	MGYLESAIEEIERVLLGNKS RDTEEVYLNNAIRYIKKELKK KEVEPTWLNEPQTLFLNWF NELYAVGGLTHVTEAVGFLE STGGRMKYPEAYSAFSNLS ENELLEVYSKFYTGLFLKAQ GGELE (SEQ ID NO: 272)	124	hypothetical protein EFP_gp100 [*Enterococcus* phage phiEF24C]	YP_001504209.1	1e-51 (113/124)		**No putative conserved domains have been detected**
143	111962	112219	MNFHGKVFHDKVFDILSRD YPDWQRYQTEKRPHPNEL RKDFAIDSTDSRYEEYVMG EFNVETASGDVKVYAVGIRR VVHKRAEEE (SEQ ID NO: 273)	85	hypothetical protein EFP_gp101 [Enterococcus phage phiEF24C]	YP_001504210.1	2e-26 (55/73)		**No putative conserved domains have been detected**
144	112225	112818	VEYTEKDIKEGMKLRCTDNS NVGYWEVDKVYEVTRNKDL GLVIAGEGERSHRTVKYILE VLNGDSKIKFEVVEEKPVRF AKVTCVYPPDRGLVEVGHC YEVLKEFPTGSVRIYLNSKL GNHSLLPDQFVFVDEPSND GEKDVEELDVEAKILADIEQL KTEAECLFAKRDRVNEQAL NLNAKARKLEESLEVLREYM (SEQ ID NO: 274)	197	putative cytidine deaminase [Enterococcus phage phiEF24C]	YP_001504212.1	3e-77 (153/197)	cytidine deaminase	**No putative conserved domains have been detected**
145	112860	113702	MIYYINFLEDFASSWSADKR YRVRRIMTTGSYAIIDNYGH VRFSSDTARGVLKNIEQEYA TNKVELTLVEEEAMNKPRFK VGERVKVSNDLQAFGIEYKT HIASKMLGYAGKEATITRVW GSNVRYFINIDGTHQDWCW TEDMLDKIEEEPTLSVRCVE AVHPFWTKGKDYEINLTSD GRYRVWDDEEDGSSGKSIK ELLDVINSSGNKFELLDETP SEAEPRLNHDMSDLEKIEAK ITALSEESYQLFEKSEEL (SEQ ID NO: 275)	280	hypothetical protein EFP_gp104 [Enterococcus phage phiEF24C]	YP_001504213.1	1e-155 (264/280)		**No putative conserved domains have been detected**

FIG. 5AJ

146	113715	114017	LNKKETLLNTTVTFLGGTSQ SSRPKGKQTLCEMQKSDGS VEFIFDGTVFYVHSMVVVYM ANKKHSMQATVSAIDGNYK YAGITFKLKVDYKENTLLLEE I (SEQ ID NO: 276)	101	**No significant similarity found.**				**No putative conserved domains have been detected**
147	114018	114647	MRKNVICRLECVSKDKDNL GEWTVDNIYPVFESELGKV YILDDEGTTCSRDSVSLIISS MASFGVTFRVAKDKAEDPIP SNPQSSTSLEIVKGYEHLEE FIDSLSSNQRVVSHSVDPNS QWHYIIYETKSAELGGVTLE ELLDTLVYNVHVVVMERSK RTYEPLESHTFKWEYGTKN TEDWEKIVPLLGYKVFNTNL NSNRGFHITILK (SEQ ID NO: 277)	209	hypothetical protein EFP_gp105 [Enterococcus phage phiEF24C]	YP_001504214.1	3e-116 (205/209)		**No putative conserved domains have been detected**
148	114810	114968	MYFVIVVNGQHRTLLKVTGK EWEMSPHTEEAVIEVALDT CYTYIENQEAQKN (SEQ ID NO: 278)	52	hypothetical protein EFP_gp106 [Enterococcus phage phiEF24C]	YP_001504215.1	6e-23 (51/52)		**No putative conserved domains have been detected**
149	114985	115125	MIGDFILWFKQAWKETFCIH DYTVKGVYKTLDNHGYLKC KKCGRIK (SEQ ID NO: 279)	46	hypothetical protein EFP_gp107 [Enterococcus phage phiEF24C]	YP_001504216.1	3e-16 (41/46)		**No putative conserved domains have been detected**
150	115138	115470	MNQRQIKKRMKKVLAILNEV EVVDSDYDSGMVLYVDVAD NEQNRDIIKEVCGILGLDKEK FIAECKESRLYEETLNLASC WHYLMQKEPKKLTIWHSVS KGFSLERYSED (SEQ ID NO: 280)	110	**No significant similarity found.**				**No putative conserved domains have been detected**

FIG. 5AK

151	115535	116176	MFKKDKKEEKTYREGDLLK TVGGYYPDARLSLGITYPLY KTTNEGWYIINNEGSRVTLIE MDALGIDYAVMEEPLLELKE GDPLLVVSDLKRGVRGLAG AEVQCLNITGEMASLAGTVV HYDKDMSHIAKGLFTVKEN DSYWCVAIAIPLNKVADPDF ALEHLLATLNKKASTKRLILN EIKYDLNLLHQELDEVSNEL EKLTKNIETIYNNR (SEQ ID NO: 281)	213	hypothetical protein EFP_gp109 [Enterococcus phage phiEF24C]	YP_001504218.1	6e-114 (203/213)		**No putative conserved domains have been detected**
152	116188	116631	MSMPSDLGKTLKKPIVINKN PDFYELAVGGKVIYNEEVME IAKAFSNKKTKYYLLNTRSN KQVCVPVYHVRPYDTQVEG LKLGDVLDAMHIMTTVTLRA VNKHGFVVDEDIIECLVDDV PENALIVTSEVSRIQPEDFG KVTIDYFV (SEQ ID NO: 282)	147	hypothetical protein EFP_gp110 [Enterococcus phage phiEF24C]	YP_001504219.1	3e-79 (144/147)		**No putative conserved domains have been detected**
153	116795	117226	MSYVNEFETIGDWLDREIYD VLLRDGHDIDELDNWGMAL FALSEGYVLTDGLDKPFLEL TREDLVAGYNHFKEELNGW LRGGKLLEVSGNLATIQGFS FDHDDVLFLEDNNKAYAML VGIIIEARDTYKNGFCKGYYV IPYQD (SEQ ID NO: 283)	143	hypothetical protein EFP_gp111 [Enterococcus phage phiEF24C]	YP_001504220.1	9e-75 (138/143)		**No putative conserved domains have been detected**
154	117581	117880	MNKYKFTYADIKNLSEEEKE KELKNRCGVLAVECLSTKQL QKKKPRFMVFLNTVIFDSTA ETGGQYATATVKTEPIGDG RFRVCDGWGQLSNGIIELLK (SEQ ID NO: 284)	99	hypothetical protein EFP_gp112 [Enterococcus phage phiEF24C]	YP_001504221.1	6e-42 (96/99)		**No putative conserved domains have been detected**
155	117959	118249	MFKRLEEYRKNLSNEELKIF NNTMKLLNDNKTDFQERTK NFDKELQYTELENEKEKILIV LDTIRVSNENYKNVISENLY HSIKEMTIIFELLYNL (SEQ ID NO: 285)	96	hypothetical protein EFP_gp113 [Enterococcus phage phiEF24C]	YP_001504222.1	7e-45 (96/96)		**No putative conserved domains have been detected**

FIG. 5AL

156	118333	118656	MNELEEVKEWNNKIEEQQE VLNKVIVTFYKEIDLKVKMVN RGLLGQLSAFNELKGMLSGI ELTAKVIAPDNVLPITTHNFL EYLFLGDNEQRAYAKEYLD GFLKSVE (SEQ ID NO: 286)	107	hypothetical protein EFP_gp114 [Enterococcus phage phiEF24C]	YP_001504223.1	1e-51 (103/107)		**No putative conserved domains have been detected**
157	118750	118890	MMNGLKRLMKAKRYKKEVK EIITMQKKAINELETLNKNLK LINQNY (SEQ ID NO: 287)	46	hypothetical protein EFP_gp115 [Enterococcus phage phiEF24C]	YP_001504224.1	1e-15 (44/46)		**No putative conserved domains have been detected**
158	118949	119215	MTKEELKSYLENYNKPFSTS MDNVFSLFINDVRAVADDFR KGEAFIYTCAELIEEQAETLE KSDLEELEEKSGESLVIQDIN GYLYFV (SEQ ID NO: 288)	88	**No significant similarity found.**				**No putative conserved domains have been detected**
159	119297	119524	MIIAENELYLVKNPLNEWDM NYHLIEKETGKDFLIDIGDVA DNEEEREKYELGLLFSDLKN LIVDLLIEYSWKTI (SEQ ID NO: 289)	75	**No significant similarity found.**				**No putative conserved domains have been detected**
160	119606	119899	MTEQQFKKEHLLEPTEWRS GGYLDTSLIDQSQSYYIESR PRVYGGCYVYQYVTMKDG TVYELYSMTASTRGIVAHNC HARNVLQRDVKQYRDSAIH Y (SEQ ID NO: 290)	97	hypothetical protein EFP_gp116 [Enterococcus phage phiEF24C]	YP_001504225.1	7e-51 (95/97)		**No putative conserved domains have been detected**
161	120012	120218	MKLSDIILVGLLVSIVLLWGY LSIMICLQVFRALGGWDIRTL TVCSGLLFAYVFGLKGIWEQ GTGKSK (SEQ ID NO: 291)	68	hypothetical protein EFP_gp117 [Enterococcus phage phiEF24C]	YP_001504226.1	9e-29 (65/68)		**No putative conserved domains have been detected**
162	120300	120542	MKLNVIHLLFCLFQEQESYSI LSYESIDEFYSRLGYDLESE WLLRDLGINGTSGLAELLTD YNNLLENEITKAVFSDKWL (SEQ ID NO: 292)	80	hypothetical protein EFP_gp118 [Enterococcus phage phiEF24C]	YP_001504227.1	1e-37 (79/80)		**No putative conserved domains have been detected**
163	120619	120864	MNELECIYDSRKSFYGKANL VEEENGISLYSYDTKVATIYT NGLAKVFGTYSQTTLRHIKE FFKQNGLKADTKKQIEKDYL (SEQ ID NO: 293)	81	hypothetical protein EFP_gp119 [Enterococcus phage phiEF24C]	YP_001504228.1	3e-39 (80/81)		**No putative conserved domains have been detected**

FIG. 5AM

164	120930	121160	MLKITKEITLGEFEAWEGGK DRLETIKELDILDEAQQEIEL MIEGAEEVTEMTINDILWFE MDEFIAQFEEEEEEE (SEQ ID NO: 294)	76	hypothetical protein EFP_gp120 [Enterococcus phage phiEF24C]	YP_001504229.1	4e-31 (75/76)		**No putative conserved domains have been detected**
165	121210	121416	MTTEEKALNIAENKGITDYK VKGNVLSYYTSYPMEKCTY LVTIDIETLEEERKELKKYYK KGLQNACL (SEQ ID NO: 295)	68	hypothetical protein EFP_gp121 [Enterococcus phage phiEF24C]	YP_001504230.1	5e-30 (66/68)		**No putative conserved domains have been detected**
166	121435	121605	VAVTINNRIKKLQYERIRKLE KRKRGEPPEFIFNGNYSLEE IELFLHFRKKSEGKK (SEQ ID NO: 296)	56	hypothetical protein EFP_gp122 [Enterococcus phage phiEF24C]	YP_001504231.1	2e-21 (53/54)		**No putative conserved domains have been detected**
167	121750	122046	MTKTELQYKKAIGVAIFATSE EDKKQLGNVAPFSIYEILEID LNKNRVYYALNCGERHAVC FTKLRKEEETGDNFILINKQP FFLKDIHKGLTWSKSL (SEQ ID NO: 297)	98	hypothetical protein EFP_gp124 [Enterococcus phage phiEF24C]	YP_001504233.1	8e-50 (95/98)		**No putative conserved domains have been detected**
168	122114	122344	MKIGKKEELEANNIFNRADE LLGAVTMEELERDNGGSIFY ADGSPDTVLWHMKKEFSLK PFHCYYFDGWYIALINI (SEQ ID NO: 298)	76	hypothetical protein EFP_gp125 [Enterococcus phage phiEF24C]	YP_001504234.1	5e-33 (68/76)		**No putative conserved domains have been detected**
169	122428	122862	MTKENNVFLNEKELMKEIIE TLENGFDGCYCDLHNEVFN YGTNTDTEELEEYGIFNAIG EIQEYEEEHFGATLTDLGNA SAVADMLYYIKGHEFLFDRL DFNDVLADVAEGLKLDKDL WNEEATEEVNKAIIKCLKRE VPWLVD (SEQ ID NO: 299)	144	**No significant similarity found.**				**No putative conserved domains have been detected**
170	122925	123356	METLENFGYTWQGIKEVTK EEAEKNVKNGVDTFLLYPD NTESLVISLDELETEGVRFG VEKPVQLLFKVSNSYHNTEE VYYGENVEEIEKKLHDSLEIT AENLTGQEIEEDWENYYKT YEEAWEATYNGILSQLKSEC TIEKM (SEQ ID NO: 300)	143	hypothetical protein EFP_gp126 [Enterococcus phage phiEF24C]	YP_001504235.1	1e-73 (137/143)		**No putative conserved domains have been detected**

FIG. 5AN

171	123438	123635	MKLTEKELNTILRDDETGNG GTAFLGETLADFLEESGIDF TNLTILEVNELLENNGIRPIE VVPC (SEQ ID NO: 301)	65	hypothetical protein EFP_gp128 [Enterococcus phage phiEF24C]	YP_001504237.1	1e-24 (59/62)		**No putative conserved domains have been detected**
172	123629	123826	MLKNIKKSDKLTRKDIQGFW GDEAKTLEEWYKSISKESDT DKMINTLKEYANNNEFHFVK GEQGQ (SEQ ID NO: 302)	65	hypothetical protein EFP_gp129 [Enterococcus phage phiEF24C]	YP_001504238.1	1e-25 (60/70)		**No putative conserved domains *have been detected***
173	123823	124128	MTNTNNQQWNQKFNDGTM NQNNQQKEVITLQVAESFV SQILTKEYSVIGLVILMFYFM FGMFGIFGGAIYIAFTHTNRK IGAWQQVRSVYTIKEEQEE WNN (SEQ ID NO: 303)	101	**No significant similarity found.**				**No putative conserved domains have been detected**
174	124116	124307	MEQLKGLTIRELIKKLEEVPE ENKDLPIYTFENENSLPIKGI SLYDENGKHSQENPLSFDVI R (SEQ ID NO: 304)	63	hypothetical protein EFP_gp130 [Enterococcus phage phiEF24C]	YP_001504239.1	8e-27 (61/63)		**No putative conserved domains have been detected**
175	124320	124679	MNSFMNKQAKQVERSKEIK LVEEVRRENVKKRFSEEVK KYLEKGYTIRLENKVFPFALI SIDLEKGEKVISLILVNEYDGI ANYTVMKKVTLREKGNRAIL KRMLTDKDVKVVSMWKGI (SEQ ID NO: 305)	119	hypothetical protein EFP_gp131 [Enterococcus phage phiEF24C]	YP_001504240.1	8e-58 (114/119)		**No putative conserved domains have been detected**
176	125592	125858	MKLKEFIKLAESKGATLEAY NELGGYELTRGDIVDQNPVL IAYMQGTHSVEISNEELENK ELTELAFVYKNASFIYPNEK ELLSGLGL (SEQ ID NO: 306)	88	hypothetical protein EFP_gp134 [Enterococcus phage phiEF24C]	YP_001504243.1	3e-40 (83/88)		**No putative conserved domains have been detected**
177	125956	126123	MLEVGKFVRGNNGARTWV GQIVGIDRLAGEYRVRDVVT GIYFYVSCSAVYECARP (SEQ ID NO: 307)	55	hypothetical protein EFP_gp135 [Enterococcus phage phiEF24C]	YP_001504244.1	9e-24 (54/55)		**No putative conserved domains have been detected**

FIG. 5AO

178	126213	126389	VDTVTDIIDVLGIIKQDIEYKG ERIKELEGQGKQEQAELLEA EVKGMREVVQDIEQAL (SEQ ID NO: 308)	58	hypothetical protein EFP_gp136 [Enterococcus phage phiEF24C]	YP_001504245.1	4e-18 (49/58)		**No putative conserved domains have been detected**
179	126471	126647	MNNNKLDELLEEEYSTLDEL LDSKEFKKQMNNLNHVPQM QPQSHNSNTLADTGRYPEK (SEQ ID NO: 309)	58	hypothetical protein EFP_gp137 [Enterococcus phage phiEF24C]	YP_001504246.1	3e-22 (52/53)		**No putative conserved domains have been detected**
180	126728	126862	MTIEQINAEVKQQEMLGNKL EVIQLGNDIYMYINGEPYKTI ELI (SEQ ID NO: 310)	44	**No significant similarity found.**				
181	126943	127101	MTIEQVKDYGKAYGKELSTK EVKEFFEKHNDMPSLMDLA KFCGAMNEDGTKN (SEQ ID NO: 311)	52	hypothetical protein EFP_gp141 [Enterococcus phage phiEF24C]	YP_001504250.1	2e-21 (50/52)		**No putative conserved domains have been detected**
182	127235	127474	MTPELAEMNLTKNDSPFSFI NESGVFIEPIKNPFSCEGTY LQACKDVAGELETNKEVGN EIDNYLKMQNWLNKLAYEYI (SEQ ID NO: 312)	79	hypothetical protein EFP_gp142 [Enterococcus phage phiEF24C]	YP_001504251.1	6e-37 (73/79)		**No putative conserved domains have been detected**
183	127554	127778	MKSIIIKQIKDGYKGILERRN NGWADEELNSYTTGVSNTL FELINDLQDNGVISEEEAEEI EEVFSNTIDILNF (SEQ ID NO: 313)	74	hypothetical protein EFP_gp138 [Enterococcus phage phiEF24C]	YP_001504247.1	5e-17 (52/74)		**No putative conserved domains have been detected**
184	127876	128571	MTEWANMNKEEVLELLND WFGVSDYDTVMGELEEMK KVTFTGSTNQPLLGGNNDLI GLPQFFKDNEAESELPTYEE LLEELEKDTWNLEAEDNTY NYSGFLESESDFKVIQAENS DTTIAFFAIHTGIDIRAGYSKA IPVIFETYYDFQEFLGNYFYS QGYYAFKHDNKEYTISLDVS ATSEYVRIYITDNNNNELQL DYEQETCMELDKESVAEYL TSQGIEFKDLKPAL (SEQ ID NO: 314)	231	hypothetical protein EFP_gp144 [Enterococcus phage phiEF24C]	YP_001504253.1	9e-110 (205/231)		**No putative conserved domains have been detected**

FIG. 5AP

185	128793	128987	MSRKYRGFDTAFTKDGVCV YVIKDDKEKGTALVRDTRG GDEYTVSNEGMIYTKDMESI DVYMPW (SEQ ID NO: 315)	64	hypothetical protein EFP_gp146 [Enterococcus phage phiEF24C]	YP_001504255.1	1e-29 (64/64)		**No putative conserved domains have been detected**
186	129086	129235	MEINKAYERLLKEVELLQND LMDIEDYSEEVYQAFQKVID ELEYVIEEG (SEQ ID NO: 316)	49	**No significant similarity found.**				
187	129752	129525	MLNSRGEPLLPINTQVRLNN FTFECNGRGRSPMGRVIGY DNSVCKEFTDYYIVESGDLQ GYAHYTNVTEVVLGGT (SEQ ID NO: 317)	75	hypothetical protein EFP_gp148 [Enterococcus phage phiEF24C]	YP_001504257.1	4e-35 (71/75)		**No putative conserved domains have been detected**
188	129782	130054	MLNIFYNVWGGFISHPVLITL SIVGIYVLGYALVKFIVGIVVL SNSLNTKWVIASAIFTTVLSI VFTIYSFLVEIYVVLVVISGLV VLLT (SEQ ID NO: 318)	90	hypothetical protein EFP_gp149 [Enterococcus phage phiEF24C]	YP_001504258.1	2e-38 (89/90)		**No putative conserved domains have been detected**
189	130400	130059	METTLIDKERLNKLKVGDTIF TKPELRDPILGCDKATVTSV TPGSVWISLNGTEYEVHKD EKTKVPLYRNQSGEIVGEYF LDFADFHKYWTYFAKTMVE QVSLRGE (SEQ ID NO: 319)	106	hypothetical protein EFP_gp150 [Enterococcus phage phiEF24C]	YP_001504259.1	5e-51 (95/106)		**No putative conserved domains have been detected**
190	130744	130433	MDKNTKDELANALGKFFGT LVLVVLTLVIGGYVTMFLWN GLIAPTFGVLTLTWAQAIGL DVFISFITAKTTTNTEDSILM VFAKATVSTLLFMLIGWVVM FFI (SEQ ID NO: 320)	103	hypothetical protein EFP_gp151 [Enterococcus phage phiEF24C]	YP_001504260.1	5e-49 (102/103)		**No putative conserved domains have been detected**
191	131000	130737	MKYLIYATLVVYGLITLLTSYI LTYGVYWQLTNELSNPMPW FVIVLCGGIVLVLITAFIILVVN VIQLNKIENQEVNIAIIKEEND G (SEQ ID NO: 321)	87	hypothetical protein EFP_gp152 [Enterococcus phage phiEF24C]	YP_001504261.1	2e-39 (84/87)		**No putative conserved domains have been detected**
192	131306	131001	MAQCYHDQLTREEEKQLKR KYEVLQSGSCWHCNKPLW MYPPDRVVNLTTQLDLSIPN EYTVPTRLHYNPITGERMGL VHVRCDYYLKELNNSLLNH SMEGK (SEQ ID NO: 322)	101	hypothetical protein EFP_gp153 [Enterococcus phage phiEF24C]	YP_001504262.1	9e-50 (95/101)		**No putative conserved domains have been detected**

FIG. 5AQ

193	131716	131525	MKLKDLIKLMKPGVDVLVTY PTAGATITVRTKIGSNNEVLE PYLDYEIANVSKTNHYIAIDII (SEQ ID NO: 323)	63	hypothetical protein EFP_gp154 [Enterococcus phage phiEF24C]	YP_001504263.1	5e-27 (60/63)		**No putative conserved domains have been detected**		
194	131984	131760	MKVEQGELAITLPQNPEENA TATIYFSVDDYGDIAITTTGE EGYTQFDFNFTEEQWAVIV DTISVQLRAQKLSS (SEQ ID NO: 324)	74	hypothetical protein EFP_gp155 [Enterococcus phage phiEF24C]	YP_001504264.1	1e-34 (73/74)		**No putative conserved domains have been detected**		
195	132249	131998	MEKPYVAVRSIHTGRVEYC TEDWLFCGSERNAMPCKEI RYVDMLHCGMESYYEVTFK ANQYTYTEELPVYAFTGIKM IEKEES (SEQ ID NO: 325)	83	hypothetical protein EFP_gp156 [Enterococcus phage phiEF24C]	YP_001504265.1	6e-40 (77/82)		**No putative conserved domains have been detected**		
196	132630	132250	MAKKVEIPSFVARAIKKYDS MLSLLANEYFDPYDEAPDD KLAEWIDEGNQYVLARAYM YGYTIKRQFKVIGDTRYDHG FTIGDTVYLEKVYPDGVYAV RGNSRHSLKIVTLDVHPCDL EEITQEEE (SEQ ID NO: 326)	126	**No significant similarity found.**				Protein of unknown function (DUF1642)	pfam07852	1e-05
197	133063	132866	MGHLPDDVGSWATHCINLV CDGELLEDKKSQTYTCEDC GEVVTLDELNEHLEKEAESY LKFFGYK (SEQ ID NO: 327)	65	hypothetical protein EFP_gp157 [Enterococcus phage phiEF24C]	YP_001504266.1	7e-29 (61/65)		**No putative conserved domains have been detected**		
198	133578	133063	MDKNEFINLLGDEIFTQVGC DGTLNPHALGYNAGIAKAVS LAYGLDEPEKVVIPYKVGEYI DKCKEENLTFINMIDKGSYP SKMYFWLANNPENHEKLAK AWVLGHTVEEEEDEYYIIIAK DKDGWGYSYIDRLGSPDFT NYLKDIPTFTEKEIRKMDER FMAFAVKVGDV (SEQ ID NO: 328)	171	hypothetical protein EFP_gp158 [Enterococcus phage phiEF24C]	YP_001504267.1	4e-82 (159/171)		Protein of unknown function (DUF1642)	pfam07852	2e-10
199	133839	133591	MSYEITYDSNTSVNIQEKIIA VNNSALYKVCVEKKASRVN EKTEVKYTLEVSSAESQEST KLELPHEVMLRLSELIENSLE F (SEQ ID NO: 329)	82	hypothetical protein EFP_gp159 [Enterococcus phage phiEF24C]	YP_001504268.1	3e-37 (79/82)		**No putative conserved domains have been detected**		

FIG. 5AR

200	134394	133852	MNKQELINALEELKFSHVPV VQELSNRSQCYNEAIKAAIL LAKKLDEPKKVIVPKFVAEW YEGNKHALDLAIFTQIRMLD GNSYPHESEFDCWLDQSK NNPIETLIRMKDGYEVEKEP LYHIVFTGLGNKGEDCYLW VDKSHNNEVYFSNKPNMGK NKFTEQEIKEIDERYWAFAV PVYK (SEQ ID NO: 330)	180	hypothetical protein EFP_gp160 [Enterococcus phage phiEF24C]	YP_001504269.1	5e-83 (154/180)		*Protein of* unknown function (DUF1642)	pfam07852	2e-19
201	134787	134395	MIKFKEFDVGDIHYEEQLEK FQNEHPSAEFVTITGGQTTY EKIWFKYTDDKVAQVELSD NQQIVLGWLKEKYTLTDIEPI ELFWRLRANSIKPDYRNSPV YKNYRYMTEIAQLQVLQAFS QWAIERKERN (SEQ ID NO: 331)	130	hypothetical protein EFP_gp161 [Enterococcus phage phiEF24C]	YP_001504270.1	6e-69 (127/130)		**No putative conserved domains have been detected**		
202	135140	134784	MSRQRYNEIIDRVCYMYME ANGEINFPNSFEGDLLKIAY KTAVEAVKKPELNKNQKQV FEWLKVGYCSKDSLFEALE RIGETYEDPKTEEAYYSLSV TEEAQVIQAFTDWFLEQEG VQ (SEQ ID NO: 332)	118	hypothetical protein EFP_gp162 [Enterococcus phage phiEF24C]	YP_001504271.1	5e-61 (114/114)		**No putative conserved domains have been detected**		
203	135314	135144	MRKINVYIETTWAGIGEIETV EVPDNATNEEIDEVARDVFS SYCSFGWGDVEDEEE (SEQ ID NO: 333)	56	hypothetical protein EFP_gp163 [Enterococcus phage phiEF24C]	YP_001504272.1	1e-23 (55/56)		**No putative conserved domains have been detected**		
204	135844	135302	MDNKFATKDDRYLVQVIVN GEVKVSKTINGLAQAKAEKE RLTKHNRRNLVIDSEEYRDQ QNNLYGSRGGRHTVISINLQ KLNHQVEGNELNTIIFDLVSK LEVTHNLKIAPTYFKAVKEG RKLFEIRKNDRHYHVGDILLL NEYTCGSYTGEFVKAKVTYI TDYAQKDDYVVLGIKLCEK (SEQ ID NO: 334)	180	hypothetical protein EFP_gp164 [Enterococcus phage phiEF24C]	YP_001504273.1	1e-91 (166/180)		ASCH domain	pfam04266	0,001

FIG. 5AS

205	136311	135847	MKYTCIKPFKTERVSVDVNS VWYGVDVNNMWYELDDPC YPDIKCPKYILIGGSAGASICI DLHTLLNNFMKVDNSYESV EIKLRERGIFGKEHTITFDYM GYAHFKQRFLKRFGNISSD RKLKKEIVNTNSLNDLERVF SNNDNWSIKIMKERY (SEQ ID NO: 335)	154	hypothetical protein EFP_gp165 [Enterococcus phage phiEF24C]	YP_001504274.1	4e-80 (144/154)		**No putative conserved domains have been detected**		
206	136778	136308	MVINRYILCIKSLSMEDMRY VVEKVSSKTDFGGLSEDCLL PQLYRPITLVFVPSKKYVYQ SLGVTTYKDEKALVYSYGTD GDGLDQLLKDIEEAKKVTTF EEGLKRRYNRQIKRKTKRIN NLLEQDKRGYGWHELGYLQ GVVTTLEDVLDDLEERQ (SEQ ID NO: 336)	156	**No significant similarity found.**				**No putative conserved domains have been detected**		
207	137345	136980	MSNCIEELLSKEAIYVDRFIV ARDNSYFANIVMQSFHTKN VFHVKRNDEYFMGIRANNF VVELGELDFEVPISKEDHEL LASVLGTKLDTATFVLVTGN HKGVRYTTIWAIPKTILDKEL L (SEQ ID NO: 337)	121	hypothetical protein EFP_gp167 [Enterococcus phage phiEF24C]	YP_001504276.1	7e-65 (120/121)		**No putative conserved domains have been detected**		
208	137521	137342	MIECLMCQVPLEETCGDFYL DEMLCGLCAMHLLLDGIEQ SLMMEIYVSELLLEEEENML (SEQ ID NO: 338)	59	hypothetical protein EFP_gp168 [Enterococcus phage phiEF24C]	YP_001504277.1	1e-23 (59/59)		**No putative conserved domains have been detected**		
209	138053	137535	MSKYILFWGHTPSKRNKLG KECLSQWYPSQFSAPIKGL GEDIIFPTAEHYMMVRKAML FNDVDTAKRILKTESPKDAK RLGRQVKNFEENLWVKHRK SIVLDGNTYKFTQNDSLRNF MLSIPKGTKFAEASPFDKVW GIGLRESDPRSRDTSKWEG LNILGEVLTEVRENLN 339	172	hypothetical protein EFP_gp169 [Enterococcus phage phiEF24C]	YP_001504278.1	2e-95 (167/172)		Domain of unknown function (DUF1768)	pfam08719	9e-39

FIG. 5AT

210	138527	138054	MIKVKVIDSDTPYGLSKELE KFLANHKHTSINYSVAYKNP STIYSALVTYKQEDVSVDSL VPLKAKGFLKIISFDKYRTLE ECHRRVPLSTYKLNLNDGD KIPLFFKDKPVIAISPTGEEP YYFYEHPEHIEANGGLPSPH FAFEHKGNYYEYWEEH (SEQ ID NO: 340)	157	hypothetical protein EFP_gp170 [Enterococcus phage phiEF24C]	YP_001504279.1	4e-73 (136/157)		**No putative conserved domains have been detected**
211	139231	138524	MCFGYICPVCETAIVGDPDN GGELCQLTHIRHSKVIGTTR GHYNGLGGVVEDCYFGGR SGRNSQEEIFRSEYEFKDSY RIGKRRQAPSGREVRAYEP LNDLTVGSPERECFEIAIEGL NKELKGYANTILALEDELLQ SAIGGLSCMGQDYYEKMMI LANMKSSSNRYWLVLSKLY NDYILTLPDSMEAKSGVIAV HVACLKTLSKEERASLPFSK PDPDQSIGTVREAYREDNT (SEQ ID NO: 341)	235	hypothetical protein EFP_gp171 [Enterococcus phage phiEF24C]	YP_001504280.1	3e-129 (225/235)		**No putative conserved domains have been detected**
212	139700	139260	VEFVEKAEYVFPKPILDFNL GHRVAIVLKEEELSCLERSY YKTRLYGSIYLVASDKISIEV YNESIKLGFNDEEVLGCVIG YPVECAKWFAKASREELSN SGVMMSGSYTFKCPEHLVD YAKEYMLEHYGLKAYYDIPC EKIVTFS (SEQ ID NO: 342)	146	hypothetical protein EFP_gp172 [Enterococcus phage phiEF24C]	YP_001504281.1	3e-78 (142/146)		**No putative conserved domains have been detected**
213	139884	139750	LNKQRENHKEKIKEHTEIIGH IEEKIENILYIPEEEEYNRDLP F (SEQ ID NO: 343)	44	hypothetical protein EFP_gp173 [Enterococcus phage phiEF24C]	YP_001504282.1	1e-14 (42/44)		**No putative conserved domains have been detected**

FIG. 5AU

Phage	Titer (pfu/ml)	Phage sensitivity (%) of EFS strains (n=105)					Total of infected strains (%)
		++++	+++	++	+	-	
F170/08	$1x10^{10}$	48	21	13	8	10	**90**
	$1x10^{9}$	43	26	8	7	16	**84**
	$1x10^{7}$	31	30	6	2	31	**69**
	$1x10^{5}$	55	1	1	0	43	**57**

FIG. 6A

Phage	Titer (pfu/ml)	Phage sensitivity (%) of EFM strains (n=56)					Total of infected strains (%)
		++++	+++	++	+	-	
F170/08	$1x10^{10}$	2	8	14	14	62	**38**
	$1x10^{9}$	5	4	5	4	82	**18**
	$1x10^{7}$	0	2	7	2	89	**11**
	$1x10^{5}$	3	0	0	2	95	**5**

FIG. 6B

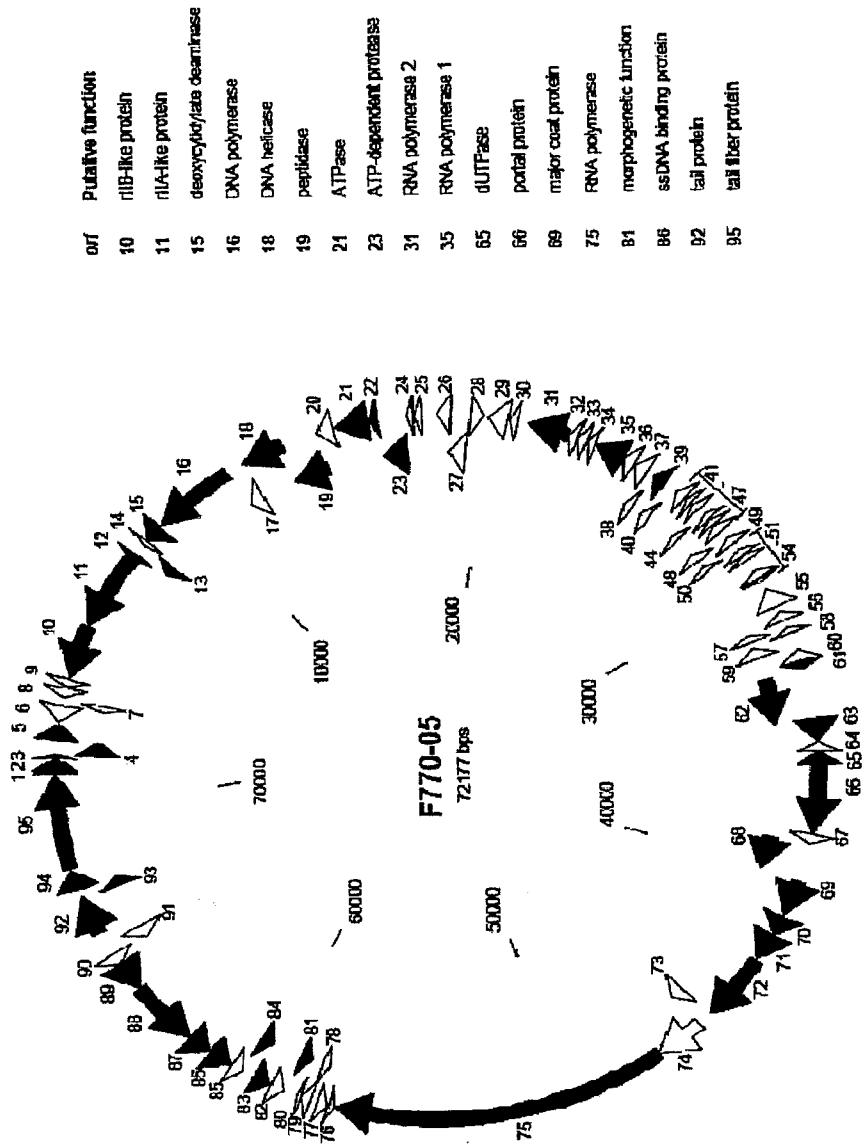

orf Putative function
10 rIIB-like protein
11 rIIA-like protein
15 deoxycytidylate deaminase
16 DNA polymerase
18 DNA helicase
19 peptidase
21 ATPase
23 ATP-dependant protease
31 RNA polymerase 2
35 RNA polymerase 1
65 dUTPase
66 portal protein
69 major coat protein
75 RNA polymerase
81 morphogenetic function
86 ssDNA binding protein
92 tail protein
95 tail fiber protein
F770-05
72177 bps
10000
20000
30000
40000
50000
60000
70000

FIG. 7

orf	Start position	Stop position	Product aminoacidic sequence	Size (aa)	Homologous/similar proteins				Conserved Domains		
					Name[organism]	Acc No	E value and identity	Predicted function	Name	Acc No	E value
1	<3	98	GILLVDSQQALECCAL SSQWGSGNNGIHHQA (SEQ ID NO: 344)	31	No significant similarity found						
2	100	528	MQVDVPGKERISALSV RGTVLILDGQEHDFAPI WDGGYLPPEAYIGRTP FQEIKVVDGDVFVRYIH QVTVEILDAEPGEVKP FKVTEDGPVEMPFEYY RLGLGTNSERSGDGE VPGSTEYGQEPSGES LPGGERADSDRIGS (SEQ ID NO: 345)	142	hypothetical protein [Pseudomonas aeruginosa]	BAB03223.1	1e-21 (51/94)		No putative conserved domains have been detected		
					hypothetical protein PPF10_gp026 [Pseudomonas phage F10]	YP_001293370.1	0,14 (32/93)				
3	533	625	MDKGEVADLTAWLEK VKEIQERYPLPEEPK (SEQ ID NO: 346)	30	hypothetical protein D3112p55 [Pseudomonas phage D3112]	NP_938262.1	6e-05 (15/20)		No putative conserved domains have been detected		
4	622	1146	MTADQVFNQVLPEAY KLLPASMNSPEASVML LAIGLQESRFASRRQL VNSINSEGRKVLLPLG PAKGYWQMEKGGAVK GLLNFWKPATKELVHS VCKARGVPATQDAVW DALEHDDVLACALARIL LYTDPHRLPPIKAQAE AWDLYLRQWRPGQPH EATWPELYRKAVRVVT Q (SEQ ID NO:)347	174	hypothetical protein Daci_3261 [Delftia acidovorans SPH-1]	YP_001564284.1	9e-30 (85/179)		No putative conserved domains have been detected		

FIG. 8A

5	1143	1655	MTISARQIRWIAEVLLF AIIALYAYNKGFVKAES KTNAEWELRMMQAER AAEENKKALEQSLLEA MNEVKKDADEQLADQ ASRIAAADAQSRSLRE QVARLRDDLIADGARA STERHASNAASVVLAD LYGSCVSHRQELAGA LDRSHAAGLTCQKSY AIVKSLGHAPPQ (SEQ ID NO: 348)	170	hypothetical protein SPAB_01000 [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]	YP_001587255.1	1e-04 (51/165)		Protein of unknown function (DUF2514)	pfam10721	1e-05
					Protein gp55 precursor [Phage Gifsy-1]	AAX65118.1	0,011 (47/166)				
6	2275	1718	MSKYEPVFDSSKVTR FYHVRGFAERNGRQV RFFKTTWGFLETDR AYWVVDEDDLKELEH VVRIRKITAASDIRDLA KERYGAFLALKDGSTK RARTSVKAAFFSMICR RERQLTFLERDLNRA QSILLGTRLDTKVAER LEMLNTTTVEIPSSWDI DQQILAEHKRIHENEG HEEGALVWEPDF (SEQ ID NO: 349)	185	**No significant similarity found**				**No putative conserved domains have been detected**		
7	2459	2268	MAEVITTVLEMPNTVIA TAVGDKIMEADAYRHY LESINVDPRFVLEEYIA MVAEKDQEVWKHV (SEQ ID NO: 350)	63	**No significant similarity found**				**No putative conserved domains have been detected**		
8	2826	2509	MPWKSDPNIWGVLSAI ALSVLSGVISLTSRIAK GHPPKFVWVVSELSS AILVGYLIYDVYPVIQH LLYEWMTMPICIAVGG HLGGRVFQWVEFKYK EKFGIPDSY (SEQ ID NO: 351)	105	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 8B

9	3134	2910	MNYYLLYLALGAAWFF VAIGHIFRVPSKQTVE RIITPPILISLSFFSTFM FYVFLWPLALLIDIWRR MIKKSTT (SEQ ID NO: 352)	74	**No significant similarity found**				**No putative conserved domains have been detected**		
10	4960	3182	MSNKVTVVGAVLDER YLTLYVKGSAEQIRIPQ GDPRVAVFVDKYVPIL SQGGEVDYSEDLLVIN NVYEAAEKKSGGIMRF FRVAKKKVAEFFSAAS ASEPAAPVAPVTAGAV PGDCAPDTDAGQDVG EEVAEKVTIKDPALAK AVDEILAHAVPASAPQ FSSVDLENLSEDGVES EDPDDDVGEGDTIIAV TDQGTIVPDAQKLKTQ LTAAVQSKAKGSTVGI ENFLRRAGSVAAKRQ HSVQDLMRFIERGDLP I (SEQ ID NO: 353)	592	rIIB-like protein [Enterobacteria phage N4]	YP_950512.1	2e-53 (158/441)	rIIB-like protein	**No putative conserved domains have been detected**		
11	7488	4972	MQVTHQKDYATHVVI GGKQAISMGISDDPAF FQVLSSSLYTDKILAVV RETLCNAYDAHKMVGI EKETPVEITLKDDEFVI RDFGPGIHPDDVGTIY GVYGGSTKKHDGSQT GGFGLGCKSPFAYVD NFQVTIHHEGKTNVYR MQKASIQNGGRPAITP VVTDIPTDQTGLEVRIN IKNEDVRRFGTLIRRIV ANAEMLANFNGVKLP TLPFSQVTEDWSIATE QVLEYNGHIICVRYGD VIYPVERDEFIAEVY (SEQ ID NO: 354)	838	rIIA-like protein [Enterobacteria phage N4]	YP_950511.1	4e-61 (131/335)	rIIA-like protein	HATPase_c, Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	pfam02518	1e-05

FIG. 8C

12	7683	7492	MSLDGQTVAVHIVMFT NYFGYVPGKKQIDHLC GQRLCCNPAHLEMVT HLTNQKRRAKRAKSK E (SEQ ID NO: 355)	63	gp22 [Enterobacteria phage N4]	YP_950500.1	5e-18 (39/62)		**No putative conserved domains have been detected**		
13	8078	7680	MAKKAKLKADWTPGK LGHAPVNGRYFFVNR ETRMTHTWTIGQLPVP EGYEQVTMQEYDSFR KFNGTLSKKKLMAFIR GEAKCSKDAGKKSGS ESKPAAKSKTRASSST TSPAPATSGKARIQVR AGVVVTGG (SEQ ID NO: 356)	132	**No significant similarity found**				**No putative conserved domains have been detected**		
14	8221	8081	MIKHFGGIEEAEAAIAS GKAVYGKPTVPKGYIL GTDIKGMYVLHKE (SEQ ID NO: 357)	46	**No significant similarity found**						
15	8822	8253	MNAAAFGLPATLREVS TVLKAPDPRSMKYRR LYMSIATNAAKQSVAE RHQVGGVLVTTTGAL FTGWNGTMPGTDNC CENGEYLREETRFKTT PYGVIHAEHNILAWAS RSGVPLDNSVLWITRA PCVRCAEMIATHGVHL VLFRDDHDEPEGMTV LAMGNVKAMSWSTLD SLITEHGGHYVVSKTL LAN (SEQ ID NO: 358)	189	deoxycytidylate deaminase [Bacteroides vulgatus ATCC 8482]	YP_001299900.1	6e-15 (41/146)	deoxycytidylate deaminase	Deoxycytidylate deamina se domain	cd01286	9e-20
					dCMP deaminase [Vibrio phage KVP40]	NP_899367.1	3e-11 (36/120)				

FIG. 8D

16	11519	8904	MKYITWEEQDSYPVAI LIKEAAVSRSAAESTYI KQLEGLGVPRKNVIVI SLDYEGKKVSAKAIKE CIKDRDQLLRDLGVQY AYVADSKYFKEWTKR KTDADFGNLSPPAGY DPGYLVTPGVNHQVL LFDPGQMHRLSRGFK AIVDHAHGVYRPVGS DLLHDVTYIYRGHVSQ AKEALARLMDKPEISC DIEGFSLSMFDSGIATI GFAWNEHDAVQIQCD YREMIQDENKHHGYY EPNAEMREVLKWFFT EYPGR (SEQ ID NO: 359)	871	DNAP [Enterobacteria phage N4]	YP_950517.1	4e-175 (348/871)	DNA polymerase	DNA polymera se family A	pfam00476	2e-34
17	12046	11519	MQARTPEFLIFKRAVK DCLDGFLYVPVRKAF QAKLNELIIADAVARG DGIRAFCHRGRNFMIP GEKPNFRYFPPRLSRG NRVLVDSLLSEYDPVLI DERDSVLTFISQVLNK SDEPSEYLKMFPSGL REPLKRVYEHFGLPVE GVEFPTESPIGSNQAG WDKLCTRVGINLVLGG L (SEQ ID NO: 360)	175	No significant similarity found					No putative conserved domains have been detected		

FIG. 8E

18	13383	12046	MVDSPVQQEIELESPV RASDHVRSEGVDKPA PFVLTPGQEAGFQTFI NFYSNPDAQVMVLKG WSGTGKSTLIRRILDE METLDRALSTLDDNFE PFEPLLTATTNQACEA LAVAMKEFNHEVKTIH RALGLRLRTDYKTGKS ELMPISRFELPYRCLIV VDEASYIDPALLQFCF DRTDCCKFIFVGDDC QLTPVGTNIMPAFAMK DIVVELIEVKRQNSGPL LDLCNAFRHTVKTGE WPKIQLDGDQLIHVPR D (SEQ ID NO: 361)	445	DNA helicase [Enterobacteria phage N4]	YP_950515.1	1e-36 (129/430)	DNA helicase	ATP-dependent exoDNAse (exonuclease V)	COG0507	2e-13
19	14531	13302	MTDRSAEDIALSKAKI RIIGDSKVSFYANIMM GLKYVWEEGMGTAAI DGITMFIDPKFFMSLD EMSRKTVILHEIEHVW RHHIGKVRMGDRDPM LYNIAGDHVINNNLLAC GYGPISWTDYRTGAK CNWCDPKYANMSTE DVYADLYQEQQTQGG GGLSSSTQGNSGSGN PVPFDDISRPAPAKDD GTPMSETEIQGAINDLI LSAATAARANGNPGSI PGEVQVFIDSLMFPKL PLPHLLRQFFQVVKRG GFT (SEQ ID NO: 362)	409	gp25 [Enterobacteria phage N4]	YP_950503.1	4e-40 (115/386)	peptidase	Uncharacterized protein conserved in bacteria	COG3864	3e-19
					metal-dependent peptidase [Clostridium acetobutylicum ATCC 824]	NP_348481.1	2e-09 (80/357)				

FIG. 8F

20	16049	14531	VSGRWELFMVRQEDL TGQAIVDEYANSDSPN RLLTGDFEGWRVSIYE KGIQKGIKFGTKSVLE KLASEFCPYVVTVKPP DGSYVTPGLYVGHCR NSESQYNQSYSRLGG TAASINEVVELIRITNPL NGHWIFDEEEVFVAQ SLAVPSLIPETHNQVE WCKFAKAMAIIGGE (SEQ ID NO: 363)	172	**No significant similarity found**				**No putative conserved domains have been detected**		
21	16131	15061	MHFPQEQEVSIFDAKF IAESFLRAGLKPMIHG SPGIGKSAVARQIAKE NNLKLIDLRLTQMDPA DLNGLPNLSGERAKF QVFEQFPLVGDELPV NPETKEPFAGWLLFLD ELTSADDDRQAAAYKL ILDRQIGNEDLHPKCL VMGAGNLETDGAIVN PMSSALISRLHHIVVR NDLKRWLQVVAPKLDI ATKVQAFLEFSPRAFY TFDPQNSGRVYACPR TWEDFSKWFLKMSPE QDPRALDDMLNLAAA MGIIG (SEQ ID NO: 364)	356	gp24 [Enterobacteria phage N4]	YP_950502.1	5e-51 (129/331)	ATPase	The AAA+ (ATPases associated with a wide variety of cellular activities) superfamily	cd00009	2e-05
22	16404	16177	MSKLQDLPVLIDRPGN YVTRDGSRVVIFTVTE RPEGYSMLTFDARGS YTRVNNTAKPECWHV SGRLHAFREHRKT (SEQ ID NO: 365)	75	hypothetical protein pQBR0228 [Pseudomonas fluorescens SBW25]	YP_001201975.1	1e-04 (27/68)		**No putative conserved domains have been detected**		

FIG. 8G

23	17234	16401	VSQANEKTIERIGKILLI FKASEGEIRPHFWLTG PSGSGKSFNIMDQCN RLDIMLPMTEVNCASL TKEGYSGLSLSKALAP LATLGNVPNVVFCDE MDKLFLSGNSNDSHA NEISIGVQNEFLRVLE GSTTQTFGDYGKYNT VCVERSLFIFAGAFNG QENMDATELLKCGVK TEFIGRTGLVYNLEKP TLEAMVQYLKESELW ANYRSLFPKEDHKKAE KWLIKEIGRQYPDSNI GVRLINTLIHQYYINAG ED (SEQ ID NO: 366)	277	ATP-dependent protease ATP-binding subunit [Helicobacter pylori Shi470]	YP_001910850.1	4e-12 (79/270)	ATP-dependent protease	ATPase family associated with various cellular activities (AAA).	pfam07724	1e-06
24	17478	17293	MQFSDLSPVEQKLYP THSSLKEALEEARHLL PGGSHHDFMRAMMG YHNTFLLFVGEWTPSE (SEQ ID NO: 367)	61	**No significant similarity found**						
25	17720	17487	MSGDAIAMIVAYFATAI VAAGLFDFVLYDDYDD KADRSVTLGILWPIALP IVFGLTVTKIIKTAWKG FKDLCKYGIK (SEQ ID NO: 368)	77	**No significant similarity found**						
26	18621	18178	MLSEERIEHELSSLKN VLDGLRRKITVLHNKR SILSEEIDTTERHVQSY VKRLEELDKEFFELRQ NQTIVHPDVQGQGQD EQTTAVLKDAVVTQM GNKLAEVLDALGFGKE HVQKHGLDETVYDAC LYVQSLKGGEALLNNL RSMLK (SEQ ID NO: 369)	147	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 8H

27	19199	18621	MEKITWFQRGNPIDVP IDRCLYFLADGKLVQF AYHNDLGQLQIAFMTG ISVGKLYAALKGKFVY VRHGFIVANQRVGIKV GRSSHNIPIAVYVKGQ EHLCVQLTAGAKELVK AQFTGDHVLWSTKIKP GDTLVMLPGEPGERV RKKVVIEEIGTETHYN WCGHACFEIAVIDKHG YRYTELNDHFQLYGV NK (SEQ ID NO: 370)	192	**No significant similarity found**	**No putative conserved domains have been detected**
28	19226	19639	MSLRQVLAGTEQEVRI VALLEVGVLPHDGMN QGVHGQFSIATALLAN LVLEPLDFLHGFGELL LQASIHRLEDCLFRDD LGSSFRLHGERLGEF GDLLVACFDGRLQLA DLGLQAIIIALSTRVDP TVVLGFRECCV (SEQ ID NO: 371)	137	**No significant similarity found**	**No putative conserved domains have been detected**
29	20325	19750	MHTFEPGDPMTVIHD SFEHIDSTEGLEAELR AFGAMWWLRGETSW WSRFRQAEERPEHVM YYDIANFIMENDFLIDN VGKRFKLGDEEEEFLE MLRKLVEEAMERDSQ YRNKPVARSVLHQAS VLAMDWVRVGYRAAR RKYPDNFAVADLMYY LYERVRYISHDAYEGS TLQLKYTLNGKYVQVY LDGELR (SEQ ID NO: 372)	191	**No significant similarity found**	**No putative conserved domains have been detected**

FIG. 8I

30	20604	20380	MRKSYLKFLDTMAWIV AVLVFVVVAVASLTVY NGLVALFVMLGAAVGI GMTFGFWFLGYGIYE ELQKLNARVRA (SEQ ID NO: 373)	74	**No significant similarity found**						
31	22168	20927	MTPYTAFEYLLIDAAN QMGHDKWLFEQRIQ WCYDNFDDLENLECN EKTRPQYLKAVMAIRA AQRGEPVGHLVGLDA CCSGMQIMSALGGCE SGAQATNLINTGFRQD AYSLVTTAASTHLGES VGEIKRSDIKTATMTH FYGSKAEPKNLFGEDT PELEAFYQGVEMVAPI ANEMRDDLINTWQPY AMKHSWVLPDNFHSI VKSVDVFETRVEVDE MEGASFEYIYKQDCG VERAVKNAANVIHSID AYVLRSMH (SEQ ID NO: 374)	413	RNAP2 [Enterobacteria phage N4]	YP_950494.1	4e-51 (137/419)	RNA polymerase 2	T3/T7-like RNA polymerase	PHA00452	2e-16
32	22475	22203	MNVAAWLHNGEWHL FTDEMNRVVSDQAYY QAGLKGPDKRDLVLL RMTAKRRNTAYWFHF RKDNPFNKYMPVAYT EEIPKELQALLTIYGL (SEQ ID NO: 375)	90	**No significant similarity found**				**No putative conserved domains have been detected**		
33	22763	22479	MELVVWKDGDNWRV FADDAVPALDGTVDR VAEGLATLYRKEKEPV VFTRRKTAFYDGQYW LMWKYYPTYGRAYGK EASDEMIKEPSAIALLA GY (SEQ ID NO: 376)	94	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 8J

34	23058	22798	VSHYAFYKEDDTWKF VKYGGLLELVQAASM MAYSPKEAAACTCYK LNGVRWWWMGMTDK DAIEDVNLLPADLRAM LVIWSLDQLLE (SEQ ID NO: 377)	86	**No significant similarity found**				**No putative conserved domains have been detected**		
35	24003	23071	MTITHMLPEDMQRAN EYRFARAHIDGYIREFI RGDEDLPALMERGIAL LEEYRTTEYSYNSKNL RMETVRNLDLEHIVFEI IVASAYCQVPDMFISF TAKLAGVLGFDDKADS IKTIAEMVAVLAELDVY DIEQVYKYGTYKVISNI QLPEKLQHAVERAMY LPPMVCKPSKLTGNK SKLHLTLEKESLILNNN HHNEDICLDVLDKMNA VELCLNTEFLSTVEEE SHKYLDTQDKKDDWY RFVSESHEMYKLMV (SEQ ID NO: 378)	310	RNAP1 [Enterobacteria phage N4]	YP_950493.1	5e-23 (63/197)	RNA polymerase 1	T3/T7-like RNA polymerase	PHA00452	0.001
36	24362	24015	MRINAHNKDMFTMVGI REAEQNMARKFNTMLI SDSLRKGESCLYIFDG LTEEVFRKDLSNVASG LMMSRLKSYTDPFKKL YTKHNGRWFVFSSDF NPVAEKLVPPEIRAQS LLFD (SEQ ID NO: 379)	115	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 8K

37	24842	24402	MPQFVVGNMWEAFD KADHFIVLSNSTLTST GAVVMTAGMAAELVA RFHDAGIQTSVGQYIA ENGGAGGIFGCRCQS KVGVFQDKRHYRDPT DLGCVSTSTTQLMWR AQENPTHQYHLEQPG QNEPWWLIKDILARLP GNVTIWSRP (SEQ ID NO: 380)	146	**No significant similarity found**			**No putative conserved domains have been detected**		
38	25093	24842	MTRTYLKRVVIRDDNG MFVSDGDTLIDALREV KLKNLLKQLTVIDQDD GHRWMFQYSHVNNHI VLTKQSPDCCDGIIRM GDLL (SEQ ID NO: 381)	83	**No significant similarity found**			**No putative conserved domains have been detected**		
39	25494	25093	METNHMIFVFGSNTA GIHGAGAALYARNNK GAEMGVGEGPTGMS YALPTKYRAHGGRLVT CHISDVAKAVQRFMDF AKEHSYMSFQVTRIGC GLAGFHDSDIAPLFQA APDNCYFSEAWKPWL KPTTKYWGNE (SEQ ID NO: 382)	133	gp14 [Enterobacteria phage N4]	YP_950492.1	3e-23 (59/125)	Hypothetical protein	PHA00684	9e-24
40	25787	25494	MPTDLKTPTGGTVTG RLVVDRDYLNKLLEVR KYSDRKIDMVYIDMTA LEERVMAHMLDQIPKP VKKSKRRPKWEMPVR NHETNHLGKGPRNKF GGFN (SEQ ID NO: 383)	97	**No significant similarity found**			**No putative conserved domains have been detected**		

FIG. 8L

41	26262	25972	MALKKSNARTNTAAQ SDDTRAASFINISIGTR GGDPVRLGNGIPLRLS EAVEAQLHEYLAEAKD DKDLAKRIENLRSRLIL SFRVVRDKSELQLDL (SEQ ID NO: 384)	96	**No significant similarity found**	
42	26541	26356	MIVLITRKATSILDRGY RECLDAESVARELHAI GMSAVTEEDVLNHWA DWDNDLSDEPRWV (SEQ ID NO: 385)	61	**No significant similarity found**	
43	26835	26614	VTDVEILNLLCLYIASS VAVLNGYMKWSSNNY TMQQTWMGLVIDILVM HVLTFSGMFALIGAVCI FFNLVGLL (SEQ ID NO: 386)	73	**No significant similarity found**	
44	27065	26832	VIILIMFLLFAVGLSMLV IGLHRQWVINEMLRFP LSISRRHDLEMRRIHA WVMAVCGLGLLFAGC GPLFIFLAGGLL (SEQ ID NO: 387)	77	**No significant similarity found**	**No putative conserved domains have been detected**
45	27280	27062	MTIVQLLAVIAVLLLVV PTVLSFLRMLVWAAET WVRCETGRGNRGTA AVATVLYGVATWVCA YLFFVVGAYL (SEQ ID NO: 388)	72	**No significant similarity found**	
46	27503	27300	MLTIACIVLIVFCGYLFL VKCLASLTCFGALFVL PGAEKVAAVVGLVWN VFWAAVWVTAINFLFH VA (SEQ ID NO: 389)	67	**No significant similarity found**	

FIG. 8M

47	27803	27507	MSTNLNLTGRLFDIKII PTNGKLTGFRVRMTLF NMDCPNTVLTHVVMC GDEYTAKSLKTAILQR RRLNLKHWHWTEVNK DLPGACTNRLKTKPFT LEI (SEQ ID NO: 390)	98	**No significant similarity found**	
48	28095	27787	MRTIAELIKIGLEWQQA NRGETYMCFVLSDLA NGVVVGPPITWDEYR SFKNWLWEKLHFRGS DSVLGLLERVGLDDSE ENWVQFYAWAYYDLI KRNTYEHQP (SEQ ID NO: 391)	102	**No significant similarity found**	**No putative conserved domains have been detected**
49	28350	28099	MMYKYARIKRVRNITV YDIACQCWARDFQYD QCLFLLIQHGFSPIQSL EEFQRVWNMLDQAFA DFCNERGCPADPIGFA DVRI (SEQ ID NO: 392)	83	**No significant similarity found**	**No putative conserved domains have been detected**
50	28592	28350	MNTLYHKMQEHVCFV GFTRDGVNYQTNRVR TFGEARHFITFNCSPS DKDIRIFYRIPHEGAED VEVVIARLDLTETKEN N (SEQ ID NO: 393)	80	**No significant similarity found**	**No putative conserved domains have been detected**
51	28819	28589	MSNPHSVFRVNKCFV RMVTNGELITSPTIHNL EEMRDYNRNNCKPTD TGIRLSYMSETEGCEV VLARFDHNGKVLV (SEQ ID NO: 394)	76	**No significant similarity found**	**No putative conserved domains have been detected**
52	29025	28834	MDQNIYTLLYTNECLH SIEHEFEAVSDEVARIK ATAMCRGQEGLWSGI YLTDPQGEAITFDPF (SEQ ID NO: 395)	63	**No significant similarity found**	

FIG. 8N

53	29726	29472	MFKALNQFFAMLESM FRAVTNLTKAAENVTE WAEEESAHFNNKARL QREQAIALLNIENAQEL QEKGLTEAVESVRKE RTKAKA (SEQ ID NO: 396)	84	**No significant similarity found**	**No putative conserved domains have been detected**
54	29750	29857	MVVVTQDQSTAQPKA SLDLEVQTDDWVEVE LNKVG (SEQ ID NO: 397)	35	**No significant similarity found**	
55	30797	30147	MNNKAVLNIKLPGQEL VEIDLGISWHEYINNA GDDNTGLVYVKLAEY AELFDVVPNNPAEKKI AELEAKVKELEDKLKA TSTEENRESFLCRVAS RGSRKQADIVKKDGLF YWVGTIRGTTLRMEST FMDADFDPVLRDARD WVKTPTVMSGGLGVL VMSDRARNHRLELYW FAATGLFTGVATHTET GLAYVSPVKHRDWKD AWREIGCYIQGKD (SEQ ID NO: 398)	216	**No significant similarity found**	**No putative conserved domains have been detected**
56	31309	31001	MELNDTGKIRIVLTIQG KAYYLDALLTRDEWDT MTDAQKTKYMNEWVL ASVSIRPQMPSSESDI LKHKIHELELEVSRLKK QATPTFRYPPGVTIGH LPDQR (SEQ ID NO: 399)	102	**No significant similarity found**	**No putative conserved domains have been detected**
57	31560	31300	MKADWVSNLIFALVW SLYVPKPASEEHLWLF HLLHFLFALLLWTAIDV TRYSPEWKEKPVFAF FIFAPMVPMNLYGAM MLLELLWN (SEQ ID NO: 400)	86	**No significant similarity found**	**No putative conserved domains have been detected**

FIG. 8O

58	31769	31557	MDISYAHVQMKLKNG KTTSHKVEIPYSLSEV QDDFYSTVAQILNLVR RGTGISVLNVTHSRVL FTAGPNQ (SEQ ID NO: 401)	70	No significant similarity found			
59	32200	31769	MQLEPYARHIVNGEL MSRNARVECGTKVFL LRDTLTHNPDTGRKLA LGAGSQVIVMGLCIQY TEKGNIPIJAVHSINED GDLFHALVDPNHLCYA ECPVDRVLKLVQVEE MTVMLRNKGYEQSEK VAELLYSYGIHQLQEG KL (SEQ ID NO: 402)	143	No significant similarity found			No putative conserved domains have been detected
60	32722	32333	MVDRLLLDVSIEHMA WDQCLFQDEVHQLRL VVAGDVAGHVLVGHT LLGPPLDLGGEGTGV SLGVVQPHQLIGHVLR SMEVVVQLELTFLHH MGVPNDVVPEGFRHV RIGQHVIECLQYFRGD GLLHLVR (SEQ ID NO: 403)	129	No significant similarity found			No putative conserved domains have been detected
61	32735	32992	MQNAQSEKVQQESAN SLLTHLKSPEKTELKID VSDRAADADIMRQNA EALARLQQEMIAGKQL SAKDVAERSMDFGEVI EGELA (SEQ ID NO: 404)	85	gp69 [Enterobacteria phage N4]	YP_950547.1	0,050 (26/77)	

FIG. 8P

62	32992	34644	MNLDATPIAKAVADEV DFAGLDEAAKSVEQW LREVVYGDDSSYIPSIF ALQFVDFIKMVNGNEG EENKTPVLHLRMLDQI GSGQTRIANMVFRGA AKTTVMGEYLFLYIALY GELPGFGKVDLALYVS DSIDNGVKNMRKNLEF RWENSEFLKKYIPQTN FTDIRWKFTNLDGKVF IVKGYGAKTGVRGAKE MGKRPQLAVLDDLVS DEDARSPTVIAAIEDTV YKAVDYALHPKKNMII WSGTPFNAKDPLYKA (SEQ ID NO: 405)	550	gp68 [Enterobacteria phage N4]	YP_950546.1	5e-157 (282/527)		Terminase-like family	pfam03237	0.003
63	34641	35375	MTIQLKQVIDLLAEGEL SNIKYVNIDTGALVLER VPSLIRAINLGVLDLHK RFLLKEGMLKIQLEEG RRLYPLRPAYQVGQK PKPGVPQFITDGNKLG RQSILKIEKIIGDNGVE YYLNDTWQPLNITTPE FDVLEISEEFYCHSSS KTLEVRYRRAPTPMKI CVDNLDSWGCIDIDLP YTHLQALLYFVASRCQ TPIGFMENTAQDGFNF SQKYEAECANLDAQN LRIDPVGNQDRFTRG GWV (SEQ ID NO: 406)	244	30 kDa protein [Enterobacteria phage N4]	YP_950545.1	5e-10 (65/236)		No putative conserved domains have been detected		

FIG. 8Q

64	35707	35408	MQLIKEYEHAQPLKFK GWQVSEDHEQNVQA LQEMLGSFPFITAAFG DNADGERVYSLSNFN EGATLDVKAGEWIFVN EEGSIEGWSAEVGAV RFKEIQA (SEQ ID NO: 407)	99	**No significant similarity found**				**No putative conserved domains have been detected**		
65	36097	35711	MPVRASDTAGGYDIF MPEGGVAYPNQPTKV KLGFSAAVPEGHVALL LPRSGTGSKAGLRLR NTCGVIDSDYRGEWV AVVSTDREPFHWEAG NRVLQMLLVPVATPEL QLVEELSETNRGDGG FGSTGE (SEQ ID NO: 408)	128	hypothetical protein COLSTE_02170 [Collinsella stercoris DSM 13279]	ZP_03298245.1	4e-19 (58/128)	dUTPase	dUTPase [nucleotide transport and metabolism]	COG0756	1e-29
66	36165	38345	MADVDEDYLTLPNED GDPSKRLQPEWSNAP SLAQLKQDYQEAKQV TDEKITQINRWLDYMH VRGEGKPKTEKGKSA VQPPTIRKQAEWRYS SLSEPFLSSPNIFEVNP VTWEDAESARQNGLV LNQQFNTKLNKQRFID EYVRAGVDEGTIIVKV GWNYQSRTVKEQVVT YEMMPDSSEELAQIY QTAAQIREESPSEYPE IPEDVRLGLEETEANGI QVRAVPVGSEEEERE ETVENHPTAQVCDYN NIVIDPS (SEQ ID NO: 409)	726	94 kDa protein [Enterobacteria phage N4]	YP_950537.1	0,0 (345/706)	portal protein	**No putative conserved domains have been detected**		
					putative portal protein [Burkholderia multivorans CGD2M]	ZP_03572553.1	8e-09 (146/671)				

FIG. 8R

67	38415	38753	MNEEHAIQITRKNAEK FVRLRDAMLRLHKNR DFQALILNDFLKDNAA RLVLLKADKNMESPE MQARIIREIDAVGALHT YFQLIGVRGDEAEQAI KDCDAELERVREEED EE (SEQ ID NO: 410)	112	No significant similarity found		No putative conserved domains have been detected
68	38753	39949	MADFLEMSDDDLPEF YEVEEQTRSDQEEPE QEQQNDEQSEEVVQE EEPADEEQEEEQEEE QDPLNSPDDELGDLP VEEKPTEEESEQEEEE EDGDKEESEETPTEE KPEAKKSEATKQEVD PADFMAKITAPFKANG RDLQVKTPEEAIRLMQ MGANYNHKMSALKPN LHMMRQLDDAGLLNP DTIANVVDLLKHKKPE AIAKLAKDAGVDPLDL DEKSVADYKPTAVPFN QVREALDEQLDSIEHS PSYNRVVT (SEQ ID NO: 411)	398	gp57 [Enterobacteria phage N4]	YP_950535.1	8e-34 (91/270)

FIG. 8S

69	39984	41183	MAGPVDNIKPMKYND PANGVESSIGPQIHTR YWYKRALIDAAKEAYF GQLADTFSMPKHYGK EIVRLHYIPLLDDRNVN DQGIDASGATIANGNL YGSSRDVGNITAKMPT LTEIGGRVNRVGFKRV EIKGKLEKYGFFREYT QEQLDFDSDPAMEGH VTTEMVKGANEITEDL LQIDLLNSAGTVRYPG AATSDAEVDASTEVTY DSLMRLRLDLDNARA PTKIKMITGTRMIDTRT VGNARALYVGSDLVP TI (SEQ ID NO: 412)	399	major coat protein [Enterobacteria phage N4]	YP_950534.1	2e-121 (218/400)	major coat protein	No putative conserved domains have been detected
70	41240	41905	MSLDELQNLSEAPLES PDTRSELEVLQEKATA LGISFRSNTGVEKLRE KINAVLNDEAVGDEEE DEATEATSSIPKPSAE AGAAALKAAEAPRPKT EGELRRDRRLAAHRLI RCRITCHNPNKNDWD AEYFSIGNDEIGTIRRL VPYEVDWHVPEALLN FIKSKQYQHFYTVTEQ TPMGPQKVRRSKSVR EFSVEILPQLSEDELES LRKQQAVNGSYKED (SEQ ID NO: 413)	221	gp55 [Enterobacteria phage N4]	YP_950533.1	2e-19 (63/200)		No putative conserved domains have been detected

FIG. 8T

71	41909	42874	MAVEPITIADLTEVKLD GKGALDQLLQVTRLHL AKEHDAGRLKGQEYA AVLTGGITAVLQNAVM FLLQKDEAANKAALVE AQIKLTEKQGELLDKQI AQADKDAELIAAKVKL TLEQAKLPDSQIRSAG FQDLLVQEQTKVQTA QTRRIDQEILSAGFQD LLVKEQTAKTKQDVLT AVQQTKVMEQQVLES TQKVLNMKQELLNLVA QECLLKAQFDLTKDQ GLNTQEQTILVRQKVA SERAQTIGAGVDADSV I (SEQ ID NO: 414)	321	gp54 [Enterobacteria phage N4]	YP_950532.1	2e-11 (84/298)		No putative conserved domains have been detected
72	42932	45154	MGLFSSKKKTVVNTTV QRVFDDAHIPDSPRTG VIQGITHETGIVENILEK LSDSIGVRANTAYLWA QRNNYYWGLPESKVV NGVDARTVVVQTIARS EGTITTYYNQFGPLNS LHWGFTELVRLYQYN PLTNELPGLSTTKGSK VYLFDMIPVFQTDTVA WADETANKGMLQDFG FSPKSGYTPSRPYNTI GGMGQFAGWSPYRT DNSFGEDYVLLTYEW KDAQGVIKQETIRMIM NLDLSLDYHQVRFRR QNGT (SEQ ID NO: 415)	740	gp53 [Enterobacteria phage N4]	YP_950531.1	1e-10 (119/562)		No putative conserved domains have been detected

FIG. 8U

73	45135	45602	MAYPYSDMPFGVELD TSTLGSFGLGGPQTQ LQMQMPAVDVNAAAS GSGGFMSGFSNIFSR DSMFGGVAPSGAQTG GWVMPALGIGQAVFG AIGANRQQRAARDQL AESRRQFDMNYGAQR QSINTNLEDRQRARVA SNPTAYESVDSYMER NRIR (SEQ ID NO: 416)	155	No significant similarity found	No putative conserved domains have been detected
74	45602	47167	MAQEITWRNIGATVSP GSASSMSAGTTGVQQ ALGALGDIISRQQEMN VNNAKLQREANTQSY LDQVAASTLEQLSNAD YRSGLEAQRDAMGM NLDRAATRDAITKQISA QQNQAAATQKFDDM QAEVGQRGIVDQLRTL AAEGRAGEVNQILAEQ QLINEGEIRKELTGVQ DAIQNRQYRAAGEQR AQAAANRAAEAHSLS MAAGRENLAFTREQR DELRRDRDEAKLVSG TIATTFQDYDESRQAQ SEIMRIVG (SEQ ID NO: 417)	521	No significant similarity found	

FIG. 8V

75	47168	57364	MADFDLDQFLSDRQE ANAGATPAFDALDFAS AGLDMKGSQKAYDLD GIRERKKRNVEESLIG KMGITPGAAGTEILNT AASFVSGTGRALGDVI ALPINAAADMGQAGVT NEAIEAYNRYVSAQM QEGDEAILSQTAAGDD GVPQTMLQRMQGVD ELRKFSTNVDKFFDW SSIVDTTRRDQLSDDI ADATAGGVERLRNAG ESFSRGEILDGLVQGA LGVGQTAATAIGASAT NPLAVGEYTVENAPQI LAYAAN (SEQ ID NO: 418)	3398	virion RNA polymerase [Enterobacteria phage N4]	YP_950528.1	3e-38 (238/1065)	RNA polymerase	Cell envelope integrity inner membrane protein TolA	PRK09510	6e-04
76	57583	57380	MGVLKGLFGAGALAG AVIGILFIGFVFSWIFRI LGVVVALFIVLLILCWV GWEWLKYCFSRKKEG EQ (SEQ ID NO: 419)	67	**No significant similarity found**				**No putative conserved domains have been detected**		
77	57910	57593	MSLVDAVVEAKRQGV QHSLRGSNYESDIPPS LKALLDEALRLANEHSI PLYWSASLPNGVMTR AALGEKGENIHIQYLM SYAAAVQDPALAQEV VQKGMAFLDKK (SEQ ID NO: 420)	105	**No significant similarity found**				**No putative conserved domains have been detected**		
78	58143	57907	MGDLSKACMLKNMHV TRVLHLIEMRNKLTNT LRDNATDDGMATLEM FDAALKQETDRFLRAL RAVGNENINEIKKAAE (SEQ ID NO: 421)	78	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 8W

79	58142	58399	MAKFLLVGCKGWSALVWTPLRGGGCTRCNGPEHSLMPTGSIDIRKPAGGSWLGLQRHQLREVVNGPLDLGGQGGLGSGIQGPMRW (SEQ ID NO: 422)	85	No significant similarity found				No putative conserved domains have been detected
80	58444	58599	MAVNTKKSPPTRNHYENFRKGMKVVTYQRTKGNTLFTVDCDPVEVADLHAC (SEQ ID NO: 423)	51	No significant similarity found				No putative conserved domains have been detected
81	58954	58550	MKAKSYYLLAFAAPTGVGTVFQSAIHAFEQGKSHDFTVPLIAQIKERSGIGANSIMLSVSFLGTMTEAEFNPPFRPGMDATVAYLEGVRAGLENSEKDNPYPTGSVEAADYRNGRISGFSMREGGQQPPQDHSPQ (SEQ ID NO: 424)	134	PmgR [Enterobacteria phage P1]	YP_006558.1	0,059 (22/66)	morphogenetic function	No putative conserved domains have been detected
82	59449	59012	MKIELQQAEVAAGIATYLTANGLKADASQLSISFQTTRKGDGGIVAFVEVPELAVASLVGTKAPVATEPQTVEVVEKPKKAEKKVVNTEAAAGLATAVAESKASEAAPVEVATEEPEPATEMEAKEEEPVAEQAAPASTGGSLFS (SEQ ID NO: 425)	145	No significant similarity found				No putative conserved domains have been detected

FIG. 8X

83	60021	59461	MARLNVIGMDPSMSN WGLACGQYDTTSNTL SLRHIEVIQTSKTKDKQ IRVNSDDLNRSTEITTR VMEVIKEANVIFVEVPV GSQSAAAMKSYGMCI GILSAVRASGKPFHLL TPTDLKVMACNSKTAS KEAMIEWAVKKYPHLN WPRTSKGEVIASRAE HMADACAAAEYGVFH HNDFKLALAMLT (SEQ ID NO: 426)	186	gp46 [Enterobacteria phage N4]	YP_950524.1	3e-36 (79/171)		**No putative conserved domains have been detected**		
84	60452	60009	MKVNPQDVKNMIVEE SFTILPSGLTTVCQLTL VNGWTVTGQSSCVDP IEFDAEIGKEVARRNA EDEVWKFAGYELMQK LHKQNMGPKERLKLE LDELKARQESLYSFLR SDAAASVHAYMGSLL VQQKDVQNNLIEILEE RLQQWQD (SEQ ID NO: 427)	147	hypothetical protein RSL1_gp284 [Ralstonia phage RSL1]	YP_001950159.1	2e-15 (35/81)		Hypothetical protein	PHA01971	3e-17
85	60814	60449	MKVRELLDSLKRQLSY CTNPQQRERLLDHTL RIPVLRPGTVGARPSV DVLSVVPGFDWDDGS MFCEPNSDIKLTVLTP EEVKTIMASYSKGTSW FAYQETKKLREEINRL KKQLELLGGSE (SEQ ID NO: 428)	121	hypothetical protein P91278ORF_144 [Photobacterium damselae subsp. piscicida]	YP_908742.1	1e-13 (40/91)		**No putative conserved domains have been detected**		

FIG. 8Y

86	61564	60818	MFGNLSTSNNSDIKEA KDSIGGGSRIFDTDIYA FKILAAYGSESSGGAL AVNFEFEEHGTGRKL KIQQYVTSSKEKGQN NYYVNAEGEKHYLPG FNIVNAICLMTAEKELA ACVPEQRTLKIYDYDA KAEVPKQVPVLADLTG KDIYLALEKIIENKRVK NEATGQYEDSSETRE LNDVAAVFHFGTKKTL NEARAKAEPEFFDKW KEAKAGTVRDKTKKV AGGGAASGRPAPAGG QAGGGKPASLFS (SEQ ID NO: 429)	248	single-stranded DNA-binding protein [Enterobacteria phage N4]	YP_950523.1	2e-25 (87/263)	ssDNA binding protein	No putative conserved domains have been detected
87	62325	61591	MTQVNDHLVLVSGLS ATGKSACLRNLREPEK VIYLNCEAGKRLPFKS RFIERTVTDPYQIPTVF DAVVEGKVEAHTIIIDT LTYLLDMYESQYIYRA ANGQAAWMDFQQFF KDLMQQKVASSPCKVI FLAHTKEEYNKATMA MDVCVPVKGALKNNG IESYFSTVISTKKVELG KLEPFKENNKLLEITPQ EEMLGYKHVFQTQITK ETVGERIRGPMGMWT HEQTFIDNDIQKVLDH LDWYYN (SEQ ID NO: 430)	244	gp44 [Enterobacteria phage N4]	YP_950522.1	2e-73 (131/242)		No putative conserved domains have been detected

FIG. 8Z

88	64542	62374	MLKYEEMQHHPTSERI VEILCEKTQSKNHRFF RILVGFQFSMMAAHM RCHIKTHERGEIPVNM YALNLMPSGAGKGFS TKVMEDQITYGFRHRF METFDTAAEKHLDDLA FKRHIRKGSELPDEQE AVRKEFKSLGPLLYDF DSGTGPAVKQMRHKL LMANAGAVNLVVDEIG LNLPAMTEIMPTFLELF DVGSVKQKLVKNTND NLRGEEIIGRTPTNLM AFGTPGKLLDGGKTE DQLMELLETGYARRC FFGM (SEQ ID NO: 431)	722	gp43 [Enterobacteria phage N4]	YP_950521.1	0,0 (324/721)		No putative conserved domains have been detected

FIG. 8AA

89	65567	64557	MGQIYTNQTGIPMAM ALWLASDYYDYSEAG LSATTLLKPIRQVVLAR RIKPSDSMADIEGMIA NRMGAAIHDSIEKAWT VNKDRALDALGIPASV AKRVLVNPTEAELKAF NEANEQPAITVYMEQ RSKKEYAGVMVSGKY DFVADGQVEDFKSTT TFSYIKDSKDSDYILQG SIYRALNPGLITKDTMR IHFIFTDWQKFMAKQN KDYPQSRVASKVFNL MPIAETEEWITNRVKW LMSLKDTPEADLPLCS DE (SEQ ID NO: 432)	336	gp42 [Enterobacteria phage N4]	YP_950520.1	2e-73 (138/322)		**No putative conserved domains have been detected**
90	65949	65569	MRDPRYSPHPVCKAQ HPQGQPCEDCEKLHR RLPVKSAEPAHKVQR DTAPLNRYQRPIPRA WKFVDVYRINMLFPLG ELDPSGALDHARKKL MAPGQRSGGKSLWQ DVKEARDTLNRWLED NAGEDD (SEQ ID NO: 433)	126	**No significant similarity found**				**No putative conserved domains have been detected**
91	66374	65946	MEKLTPEDVPFKDFPI DSMPNLLAQMGKARA DTIRFHGLDRRSIGGP RTRWFTNPHAKRLQG LPDAFSDRGVEDILSGI ASATEGSQRPLSAARL FVLLQEPQLCYDLLMG GMALEKRQALRYMAA AKLAVFHLNRYFGASQ (SEQ ID NO: 434)	142	**No significant similarity found**				**No putative conserved domains have been detected**

Fig. 8AB

92	66766	68055	MVDTCNINGVCGTGD WNGPKPGDPNMNDLL LKATPAFGGIDIEFTW PTTNPGAVGTTRLFRS TDANFAGATIRAFVNG NFYFDKTDPGSKVDQ RYYYWIQLVSINGTDG DIIGPASATARPLIEQM IEQLTGEIDSGLLSQEL RKEIAQIELNKLGITQE EIERAKNDDALGVRLT QIDAKMDQNTAILQEE VRARVTADSSLVQTV NTMYADFNGNIAAIQQ ENTALATKVNALASSV TTINATVNGDSASGKV (SEQ ID NO: 435)	429	prophage LambdaSo, host specificity protein J, putative [Shewanella oneidensis MR-1]	NP_716509.1	2e-24 (98/281)	tail protein	Phage-related protein	COG4733	4e-04
					BcepGomrgp22 [Burkholderia phage BcepGomr]	YP_001210242	2e-16 (101/363)				
					putative phage tail protein [Escherichia coli]	YP_002519295.1	2e-14 (91/301)				
93	68052	68351	MSYGFRFYDANGNVT VDSTNKSFRSVYRQQ VFPVLGGTTNLPPGFD ASKGDIFFFTWFQLAP NPWPQFVDFGFVNNQ IQWYDTYSTSYGKAYL NVVSFR (SEQ ID NO: 436)	99	hypothetical protein PSPA7_2427 [Pseudomonas aeruginosa PA7]	YP_001347794.1	2e-05 (22/55)		**No putative conserved domains have been detected**		
94	68348	69019	MTYGIKLTNENSDICID ELNPVYVVVFEGSYKY DSPGQDFIYVQFPTPI RSQSLPIFFAKQDGPH GFMDFTWFGSNGNW TGCRFVLTNFAGMAP SVYSGKYKIVAVHMPK TAGWGMQVFDADGN GVFDTGYTPAVFLGGI QRFLPYGYNPNFPGG RTLGSWYADATKIKQ GAYFRVDFGNTTFRH NGFTIGMLNGPTGWM YIAAFISGNKPGYTIDH PLLAIE (SEQ ID NO: 437)	223	hypothetical protein PACL_0538 [Pseudomonas aeruginosa]	ACD38786.1	5e-10 (40/117)		**No putative conserved domains have been detected**		

Fig. 8AC

95	69058	72177	MTTKVIFTFHNPDGSP QANEKFTVRLTRPGM SDAEHCVVIPETYEMV TDAKGEFTMDLESSTS AYRVTAIGDDDEYEDD PCSQYTFTFVVPDSVD PVYVQELILMPPPNNL PWDEEAMNKITQAVV DARNARDDAEESADR AEAQVGLAAEQVTLAK AEVTKATAQADRSKTE ADRATTQATNAANSA TAAANSATQANTQAN RAKTEADRSKSEADR ARDLADAVAEKVEGG SLPPLVGMNETFTYEG TDPYRWTVSGPATAV SDGSVMRLTKTDGSG SRAFVRQAVSFPDSH WVVYMRVKTQTGTAS RNCSAQIRFIAADNKN CVVYFNVNANGLVEP NTIHMQGTEGDTRNA ATMFTGLGTEDWLDL AVKYDAVNRHIELFRR MPNGTWQKGGGRLM VDAIKPAFIEISSMPVA PQNWWLDTDFISVCK PNLICYGDSIAAGQNE YGVTRGNNPYNNNRN WAGTWFGKVPLYATN RNNLVLVQGVEGRRT WQYLSQLSEISNSGVK VVFIHASTNDVNDATM TMAKRTSDTQAIIDQL HAVGAQVVLFNSMQG TKAYNDASSTTVKLRD YTDQWWNTELPKVNG LAQTLDIARLIAKDGYM DPALGASDGLHLTNAS AQKIADKLGQFFSNSS DTNGFASLDSPAFTGI PTVPTQTPFLPYGKQI	1040	tail fiber protein [Pseudomonas aeruginosa]	BAB03222.1	3e-75 (140/256)	tail fiber protein	SGNH_ hydrolase
					gp17 [Yersinia phage Yepe2]	YP_002003351	3e-07 (47/125)		

Fig. 8AD

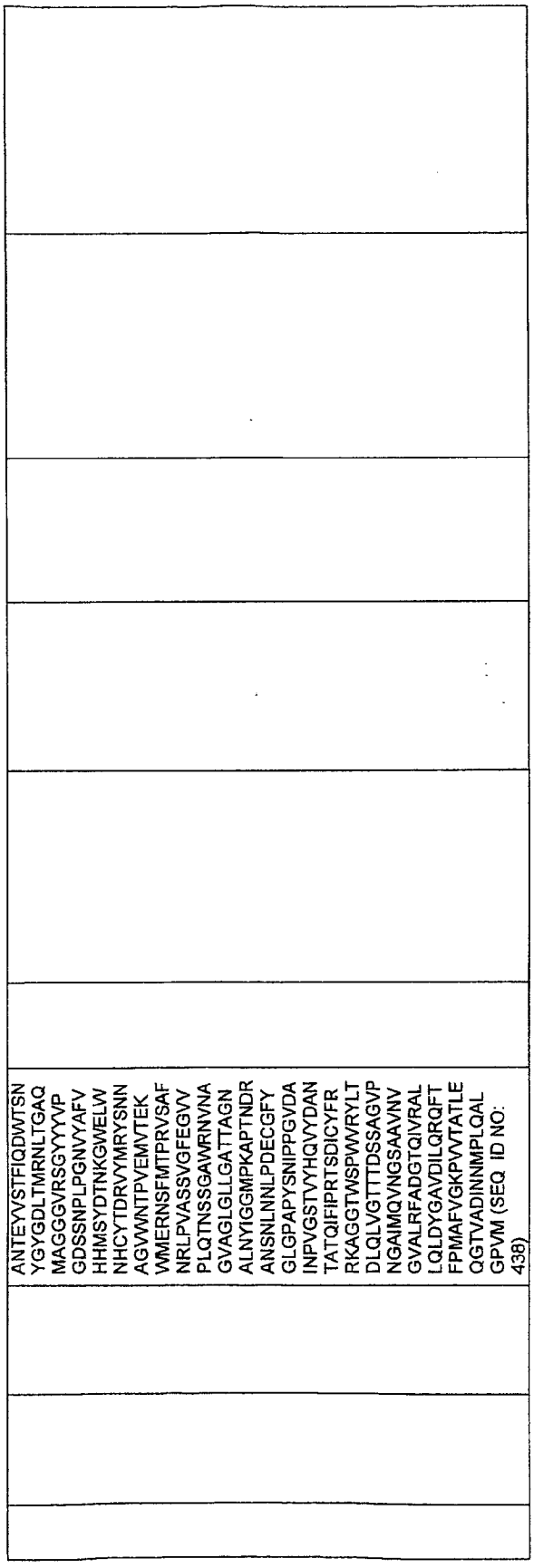
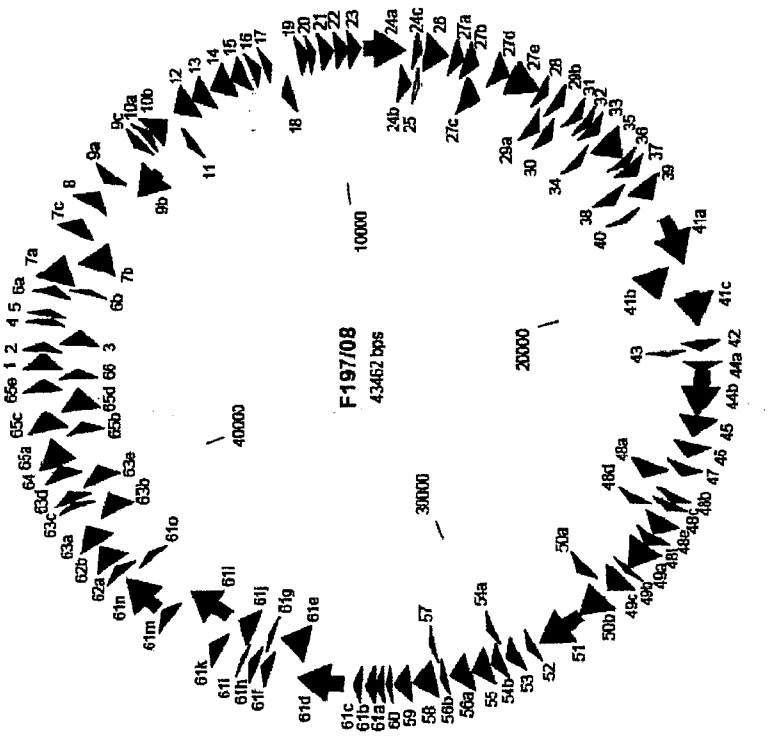

ANTEYVSTFIQDWTSN
YGYGDLTMRNLTGAQ
MAGGGVRSGYYYVP
GDSSNPLPGNVYAFV
HHMSYDTNKGWELW
NHCYTDRVYMRYSNN
AGVWNTPVEMVTEK
WMERNSFMTPRVSAF
NRLPVASSVGFEGVV
PLQTNSSGAWRNVNA
GVAGLGLLGATTAGN
ALNYIGGMPKAPTNDR
ANSNLNNLPDECGFY
GLGPAPYSNIPPGVDA
INPVGSTVYHQVYDAN
TATQIFIPRTSDICYFR
RKAGGTWSPWVRYLT
DLQLVGTTTDSSAGVP
NGAIMQVNGSAAVNV
GVALRFADGTQIVRAL
LQLDYGAVDILQRQFT
FPMAFVGKPVVTATLE
QGTVADINNMPLQAL
GPVM (SEQ ID NO:
438)

Fig. 8AE

Phage	Titer (pfu/ml)	Phage sensitivity (%) of PSA strains (n=100)					Total of infected strains (%)
		++++	+++	++	+	-	
F770/05	$7,7x10^{12}$	2	52	2	2	42	58
	$7,7x10^{11}$	1	52	1	1	45	55
	$7,7x10^{9}$	1	44	4	1	50	50
	$7,7x10^{7}$	1	28	2	1	67	32
	$7,7x10^{5}$	0	21	6	3	70	30

FIG. 9



orf	Putative function
2	tail protein
6a-6b	holin
7a-7c	CHAP/amidase endolysin
9a-9c	integrase
10a-10b	Na/K ATPase
13	lipoprotein
15	ci-like repressor
16	cro-like repressor
19	DNA binding protein
27a-27e	DNA polymerase
29a-29b	DNA binding protein
35	dUTPase
40	transcriptional activator
41a-41c	ATPase
orf	Putative function
42	diacylglycerol kinase
44a-44b	helicase
45	transcriptional regulator
46	endonuclease
47	terminase small subunit
48a-48f	terminase large subunit
49a-49c	portal protein
50a-50b	Clp protease
51	major capsid protein
54a-56b	major tail protein
58	major tail protein
61a-61o	tape measure protein
62a-62b	holin
65a-65e	minor structural protein

FIG. 10

orf	Start position	Stop position	Aminoacidic sequence	Size (aa)	Homologous/similar proteins				Conserved Domains		
					Name[organism]	Acc No	E value and identity	Predicted function	Name	Acc No	E value
1	3	377	NYPRDVSTNGTVEYLVV TSDYKRMTYRPNGTNKV FVKRKEAGSWSEWSELA INDYNTPFETVQSAQSKA NMAESNAKLYADDKFNK RYSVIFDGTANGVGSTLY LNESLDQFILLIFLWDFSR W (SEQ ID NO: 439)	124	hypothetical protein SACOL0384 [Staphylococcus aureus subsp. aureus COL]	YP_1852761.1	1e-63 (118/121)		No putative conserved domains have been detected		
					ORF007 [Staphylococcus phage 3A]	YP_239954.1	5e-63 (117/121)				
2	421	609	LNPSNLPDGDGNGGGVY EFGLTKSSRTSLTISNDV YFDLGSQRGSGANANRG TINKIIGVRK (SEQ ID NO: 440)	62	hypothetical protein SPTP3102_gp61 [Staphylococcus phage tp310-2]	YP_001429956.1	4e-28 (62/62)	tail protein	No putative conserved domains have been detected		
					tail protein [Staphylococcus phage phiSauS-IPLA88]	YP_002332529.1	8e-14 (39/61)				
3	609	977	MQILVNKRNEIISYAIIGGF EEGIDIENLPENFSQVFR PKAFKYSNGEIVFNEDYS EEKDDLHQQIDSEEQNT VASDDILRKMVASMQKQ VVQSTKLSMQVNKQNAL MAKQLVTLNKKIRRG (SEQ ID NO: 441)	122	SLT orf 129-like protein [Staphylococcus phage phi 12]	NP_803352.1	3e-62 (118/119)		No putative conserved domains have been detected		
4	992	1156	MLKLISPTFEDIKTWYQLK EYSKEDIAWYVDMEVIDK EEYAIITGEKYPENLES (SEQ ID NO: 442)	54	ETA orf 59-like protein [Staphylococcus phage phi 12]	NP_803353.1	1e-22 (54/54)		Phage_XkdX, phage uncharacterised protein	pfam09693	4e-07

FIG. 11A

5	1203	1331	MFGFTKRHEQDWRLTRL EENDKTMFEKFDRIEDSL RTQEKNL (SEQ ID NO: 443)	42	hypothetical protein SAPPV1_gp59 [Staphylococcus phage phiNM]	YP_874008.1	6e-15 (40/40)		**No putative conserved domains have been detected**		
6a	1642	1851	MDAKVITRYIVLILALVNQ FLANKGISPIPVDEESVSS IILTVVALYTTYKDNPTSQ EGKWANQKIKEI (SEQ ID NO: 444)	69	holin [Staphylococcus phage phiSLT]	NP_075521.1	1e-30 (66/68)	holin	Phage_holin, phage lysis protein	pfam04688	3e-09
6b	1850	1945	KAESKYRKATGQAPIKEV MTPTNMNDTNDLG (SEQ ID NO: 445)	32	holin [Staphylococcus phage phiSLT]	NP_075521.1	4e-10 (31/31)		**No putative conserved domains have been detected**		
7a	1949	2527	MTNVDNKKTKQKKWFDN SLGKQFNPDLFYGFQCY DYANMFFMIATGERLQG LYAYNIPFDNKARIEKYG QIIKNYDSFLPQKLDIVVF PSKYGGGAGHVEIVESA NLNTFTSYGQNWNGKG WTNGVAQPGWGPETVT RHVHYYDDPMYFIRLNFP DKVSVGDKAKSVIKQATA KKQAVIKPKKNYACSRS WL (SEQ ID NO: 446)	192	amidase [Staphylococcus phage tp310-1]	YP_001429893.1	6e-99 (171/176)	CHAP/amidase endolysin	CHAP domain	pfam05257	9e-17
7b	2502	3143	MLVAGHGYNDPGAVGN GTNERDFIRKYITPNIAKY LRHAGHEVALYGGSSQS QDMYQDTAYGVNVGNK KDYGLYWVKSQGYDIVL EIHLDAAGESASGGHVIIS SQFNADTIDKSIQDVIKNN LGQIRGVTPRNDLLNVNV SAEINMNYRLSELGFITN KKDMDWIKKNYDLYSKLI AGAIHGKPIGGLVAGNVK TSAKNQKKSTSASRLYTR (SEQ ID NO: 447)	213	putative endolysin [Staphylococcus phage phiSauS-IPLA35]	YP_002332423.1	5e-113 (201/202)		N-acetylmuramoyl-L-alanine amidase or MurNAc-LAA	cd02696	7e-21
					amidase [Staphylococcus phage tp310-1]	YP_001429893.1	7e-113 (201/202)				

FIG. 11B

7c	3079	3414	MLKHQLKTKKNPPVPAG YTPDKNNVPYKKETGYY TVANVKGNNVRDGYSTN SRITGVLPNNTTITYDGAY CINGYRWITYIANSGQRR YIATGEVDKAGNRISSFG KFSTI (SEQ ID NO: 448)	111	truncated amidase [Staphylococcus phage phiPVL108]	YP_918945.1	3e-52 (100/110)		SH3_5, bacterial SH3 domain	pfam08460	1e-05
					amidase [Staphylococcus phage tp310-1]	YP_001429893.1	1e-49 (97/110)				
8	3774	4085	MLYLLLYSRSELYSRAEA MYLTVGPTGDIFLVITRYI YLNNIEMLHSLQPYLNRY GYIYSPTTNKTTDPINLGL WLFFCVFFGAKKRADYL KKGQTLVENLKG (SEQ ID NO: 449)	103	hypothetical protein SPTP3102_gp67 [Staphylococcus phage tp310-2]	YP_001429962.1	1e-39 (82/92)		**No putative conserved domains have been detected**		
9a	4564	4319	MLTEGSYSQQKKGNPLC NNQIAGVLKKTTKALNMN KKVTTHTFRHTHITLLVE MNVSLKAIMKRVGHVDE KNNHSHIYSCN (SEQ ID NO: 450)	81	integrase [Staphylococcus phage PVL]	NP_058467.1	2e-28 (61/61)	integrase	Tn1545-related conjugative transposon integrases	cd01199	3e-13
9b	5270	4512	LTFHALLDEWLEYHIKTS GSKLTTLNNIKIRIRNIKRY SSENLLLNKLDTKYMQIFI NKLSDIYSQNQVTRQLG DMKGAIKYAVKFYNYPNE YLLTNVKIPKRRKTIEDIE KDESKMYNYLEMNQVLQ IRDHILNDNKLHKRNRILIA SILEVQALTGMRIGELQA LQEKDIDLLNKTINITGTIH RIKYEEGFGYKDTTKTISS KRSISINSRTVEIFKKILE NKMLKRWNSSYVDRGFI FTTKKRESFM (SEQ ID NO: 451)	252	integrase [Staphylococcus aureus]	BAA24009.1	9e-140 (247/247)		Tn1545-related conjugative transposon integrases	cd01199	3e-23

FIG. 11C

9c	5479	5300	MWIEKFKNKNNETKYRY YEKYKDPYTDKWKRVSV VLNKNTKQSQKRSNVSF RRKNKRKN (SEQ ID NO: 452)	59	integrase [Staphylococcus phage tp310-2]	YP_001429896.1	3e-19 (48/58)		**No putative conserved domains have been detected**
10a	5605	5754	MTQFLGALLLTGVLGYIP YKYLTMIGLVSEKKQGYQ YSCIIDFFLLKHV (SEQ ID NO: 453)	49	Na/K ATPase [Staphylococcus phage phi 12]	NP_803308.1	2e-09 (31/33)	Na/K ATPase	**No putative conserved domains have been detected**
10b	5795	6214	LNLIQLLTGLKANILFLFIF VLTVFVFNPLIVKFIIWLINI TRKFMKLDCISLLDKRDK LFNNNGKPVFIVIKDFEN RIIEEGELKTYNSAGSDF DLLEVERQDFKVSDLASN DELYIKHTLVDLKQQIKLD LYLMNEY (SEQ ID NO: 454)	139	Na(+)/K(+) ATPase [Staphylococcus phage phi2958PVL]	NP_075465.1	2e-71 (138/139)		**No putative conserved domains have been detected**
					Na/K ATPase [Staphylococcus phage phi 12]	NP_803308.1	9e-63 (123/129)		
11	6358	6197	LNGGENFMVDKNKKQET TRSNPLNKSFEKSGASE KLKSTLSEKAKKKRLVFIH (SEQ ID NO: 455)	53	hypothetical protein SAOUHSC_01579 [Staphylococcus aureus subsp. aureus NCTC 8325]	YP_500095.1	1e-14 (41/47)		**No putative conserved domains have been detected**
					ORF130 [Staphylococcus phage 3A]	YP_239962.1	5e-11 (36/40)		
12	6845	6450	METNKTIDLMNYVEFPKR YTEAKGKLVAQPITTINSA RRVENEDMTVCYILDQD DDVMDFIFDRDIITVYCPE NGTATDEYFCEIIFNSDD TFTLKRLSNYVTIKDRSY PMSKINDVNITGKVVRLF RDFK (SEQ ID NO: 456)	131	hypothetical protein phiSLTp03 [Staphylococcus phage phiSLT]	NP_075466.1	5e-70 (131/131)		**No putative conserved domains have been detected**

FIG. 11D

13	7260	6874	VKKEKTKKKKKIKKSQTQ KHKDSKPKTQQEKNEKK LKIKNPPNNSIQNNSNNQ NQSQNNQLNNNSDPSN NTPANINENDSQNTNLND EYVVSPGWTKDEQAKAF EEYKKGKEEEARAGASA VPGANIN (SEQ ID NO: 457)	128	putative liporotein [Staphylococcus phage phiPVL108]	YP_998895.1	4e-38 (107/114)	lipoprotein	**No putative conserved domains have been detected**		
14	7795	7334	LGLYEELCINNEKIKIEET DQLPNFQPGCYMNGKIYI RRNLSEVRKAEVLYEELA HHKLTYGNILDQTKWINR KFENYARRHGFTSAVPL HEIVEAHNYGVRNLYELS EYLQLSESYILEAIEQYKK IYGIGTHYGEYSITFEPLR VFKYKEI (SEQ ID NO: 458)	153	phiSLT ORF153-like protein [Staphylococcus aureus subsp. aureus USA300]	YP_494132.1	2e-83 (151/153)		Domain of unknown function (DUF955)	pfam06114	1e-04
					hypothetical protein SauSIPLA35_gp05 [Staphylococcus phage phiSauS-IPLA35]	YP_002332368.1	2e-64 (122/123)				
15	8137	7808	MENNKVRKILSENLQELM NDKNIDQRELAEAIGVSQ PTVSNWIQQTKYPRIKRI QQLADYFNVPKSRITESK KDIHQETIAAHFDKEGLT EEEIEEVNRFIEWVRNRD K (SEQ ID NO: 459)	109	hypothetical protein SAV0851 [Staphylococcus aureus subsp. aureus Mu50]	NP_371375.1	6e-57 (109/109)	cI-like repressor	HTH_XRE, helix-turn-helix XRE-family like proteins	cd00093	5e-08
					repressor [Staphylococcus phage phiSauS-IPLA35]	YP_002332369.1	3e-35 (74/84)				
16	8298	8489	MPEQLSVRKWRLVRDLK QQEVADILGVNAKTVGH WEKDDTNLSNVTVYALA KLYDIEVDQIKV (SEQ ID NO: 460)	63	cro [Staphylococcus phage phiSauS-IPLA35]	YP_002332370.1	2e-28 (63/63)	cro-like repressor	HTH_XRE, helix-turn-helix XRE-family like proteins	cd00093	3e-06

FIG. 11E

FIG 11E

17	8573	8749	MNEEKLKMILLLLEDIPRD EWNRLVNEVNNQYSYQA DKVGLASDNCQQIANNY KHYGF (SEQ ID NO: 461)	58	hypothetical bacteriophage protein [Staphylococcus aureus subsp. aureus USA300_TCH1516]	ZP_02761849.1	2e-26 (58/58)		**No putative conserved domains have been detected**		
					hypothetical protein SauSIPLA35_gp08 [Staphylococcus phage phiSauS-IPLA35]	YP_002332371.1	3e-26 (57/58)				
18	8985	8746	VISIHKRLLTQYLDKEIVTS LDLHLINGEVIKVQEHIKD AESKTLHIIHPKDRVVSLD HVLYFDINVKGEKNNDSP YPS (SEQ ID NO: 462)	79	hypothetical protein SAS0900 [Staphylococcus aureus subsp. aureus MSSA476]	YP_043027.1	8e-37 (78/79)		**No putative conserved domains have been detected**		
					hypothetical protein SauSIPLA35_gp09 [Staphylococcus phage phiSauS-IPLA35]	YP_002332372.1	8e-35 (73/76)				
19	9334	9549	VKKLYATPTQIHQLFGVC RSTVYNWLKYYRKDNLG VENLYIDYSPTGTLINISKL EEYLIRKHKKMVLGGY (SEQ ID NO: 463)	71	putative DNA-binding protein [Staphylococcus phage phiPVL108]	YP_918904.1	2e-30 (65/65)	DNA binding protein	**No putative conserved domains have been detected**		
20	9550	9711	MSDTYKSYLIAVLCFTVL AIVLMPLLYFTTAWSIAGF ASIATFIYYKEYFYEE (SEQ ID NO: 464)	53	ORF100 [Staphylococcus phage 69]	YP_239610.1	4e-21 (51/53)		Protein of unknown function (DUF1270)	pfam06900	8e-11
21	9805	10059	MAENIKTEQHYYTKDFSG YRNEEDNFVANQELTVTI TLNEYRKLIEIKAVKDKEE DTYRGKYFEEERKKRKIG KRKYKTKKQNL (SEQ ID NO: 465)	84	ORF046 [Staphylococcus phage 52A]	YP_240649.1	6e-32 (71/80)		**No putative conserved domains have been detected**		

FIG. 11F

22	10116	10376	MYYKIGEIKNKIISFNGFE FKVSAMKRHDGISIQIKD MNNVPFKSFHVIDLSELYI AMDAIHDVVNEWIEENTD EQDKLMNLVMKW (SEQ ID NO: 466)	86	hypothetical protein SPTP3103_gp13 [Staphylococcus phage tp310-3]	YP_001429975.1	1e-39 (77/86)		Protein of unknown function (DUF1108)	pfam06531	7e-32
23	10390	10638	MAILEDIFEELKLLNNNLR VLNTELSTVDSSIVQEKV KEAPMPKEETAQLESIEE VKETSADLTKDYVLSVGK EFLKKSRYF (SEQ ID NO: 467)	82	hypothetical protein MW1428 [Staphylococcus aureus subsp. aureus MW2]	NP_646245.1	1e-35 (78/79		**No putative conserved domains have been detected**		
					hypothetical protein SPTP3102_gp18 [Staphylococcus phage tp310-2]	YP_001429913.1	7e-35 (77/79				
24a	10751	11587	MKLDHSNRAHAKLSASG AKQWLNCPPSIKASEGIA DKSTVFAEEGTFAHELSE LYFSLKYEGLTQFEFNKA FQNYKRNQYYSEELREY VEEYVANVEEKYNEALS RDNDVIALFETKLDLGKY VPESFGTGDVIIFSGGVL EIIDLKYGKGIEVSAIDNP QLRLYGLGAYELLSLMYD IHTIRMTIIQPRIDNFSTEE LPISRLLQWGADFVKPLA RLAYNGGGEFKAGSHCR FCKINHSCRTRAEYMQN VPQKPPHLLSDEEIAELL YKLPDIKKMG (SEQ ID NO: 468)	278	hypothetical protein MW1427 [Staphylococcus aureus subsp. aureus MW2]	NP_646244.1	8e-163 (276/276)		**No putative conserved domains have been detected**		
					ORF012 [Staphylococcus phage 3A]	YP_239979.1	8e-160 (270/276)				
24b	11532	11807	MKRLQNFYINCLISKKWA DEVEQYALNQAKENDKN YPGWKLVEGRSRRMITD TKAMLEKLVEAGYKPEDI TETKLLSITNLEKLIGKKSI F (SEQ ID NO: 469)	91	hypothetical protein MW1427 [Staphylococcus aureus subsp. aureus MW2]	NP_646244.1	6e-36 (74/76)		**No putative conserved domains have been detected**		
					hypothetical protein phi2958PVL_gp17 [Staphylococcus phage	YP_002267987.1	5e-35 (72/76)				

FIG. 11G

					phi2958PVL]				
24c	11785	11919	LVKKAFSKITEGFIEKPQG KLTLATESDKRPAIKQSA EDDFDKL (SEQ ID NO: 470)	44	hypothetical protein MW1427 [Staphylococcus aureus subsp. aureus MW2]	NP_646244.1	1e-15 (42/42)		**No putative conserved domains have been detected**
					hypothetical protein phi2958PVL_gp17 [Staphylococcus phage phi2958PVL]	YP_002267987.1			
25	11900	12019	MILTNYKNLKGRYINMKA KVLNKTKVITGKVRASYA HIF (SEQ ID NO: 471)	39	**No significant similarity found.**				**No putative conserved domains have been detected**
26	12003	12464	MHIFFEPHSMQEGQESK YSISLIIPKSDTSTIKAIEQA IEAAKEEGKVSKFGGKVP ANLKLPLRDGDTEREDD VNYQDAYFINASSKQAP GIIDQNKIRLTDSGTVVSG DYIRASINLFPFNTNGNK GIAVGLNNIQLVEKRRTS WRCKCSRR (SEQ ID NO: 472)	153	hypothetical protein MW1426 [Staphylococcus aureus subsp. aureus MW2]	NP_646243.1	2e-74 (139/140)		**No putative conserved domains have been detected**
					hypothetical protein phi2958PVL_gp18 [Staphylococcus phage phi2958PVL]	YP_002267988.1	4e-74 (138/140)		
27a	12572	12805	MNIDIETYSSNDISKCGAY KYTEAEDFEILIIAYSIDGG AISAIDMTKVDNEPFHAD FETFKIALFDPAVKKVCIQ C (SEQ ID NO: 473)	77	DNA polymerase [Staphylococcus phage phi2958PVL]	YP_002267989.1	2e-36 (72/72)	DNA polymerase	**No putative conserved domains have been detected**
27b	12846	13118	MPPEEWICTMVNSMRIG LPASLDKVGEVLRLQNQ KDKAGKNLIRYFSIPCKPT KVNGGRTRNLPEHDLEK MATIYRLLYSRCRSRNDD CS (SEQ ID NO: 474)	90	DNA polymerase [Staphylococcus phage phi2958PVL]	YP_002267989.1	2e-37 (70/70)		**No putative conserved domains have been detected**

FIG. 11H

27c	13012	13428	MEEEQETCLNMILKKWQ QFIDYCIRDVEVEMTIAHK IKDFPVTAIEQAYWVFDQ HINDRGIKLSKSLMLGAN VLDKQSKEELLNQAKHIT GLENPNSPTQLLAWLKD DQGLDIPNLQKKTVQEYL KEATGKAKKNARN (SEQ ID NO: 475)	138	DNA polymerase [Staphylococcus phage phi2958PVL]	YP_002267989.1	5e-66 (121/122)		**No putative conserved domains have been detected**		
27d	13470	13835	MHDMMCSDERVRGLFQ FYGAGTGRWAGRGVQL QNLTKHYISDTELEIARDL IKEQRFDDLDLLLNVHPQ DLLSQLVRTTFTAEEGNE LAVSDFFCNRGKSHSMV CKRTMAFRCVQHTRKDI (SEQ ID NO: 476)	121	ORF003 [Staphylococcus phage 3A]	YP_239981.1	3e-51 (98/121)		**No putative conserved domains have been detected**		
27e	13852	14529	MFNVPVESITKGDPLRQK GKVSELALGYQGGAGAL KAMGALEMGIEENELQG LVDSWRNANPNIVNFWK ACQEAAINTVKSRKTHHT HGLRFYMKKGFLMIELPS GRALAYPKASVGENSWG SQVVEFMGLDLNRKWSK LKTYGGKLVENIVQATAR DLLAISIARLEASGFKIVG HVHDEVIVEIPRGSNGLK EIETIMNKPVDWAKGLNL NSDGFTSPFYMKD (SEQ ID NO: 477)	225	DNA-directed DNA polymerase [Staphylococcus aureus subsp. aureus JH9]	YP_001246416.1	2e-130 (225/225)		POLAc, DNA polymerase A domain	smart00482	3e-05
					DNA polymerase [Staphylococcus phage phi2958PVL]	YP_002267989.1	6e-130 (224/225)				
28	14542	14727	MQHQAYINASVDIRIPTE VESVNYNQIDKEKENLAD YLFNNPGELLKYNVINIKV LDLEVE (SEQ ID NO: 478)	61	ETA orf 26-like protein [Staphylococcus phage phi 12]	NP_803319.1	1e-26 (61/61)		**No putative conserved domains have been detected**		

FIG. 11I

29a	14724	15005	MMARRKVIRVRIKGKLMT LREVSEKYHISPELLRYR YKHKMRGDELLCGRKDS KSKDEVEYMKSQIKDEEK EREKIRKKSDFEPIPTKCE SGI (SEQ ID NO: 479)	93	hypothetical protein SauSIPLA35_gp19 [Staphylococcus phage phiSauS-IPLA35]	YP_002332382.1	1e-36 (79/80)	DNA binding protein	PVL ORF-50-like family	pfam07768	3e-11
29b	14926	15129	MKKKREKKSEKKAILNLY QRNVRAEYEEERKRRLR PWLYDGTPQKHSRDPY WFDVTYNQMFKKWSEA (SEQ ID NO: 480)	67	putative DNA-binding protein [Staphylococcus phage phi2958PVL]	YP_00226799.1	1e-27 (59/64)				1e-13
					hypothetical protein SauSIPLA35_gp19 [Staphylococcus phage phiSauS-IPLA35]	YP_002332382.1	5e-27 (58/64)				
30	15129	15386	MSIISNRKVDMNETQDNV KQPAHYTYGDIEIIDFIEQ VTAQYPPQLAFAIGNAIK YLSRAPLKNGHEDLAKAK FYVDRVFDLWEG (SEQ ID NO: 481)	85	hypothetical protein MW1422 [Staphylococcus aureus subsp. aureus MW2]	NP_646239.1	8e-44 (85/85)		**No putative conserved domains have been detected**		
					hypothetical protein phiETA2_gp29 [Staphylococcus phage phiETA2]	YP_001004289.1	4e-43 (84/85)				
31	15389	15589	MATQKQVDYVMSLQEQL ELEDCEKYTDEQVKAMS HKEVSNVIENYKTSIRNE ELYYECMSFGLPNC (SEQ ID NO: 482)	66	hypothetical protein SAR1537 [Staphylococcus aureus subsp. aureus MRSA252]	YP_040939.1	5e-31 (66/66)		**No putative conserved domains have been detected**		
					hypothetical protein [Staphylococcus phage phiMR25]	YP_001949825.1	1e-28 (63/66)				
32	15683	15847	VAHTHVVNGTYYFHGHIV PGWQSVKKTFDTAEELEI YIKQHGLEYEEQKQLTLF (SEQ ID NO: 483)	54	hypothetical protein USA300HOU_1468 [Staphylococcus aureus subsp. aureus USA300_TCH1516]	YP_001575356.1	3e-24 (54/54)		Phage_Orf 51	pfam06194	1e-18

FIG. 11J

					hypothetical protein SA1786 [Staphylococcus phage phiN315]	NP_835543.1	2e-23 (53/54)				
33	15862	16116	MNNREQIEQSIISASAYN GNDTEGLLKEIEDVYKKA QAFDEILEGLPNAMQDAL KEDIGLDEAVGIMTGQVV YKYEEEQENEEI (SEQ ID NO: 484)	84	hypothetical protein phi2958PVL_gp24 [Staphylococcus phage phi2958PVL]	YP_002267994.1	3e-39 (82/84)		Protein of unknown function (DUF1024)	pfam06260	2e-27
34	16103	16273	MKKFNVQITYTGMIEETIE AESLEEAEFEADVIARLE APFDCDEYEINVEEEQEN D (SEQ ID NO: 485)	56	hypothetical protein phiETA3_gp33 [Staphylococcus phage phiETA3]	YP_001004362.1	1e-22 (54/56)		**No putative conserved domains have been detected**		
35	16266	16793	MTNTLQVKLLSKDARMP ERNHKTDAGYDIFSAETV VLEPQEKAVIKTDVAVSIP EGYVGLLTSRSGVSSKT HLVIETGKIDAGYHGNLGI NIKNDAQVYLTTNEQCFD IQGEMENSFVNNAKKKP FTINDYYEIYKGDKLAQLV IVPIWTPELKQVEEFESV SERGAKGFGSSGV (SEQ ID NO: 486)	175	dUTPase [Staphylococcus phage phiPVL108]	YP_918921.1	7e-98 (173/175)	dUTPase	deoxyuridine 5'-triphosphate nucleotido-hydrolase	PRK00601	1e-24
36	16830	17003	VRERTKIIYRGWNKEIFIL QGKNMNVIGLRQIFDELK RSYEGYKIVVIPIEVDFEIK (SEQ ID NO: 487)	57	ORF089 [Staphylococcus phage 69]	YP_239633.1	1e-23 (56/57)		**No putative conserved domains have been detected**		
37	17020	17307	VTQYLVTTFKDSTGLPHE HITVARDNQTFTVVEAES KEEAKEKYEARNVPVDG ATNLNDIKSNIGIFHVEKV EPNEGMVDINIETMKPFE EADDD (SEQ ID NO: 488)	95	ORF054 [Staphylococcus phage ROSA]	YP_240374.1	3e-45 (89/95)		Protein of unknown function (DUF1381)	pfam07129	7e-09

FIG. 11K

38	17290	17537	MINIPKMKFPKKYTEIISK KYKNKTPEEKAKIENDFIK DINDKDSEFYSPMMANM NEHELRAMLRMMPSLIDT GDDNDD (SEQ ID NO: 489)	79	hypothetical protein SPTP3102_gp35 [Staphylococcus phage tp310-2]	YP_001429930.1	1e-34 (77/79)		**No putative conserved domains have been detected**		
39	17530	17916	MIKKLKNMNWFDIFIAGIL RLFGVIALMLVVISPIYTV ASYQNKEVHQGTITDKY NKRQDKEDKFYIVLDNKQ VIENSDLLFKKKFDSADIQ ARLKVGDKVEVKTIGYRI HFLNLYPVLYEAKKVDKQ (SEQ ID NO: 490)	129	ORF040 [Staphylococcus phage 88]	YP_240738.1	9e-67 (127/128)		Protein of unknown function (DUF1523)	pfam0750 9	4e-05
40	17913	18065	MIKQILRLLFLLAMYELGK YVTEQVYIMMTANDDVE APSDFAKIRAEVSW (SEQ ID NO: 491)	50	hypothetical protein SPTP3102_gp37 [Staphylococcus phage tp310-2]	YP_001429932.1	2e-20 (49/50)	transcriptional activator	Transcription al activator RinB	pfam0611 6	4e-17
41a	18386	19444	MLDKVTQIETIKYDRDVS YSYAASRLSTHWTNHNM AWSDFMQKLAQTVRTKE DLTEYNKMSKSEQADIKD VGGFVGGYLKEGKRRAG QVMNRSMLTLDIDYAAQ DMTDILSMFYDFAYCLYS THKHREISPRLRLVIPLKR NVNADEYEAIGRKVADIV GMDYFDDTTYQPHRLMY WPSTSNDAEFFFTYEDL PLLDPDKILNEYVDWTDT LEWPTSSREESKTKRLA DKQGDPEEKPGIIGAFCR AYTIEEAIETFIPDLYEKHS TNRYTYHEGSTAGGLVL YENNKFAYSHHNTDPVS GMLVNSFDLVRIHLYGAQ DEETKTDTPVNRLPSYKA MQQRAQNDEVVKKAIN (SEQ ID NO: 492)	352	ORF002 [Staphylococcus phage 47]	YP_240066.1	0,0 (348/351)		**No putative conserved domains have been detected**		

FIG. 11L

41b	19416	20045	MKLLKKQLINDKMSDAM QDFDEIENSDDAWSETL EITSKGTFKASIPNIEIILR NDPNLKGKIAFNEFTKQI ECLGKVPWNTNFKTRQ WQDGDDSSLRSYIEKIYD IHHSGKTKDAIISVAMQN AYHPVRDYLNKISWDGH KRLEKLFIKYLGVEDTEV NRTTTKKALTAGIARVME PGCKFDYMLTLYGPQGV GKSALLKKIRWCMVF (SEQ ID NO: 493)	209	ORF002 [Staphylococcus phage 47]	YP_240066.1	2e-114 (198/202)	ATPase	Predicted P-loop ATPase and inactivated derivatives	COG5545	1e-27
41c	20104	20835	MEMAELAATRKAEVEAIK HFISKQVDRFRVAYGHYI EDFPRQCIFIGTTNKVDFL RDETGGRRFWPMTVNP ERVEVNWSKLTKDEIDQI WAEAKYYYEQGEELFLN PELEEEMRSIQSKHTEES PYTGIIDEYLNTPIPSNWE DLSIFERRRFYQGDVDML PTGNVDYVERNKVCALE VFVECFGKDKGDSRGSM EIRKISNILRQLDNWSVYD GNKSGKIRFGKDYGVQIA YVRDESLEDLI (SEQ ID NO: 494)	244	ORF002 [Staphylococcus phage 47]	YP_240066.1	6e-141 (238/243)		Predicted P-loop ATPase and inactivated derivatives	COG5545	1e-20
42	21177	21371	MKESTLEKYLVKEITKLN GLCLKWVAPGTRGVPDR IIIMPEGKTFFVEMKQEKG KLHPLQKICA (SEQ ID NO: 495)	64	ORF053 [Staphylococcus phage 42E]	YP_239929.1	2e-27 (60/61)		VRR-NUC domain	pfam0877 4	5e-08
					diacylglycerol kinase, catalytic region [Bacillus selenitireducens MLS10]	ZP_02170287.1	1e-06 (27/61)	diacylglycerol kinase			

FIG. 11M

43	21364	21468	VHRQFENRDHTVYVLWN KEQVNTFIRMVGGTFGD (SEQ ID NO: 496)	34	ORF045 [Staphylococcus phage 3A]	YP_239996.1	1e-12 (34/34)		**No putative conserved domains have been detected**		
44a	21616	21828	MLVIAPKQVAKDTWVDE VDKWNHLNHLKVSLILGT PKERNDALNTEADIYVTN KENTKWLCDQYKKRMAI (SEQ ID NO: 497)	70	phage helicase [Staphylococcus phage phi2958PVL]	YP_002268001.1	4e-32 (65/66)	helicase	**No putative conserved domains have been detected**		
44b	21830	22819	MVVIDELSTFKSPKSQRF KSIKKKLPLINRFIGLTGTP SPNSLQDLWAQVYLIDR GERLESSFSRYRERYFK PTHQVSEHVFNWELRDG SEEKIYERIEDICLSMKAK DYLDMPDRVDTKQTVVL SEKERKVYEELEKNYILE SEEEGTVVAQNGASLSQ KLLQLANGAVYTDDEDV RLIHDKKLDKLEEIIEESQ GQPILLFYNFKHDKERILQ RFKEATTLEDSNYKERW NSGDIKLLIAHPASAGHG LNLQQGGHIIVWFGLTWS LELYQQANARLYRQGQN HTTIIHHIMTDNTIDQRVY KALQNKELTQEELMKAIK ARIAKHK (SEQ ID NO: 498)	329	helicase [Staphylococcus phage phi 12]	NP_803332.1	0,0 (327/329)		HELICc,helicase superfamily c-terminal domain	cd00079	0,002
45	22832	23269	MGNTIYDIKPGTFKYIESE IYNLNENKKEIKRLRLEIL NPTKEQDSNIVYGPLQK GEPVRTTELMATRLLTNK MLRNLEEMVEAVESEYL KLPEDHKKVIRLKYWNKE KKLKMEQIGHECHMHRN TVTTIRKNFVKAVAYHAGI K (SEQ ID NO: 499)	145	hypothetical protein phiSLTp36 [Staphylococcus phage phiSLT]	NP_075498.1	6e-79 (145/145)	transcriptional regulator	**No putative conserved domains have been detected**		
					phi SLT ORF 145-like protein, phage transcriptional regulator [Staphylococcus aureus subsp. aureus	YP_494104.1					

FIG. 11N

					USA300]						
46	23426	23758	MTKHNNIYKHGRKSYQY DWFYHSKAWKKLREIAL DRDNYLCQMCLREDIVT DANIVHHIIYVDEDFNKAL DLDNLMSVCYSCHNKIHA NDNDKSNLKKIRVLKNLN KKII (SEQ ID NO: 500)	110	ORF046 [Staphylococcus phage 42E]	YP_239933.1	4e-53 (102/103)	endonuclease	McrA, restriction endonuclease [Defense mechanisms]	COG1403	2e-04
47	23945	24178	LYIETYEFYCRLRDELKN SDLMIEHTNKAGASNIIKN PLSIELTKTVQTLNNLLKS MGLTAAQRKKIVQEEGG FGDY (SEQ ID NO: 501)	77	ORF037 [Staphylococcus phage 3A]	YP_239934.1	4e-38 (77/77)	terminase small subunit	Terminase_4, phage terminase, small subunit	pfam0511 9	2e-12
48a	24166	24516	VTIKVLNEPSPKLLTTWY AEQVTQGKIKTSKYVRKE CERHLRYLENGGKWVFD EELAHRPIRFIEKFCKPSK GSKRQLVLQPWQHFIIGS LFGWVHKETKLRRFKEA LIFMGRKKW (SEQ ID NO: 502)	116	putative terminase large subunit [Staphylococcus phage phiSauS-IPLA35]	YP_002332401.1	3e-63 (113/114)	terminase large subunit	Terminase_1, phage terminase	pfam0335 4	6e-05
48b	24604	24789	MKQARILFDESKAMIKAS PKLDKNFRTLRDEIHYDA TISKIMPQASDSDKLDGL NTHMGIF (SEQ ID NO: 503)	61	ORF005 [Staphylococcus phage 3A]	YP_239935.1	2e-28 (61/61)				0,001
48c	24818	24997	LISVIKNSRAARLQPLLIYI TTAGYQLDGPLVDMVEA GRDTLDQIIEDERTFLLFS IFG (SEQ ID NO: 504)	59	ORF005 [Staphylococcus phage 47]	YP_240002.1	6e-23 (52/52)				0.004
48d	24990	25205	LDDDDDINDSSNWIKANP NLGVSINLDEMKEEWEK AKRTPAERGDFITKRFNIF ANNDEMSFIDYPTLQKK (SEQ ID NO: 505)	71	terminase large subunit [Staphylococcus phage phi2958PVL]	YP_002268005.1	5e-34 (70/70)				7e-08

FIG. 11O

48e	25177	25563	LITQHSKKNNEIVSLEELE GRPCTIGYDLSETEDFTA ACATFALDNGKVAVLSHS WIPKHKVEYSNEKIPYRE WEEDGLLTVQDKPYIDY QDVLNWIIKMNEHYVVEK ITYDRANAFKLNQELKKL RV (SEQ ID NO: 506)	128	terminase large subunit [Staphylococcus phage phi2958PVL]	YP_002268005.1	4e-65 (117/118)				4e-08
48f	25595	25864	LSPALKDLKEMFLDGKIIF NNNPLMKWYINNVQLKL DRNGNWLPSKQSRYRKI DGFAAFLNTYTDIMNKVV SDSGEGNIEFISIKDIMR (SEQ ID NO: 507)	89	putative terminase large subunit [Staphylococcus phage phiSauS-IPLA35]	YP_002332401.1	2e-45 (89/89)				6e-08
49a	25869	26498	VNVIAKENIVTRIKKKLIDN WIDQSTSKLYDFSPWKN RSFWGVINNTLETNETIF SAITKLSNSMASLPLKMY EDYKVVNTEVSDLLTVSP NNSLSSFDFINQIETIRNE KGNAYVLIERDIYHQPSK LFLLNPDVVEMLIENQSR ELYYSIHAATGNKLIVHN MDMLHFKHIVASNMVQGI SPIDVLKNTTDFDNAVRT FNLTEMQKT (SEQ ID NO: 508)	209	portal protein [Staphylococcus phage phiSLT]	NP_075502.1	4e-117 (207/208)	portal protein	Phage portal protein	pfam0486 0	3e-39
49b	26506	26580	MLKYGSNVGKEKKAASV RRFQTVL (SEQ ID NO: 509)	24	portal protein [Staphylococcus phage phi2958PVL]	YP_002268006.1	0,007 (15/24)		**No putative conserved domains have been detected**		
49c	26728	27111	MQDQIQISRKNEELNRFY LQHTLLPIVKQYEEEFNR KLLTKTDREKNRYFKFNV KSYLRADSATQAEVYFKA VRSGYYTINDIREWEDLP PVEGGDKPLISGDLYPID TPLELRKSLKGGDKNVN ES (SEQ ID NO: 510)	127	head portal protein [Staphylococcus phage phi 12]	NP_803337.1	4e-64 (118/118) 348		Phage portal protein	pfam0486 0	5e-18

FIG. 11P

50a	27095	27343	MSMKAKYFQMKRKSKSK GEIFIYGDIVSDKWFESD VTATDFKNKLDELGDISEI DVHINSSGGSVFEGHAIY NMLKNASCKN (SEQ ID NO: 511)	82	bacteriophage protease [Staphylococcus aureus subsp. aureus USA300_TCH1516]	ZP_02759748.1	9e-38 (77/81)	Clp protease	CLP_proteas e	pfam0057 4	4e-09
					protease [Staphylococcus phage phiSLT]	NP_075503.1	1e-37 (77/81)				
50b	27324	27947	MHPAKINIYVDALAASIAS VIAMSGDTIFMHKNSFLMI HNSWVMTVGNAEELRKT ADLLEKTDAVSNSAYLDK AKDLDQEHLKQMLDAET WLTAEEALSFGLIDEILGA NEIAASISKEQYKRFENV PEDLKKDVDKITKIDDVDT SELVETPKESMSLEEKRK KEKKIKRECEILKNDNELL GGNEMPTLYELKQSLGM IGQQLKK (SEQ ID NO: 512)	207	bacteriophage protease [Staphylococcus aureus subsp. aureus USA300_TCH1516]	ZP_02759748.1	4e-89 (164/167)		CLP_proteas e	pfam0057 4	8e-27
					protease [Staphylococcus phage phiSLT]	NP_075503.1	2e-87 (173/177)				
51	27959	28978	LSQKATDPNIDMEDIKQL ETEKAGLQQRFNIVERQV QDIEEKEKAKVKDKGEAY QSLSDNEKMVKAKAEFY RHAILPNEFEKPSMEAQR LLHALPTGNDSGGDKLLP KTLSKEIVSEPFAKNQLR EKARLTNIKGLEIPRVSYT LDDDDFITDVETAKELKA KGDTVKFTTNKFKVFAAI SDTVIHGSDVDLVNWVE NALQSGLAAKERKDALA VSPKSGLEHMSFYNGSV KEVEGADMYDAIINALAD LHEDYRDNATIYMRYADY VKIISVLSNGTTNFFDTPA EKVFGKPVVFTDAAVKPI VGDFNYFGINYDGTTYDT	339	hypothetical protein phiSLTp42 [Staphylococcus phage phiSLT]	NP_075504.1	0,0 (328/337)	major capsid protein	Phage capsid family	pfam0506 5	4e-04

FIG. 11Q

			DKDVKKRRIFVCINSMV (SEQ ID NO: 513)								
52	29120	29284	MSLEEIKLWLRIDYNFEN DLIEGLIQSAKSELLLSGV PDYDKDDLEYPLFLYSD (SEQ ID NO: 514)	54	hypothetical protein phiSLTp43 [Staphylococcus phage phiSLT]	NP_075505.1	3e-20 (50/53)		**No putative conserved domains have been detected**		
53	29482	29748	MKRKKMKLYSCFCKIYNP SMKDREILKATESKSGLTI IMRSSKIEYLPQTNHLVKI DRGLYSDKLFNIKEIRIDT PDIGYNTVVLSEK (SEQ ID NO: 515)	88	hypothetical protein phiSLTp44 [Staphylococcus phage phiSLT]	NP_075506.1	9e-42 (84/87)		**No putative conserved domains have been detected**		
54a	29745	29897	MSVEIKGIPEVLKKLESVY GKQSMQAKSDRALNEAS EFFYKGFKERIREF (SEQ ID NO: 516)	50	ORF028 [Staphylococcus phage 3A]	YP_239942.1	5e-15 (42/50)		**No putative conserved domains have been detected**		
54b	29842	30102	MKHLNFFIKALKKEFESF KDTGASIEEMTKSKPYTK VGSQERAVLIEWVGPMN RKNIIHLNEHGYTRDGKKI YTKRFWSYCKNISC (SEQ ID NO: 517)	86	hypothetical protein SauSIPLA35_gp44 [Staphylococcus phage phiSauS-IPLA35]	YP_002332407.1	3e-33 (68/81)		**No putative conserved domains have been detected**		
55	30149	30544	MNILNTIKGILLSDAELKT HINSRIYYYKVTENAETSK PFVVITPVYDLPSDFMSD KYLSEEYLIQIDVESSNN QKTIDITKRIRYLLYQQNLI QASSQLDAYFEETKRYV MSRRYQGIPKNIYYKNQR IE (SEQ ID NO: 518)	131	hypothetical protein phiSLTp46 [Staphylococcus phage phiSLT]	NP_075508	3e-69 (131/131)		**No putative conserved domains have been detected**		

FIG. 11R

56a	30580	30975	MAEGQGSYKVGFKRLYV GVFNPEATKVVKRMTWE DEKGGTVDLNITGLAPDL VDMFASNKRVWMKKQG TNEVKSDMSIFNIPSDDL NTVIGRTKDKKWYILGRR EYKSTVCNSNWRIGRWF NRSAGICSLT (SEQ ID NO: 519)	131	major tail protein [Staphylococcus phage phi 12]	NP_803343.1	1e-49 (96/96)	major tail protein	Phage major tail protein	pfam0463 0	6e-26
56b	31064	31183	MNRKVDVDGTSQGIVYG YHEGKEGETEFFKKSIR WIHGQ (SEQ ID NO: 520)	39	major tail protein [Staphylococcus phage phiSLT]	NP_075509.1	6e-10 (31/31)		**No putative conserved domains have been detected**		
					major tail protein [Staphylococcus phage phi 12]	NP_803343.1					
57	31180	31281	VKIIQRILQVRYPANPQNV EVAVNSKSATVSAE (SEQ ID NO: 521)	33	ORF083 [Staphylococcus phage 42E]	YP_239867.1	6e-10 (33/33)		**No putative conserved domains have been detected**		
58	31315	31770	MTKTLKVYKGDDVVASE QGEGKVSVTLSNLEADT TYPKGTYQVAWEENGKE SSKVDVPQFKTNPILVSG VSFTPETKSITVNADDNV EPNIAPSTATNKTLKYTS EHPEFVTVDERTGAIHGV AEGTSVITATSTDGSDKS GQITVTVTNG (SEQ ID NO: 522)	151	major tail protein [Staphylococcus phage phiSLT]	YP_075510.1	2e-80 (151/151)	major tail protein	Bacterial surface proteins containing Ig-like domains	COG5492	5e-07
					major tail protein [Staphylococcus phage phi 12]	NP_803344.1	2e-77 (146/151)				
59	31829	32179	MIKFEIKDRKTGKTESYT KEDVTMGEAEKCYEYLE LVNQENKKEAPNATKMR QKERQLLVDLFKDEGLTE EDVLNKMSTKTYTKALQ DIFREINGEDEEDSETEP EEMGKTEEQSQ (SEQ ID NO: 523)	116	hypothetical protein phiSLTp49 [Staphylococcus phage phiSLT]	NP_075511.1	3e-59 (116/116)		**No putative conserved domains have been detected**		

FIG. 11S

60	32221	32331	MEQYGWTLTEVRKQPYV KLLEILNEENKEETEEKTK (SEQ ID NO: 524)	37	ORF103 [Staphylococcus phage 42E]	YP_239870.1	4e-05 (23/23)		**No putative conserved domains have been detected**		
61a	32394	32579	MNEKVEGMTLELKLDHL GVQEGMKGLKRQLGVV NSEMKANLSAFDKSEKIN GKNIRRELRG (SEQ ID NO: 525)	62	tail fiber protein [Staphylococcus phage phi 12]	NP_803346.1	6e-20 (49/49)	tape measure protein	**No putative conserved domains have been detected**		
					putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1					
61b	32580	32741	MIGLKFKKKMYSQVEDEL KQVNANYQKAKSSVKDV EKAYLKLVEANKKRKISS (SEQ ID NO: 526)	53	putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	4e-16 (44/49)		**No putative conserved domains have been detected**		
61c	32852	33016	LRDAEQKLKNSNQATTA QLKRASDAVQKQSAKHK ALVEQYKQEGNQVQKTK SAK (SEQ ID NO: 527)	54	putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	1e-19 (50/51)		**No putative conserved domains have been detected**		
61d	33223	34206	MKTFNKEQMIAQSHFGK LASQADVMSKKFSSIGDK MTSLGRTMTMGVSTPITL GLGAALKTSADFEGQMS RVGAIAQASSKDLKSMS NQAVDLGAKTSKSANEV AKGMEELAALGFNAKQT MEAMPGVISAAEASGAE MATTATVMASAINSFGLK ASDANHVADLLARSAND SAADIQYMGDALKYAGT PAKALGVSIEDTSAAIEVL SNSGLEGSQAGTALRAS FIRLANPSKNTAKEMKKL GIHLSDAKGQFVGMGELI RQFQDNMKGMTREQKL ATVATIVGTEAASGFLALI EAGPDKINSYSKSLKNSN GESKKSSRFDER (SEQ ID NO: 528)	327	tail length tape measure protein [Staphylococcus phage phi2958PVL]	YP_002268017.1	0,0 (320/322)		Phage-related minor tail protein	pfam10145	1e-35
					putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1					

FIG. 11T

61e	34166	34816	MAKVKKAADLMKDNLKG ALEQLGGAFESLAIEVGK DLTPMIRAGAEGLTKLVD GFTHLPGWVRKASVGLA LFGAAIGPAVLAGGLLIRT VGSAAKGYASLNRRIAEN TILSNTNSKAMKSLGLQT LFLGSTTGKTSKGFKGLA GAMMFNLKPINVLKNSAK LAILPFKLLKNGLGLAAKS LFAVSGGARFAGVALRFL TGPIGATITAITIAYKVF (SEQ ID NO: 529)	216	putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	6e-116 (212/212)		**No putative conserved domains have been detected**
61f	34797	35003	LRIKFFKTAYDRVEWFRN GINGLGETIKFFGGKIIGG AVRKLGEFKKLSWKYRQ KLQRKVFKRYERWL (SEQ ID NO: 530)	68	ORF001 [Staphylococcus phage 3A]	YP_239947.1	5e-17 (42/43)		**No putative conserved domains have been detected**
					putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	7e-17 (42/43)		
61g	34987	35097	MKDGYKSLSDDDLLKVG VNKFKGFMQTMGTASKK SV (SEQ ID NO: 531)	36	ORF001 [Staphylococcus phage 3A]	YP_239947.1	2e-11 (34/35)		**No putative conserved domains have been detected**
					putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	2e-11 (34/35)		
61h	35108	35257	VLGKGVSKETEKALEKYV HYSEENSRIMEKVRLNS GQISEDKAKKTFEN (SEQ ID NO: 532)	49	putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	3e-17 (45/48)		**No putative conserved domains have been detected**

FIG. 11U

61l	35404	35478	MTCELKKEQELNQKIKEL KEKSFE (SEQ ID NO: 533)	24	TP901 family phage tail tape measure protein [Staphylococcus aureus subsp. aureus JH9]	YP_001246447.1	2e-07 (17/17)		No putative conserved domains have been detected
					putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	1e-06 (16/16)		
61j	35471	35857	LSDGQISENERKEIEKLE NQRRDITVKELSKTEKEQ ERILVRMQRNRNAYSIDE ASKAIKEAEKARKARKKE VDKQYEDDVIAIKNNVNL SKSEKDKLLAIADQRHKD EVRKAKSKKDAVVDVVK KAK (SEQ ID NO: 534)	128	tail length tape measure protein [Staphylococcus phage phi2958PVL]	YP_002268017.1	3e-64 (126/126)		No putative conserved domains have been detected
61k	35924	36220	MALKVGGLTLEKTKRKKS DKYAKEQEETARRNRENI KKWFGNAWDGVKSKTG EAFSKMGRNANHFGGE MKKNVERNQRDSKQIKF RLELSQKFCRIPH (SEQ ID NO: 535)	98	putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	6e-26 (58/58)		No putative conserved domains have been detected
61l	36138	37214	MWSGIKGIPSKLSSGWS SAKSSVGYHTKAIANSTG KWFGKAWQSVKSTTGSI YNQTKQKYSDASDKAWA HSKSIWRGTSKWFSNAY KSAKGWLTDMANKSRAK WDNISSTAWSNAKSVWK GTSKWFSNSYKSLKDWT GDMYSRAHDRFDAISSS AWSNAKSVFNGFRKWLS KTYDWIRDIGKDMGRAA ADLGKNVANKAIGGLNS MSGIKIKSSAITTIKALIKD	358	putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	0,0 352/352		No putative conserved domains have been detected

FIG. 11V

			IPTLSTGTLAGKGVATDN SGALTQPTFAVLNDRGS GNAPGGGVQEVIHRADG TFHAPQGRDVVVPLGVG DSVINANDTLKLQRMGVL PKFHGGTKKKDWLDQLK GNIGKKAGEFGATAKNTA HNIKKRCRRNG (SEQ ID NO: 536)							
61 m	37207	37434	MVEAAGDKIKDGASWLG DKIGDVWDYVQHPGKLV NKVMSGLNINFGGGANA TVKIAKGAYSLLKKEISRQ SKIVV (SEQ ID NO: 537)	75	phi12 tail fiber protein-like protein [Staphylococcus aureus bacteriophage phi 3A]	AAM49603.1	7e-31 (65/67)		**No putative conserved domains have been detected**		
					putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	1e-28 (61/61)				
61n	37556	38458	MPSGTNVYAVKGGIADK VWTDYGGGNSIQIKTGA NEWNWYMHLSKQLARQ GQRIKAGQLIGKSGATGN FVRGAHLHFQLMQGSHP GNDTAKDPEKWLKSLKG SGVRSGSGVNKAASAW AGDIRRAAKRMGVNVTS GDVGNIISLIQHESGGNA GITQSSALRDINVLQGNP AKGLLQYIPQTFRHYAVR GHNNIYSGYDQLLAFFNN RYWRSQFNPRGGWSPS GPRRYANGGLITKHQLAE VGEGDKQEMVIPLTRRK RAIQLTEQVMRIIGMDGK PNNITVNNDTSTVEKIVET NCYVK (SEQ ID NO: 538)	300	putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1	2e-175 (291/294)		Lytictransglycosylase (LT) and goose egg white lysozyme (GEWL) domain	cd00254	7e-07

FIG. 11W

61o	38448	38618	MLSDKGNKLTDALIQTVS SQDNNLGSNDAIRGLEKI LSKQSGHRANANNYMG GLTN (SEQ ID NO: 539)	56	tail fiber protein [Staphylococcus phage phi 12]	NP_803346.1	2e-24 (56/56)		**No putative conserved domains have been detected**		
					putative tape measure protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332413.1					
62a	38618	38815	MQSFVKIIDGYKEEVITDF NQLIFLDARAESPNTNDN SVTINGVDGILPGAISFAP FFISIKVWL (SEQ ID NO: 540)	65	hypothetical protein phiSLTp52 [Staphylococcus phage phiSLT]	NP_075514.1	3e-25 (57/62)	holin	Protein of unknown function (DUF1306)	pfam06997	0,002
					holin-like protein [Staphylococcus phage phi 12]	NP_803346.1	4e-25 (57/62)				
62b	38907	39377	MPGVKYAVNTANVTSNL KDGSSTEIEVSLNVYKGY SESVNWTDSEFLFDSNW MFENGIPLDFTPKYTHTS NQFTIWNGSTDTINPRFK HDLKILINLNASGGFELVN YTTGDIFKYNKSIDKNTDF VLDGVYAYRDINRVGIDT NRGIITLAPGKK (SEQ ID NO: 541)	156	holin-like protein [Staphylococcus phage phi 12]	NP_803346.1	1e-84 (155/155)		Protein of unknown function (DUF1306)	pfam06997	2e-45
63a	39453	39878	MDYHDHLSVMDFNELIC ENLLDVDYGSFKEYYELN EARYITFTVYRTTHNSFV FDLLICENFIIYHGEKYTIK QTAPKVEGDKVFIEVTAY HIMYEFQNHSVESNKLD DDSSETGKTPEYSLDEYL RYGFANQKNFGQNDL (SEQ ID NO: 542)	141	hypothetical protein SPTP3102_gp58 [Staphylococcus phage tp310-2]	YP_001429953.1	2e-74 (134/134)		Protein of unknown function (DUF1142)	pfam06605	4e-45
					hypothetical protein SauSIPLA35_gp52 [Staphylococcus phage phiSauS-IPLA35]	YP_002332415.1	6e-69 (125/134)				

FIG. 11X

63b	39868	40329	MTYKIIGDFKRKVPIDELG NKNGLEYCKEAVDLFGCI IYPNDTEIGFYSPETFYQ RSEKVIRYQYNTDTVSAT VSTLELRTAIKVFGKKYTA EEKKNYNPIRTTDIKYSN GFIKEGTYRTETIGSKATI NFDCKYGNETVRFTIKKG LSRWNI (SEQ ID NO: 543)	153	ORF006 [Staphylococcus phage 47]	YP_240019.1	4e-81 (147/147)		Protein of unknown function (DUF1142)	pfam06605	8e-32
					hypothetical protein SauSIPLA35_gp52 [Staphylococcus phage phiSauS-IPLA35]	YP_002332415.1	5e-81 (147/147)				
63c	40331	40504	LILDGKQIKQISCFAKSVQ SETIDLIKNIDKGKHVLEMI FLGEDPKNRIDISSNKKS (SEQ ID NO: 544)	57	ORF006 [Staphylococcus phage 3A]	YP_239951.1	1e-24 (56/57)		**No putative conserved domains have been detected**		
					hypothetical protein SauSIPLA35_gp52 [Staphylococcus phage phiSauS-IPLA35]	YP_002332415.1	8e-24 (55/57)				
63d	40516	40710	MLELKKSTVLNLIADNSG RNQYKAIVDYVADSAKQF GIRYANTQTNEDIETQDK LLEFAKKANK (SEQ ID NO: 545)	64	hypothetical protein SauSIPLA35_gp52 [Staphylococcus phage phiSauS-IPLA35]	YP_002332415.1	1e-24 (56/57)		Protein of unknown function (DUF1142)	pfam06605	2e-12
63e	40688	41041	LQKKQINDTPKTELDVNYI GYEKIEPRDSVFFVHELM GYNTELKVVKLDRSHPFV NAIDEVSFSNEIKDMVQI QQALNRRVIAQDNRYNY QANRINHLYTSTLNSPFE TMDIGSVLI (SEQ ID NO: 546)	117	hypothetical protein SauSIPLA35_gp52 [Staphylococcus phage phiSauS-IPLA35]	YP_002332415.1	3e-62 (115/117)		Protein of unknown function (DUF1142)	pfam06605	2e-27
64	41041	41331	MATEEVKIKALLENDKQY FPATHWKAINGIPYAGSS DIDGLPQDGIISVDDKNKL DKLKIGEAGIIQNSIVQKS PNGKLWKITVDDSGKLG TVLFY (SEQ ID NO: 547)	96	hypothetical protein phiSLTp54 [Staphylococcus phage phiSLT]	NP_075516.1	5e-48 (96/96)		PRK05926, hypothetical protein	PRK05926	3e-04

FIG. 11Y

65a	41347	41973	MENLYLIKDLGALAGRDY RAKEIQNLQRIEQFALGL TTEFKLHQKAKTMQHFA EQIYYNGRSQAAVNKSL QSQINALVVAPRNNSANE IVQARVNVNGETFDTLKE HLDDWETKTQINKEETIR ELNKTKQEILDIEYRFEPD KQEFLFVTELAPLTNAVM QSFWFDNRTGIVYMTQA RNNGYMLSRLRPNGQFI DSSLIVGGGSWYT (SEQ ID NO: 548)	208	hypothetical protein phi2958PVL_gp50 [Staphylococcus phage phi2958PVL]	YP_002268021.1	1e-115 (204/204)	minor structural protein	**No putative conserved domains have been detected**
					minor structural protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332417.1	1e-114 (202/204)		
65b	41951	42169	VGGHGTHNGYRYIDDEL WIYSFILNGNNENTLVRF KYTPNVEISYGKYGMQD VFTGHPEKPYITPVINEKR K (SEQ ID NO: 549)	72	hypothetical protein phiSLTp55 [Staphylococcus phage phiSLT]	NP_075517.1	1e-34 (69/69)		**No putative conserved domains have been detected**
					minor structural protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332417.1	1e-34 (69/69)		
65c	42153	42575	MKKENKILYRIERPRSQW ELENSMNYIEIRSLDDVD KNIDKVLHKISIPMRLTNE TQPMQGVTFDEKYLYWY TGDSNPNNRNYLTAFDL ETGEEAYQVNADYGGTL DSFPGEFAEAEGLQIYYD KDSGKKSFDARCYCRW (SEQ ID NO: 550)	140	hypothetical protein phiSLTp55 [Staphylococcus phage phiSLT]	NP_075517.1	9e-71 (128/131)		**No putative conserved domains have been detected**
					minor structural protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332417.1	1e-70 (128/131)		
65d	42520	43020	MTKIVVKKALMLGVTVGG DGNRTHRIFMIGQRGILEI LHSRGVPFIMSDTGGRV KPLPMRPDKLKNLGMLT EPGLYYLYTDHTVQIDDF PLPREWRDAGWFLEVKP PQTGGDVIQILTRNSYAR NMMTFERVLSGRTGDIS DWNYVPKNSGKWERVP	166	hypothetical protein phiSLTp55 [Staphylococcus phage phiSLT]	NP_075517.1	3e-89 (156/156)		**No putative conserved domains have been detected**
					minor structural protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332417.1	4e-89 (156/156)		

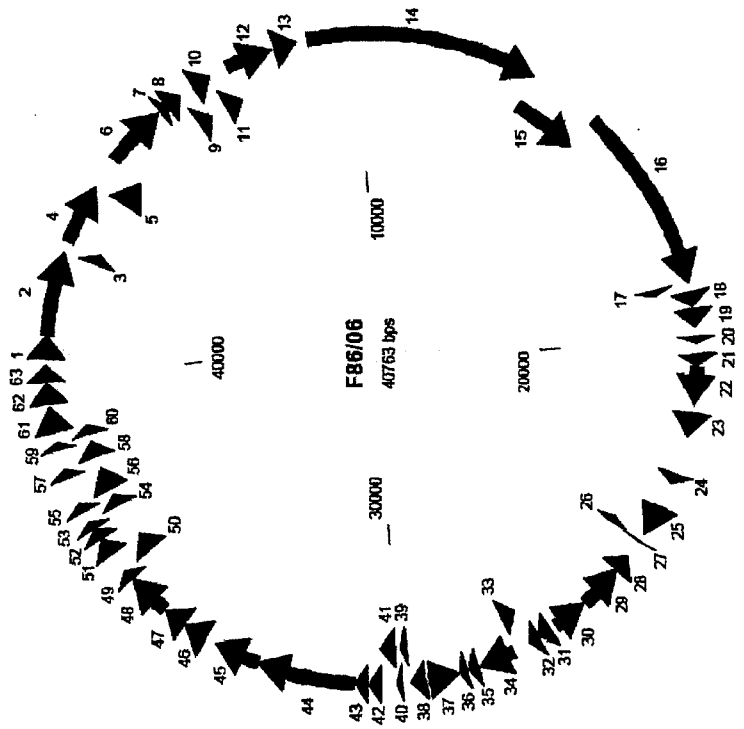
FIG. 11Z

			SFITKNVRY (SEQ ID NO: 551)							No putative conserved domains have been detected	
65e	43007	43261	MSDINIVGMSFYLTTDDT KRFTDFPTERKGVAGWN LYVEASNTGGFVHRLVR NSVTASAEILLKNYDSKT SSGPWTLHEGRIIS (SEQ ID NO: 552)	84	hypothetical protein phi2958PVL_gp50 [Staphylococcus phage phi2958PVL]	YP_002268021.1	1e-42 (84/84)			Domain of unknown function (DUF2479)	pfam10651	6e-16
					minor structural protein [Staphylococcus phage phiSauS-IPLA35]	YP_002332417.1						
66	43261	43461	MSNLEKSVAINLENTAHY ENISNLDITFRTGESDSSV LLFNIIKNNQPLLLSEENIK ARIAIRGKGV (SEQ ID NO: 553)	66	ORF005 [Staphylococcus phage 42E]	YP_239878.1	2e-30 (67/67)					

FIG. 11AA

Phage	Titer (pfu/ml)	Phage sensitivity (%) of STA strains (n=100)					Total of infected strains (%)
		++++	+++	++	+	-	
F197/08	$1,9x10^{11}$	14	61	8	14	3	**97**
	$1,9x10^{9}$	8	22	18	17	35	**65**
	$1,9x10^{7}$	2	1	8	12	77	**23**
	$1,9x10^{5}$	1	1	1	4	93	**7**
	$1,9x10^{4}$	0	0	0	1	99	**1**

FIG. 12



orf	Putative function
1	terminase small subunit
2	terminase large subunit
4	portal protein
5	prohead protease
6	capsid protein
8	DNA packaging
9	head-tail adapter
10	head-tail joining
11	structural protein
12	major tail protein
14	tail tape measure
15	tail protein
16	structural protein
21	holin
22	CHAP endolysin
23	staphylokinase
24	cell wall hydrolase remnant

orf	Putative function
25	ATPase and/or staphylococcal complement inhibitor
29	ATP-dependent helicase
30	ci-like repressor
31	cro-like repressor
34	antirepressor
45	recombinase
46	partial metallo-beta-lactamase domain
47	ssDNA binding protein
48	primosome component
50	endodeoxyribonuclease
58	dUTPase
59	transcriptional activator
62	nucleotide pyrophosphohydrolase
63	endonuclease

FIG. 13

orfs	Start position	Stop position	Product aminoacidic sequence	Size (aa)	Homologous/similar proteins				Conserved Domains		
					Name[organism]	Acc No	E value and identity	Predicted function	Name	Acc No	E value
1	58	525	MAGRPKKLLSNSNKNYTKE EIIEKERQEAQLNKFSKIDT EPPHFLDEIAKQEYLRILPH MQELPISNLDKAQLAQYCS FYSDFVKASLILEREDLILED DKGNQKVNPAFNIKEKAGI RLQQTANTLGLTIDSRLRIM VPDEKEDDDPYMEFVSD (SEQ ID NO: 554)	155	hypothetical protein PVL_01 [Staphylococcus phage PVL]	NP_058440.1	3e-85 (155/155)	terminase small subunit	Terminase_ 4, phage terminase, small subunit	pfam05119	2e-18
2	528	2222	MTDYVTKYAKKVVSGEILA SLKNIQVCKRHLSFMENPP NGCHWDNHLSNKAIKFVE MLPDPKTNQPMPLMEFQK FIVGSLYGWRRGQYRMFT KAYISMARKQGKSLIVSGM SVNELLFGQYPKFNRQIYV ASSTYKQAQTIFKMASQQV NLMRSKSKFIREKTDVRKT DIEDVLSSSVFAPLSNNPDA VDGKDPTVAILDELASMPD DEMYSRFKTGMTLQKNPLT LLVSTAGDNLNSQMYQEYK YIKRILNEEVRADNYFVYCA EMDSQEEVQDETKWIKAM PLLESKEHRKTILQNVKADI QDELEKGTSYHKILIKNFNL WQAQREDSLLDISDWEQVI TPMPNINGKDVYIGVDLSRL DDLTSVGFIFPNDDKKVFLH SHSFIGLRTNLEQKSKRDKI NYELAIERGEAETTQSDSG MIDYKQVIDFIVKFITTHDLN VQAVCYDPWNAQSFITTIE SMALDWPLIEVGQSFKALS QSIKEFRMWVADERIQHND NMLLTTSVNNAVLIRDGED NVKINKKMNRQKIDPIISITA	564	phi PVL ORF 2 homologue [Staphylococcus prophage phiPV83]	NP_061628.1	0,0 (564/564)	terminase large subunit	Terminase_ 1, phage terminase	pfam03354	2e-169

FIG. 14A

			FTEARMHEFQENWTEKYE SEEFGF (SEQ ID NO: 555)								
3	2197	2436	MKAKNSDFKGGDKMDLNKI NVFFNFLVANLVSILFLLGLF VVNVSMYKAFGQNIGLLCI GITLIVISLILNHESNQERS (SEQ ID NO: 556)	79	phi PVL orf 3-like protein [Staphylococcus phage phi13]	NP_803385.1	1e-35 (78/79)		**No putative conserved domains have been detected**		
4	2442	3692	VGIFYKNEKRDLQYNEDDL QMMVQTLPGFQGTKLRQY KDIEAIRHSDIFTAVMMIASD LARMPIRVTVNGQINYSDRI VNLLNTRPNPMYNGYIFKL VVFVSALLTSHGYIEITRDK TGEPMNLTFRKTSEIELKSD ARGRLYYFHQRIDSNGNNI ERNVKFEDMLDIKFYSLDGI NGLSLLDTLSRTIESDNNGK DFLNNFLRNGTHAGGILKM KGVLDNKKARDRAREEFH KSFSGTKQAGKVVVLDES MTFDQLEVDTEVLKLIRENK SSTREIAGVFGIPLHKFGIET ANMSITDANLDYLSTLKPYI TCVCAELNFKFNDEYVNRE FKFDTTEIRVVDEKTQAEID KINIDSGKMNIDEIRQRDGL APIPGGNGSIHRVDLNHVNI ELVDEYQMNKSRATDKKLK GGEENE (SEQ ID NO: 557)	416	portal protein [Staphylococcus phage phi13]	NP_803386.1	0,0 (416/416)	portal protein	Phage portal protein	pfam04860	2e-78
5	3685	4269	MSKETRVGNIIEVRSNDNN EMVIEGYALKFDTWSENLG GFKETISRRALENTDLSDV RCLVDHIPSQIIGRTKSGTL ELETDDVGLKYRCKLPNTT FARDLYENMRVGNINQCSF GFMLDDKGDEVRFDEQENI YKRTLTAIRELTDVSVVTYP AYKDTDVKPALRSIETVKKE QRKKELEIRLKKHSILNNIW (SEQ ID NO: 558)	194	putative prohead protease [Staphylococcus aureus subsp. aureus MSSA476]	YP_044002.1	4e-110 (194/194)	prohead protease	Peptidase_U 35, caudovirus prohead protease	pfam04586	1e-43
					prohead protease [Staphylococcus phage phi13]	NP_803387	6e-110 (194/194)				

FIG. 14B

6	4357	5604	MKTKEELQSEISDIKRQIDL KVKYATRALNNDELEKAEK LEQEITDLRSQIQEKQEELD KLKEKDGTSENNQQSVEV NEARTYRNQANINDLGISIQ NTKVTSQEVRDFTEYLETR NDIQGGSLKTDSGFVVIPEE IVTDILKLKEVEFNLDKYVTV KRVTNGSGKYPVVRQSEV AALEKVEELEENPELAVKP FFQLAYDINTHRGYFRISRE AIEDAKVNVLQELKLWMAR TIAATRNKAIIDVITKGSTGS TSSGFEKEGKKLEVKKAKS LDDIKDAINLNVKPNYEHNV AIVSQTMFAKLDKMKDKLG NYLIQPDVKEKTQQRLLGA KIEILPDEVLGQKGNNTLIIG NLKDAIVLFDRSQYQASWT DYMHFGECLMIAVRQDCRI LDYKSAIVEYDDSERGEGD LGLEA (SEQ ID NO: 559)	415	putative capsid protein [Staphylococcus phage phiPVL108]	YP_918931.1	0.0 (415/415)	capsid protein	Phage capsid family	pfam05065	6e-60
7	5640	5798	MAMYEVKKSYTDLEKGQY LKSGKRVEMTVKRAEYVNK KLKEHGVILERVKEE (SEQ ID NO: 560)	52	hypothetical protein PVL_07 [Staphylococcus phage PVL]	NP_058446.1	2e-20 (52/52)	No putative conserved domains have been detected				
8	5807	6139	MQLTAEELKLLKKHCKIDH NSEDDLLEIYYSWAFHEIAS AVTDEPSKYIDWFKSHPLF ARAIYPLASYYFENRIAYLD RDLSLAPHMVLSTVHKLRG SFEQFLESENDEI (SEQ ID NO: 561)	110	hypothetical protein MW1902 [Staphylococcus aureus subsp. aureus MW2]	NP_646719.1	3e-58 (110/110)	DNA packaging	Phage QLRG family, putative DNA packaging	pfam05136	4e-28
					DNA packaging protein [Staphylococcus phage phiPVL108]	YP_918932.1	1e-57 (109/110)					
9	6126	6461	MMKFNSNKLNERIDFCEDV SERVNGNPMKPKTKILYSC FACIQESKESDTQTNLNTG SKFIKTIIIRDTRGDYKPTNK HYVLHEGQRFNIKYVKPDY QDKSYLRIYGEVII (SEQ ID NO: 562)	111	putative phage head tail adapter [Staphylococcus phage φ310-1]	YP_00142987 7.1	2e-59 (111/111)	Head tail adapter	No putative conserved domains have been detected			

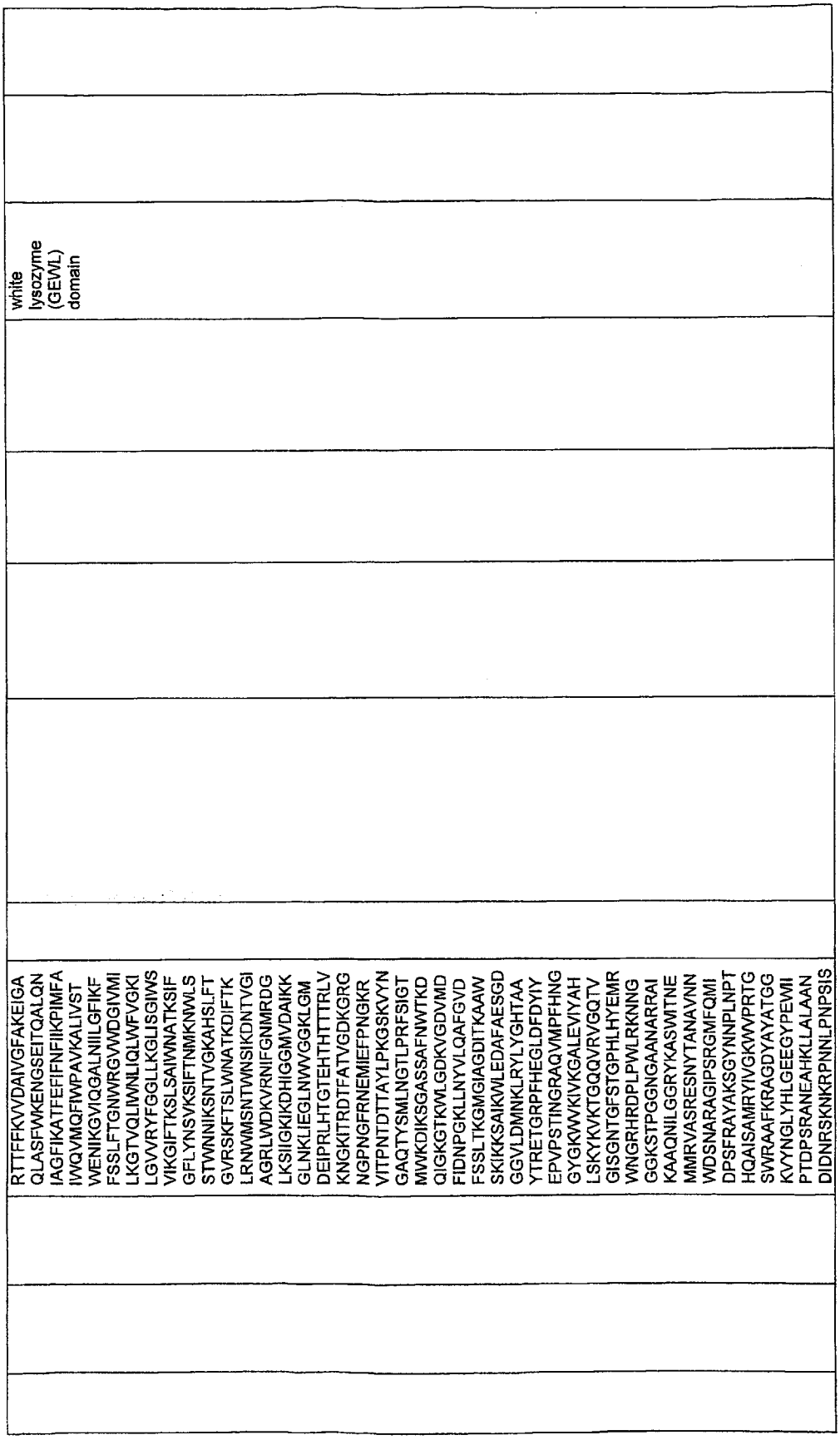
FIG. 14C

10	6461	6838	MGARIESNNIEQGLKNAVL KMNLNSNVIVKAGAMSLVP LLKSNTPFADTKKHARDHIA VSNVKTDRDTSEKIVTIGYA KGVSHRIHATEFGTMYQKP QLFITKTEKQGKNKVLKTML DTAKRLQK (SEQ ID NO: 563)	125	phi PVL ORF 11 homologue [Staphylococcus prophage phiPV83]	NP_061636.1	2e-65 (123/125)	head-tail joining protein	**No putative conserved domains have been detected**		
					head-tail joining protein [Lactobacillus phage Lrm1]	YP_00211767 7.1	4e-05 (38/115)				
11	6835	7215	MINVTKIIRNAIIANNITDEVN VFNYTIDDHFHEKTDKPIIRI YPLPFNPDTYADDNEISRE YHYQIDVWWSQDEPNEQA EKIVELLKVINFQCYYREPL YESDVMSFRHIIRAKGSILS MKLEEN (SEQ ID NO: 564)	126	phi PVL orf 12-like protein [Staphylococcus phage phi13]	NP_803393.1	1e-67 (125/126)	structural protein	**No putative conserved domains have been detected**		
					structural protein [Bacillus phage Fah]	YP_512319.1	1e-04 (27/79)				
12	7216	8169	MIEKLKQAPRFLKLNLQHFA DTGVSGIAIGVSNFYYAPIL KDTENEWETGAGTRIRFLK EIEVDRPQDTEEDYGDDMV AATAVSNGKLSVKTTFVTV PADDKAFLNGAKKGVGGY KYGAKDIPPDVAIVFERRNH DESSEWVGLFKGKFTRSSI KGQTKQDKVEFQNDDVEG NFIDRLFDESSHVTGYDKK GSTTGRDYVFMETFGKTY DEFMSSRGEQNMEPVEKE MKKTEKVEVTSVNVTDEQV TVKVDATKQLSATTEPSGQ KVTYAVTEGQTYASVTSTG LVKGLAEGNATVTATAGKQ TDTVQITVQSNLEM (SEQ ID NO: 565)	317	phi PVL orf 13-like protein [Staphylococcus phage phi13]	NP-803394.1	0,0 (317/317)	major tail protein	Bacterial Ig-like domain (group 2)	pfam02368	8e-08
					putative phagelike major tail protein [Bacillus pumilus ATCC 7061]	ZP_03055808. 1	5e-08 (51/181)				

FIG. 14D

13	8234	8680	MERTSIELITGFTKTGKPQY QKYLAKPIITLFETIQGSKLG LKLNKAFKGADFKDLTEEE FNNLSVTEQEEYKNKQEEY ENNMAVQMEVLEEVLDFIV EAFDNQFTSIELQKGLPNG QEGIEKIGQLIGRITGGEPS DTKKFVTENQK (SEQ ID NO: 566)	148	phi PVL ORF 14 homologue [Staphylococcus prophage phiPV83]	NP_061639.1	5e-78 (148/148)		**No putative conserved domains have been detected**		
14	8918	13567	MPNPIGNMVIKVDLDGSGF NRGVTGLNRQMKMVSREL SANLSQFSRYDNSLEKSKI KVEGLSKKQKVQAQITKEL KDSYDKLSKETGENSAKTQ AAAAKYNEAYAKLNQYERE LNQATQELKDMQREQKAL NTAMGKLGTNFNNFGPKL QEIGNSMKNVGRNMTMYV TAPVVAGFAVAAKKGIEFD DSMRKVKATSGATGEEFE ALKKKAREMGATTKFSASD SAEALNYMALAGWDSKQM MEGLSGVMDLAAASGEEL GAVSDIVTDGLTAFGLKAK DSGHFADVLAQTSSKANTD VRGLGEAFKYVAPVAGALG YTIEDTSIAIGLMSNAGIKGE KAGTALRTMFTNLSSPTRA MGNEMERLGISITDSNGKM IPMRKLLDQLREKFKHLSK DQQASSAATIFGKEAMSGA LAIINASDEDYQKLTKSIDSS TGASKRMADTMESGLGGK LRTLRSQLEELALTIYDRIEP ALKIIVSAFSKVVTWVTKLP TSIQLAVVGFGLFAAVLGPL VFMFGLFISVMGNAMTVLG PLLINVNKAGGIFAFLRTKIA SLVKLFPILGVSISSLTLPITL IVGALVGIGIAFYQAYKRSE TFRNIVNQAISGVANAFKAA KLALQGFFDLFKGDSKGAV TLEKIFPPETVAGIQNVVNTI	1549	tail length tape measure protein [Staphylococcus phage tp310-1]	YP_00142988.1	0,0 (1534/1550)	tail length tape measure protein	Phage-related protein [Function unknown]	COG5412	2e-124
									Lytic transglycosylase (LT) and goose egg	cd00254	8e-07

FIG. 14E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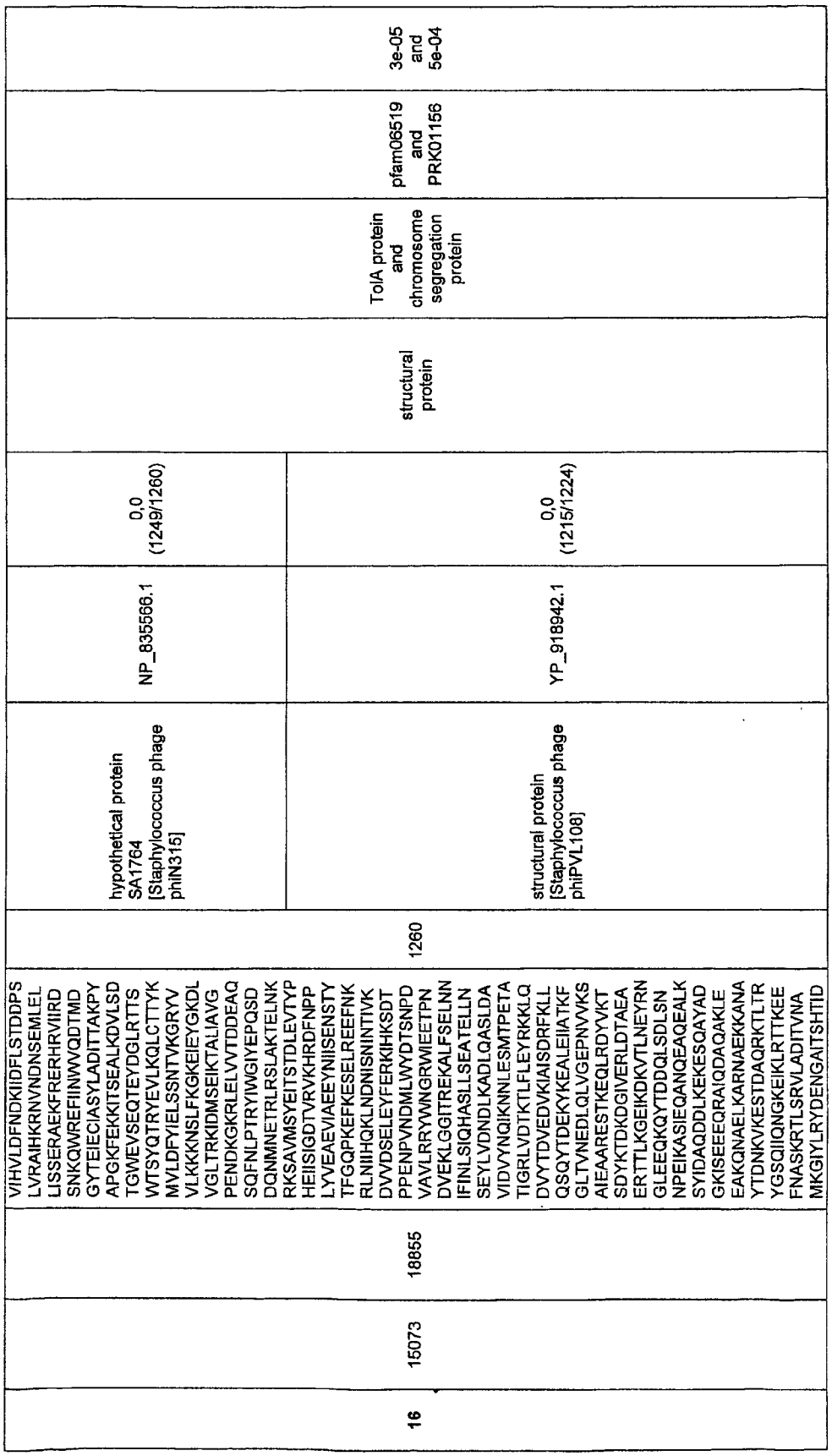
QLASFWKENGSEITQALQN
IAGFIKATFEFIFNFIIKPIMFA
IWQVMQFIWPAVKALIVST
WENIKGVIQGALNIILGFIKF
FSSLFTGNWRGVWDGIVMI
LKGTVQLIWNLIQLWFVGKI
LGVVRYFGGLLKGLISGIWS
VIKGIFTKSLSAIWNATKSIF
GFLYNSVKSIFTNMKNWLS
STWNNIKSNTVGKAHSLFT
GVRSKFTSLWNATKDIFTK
LRNWMSNTWNSIKDNTVGI
AGRLWDKVRNIFGNMRDG
LKSIIGKIKDHIGGMVDAIKK
GLNKLIEGLNWVGGKLGM
DEIPRLHTGTEHTHTTTRLV
KNGKITRDTFATVGDKGRG
NGPNGFRNEMIEFPNGKR
VITPNTDTTAYLPKGSKVYN
GAQTYSMLNGTLPRFSIGT
MWKDIKSGASSAFNWTKD
QIGKGTKWLGDKVGDVMD
FIDNPGKLLNYVLQAFGVD
FSSLTKGMGIAGDITKAAW
SKIKKSAIKWLEDAFAESGD
GGVLDMNKLRYLYGHTAA
YTRETGRPFHEGLDFDYIY
EPVPSTINGRAQVMPFHNG
GYGKWVKIVKGALEVIYAH
LSKYKVKTGQQVRVGQTV
GISGNTGFSTGPHLHYEMR
WNGRHRDPLPWLRKNNG
GGKSTPGGNGAANARRAI
KAAQNILGGRYKASWTNE
MMRVASRESNYTANAVNN
WDSNARAGIPSRGMFQMI
DPSFRAYAKSGYNNPLNPT
HQAISAMRYIVGKWVPRTG
SWRAAFKRAGDYAYATGG
KVYNGLYHLGEEGYPEWII
PTDPSRANEAHKLLALAAN
DIDNRSKNKRPNNLPNPSIS
white lysozyme (GEWL) domain

FIG. 14F

			NSDTNYIHTLENKLDAVINC LVSLVESNQVIADKDYEPVI NKYVFEDEVNNSIDKRERH ESTRVRFRRGGTII (SEQ ID NO: 567)								
15	13567	15057	MQDTIQIDNKTIEWLVVQR GFEIPSFNFVTEKESVKGR TGSIAKARYLNDIEFELPLII RNEVLAPGGQKTHDDILEE LVEFFDIDNLKPKKLKFKSQ NWYWFAYFDGPLKLPKNP RGSVKFTIKVVLTDPYKYSV TGNKNTAISDQVSVVNSGT ADTPLIVEARAIKPSSYFMIT KNDEDYFMVGDDEVTKEV KDYMPPVYHSEFRDFKGW TKMITEDIPSNDLGGKVGG DFVISNLGEGYKATNFPDA KGWVGAGTKRGLPKAMTD FQITYKCIVEQKGKGAGRT AQHIYDSDGKLLASIGYENK YHDRKIGHIVVTLYNQKGD PKKIYDYQNKPIMYNLDRIV VYMRLRRVGNKFSIKTWKF DHIKDPDRRKPIDMDEKEW IDGGKFYQRPASIIAIYSAKY NGYKWMEMNGLGSFNTEI LPKPKGARDVIIQKGDLVKI DMQAKSVVINEEPMLSEKS FGSNYFNVDSGYSELIIQPE NVFDTTVKWQDRYL (SEQ ID NO: 568)	496	hypothetical protein MW1894 [Staphylococcus aureus subsp. aureus MW2]	NP_646711.1	0,0 (496/496)	tail protein	**No putative conserved domains have been detected**			
					phi PVL orfs 18-19-like protein [Staphylococcus phage phi13]	NP_803397.1	0,0 (481/496)				
					phage tail fiber protein [Staphylococcus aureus subsp. aureus str. Newman]	YP_00133292 1.1	0,0 (441/496)				

FIG. 14G



16	15073	18855	VIHVLDFNDKIIDFLSTDDPS LVRAIHKRNVNDNSEMLEL LISSERAEKFRERHRVIIRD SNKQWREFIINWVQDTMD GYTEIECIASYLADITTAKPY APGKFEKKITSEALKDVLSD TGWEVSEQTEYDGLRTTS WTSYQTRYEVLKQLCTTYK MVLDFYIELSSNTVKGRYV VLKKKNSLFKGKEIEYGKDL VGLTRKIDMSEIKTALIAVG PENDKGKRLELVVTDDEAQ SQFNLPTRYIWGIYEPQSD DQNMNETRLRSLAKTELNK RKSAVMSYEITSTDLEVTYP HEIISIGDTVRVKHRDFNPP LYVEAEVIAEEYNIISENSTY TFGQPKEFKESELREEFNK RLNIIHQKLNDNISNINTIVK DVVDSELEYFERKIHKSDT PPENPVNDMLWYDTSNPD VAVLRRYWNGRWIEETPN DVEKLGGITREKALFSELNN IFINLSIQHASLLSEATELLN SEYLVDNDLKADLQASLDA VIDVYNQIKNNLESMTPETA TIGRLVDTKTLFLEYRKKLQ DVYTDVEDVKIAISDRFKLL QSQYTDEKYKEALEIIATKF GLTVNEDLQLVGEPNVVKS AIEAARESTKEQLRDYVKT SDYKTDKDGIVERLDTAEA ERTTLKGEIKDKVTLNEYRN GLEEQKQYTDDQLSDLSN NPEIKASIEQANQEAQEALK SYIDAQDDLKEKESQAYAD GKISEEEQRAIQDAQAKLE EAKQNAELKARNAEKKANA YTDNKVKESTDAQRKTLTR YGSQIIQNGKEIKLRTTKEE FNASKRTLSRVLADITVNA MKGIYLRYDENGAITSHTID	1260	hypothetical protein SA1764 [Staphylococcus phage phiN315]	NP_835566.1	0,0 (1249/1260)				
					structural protein [Staphylococcus phage phiPVL108]	YP_918942.1	0,0 (1215/1224)	structural protein	TolA protein and chromosome segregation protein	pfam06519 and PRK01156	3e-05 and 5e-04

FIG. 14H

		KDGVKISGDKVDITANREF NVVANNINNKVGKNDIVNS LNLSNEGLDINVNRIGIKGG NANRYVQVQNDFIELGGIV QRTWKGKRSTDDIFTRLKD GHLRFRNNTAGGSLYMSH FGISTYIDGEGEDGGSSGTI QWWDKTYSDSGMNGITIN SYGGVVALTSDYNRIIIDSY ASANIESREAPIYLSPNTKN KPGLNRFAFTLSNADSAYE TDGYIMFGSDENYKYGAGL RFSKRSNKGLVQVVNGDY ATGGDTTIESGMGKFNIVK RRDGNSYVSIQSYDLLAVG SDNAGDRVASNSIYKRTYS APANLHITSAGTIGRATSAK KYKISIENQYINEDDQFSHS KEILKLPIRTWFDKYESEIM AKELESGKKLSDDTFKLSR HTGLIAEEVEELGFNEFVIY DDNGEIEGIAYDRLWVHLIP IIKNQQSKIEKLEELINE (SEQ ID NO: 569)										
17	18848	19000	MNDSNQGLQANPQYTIHYLSQ EITRLTQENAMLKAYIQEQNEK SKSAEEE (SEQ ID NO: 570)	50	hypothetical protein SAS061 [Staphylococcus phage phiN315]	NP_835567.1	2e-20 (50/50)				No putative conserved domains have been detected	
18	19046	19333	MANEIIKKTERFILVQIDKEG TERVLYQDFVGSFTTSDSA SYAQDFKSEENAKKIAETL NLLYQLTVNQNGVKVVKEV VDRTDLSSDKSVDSEIM (SEQ ID NO: 571)	95	hypothetical protein SAS1874 [Staphylococcus aureus subsp. aureus MSSA476]	YP_043988.1	1e-45 (93/95)				No putative conserved domains have been detected	
					hypothetical protein SABPV108_gp53 [Staphylococcus phage phiPVL108]	YP_918943.1	2e-45 (93/95)					

FIG. 14I

19	19389	19763	LDDIQKIKKELSELVERVDDVEI LANETADHYLELREEHKQHHN ELRESHKELKDKQDKVVDENL EQTKILNRIEERYQTQVDVAQK NEEKTLAQNKWLVGAIWALVTI VMIAVITASITALLP (SEQ ID NO: 572)	124	hypothetical protein SA1762 [Staphylococcus phage phiN315]	NP-835669.1	2e-62 (123/124)		Ligand-gated ion channel family (belongs to the PBPb superfamily)	pfam00060	0.002
									Zinc finger-containing protein	pfam10146	0.004
20	19948	20082	MLALLKSLERRCLMITISTM LQFGLFLIALIGLVIKLIELSN KK (SEQ ID NO: 573)	44	ORF087 [Staphylococcus phage 42E]	YP_239882.1	2e-13 (43/44)		**No putative conserved domains have been detected**		
21	20294	20548	MINWKIRMKQKSFWVAILS AIFLFAQNIAKAIGYDIQVYT EQLTDGLNAILGFLVLTGVI QDPTTKGIGDSHQALEYEE PRRKY (SEQ ID NO: 574)	84	holin [Staphylococcus phage phi13]	NP_803401.1	2e-42 (84/84)	holin	Phage_holin_1, bacteriophage holin	pfam04531	1e-32
22	20560	21327	MKTYSEARARLRWYQGRY IDFDGWYGYQCADLAVDYI YWLLEIRMWGNAKDAINND FKNMATVYENTPSFVPQIG DVAVFTKGIYKQYGHIGLVF NGGNTNQFLILEQNYDGNA NTPAKLRWDNYYGCTHFIR PKYKSEGLMNKITNKVKPP AQKAVGKSASKITVGSKAP YNLKWSKGAYFNAKIDGLG ATSATRYGDNRTNYRFDV GQAVYAPGTLIYVFEIIDGW CRIYWNNHNEWIWHERLIV KEVFSFLG (SEQ ID NO: 575)	255	amidase [Staphylococcus phage phi13]	NP_803402.1	2e-146 (251/251)	CHAP endolysin	CHAP domain	pfam05257	9e-18
23	21508	21997	MLKRSLLFLTVLLLLFSFSSI TNEVSASSSFDKGKYKKGD DASYFEPTGPYLMVNVTGV DGKGNELLSPRYVEFPIKP GTTLTKEKIEYVVEWALDAT AYKEFRVVELDPSAKIEVTY YDKNKKKEETKSFPITEKGF VVPDLSEHIKNPGFNLITKV VIEKK (SEQ ID NO: 576)	163	Staphylokinase [Staphylococcus phage tp310-3]	YP_00143001 8.1	9e-88 (163/163)	staphylokinase	Staphylokinase / Streptokinase family	pfam02821	1e-17

FIG. 14J

24	22777	22983	VRDGYSTNSRITGVLPNNA TIKYDGAYCINGYRWITYIA NSGQRRYIATGEVDKAGN RISSFGNFSAV (SEQ ID NO: 577)	68	amidase [Staphylococcus phage tp310-1]	YP_00142989 3.1	1e-31 (67/68)	cell wall hydrolase remnant	SH3_5, bacterial SH3 domain	pfam08460	4e-05
25	23495	24124	MKIRKSILAGTLAIVLASPLV TNLDKNEAQASTSLPTSNE YQNEKLANELKSLLDELNV NELATGSLNTYYKRTIKISG LKANIWFLIIFVLTVLVFNPLI VKFIIWLINETRKFMNLDCIS LLDKRDKLFNNNGKPVFIVI KDFENRIIEEGELKTYNSAG SDFDLLEVERQDFKVSDLP SNDELYIKHTLVDLKQQIKL DLYLMNEY (SEQ ID NO: 578)	209	Na/K ATPase [Staphylococcus phage phi 12]	NP_803308.1	3e-70 (131/133)	ATPase and/or Staphylococcal Complement Inhibitor	**No putative conserved domains have been detected**		
					SCIN [Staphylococcus phage tp310-3]	YP_00143002 0.1	4E-38 (82/82)				
26	24267	24121	LNGGENFMADKNKKQEAT RSNPINKSFEKPGASENLK STLSEKAKKKD (SEQ ID NO: 579)	48	hypothetical protein SAOUHSC_01579 [Staphylococcus aureus subsp. aureus NCTC 8325]	YP_500095.1	4e-18 (47/48)		**No putative conserved domains have been detected**		
					ORF136 [Staphylococcus phage 47]	YP_240032.1	7e-14 (41/41)				
27	24485	24303	MKITNCKIKRETIVYEVLTS GNQPFTYELPKDLSSHNAR KYLEFISQKIDGDKLTKEDS L (SEQ ID NO: 580)	60	hypothetical protein SaurJH9_2058 [Staphylococcus aureus subsp. aureus JH9]	YP_00124741 7.1	1e-27 (60/60)		**No putative conserved domains have been detected**		
					hypothetical protein phi12p03 [Staphylococcus phage phi 12]	NP_803309.1	4e-27 (59/60)				

FIG. 14K

28	25030	24689	MIKKIFTKKHVFLVIEDENH NHSDAVFGKSILLSIYVGVN KKTNSKSGKFIYLDRSKRIV RQSDITKIESANENDVDFYN LLKKEKEIVYSKNIVDKYNL ANYIIYYEVSTKE (SEQ ID NO: 581)	113	hypothetical protein NM3_gp04 [Staphylococcus aureus phage phiNM3]	YP_908793.1	3e-56 (113/113)		**No putative conserved domains have been detected**		
29	25968	25036	MKKYDIAVLDFETMNEHMN SPCEVAVSLIKDLSIVKVYS SYINPPNNRYNLKNAKIHKI PEDVILKAPKYPDIYQEILYL LKESHLIIAHNALFDISVLKN TNNYYDLPVPNFMYVDSINI FRSFHAISSFKLENLCSLYD IDKEKLHSAKFDVLALSKML ISLAKNNQHYSVLKLIHYMP KQYIRFSKYSNSPTKLFDS GFQKIHMKISEINKIEVESVI PILKDKNVVFTGNFDTEKQ DLMILTRKKGAYIRSDVTAK TDILVEGVQDDKYKDVNGL VSKQRKAREYVGNGAKIQF LNEEDLINLIKE (SEQ ID NO: 582)	310	Pol III-like ATP dependent helicase [Staphylococcus phage phi12]	NP-803310.1	4e-177 (310/310)	ATP-dependent helicase	DNA polymerase III subunit epsilon	PRK06195	1e-35
30	26697	25984	MNKERNIIIAKNIRKFLNDSN MSQKKLAELINIKPSTLSDY LNLRSNPSHGVIQRIADVFE VGKSDIDTTYKDDNDITSIY NKLTPPRQENVLNYANEQL EEQNSKGDNVVDINSYKQE KTPVNVNGCVSAGVGERL HDETLFTEMVKGPIPTHDL ALKVNGDSMEPMFKDGEII FVEKTHNIKNGQIGIFIIEEE AYVKKVFVEDDRLTLVSLN KDYDDLHFYRNESVRLIGK VIL (SEQ ID NO: 583)	237	hypothetical protein SA1805 [Staphylococcus aureus subsp. aureus N315]	NP_375106.1	3e-134 (237/237)	cI-like repressor	Peptidase S24 LexA-like proteins	cd06529,	9e-16
					cI-like repressor [Staphylococcus phage 11]	NP_803258.1	5e-38 (96/240)		LexA repressor	PRK00215	2e-09
31	26830	27093	MKTLKELRTDYGLTQKELG DLFKVSSRTIQNMEKDSTNI KDSLLSKYMSAFNVKYDDI FLGNEYENFVFTNDKKKSII LAFKEKQTS (SEQ ID NO: 584)	88	transcriptional regulator [Staphylococcus phage phi 12]	NP_803312.1	5e-42 (87/87)	cro-like repressor	Helix-turn-helix XRE-family like proteins	cd00093	6e-07

FIG. 14L

32	27109	27324	MNIQVATKLAMEKGISIRRE NQDVYGILPTNLQRYQCLV VSRHYKKKRQTAAGRWQP SADDLIADDWILDY (SEQ ID NO: 585)	71	hypothetical protein NM3_gp08 [Staphylococcus aureus phage phiNM3]	YP_908797.1	8e-35 (71/71)		**No putative conserved domains have been detected**		
33	27642	27313	MTDEAKFVLLQLYSIYLDRI DEGMSKRSASYFGSDESS FNAFFLGFNFEDYIDAVLEL KHRDFVIASAEDGGFLEMA LSREGIAYSESESKKDYKTL MGLIRDLKKLII (SEQ ID NO: 586)	109	hypothetical protein NM3_gp09 [Staphylococcus aureus phage phiNM3]	YP_908798.1	2e-54 (109/109)		Uncharacteri zed protein conserved in bacteria (DUF2064)	pfam09837	0,005
34	27693	28445	MQALQTKSNIGEMFNIQEK ENGEIAISGRELHQALEVKT PYKKWFERMSDYGFEENID YIVTDIFVHNPLGGRQNQT DHALTLDTAKEIAMIQRSEP GKRARQYFIQVEKAWNSP EMIMQRALKIANNTINQLET KIERDKPKIVFADAVATTKT SILVGELAKIIKQNGINIGQR RLFEWLRQNGFLIKRKGVD YNMPTQYSMERELFEIKET SITHSDGHTSISKTPKVTGK GQQYFVNKFLGEKQTS (SEQ ID NO: 587)	250	anti repressor [Staphylococcus phage phiN315]	NP_835526.1	2e-145 (250/250)	antirepressor	ANT, phage antirepresso r protein KilAC domain	pfam03374	7e-36
35	28461	28658	MQAQNKKVIYYYYDEAGN RRPVNIQYNDGYDLMIDPR FIEMTLERHPHLKNNFYGLI DGKEFKLD (SEQ ID NO: 588)	65	phi PVL orf 35-like protein [Staphylococcus phage phi13]	NP_803363.1	1e-30 (65/65)		**No putative conserved domains have been detected**		
36	28689	28829	MLQKFRIAKEKNKLKLKLLK HASYCLERSNNPELLRAVA ELLKKVN (SEQ ID NO: 589)	46	hypothetical protein MW1930 [Staphylococcus aureus subsp. aureus MW2]	NP_646747.1	1e-16 (46/46)		**No putative conserved domains have been detected**		
					ORF124 [Staphylococcus phage 88]	YP_240709.1	1e-10 (36/46)				

FIG. 14M

37	29476	28844	VYIDPLKNVRFSINNVISNV EISKSMAIKQSLKPKYQLDII NRNNINLFSDFKVDFHLNN LIEMNFNLRNSFSSLTFQR NLFSEETIKSFKELYRFDDE IVLQAQQTIRDFYINPTAIST LAEAINSTYPINEQSTYKRH DEFVKRIENDFPHPFKKLIR WSNGIAAGADIQIFVTNYIN ENDLHIQNSLIVAIVCLLSFL STYCSHSKK (SEQ ID NO: 590)	210	hypothetical protein SAV1992 [Staphylococcus aureus subsp. aureus Mu50]	NP_372516.1	1e-117 (210/210)		**No putative conserved domains have been detected**		
					hypothetical protein NM3_gp12 [Staphylococcus aureus phage phiNM3]	YP_908801.1	4e-117 (209/210)				
38	29535	29855	MPHILNVTVPIPETHVLITKD EYDELIGYSLDPVWNMSDL KKKLKIASDETIKDRLLFHP RFEKELRAQGIVHYPDENF NRWRFNARKMNKFVDEHF NEIYKERIK (SEQ ID NO: 591)	106	hypothetical protein NM3_gp13 [Staphylococcus aureus phage phiNM3]	YP_908802.1	9e-56 (106/106)		Domain of unknown function (DUF771)	pfam05595	3e-33
39	29852	30013	MSNIYKSYLLAVLCFTVLAIV LMPLLYFTTAWSIAGFASIA TFIFYKEYFYEE (SEQ ID NO: 592)	53	ORF105 [Staphylococcus phage 71]	YP_240424.1	2e-21 (53/53)		Protein of unknown function (DUF1270)	pfam06900	4e-11
40	30010	30111	MKKLLLAPTSNSDKRLTKLI HFQYKTKNGGSQL (SEQ ID NO: 593)	33	hypothetical protein NM3_gp15 [Staphylococcus aureus phage phiNM3]	YP_908804.1	3e-10 (33/33)		**No putative conserved domains have been detected**		
41	30108	30434	MTKNYKDMTQEELRDLLAE KNGELFEVVNEINKETEFAV LLFSTVGVSNGDTTSSSHC ALGDIVGLANLLNNENDYH DIANVIEMYKLKKLLGLADN KEDENDVLQNG (SEQ ID NO: 594)	108	hypothetical protein NM3_gp16 [Staphylococcus aureus phage phiNM3]	YP_908805.1	2e-54 (108/108)		Hypothetical protein of unknown function (DUF2482)	pfam10655	3e-40

FIG. 14N

42	30415	30675	MYYKTGDVCQKIINVDGFD FRLRVKKRAYSVEIVVLDHE GNSIDGILVSDENDLYTALD ILKQSIYEWIENNTDEQDKL MNLVMKW (SEQ ID NO: 595)	86	hypothetical protein NM3_gp17 [Staphylococcus aureus phage phiNM3]	YP_908806.1	1e-42 (86/86)		Protein of unknown function (DUF1108)	pfam08531	2e-35
43	30684	30847	MRDTERNILNIFKTLFDEYT LSNQRALLEIERNHHGYLSI NFLHYHDSYKTNNKLVQIH EINPDSHERIKNLIIEVLRGH RKIKKGA (SEQ ID NO: 596)	87	hypothetical protein NM3_gp18 [Staphylococcus aureus phage phiNM3]	YP_908807.1	4e-43 (87/87)		No putative conserved domains have been detected		
44	30956	32899	MKINKLTISNFAGIKEVTFNF DGKDAKIYGNNATGKTTTA TALQWLLFDKGLDGSTKSF NPVPLNEKNAENYELIPTVF AEFEIDGKITTFKKESHPKY TINQKTNRKEYSRSRTKKQ YINDESIKVKDYKARIDELID EDVFKLITNPQAFNLLDWK KRRSLLFEIAKPINDEDVIKT NDDFKELNNILGDHEIETKK KILTDKIKQINKDIKDIPIRIN QTQQNKQDVPEFDNDRYAI IKQEIEQLENERIDIQNGKE EINLRNQLADKQSELKRIED NNSASNENKIHALTNELHV ENGTVANLKTRLKQNKQQI THEENRRNQLLENHKGLKS DLEKSKNQKFEHLDDNVCS CCGQQLPTEQVNEAREKA LQKFNVKKSKELETIQTSIN HIISEGKKIKPIIEKLEDDNN NLQIKINEAEERSARIQNKIN KLKTTHVDVTQTDEYKAVM LEINEINQKRSNIRKTIQDKV SGIDDKISELTQEKSEIEVS RSIEKSNKHLDDVISELRNE EDRLLDEKEKYSHDLYILKK EFTTTKVKMLTENINNEFDIA EFKLFNTLVNGELEETCSTT	647	hypothetical protein NM3_gp19 [Staphylococcus aureus phage phiNM3]	YP_908808.1	0.0 (646/647)	SMC_N, RecF/RecN/ SMC N terminal domain	pfam02463	2e-06

FIG. 14O

			VNGVEYDSGLNNASRINVG LDIINTLSKHFKVTAPIFIDNA ESVTELIKTESQQIQLIVNE QDKKLRMETI (SEQ ID NO: 597)								
45	32901	33821	MTENNKLQTIEQQLVQEKN VSDNVLNKVRVLESQGNLE LPNDYSPSNAMKQAWLQIS QDNKLMSCNDTSKANALLD MVTQGLNPAKNQCYFIPYG NKMQLQRSYHGNVMMLKR DAGAQDVVAQVIYKGDTFK QEMGETGRIKAIKHEQDFF NIDKENIIGAYCTIVFNDGR DNYIEVMTIEQIKQAWMQS SMIKDEKALQNSKTHNNFK EEMAKKTVINRAAKRYINTS TDSNIFKYAQESEQRQRKE VLDAEVEENANQEQLDFEQ	306	RecT protein [Staphylococcus aureus phage phiNM3]	YP_908808.1	1e-179 (306/306)	recombinase	RecT family	pfam03837	3e-44

FIG. 14P

			PVLEEAQYTELENDKPIDVS DFEEIKEPATEKESEEEPF (SEQ ID NO: 598)											
46	34034	34519	MTAGTQQAMNFESHRLCTI KAKQELRIGTWSILPFDIEH DANEPVAFLLQSTLGYKVL YVTDTKYLKYKFNGITHMM LEVNYIYEQMQENIKNGSV HSTLANRIMESHFSLEHAIG MLKANDLTRLEEIHLLIHLSS QNSNAKYIKSEIQKVTGVPV YVGGL (SEQ ID NO: 599)	161	hypothetical protein NM3_gp21 [Staphylococcus aureus phage phiNM3]	YP_908810.1	1e-90 (160/161)	partial metallo-beta-lactamase domain		PhnP, metal-dependent hydrolases of the beta-lactamase superfamily	COG1235	3e-14
47	34520	34990	MINRTILVGRLTRDPELRTT QSGVNVASFTLAVNRTFTN AQGEREADFINVIVFKKQAE NVNKYLSKGSLTGVDGRLQ TRNYENKEGQRVYVTEVIA DSIQFLEPKNSNDTQQDLY QQQVQQTRGQSQYSNNK PVKDNPFANANGPIEIDDD DLPF (SEQ ID NO: 600)	156	ssDNA binding protein [Staphylococcus phage PVL]	NP_058484.1	3e-85 (156/156)	ssDNA binding protein		single-strand DNA-binding protein	PRK06751	7e-41

FIG. 14Q

48	35020	35913	MTGWISIDRSIQNHWLFKE KRTFSKFEAWIYLLMEANH SKAKVPIGNQIVTVERGQR LTSILTLSDLFNWSRFKVKT FLDLLESDGMLEVKTTSKY TLITIVNYDFYQSEQGRNQ HQNDIKPTSKQHQSNINPT SKQHQTNTNNNDNKDNNE KNVNNEKKKVTAFDFFQDN GFGFITPYNLDDLNYYLDSF ENDSDQIVTASLKIAKDRNK VTWGYAKSILNTWLNANLK SIEQVRAFEKQQLESKKQN YKPFVKQSKEKTPKWLTDS TRETKTPEVDENLEKDREA FIKRLNSKWE (SEQ ID NO: 601)	297	hypothetical protein PVL_46 [Staphylococcus phage PVL]	NP_058485.1	1e-171 (297/297)	primosome component	DnaD, putative primosome component and related proteins	COG3935	2e-41
49	35920	36138	MDAFDKYYLFDHDGNKMF SVTPHFKDGRHLVVGLKHT KFNGRRWYLDDYELKTLID NEQMELGHQTSLFEYI (SEQ ID NO: 602)	72	hypothetical protein PVL_47 [Staphylococcus phage PVL]	NP_658486.1	3e-35 (72/72)		**No putative conserved domains have been detected**		
50	36135	36551	MRDYMEIEIKFNEVFNAPM GSPRPRFRNTGRYAHTYM PTKYTEHKKYLQNQMPKLN LENALKIELEFYFPLLKSWS KKKKNEMVGQYKVTKPDID NLIKTVLDACNGHLWKDDN QITEITSSKRYGIEPKIIIRIEE I (SEQ ID NO: 603)	138	hypothetical protein PVL_48 [Staphylococcus phage PVL]	NP_058487.1	5e-73 (132/134)	endodeoxy-ribonuclease	Endodeoxy-ribonuclease RusA	pfam05866	2e-23
51	36564	36932	MARKARIVTINDKPYRFSKF EMELIESHGITAGMVSKRV KDGWELHEAMDAPEGTRL SEYREKKTIERLEQARLER KLERERKKEAELRRKKPHL FNVPQKHPRGRYACYLLEN DIFVKVKK (SEQ ID NO: 604)	122	hypothetical protein SAR2077 [Staphylococcus aureus subsp. aureus MRSA252]	YP_041447.1	5e-64 (120/122)		PVL ORF-50-like family	pfam07768	4e-30
					hypothetical protein PVL_49 [Staphylococcus phage	NP_058488.1	4e-62 (117/122)				

FIG. 14R

					PVL]						
52	36936	37178	MTDNARKEYLNQFFGFKR YLYQDNERVAHIHVVNGTY YFHGHIVPGWQSVKKTFDT AEELEIYIKQHGLEYEEQKQ LTLF (SEQ ID NO: 605)	60	hypothetical protein NM3_gp27 [Staphylococcus aureus phage phiNM3]	YP_908816.1	2e-40 (80/80)		Phage conserved open reading frame 51	pfam06194	5e-32
53	37184	37357	MEMMNAEKHMQMMQMLQ NCVIDKYVSHDEYEELIAID KHGNKMFIKFYPNTEDDTN E (SEQ ID NO: 606)	57	similar to phage phi PVL ORF51 [Staphylococcus phage phiETA]	NP_510923	1e-25 (56/56)		**No putative conserved domains have been detected**		
54	37350	37601	MNNREQIEQSVISASAYNG NDTEGLLKEIEDVYKKAQA FDEILEGMTNAIQHSVKEG VELDEAVGIMAGQVVYKYE EEQENEH (SEQ ID NO: 607)	83	hypothetical protein NM3_gp29 [Staphylococcus aureus phage phiNM3]	YP_908818.1	1e-39 (83/83)		Protein of unknown function (DUF1024)	pfam06260	9e-26
55	37591	37773	MSISVGDKVFNPETNSTLEI VQLVGDIRDTHYKLSDGSII SLIDFVVKPIHLIKEEQEND (SEQ ID NO: 608)	60	hypothetical protein NM3_gp30 [Staphylococcus aureus phage phiNM3]	YP_908819.1	3e-26 (60/60)		**No putative conserved domains have been detected**		
56	37766	38308	MTNTLQVRLLSENARMPER NHKTDAGYDIFSAETVVLE PQEKAVIKTDVAVSIPEGYV GLLTSRSGVSSKTHLVIETG KIDAGYHGNLGINIKNDEER DGIPFLYDDIDAELEDGLISI LDIKGNYVQDGRGIRRIYQI NKGDKLAQLVIVPIWTPELK QVEEFESVSERGAKGFGS SGV (SEQ ID NO: 609)	180	putative dUTP pyrophosphatase [Staphylococcus aureus phage phiNM3]	YP_908820.1	2e-99 (180/180)	dUTPase	dUTPase	pfam00692	1e-21

FIG. 14S

57	38345	38551	VTQYLVTTFKDSTGRKHTHI TKAKSNQRFTVVEAESKEE AKEKYEKQVKRDAVIKVGQ LFENIRECGK (SEQ ID NO: 610)	68	similar to phage phi PVL ORF55 [Staphylococcus phage phiETA]	NP_510929.1	6e-31 (67/68)		Protein of unknown function (DUF1381)	pfam07129	5e-08
58	38548	38934	MIKKLKNMDGFDIFIVGILSL FGITALLLVVALPIYTVASYQ NKEVHQGTITDKYNKRQDK EDKFYIVLDDKQVIENSDLF FKGKFDSADIQARLKVGDK VKVKTIGYRIHFLNLYPVLY EVKKVDKK (SEQ ID NO: 611)	128	hypothetical protein phiETA_36 [Staphylococcus phage phiETA]	NP_510930.1	6e-66 (128/128)		Protein of unknown function (DUF1523)	pfam07509	2e-05
59	38931	39080	MIKQILRLLFLLAMYELGKY VTEQVYIMMTANDDVEAPS DYVFRAEVSE (SEQ ID NO: 612)	49	hypothetical protein SAS062 [Staphylococcus phage phiN315]	NP_835548.1	4e-20 (49/49)	transcriptional activator	Transcriptional activator RinB	pfam06116	2e-15
60	39080	39280	MWITMTIVFAILLLVCISINS DRAREIQALRYMNDYLLDE VVKTKGYNGLKEYRIELKR MNNDIKK (SEQ ID NO: 613)	66	hypothetical protein NM3_gp35 [Staphylococcus aureus phage phiNM3]	YP_908824.1	3e-30 (66/66)		Protein of unknown function (DUF1514)	pfam07438	4e-22
61	39303	39839	MYNRKEIREMIDNYKWMK NIIDSKVYDNESTSIAQYGY QSAMPKAKGTTSNKVLVKV INKNKALRKYDYLINKIAFID EYEEYITNEKDYHILQMLKQ RESHNRIMSILDIGRDNFYS RVKDIVNILYNLQTRNRHIV HIGQFGHIVQIVQIVHIGLIL MLHIVFYYNCYVAKHLYLF (SEQ ID NO: 614)	178	hypothetical protein MW1912 [Staphylococcus aureus subsp. aureus MW2]	NP_646729.1	5e-70 (131/131)		**No putative conserved domains have been detected**		
					hypothetical protein PVL_60 [Staphylococcus phage PVL]	NP_058499.1	2e-69 (130/131)				

FIG. 14T

62	39889	40341	MEISKYQEIATRTHNDELNL NESITCYGLGLTQSTGNVT DLIKQHMFCNVPIDKGIMIN ELSEALWNIANLTNVLGINL DEIAGHSVNTILMNKPNQTI NLDNGIKQGDKVLFQGSKY LVDGSIGNLLLISNDKDDRQ VTVQDVKKVDKE (SEQ ID NO: 615)	150	hypothetical protein SABPV108_gp35 [Staphylococcus phage phiPVL108]	YP_918925.1	6e-81 (150/150)	nucleotide pyrophosphohydrolase	No putative conserved domains have been detected				
					MazG nucleotide pyrophosphohydrolase [Chloroflexus aggregans DSM 9485]	YP_00246389 0.1	5e-08 (29/95)						
63	40348	40701	LSIMKRCGHPTCNVLINHN ESYCDKHKQYANENYNDL RRRNDPEYLRFYKSKTWQ NMRRIVLLEHDFICVSCGN QATMVDHIVPTKIDWARRL DKSNLQPLCDACHNQKTK EDLKKY (SEQ ID NO: 616)	117	phage endonuclease [Staphylococcus phage phiPVL108]	YP_918926.1	3e-64 (117/117)	endonuclease		McrA, restriction endonuclease [defense mechanisms]	COG1403	3e-05

FIG. 14U

Phage	Titer (pfu/ml)	Phage sensitivity (%) of STA strains (n=100)					Total of infected strains (%)
		++++	+++	++	+	-	
F86/06	$3,0x10^9$	0	19	22	21	38	62
	$3,0x10^8$	0	5	6	6	83	17
	$3,0x10^6$	0	1	0	0	99	1
	$3,0x10^4$	0	0	1	0	99	1

FIG. 15

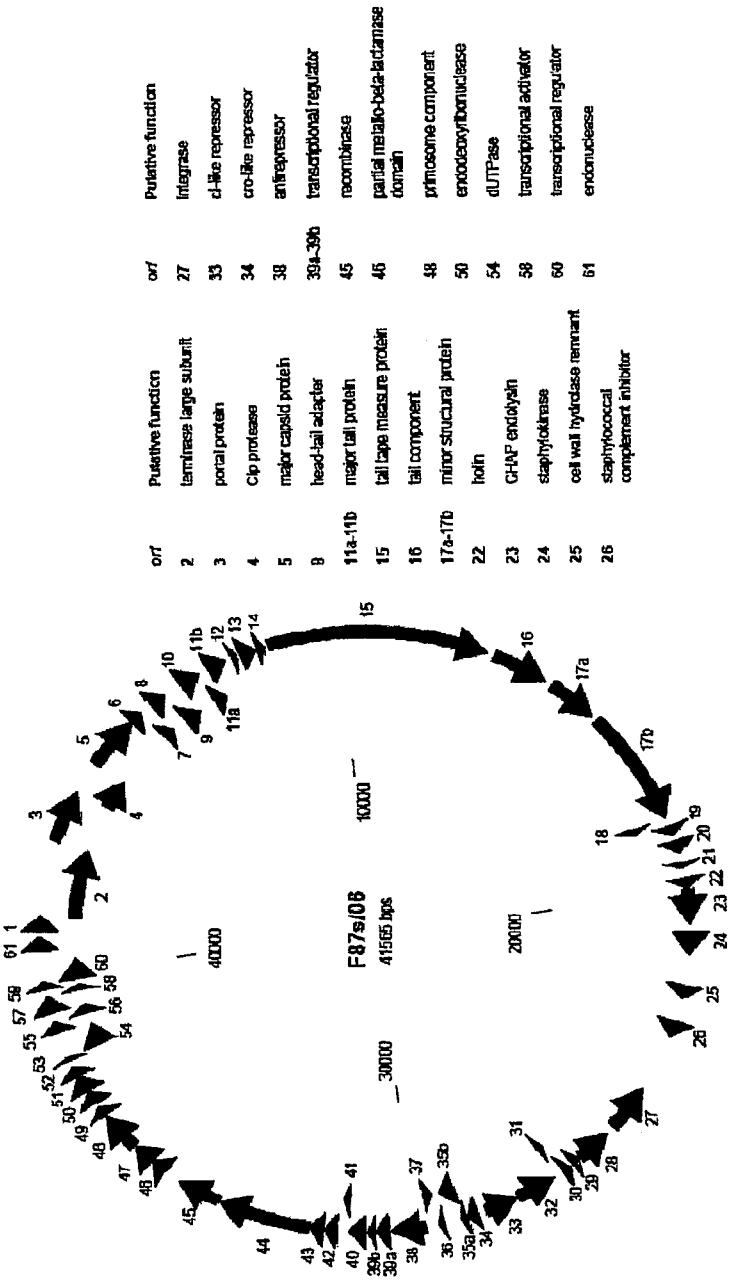

F87s/08
41565 bps
10000
20000
30000
40000
orf Putative function
2 terminase large subunit
3 portal protein
4 Clp protease
5 major capsid protein
8 head-tail adapter
11a-11b major tail protein
15 tail tape measure protein
16 tail component
17a-17b minor structural protein
22 holin
23 GH-NF endolysin
24 staphylokinase
25 cell wall hydrolase remnant
26 staphylococcal complement inhibitor
orf Putative function
27 integrase
33 cI-like repressor
34 cro-like repressor
38 antirepressor
39a-39b transcriptional regulator
45 recombinase
46 partial metallo-beta-lactamase domain
48 primosome component
50 endodeoxyribonuclease
54 dUTPase
58 transcriptional activator
60 transcriptional regulator
61 endonuclease

FIG. 16

orf	Start position	Stop position	Product aminoacidic sequence	Size (aa)	Homologous/similar proteins				Conserved Domains		
					Name[organism]	Acc No	E value and identity	Predicted function	Name	Acc No	E value
1	79	423	MEIIVDENLVLKEKERL QVLYKDIPSNKLKVVDG LIIQAARLRVMLDYMWE DIKEKGDYDLFTQSEKA PPYERERPVAKLFNAR DAAYQKIIKQLSDLLPE EKEDTETPSDDYL (SEQ ID NO: 617)	114	hypothetical protein SA1778 [Staphylococcus phage phiN315]	NP_835552.1	3e-58 (114/114)		No putative conserved domains have been detected		
2	420	2081	MISNKYVDEYINLWKQ GKIILNKERIDLFNYLQK HIYSRDDVYFDEQKIED CIKFIEKWYFPTLPFQR FIIANIFLIDKNTDEAFFT EFAIFMGRGGGKNGLIS AISDFLSTPLHGVKEYHI SIVANSEDQAKTSFDEI RTVLMDNKRNKTGKTP KAPYEVSKAKIINRATK SVIRYNTSNTKTKDGG REGCVIFDEIHYFFGPE MVNVKRGGLGKKKNR RTFYISTDGFVREGYID AMKHKIASVLSGKVKN SRLFAFYCKLDDPKEV DDRQTWEKANPMLHK PLSEYAKTLLSTIEEEY NDLPFNRSNKPEFMTK RMNLPEVDLEKVIAPW KEILATNREIPNLDNQM CIGGLDFANIRDFASVG LLFRKNDDYIWLGHSFV RQGFLDDVKLEPPIKE WEKMGLLTIVDDDVIEI EYIVDWFLKAREKYGLE KVIADNYRTDIVRRAFE DAGIKLEVLRNPKAIHG LLAPRIDTMFAKHNVIY	553	77ORF003 [Staphylococcus phage 77]	NP_958603.1	0,0 (553/553)	terminase large subunit	Terminase_ 1, phage terminase	pfam033 54	2e-37

FIG. 17A

			GDNPLMRWFTNNVAV KIKPDGNKEYIKKDEVR RKTDGFMAFVHALYRA DDIVDKDMSKALDALM SIDF (SEQ ID NO: 618)								
3	2097	3260	MSILEKIFKTRKDISYML DLDMIEDLSQQAYVKR LAIDSCIEFVARAVAQS HFKVLEGNRIQKNDVY YKLNIKPNTDLSSDSFW QQVIYKLIYDNEVLIVVS DSKELLIADSFYREEYA LYDDIFKDVTVKDYTYQ RTFTMQEVIYLKYNNNK VTHFVESLFEDYGKIFG RMIGAQLKNYQIRGILK SASSAYDEKNIEKLQAF TNKLFNTFNKNQLAIAP LIEGFDYEELSNGGKNS NMPFSELSELMRDAIK NVALMIGIPPGLIYGETA DLEKNTLVFEKFCLTPL LKKIQNELNAKLITQSM YLKDTRIEIVGVNKKDP LQYAEAIDKLVSSGSFT RNEVRIMLGEEPSDNP ELDEYLVTKNYEKANE NGSTLKGGDEDESGD (SEQ ID NO: 619)	387	hypothetical protein SA1776 [Staphylococcus phage phiN315]	NP_835554.1	0,0 (381/395)	portal protein	Phage portal protein	pfam04860	2e-45
4	3244	3981	MKVEIKGVIVSNEDKW VYEMLGMDSTCPKDVL TQLEFSDEDVDIIINSNG GNLVAGSEIYTHLRAHK GKVNVRITAIAASAASLI AMAGDHIEMSPVARM MIHNPSSIAQGEAKDLN HAAETLEHVGQIMAEA YAVRAGKNKQELIEMM AKETWLNADEAIEQGF ADSKMFENDNMQIVAS DTQVLSKDVLNRVTAL	245	peptidase S14, ClpP [Staphylococcus aureus subsp. aureus JH9]	YP_001247381	1e-139 (245/245)	Clp protease	ATP-dependent Clp protease proteolytic subunit	CHL00028	3e-07
					77ORF015 [Staphylococcus phage 77]	NP_958605.1	1e-138 (243/245)				

FIG. 17B

			VSKTPEVNIDIDAIANKV IEKINMKEKESEIDVADS KLSANGFSRFLF (SEQ ID NO: 620)								
5	4004	5149	MTINLSETFANAKNEFI NAVNNGEPQERQNELY GDMINQLFEETKLQAK AEAERVSSLPKSAQTL SANQRNFFMDINKSVG YKEEKLLPEETIDRIFED LTTNHPLLADLGIKNAG LRLKFLKSETSGVAVW GKIYGEIKGQLDAAFSE ETAIQNKLTAFVVLPKD LNDFGPAWIERFVRVQI EEAFAVALETAFLKGTG KDQPIGLNRQVQKGVS VTDGAYPEKEEQGTLT FANPRATVNELTQVFK YHSTNEKGKSVAVKGN VTMVVNPSDAFEVQAQ YTHLNANGVYVTALPF NLNVIESTVQEAGKVLT YVKGLYDGYLAGGINV QKFKETLALDDMDLYT AKQFAYGKAKDNKVAA VWKLDLKGHKPALEDT EETL (SEQ ID NO: 621)	381	77ORF006 [Staphylococcus phage 77]	NP_958606.1	0,0 (381/381)	major capsid protein	**No putative conserved domains have been detected**			
					major capsid protein [Listeria phage B025]	YP_00146962 1.1	1e-111 (191/293)				
6	5169	5453	MVKFKVVREFKDIEHN QHKYKVGELYPAEGYN NPRVELLTNQIKNKYDK VYIVPLDKLTKQELLEL CESLQKKASSSMVKSEI IDLLNGEDNDD (SEQ ID NO: 622)	95	77ORF045 [Staphylococcus phage 77]	NP_958607.1	3e-47 (94/94)		**No putative conserved domains have been detected**		

FIG. 17C

7	5443	5727	MTIDDLLVKFKSLEKIDH NSEDEYLKQLLKMSYE RIKNQCGVFELENLIGQ ELILIRARYAYQDLLEHF NDNYRPEIIDFSLSLME VSEDEESV (SEQ ID NO: 623)	94	hypothetical protein SA1772 [Staphylococcus phage phiN315]	NP_835558.1	2e-46 (94/94)		**No putative conserved domains have been detected**
8	5711	6073	MKKVFKKPRITTKRLNT RVHFYKYTENNGPEAG EKEEKLLYSCWASIDG VWLRELEQAISNGTQN DIKLYIRDPQGDYLPSE EHYLEIESRYFKNRLNI KQVSPDLDNKDFIMIRG GYSS (SEQ ID NO: 624)	120	hypothetical protein SA1771 [Staphylococcus phage phiN315]	NP_835559.1	2e-65 (120/120)	head-tail adapter	**No putative conserved domains have been detected**
					phage head-tail adaptor, putative [Staphylococcus aureus subsp. aureus JH9]	YP_00124737 7.1	2e-65 (120/120)		
9	6070	6477	MSVKVTGDKALERELE KHFGIKEMVKVQDKALI AGAKVIVEEIKKQLKPS EDSGALISEIGRTEPEW IKGKRTVTIRWRGPFER FRIVHLIENGHVEKKSG KFVKPKAMGGINRAIRQ GQNKYFETLKRELKNC D (SEQ ID NO: 625)	135	77ORF029 [Staphylococcus phage 77]	NP_958610.1	4e-69 (132/134)		**No putative conserved domains have been detected**
10	6470	6886	VIDILYKVHEVISQDRIIR EHVNINNIKFNKYPNVK DTDVPFIVIDDIDDPIPT TYTDGDECAYSYIVQID VFVKYNDEYNARIIRNKI SNRIQKLLWSELKMGN VSNGKPEYIEEFKTYRS SRVYEGIFYKEEIKWQ (SEQ ID NO: 626)	138	hypothetical protein SA1769 [Staphylococcus phage phiN315]	NP_835561.1	2e-70 (133/134)		**No putative conserved domains have been detected**

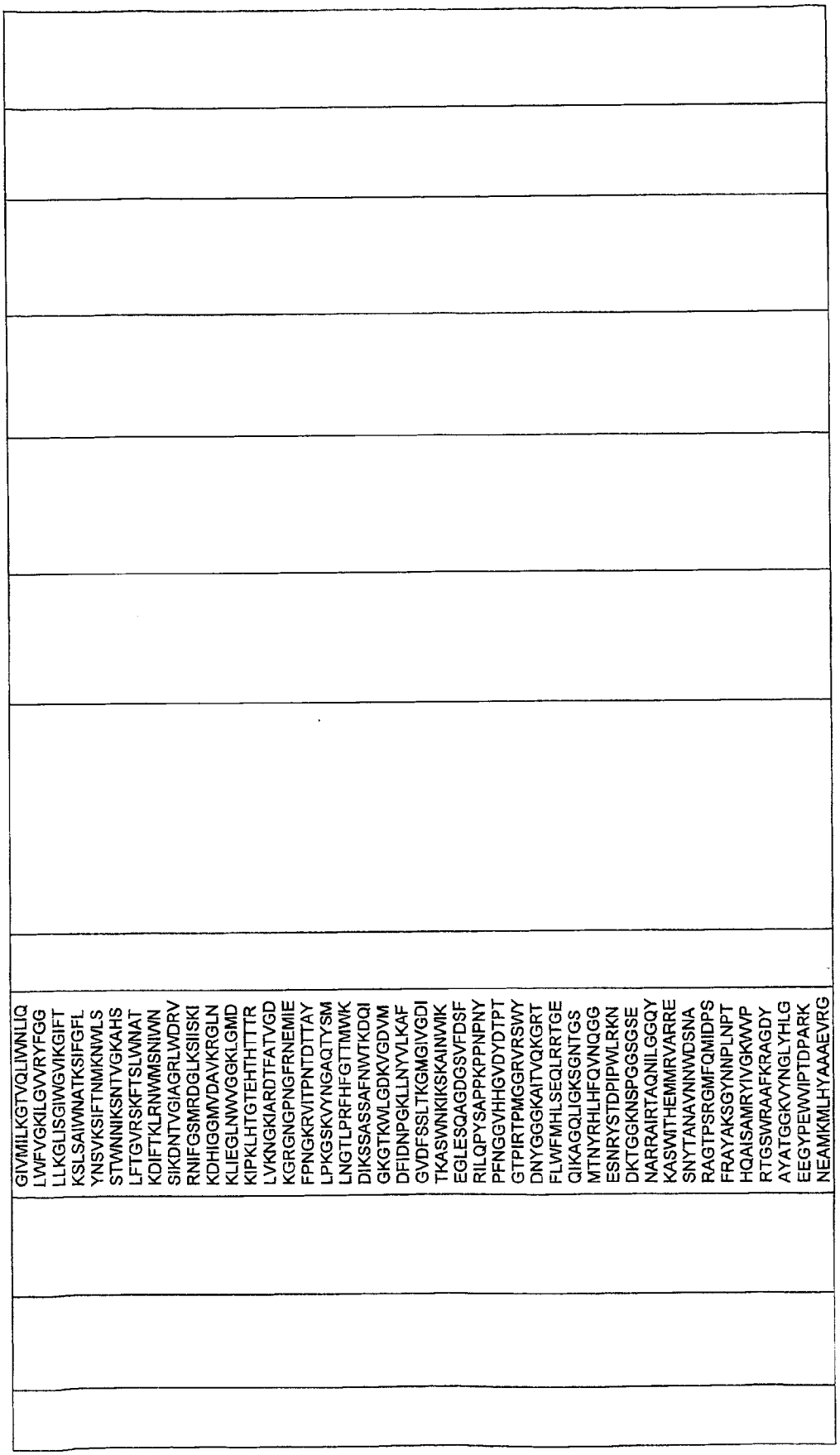
FIG. 17D

11a	6877	7206	MAIKHASAPKAYFNITG LGFAKLTKEGAELKYSD ITKTRGLQKIVLNWWRT KNKLMLMVVQSNQGT QTEKVKFRYKCMLSLK RFAKLFLMKIMMKMAF TKRNKVNKTIT (SEQ ID NO: 627)	109	phi13 family phage major tail protein [Staphylococcus aureus	YP_00124737 4.1	6e-18 (44/44)	major tail protein	**No putative conserved domains have been detected**
					hypothetical protein SA1768 [Staphylococcus phage phiN315]	NP_835562.1	6e-17 (42/44)		
11b	7104	7520	MHAFPKEIRKIVFNEDY DEDGVYEEKQGKQNN YVAVWFRQERRDGTF RTVLLPKVMFTNPKIDG ETAEKDWDFSSEEVEG EALFPLVDNKKSVRKYI FDSANMTNHDGDGEK GEEAFLKKILGEEYTGN VTEGNEETL (SEQ ID NO: 628)	138	hypothetical protein SA1768 [Staphylococcus phage phiN315]	NP_835562.1	7e-76 (138/138)		**No putative conserved domains have been detected**
12	7646	7786	LKYTTDQTNIVSINSDG QVTAEAQGIATVKATV GNMSDTITINVEA (SEQ ID NO: 629)	46	hypothetical protein NM3_gp49 [Staphylococcus aureus phage phiNM3]	YP_908838.1	1e-16 (45/46)		**No putative conserved domains have been detected**
13	7836	8186	MAKLKRNIIQLVEDPKA NEIKLQTYLTPHFISFEI VYEAMDLIDDIEDENST MKPREIADRLMDMVVKI YDNQFTVKDLKERMHA PDGMNALREQVIFITQG QQTEETRNFIQNMK (SEQ ID NO: 630)	116	hypothetical protein SA1767 [Staphylococcus phage phiN315]	NP_835563.1	2e-61 (116/116)		**No putative conserved domains have been detected**
14	8213	8374	MLKNMDTLMMDLIENG KDANEVLKMPFHYVLSI YQNKNNDISEEKAEALI DAF (SEQ ID NO: 631)	53	77ORF100 [Staphylococcus phage 77]	NP_958614.1	3e-22 (53/53)		**No putative conserved domains have been detected**

FIG. 17E

15	8431	12975	MGERIKGLSIGLDLDAA NLNRSFAEIKRNFKTLN SDLKLTGNNFKYTEKST HSYKQRIKELDGTITGY KKNVDDLAKQYGKVSQ EQGENSAEAQKLRQEY NKQANELNFLEKELEKT TTEFEEFKKAQVEAQR MAESGWGKTSKVFES MGPKLTKMGDGLKSIG KGLMIGVTAPVLGIAAA SGKAFAEVDKGLDTVT QATGATGGELKKLQNS FKDVYGNFPADAETVG GVLGEVNTRLGFTGKE LESATESFLKFSHITGS EGVQAVQLITRAMGDA GIEADEYQSVLDMVAK AAQASGISVDTLADSIT KYGAPMRAMGFEMKE SIALFSQWEKSGVNTEI AFSGLKKAISNWGKAG KNPREEFKKTLAEIEKT PDIASATSLAIEAFGAKA GPDLADAIKGGRFSYQ EFLKTIEDSQGTVNQTF KDSESGGSERFKVAMNK LKLVGADVWTSIESAFA PVMEELIKKLSIAVDWF SNLSDGSKRSIVIFGGIA AAIGPVVFGLGAFISTIG NAVTVLAPLLAGIAKAD GLISFLSTKVPILGTVFT ALTGPIGIVLGVLAGLAV AFTIAYKKSETFRNFVN GAINSVKQTFSNFIQFIQ PFIDSVKNVFKQAVSAI VDFAKDIWSQINGFFNE NGISIVQALQNICNFIKAI FEFILNFVIKPIMFAIWQ VMQFIWPAVKALIVSTW ENIKGVIQGALNIILGFIK FFSSLFTGNWRGVWD	1514	TP901 family phage tail tape measure protein [Staphylococcus aureus subsp. aureus JH9]	YP_00124737 0.1	0,0 (1327/1526)	tail tape measure protein	COG5412, phage-related protein [function unknown]	PhageMin_Tail, phage-related minor tail protein	COG5412	pfam10145	9e-153
					phage tail tape measure protein [Staphylococcus aureus phage phiNM3]	YP_908841.1	0,0 (1325/1526)		Peptidase family M23	pfam01551	7e-25		
									Lytic transglycosylase (LT) and goose egg white lysozyme (GEWL) domain	cd00254	2e-18		
											3e-07		

FIG. 17F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SIKDNTVGIAGRLWDRV
RNIFGSMRDGLKSIISKI
KDHIGGMVDAVKRGLN
KLIEGLNWVGGKLGMD
KIPKLHTGTEHTHTTR
LVKNGKIARDTFATVGD
KGRGNGPNGFRNEMIE
FPNGKRVITPNTDTTAY
LPKGSKVYNGAQTYSM
LNGTLPRFHFGTTMWK
DIKSSASSAFNWTKDQI
GKGTKWLGDKVGDVM
DFIDNPGKLLNYVLKAF
GVDFSSLTKGMGIVGDI
TKASWNKIKSKAINWIK
EGLESQAGDGSVFDSF
RILQPYSAPPKPPNPNY
PFNGGVHHGVDYDTPT
GTPIRTPMGGRVRSWY
DNYGGGKAITVQKGRT
FLWFMHLSEQLRRTGE
QIKAGQLIGKSGNTGS
MTNYRHLHFQVNQGG
ESNRYSTDPIPWLRKN
DKTGGKNSPGGSGSE
NARRAIRTAQNILGGQY
KASWITHEMMRVARRE
SNYTANAVNNWDSNA
RAGTPSRGMFQMIDPS
FRAYAKSGYNNPLNPT
HQAISAMRYIVGKWVP
RTGSWRAAFKRAGDY
AYATGGKVYNGLYHLG
EEGYPEWVIPTDPARK
NEAMKMLHYAAAEVRG

FIG. 17G

			RKASKNKRPSQLSSVN GFDDPSLLLKMIEQQQ QQIALLLKIAQSNDVIAD KDYQPIIDEYAFDKKVN ASIEKRERQESTKVKFR KGGIAIQ (SEQ ID NO: 632)							
16	13144	14328	VVRNDYLSHNGFKTHD DVLNELVKFFNYEEQV KLQFKSKDWYWNAYF EGPIKLHKEFAIPVKFTI KVVLTDPYKYSVTGYK NTAISDQVSVVNSGTA DTPLIVEARAIKPSSYF MITKNDEDYFMVGDDE VTKEVKDYMPPVYHSE FRDFKGWTKMITEDIPS NDLGGKVGGDFVISNL GEGYKATNFPDAKGW VGAGTKRGLPKAMTDF QITYKCIVEQKGKGAGR TAQHIYDSDGKLLASIG YENKYHDRKIGHIVVTL YNQKGDPKKIYDYQNK PIMYNLDRIVVYMRLRR VGNKFSIKTWKFDHIKD PDRRKPIDMDEKEWID GGKFYQRPASIIAIYSAK YNGYKWMEMNGLGSF NTEILPKPKGARDVIIQK GDLVKIDMQAKSSCHQ (SEQ ID NO: 633)	384	phi77 ORF004-like protein, putative phage tail component [Staphylococcus aureus subsp. aureus USA300]	YP_494580.1	0,0 (389/390)	tail component	No putative conserved domains have been detected		
					hypothetical protein SA1765 [Staphylococcus phage phiN315]	NP_835565.1	0,0 (388/390)			

FIG. 17H

17a	14474	15565	VIHVLDFNDKIIDFLSTD DPSLVRAIHKRNVNDN SEMLELLISSERAEKFR ERHRVIIRDSNKQWRE FIINWVQDTMDGYTEIE CIASYLADITTAKPYAP GKFEKKTTSEALKDVLS DTGWEVSEQTEYDGL RTTSWTSYQTRYEVLK QLCTTYKMVLDFYIELS SNTVKGRYVVLKKKKNS LFKGKEIEYGKDLVGLT RKIDMSEIKTALIAVGPE NDKGKRLELVVTDDEA QSQFNLPTRYIWGIYEP QSDDQNMNETRLRSLA KTELNKRKSAVMSYEIT STDLEVTYPHEIISIGDT VRVKHRDFNPPLYVEA EVIAEEYNIISENSTYTF GQPKEFKESELREEFN KRLNIIHTKVKR (SEQ ID NO: 634)	363	phi PVL ORF 20 and 21-like protein [Staphylococcus aureus subsp. aureus Mu50]	NP_372477.1	0,0 (357/361)	minor structural protein	No putative conserved domains have been detected			
					phage minor structural protein [Staphylococcus aureus phage phiNM3]	YP_908843.1	0,0 (354/361)				
17b	15675	18260	MLWYDTSNPDVAVLRR YWNGRWEATPNDVEK LGGITREKALFSELNNIF INLSIQHASLLSEATELL NSEYLVDNDLKEDLQA SLDAVIDVYNQIKNNLE SMTPETATIGRLVDTQA LFLEYRKKLQDVYTDVE DVKMAISDRFKLLQSQ YTDEKYKEALEIIATKFG LTVNEDLQLVGEPNVV KSAIEAARESTKEQLRD YVKTSDYKTDKDGIVER LDTAEAERTTLKGEIKD KVTLNEYRNGLEEQKQ YTDDQLSDLSNNPEIKA SIEQANQEAQEALKSYI	861	77ORF002 [Staphylococcus phage 77]	NP_958617.1	0,0 (859/861)		TolA protein and chromosome segregation protein	pfam06519 and PRK01156	9e-05 and 6e-04
					phage minor structural protein [Staphylococcus aureus phage phiNM3]	YP_908843.1	0,0 (855/860)				

FIG. 17I

18	18250	18402	MQDNKQGLQANPEYTI HYLSQEIMRLTQENAM LKAYIQENKENQQCAE EE (SEQ ID NO: 636)	50	hypothetical protein phiPV83p56 [Staphylococcus prophage phiPV83]	NP_061644.1	2e-20 (50/50)		No putative conserved domains have been detected

DAQDDLKEKESQAYAD GKISEEEQRAIQDAQAK LEEAKQNAELKARNAE KKANAYTDNKVKESTD AQRKTLTRYGSQIIQNG KEIKLRTTKEEFNATNR TLSNILNEIVQNVTDGT TIRYDDNGVAQALNVG PRGIRLNADKIDINGNR EINLLIQNMRDKVDKTDI VNSLNLSREGLDINVNR IGIKGGDNNRYVQIQND SIELGGIVQRTWRGKR STDDIFTRLKDGHLRFR NNTAGGSLYMSHFGIS TYIDGEGEDGGSSGTI QVWWDKTYSDSGMNGI TINSYGGVVALTSDNN RVVLESYASSNIKSKQA PVYLYPNTDKVPGLNR FAFTLSNADNAYSSDG YIMFGSDENYDYGAGI RFSKERNKGLVQIVNG RYATGGDTTIEAGYGK FNMLKRRDGNRYIHIQS TDLLSVGSDDAGDRIAS NSIYRRTYSAAANLHIT SAGTIGRSTSARKYKLS IENQYNDRDEQLEHSK AILNLPIRTWFDKAESEI LARELREDRKLSEDTY KLDRYVGLIAEEVENLG LKEFVTYDDKGEIEGIA YDRLWHLIPVIKEQQL RIKKLEESKNAG (SEQ ID NO: 635)

FIG. 17J

19	18449	18670	MAKEIINNTERFILVQID KEGTERVVYQDFTGSF TTSEMVNHAQDFKSEE NAKKIAETLNLLYQLTN KKQRVK (SEQ ID NO: 637)	73	hypothetical protein PVL_21 [Staphylococcus phage PVL]	NP_058460.1	4e-35 (73/73)		**No putative conserved domains have been detected**		
20	18793	19089	LGWFKKHEHEWRIRRL EENDKTMLSTLNEIKLG QKTQEQVNIKLDKTLDA IQKEREIDEKNKKENDK NIRDMKMWVLGLVGTI FGSLIIALLRMLMGI (SEQ ID NO: 638)	98	phi PVL ORF 17 homologue [Staphylococcus prophage phiPV83]	NP_061646.1	9e-48 (97/98)		**No putative conserved domains have been detected**		
21	19281	19415	MVALLKSLERRRLMITI STMLQFGLFLIALIGLVI KLIELSNKK (SEQ ID NO: 639)	44	hypothetical protein SAR2042 [Staphylococcus aureus subsp. aureus MRSA252]	YP_041413.1	8e-15 (44/44)		**No putative conserved domains have been detected**		
					ORF087 [Staphylococcus phage 42E]	YP_2398821.1	4e-14 (43/44)				
22	19627	19881	MINWKIRMKQKSFWVA ILSAIFLFAQNIAKAIGYD IQVYTEQLTDGLNAILG FLVLTGVIQDPTTKGIG DSHQALEYEEPRRKY (SEQ ID NO: 640)	84	holin-like protein [Staphylococcus aureus subsp. aureus Mu50]	NP_372470.1	2e-42 (84/84)	holin	Phage_holin_1, bacteriophage holin	pfam04531	1e-32
					holin [Staphylococcus prophage phiPV83]	NP_061647.1	8e-42 (83/84)				
23	19893	20648	MKTYSEARARLRWYQ GRYIDFDGWYGYQCA DLAVDYIYWLLEIRMW GNAKDAINNDFKNMAT VYENTPSFVPQIGDVAV FTKGIYKQYGHIGLVFN GGNTNQFLILEQNYDG NANTPAKLRWDNYYG CTHFIRPKYKSEGLMN KITNKVKPPAQKAVGKS ASKITVGSKAPYNLKW	251	amidase [Staphylococcus phage phi13]	NP_803402.1	2e-146 (251/251)	CHAP endolysin	CHAP domain	pfam05257	1e-17

FIG. 17K

			SKGAYFNAKIDGLGATS ATRYGDNRTNYRFDVG QAVYAPGTLIYVFEIIDG WCRIYWNNHNEWIWH ERLIVKEVF (SEQ ID NO: 641)								
24	20839	21330	MLKRGLLFLTVLLLLFS FSSITNEVSASSSFDKG KYKKGDDASYFEPTGP YLMVNVTGVDGKGNEL LSPHYVEFPIKPGTTLT KEKIEYYVEWALDATAY KEFRVVELDPSAKIEVT YYDKNKKKEETKSFPIT EKGFVVPDLSEHIKNPG FNLITKVVIEKK (SEQ ID NO: 642)	163	staphylokinase precursor [Staphylococcus aureus phage phiNM3]	YP_908850.1	9e-88 (162/163)	staphylokinase	Staphylokinase/Streptokinase family	pfam02821	3e-18
25	22020	22316	VPAGYTLDKNNVPYKK ETGYYTVANVKGNNVR DGYSTNSRITGVLPNN ATIKYDGAYCINGYRWI TYIANNGQRCYIATGEV DKAGNRISSFGNFSAL (SEQ ID NO: 643)	98	truncated amidase [Staphylococcus aureus subsp. aureus Mu3]	YP_001442518.1	5e-49 (97/98)	cell wall hydrolase remnant	Bacterial SH3 domain	pfam08460	7e-05
					peptidoglycan hydrolase [Staphylococcus phage phi 12]	NP_803355.1	4e-47 (93/98)				
26	22826	23176	MKIRKSILAGTLAIVLAS PLVTNLDKNEAQASTSL PTSNEYQNEKLANELK SLLDELNVNELATGSLN TYYKRTIKISGQKAMYA LKSKDFKKMSEAKYQL QKIYNEIDEALKSKY (SEQ ID NO: 644)	116	hypothetical protein SAV1942 [Staphylococcus aureus subsp. aureus Mu50]	NP_372466.1	1e58 (116/116)	Staphylococcal Complement Inhibitor	**No putative conserved domains have been detected**		
					Staphylococcal complement inhibitor [Staphylococcus aureus phage phiNM3]	YP_908853.1	1e-58 (116/116)				

FIG. 17L

27	25470	24430	MKTRCYDGKKWQYEF KYEGKRYRKKGFRTKR EANSAGLDKLNELRSG FNIDNYITLEEYFENWIK TYKQPVVKENTYRHYR NALQHIQKHKIGKMELS KINRQVYQKFINDYSKE HAKETIRKTNGAIRSAL DDALYDGLIFKNPAYKV NYKAGKPTKSEQEKFIS VTEYEILKDHVRKKKRTR SSLALFIMICTGCRVSG ARNIKIEHINQVKNTIFID ERKTDTSPRYISIAKSD MKHIMDVISTFAISYDG YIFKEAGSIINLHAINNAL KSACRVNNIPIITSHALR HTHCSYLLAKGVSIHYI SKRLGHKNIAITTSVYS HLLEEKFNEEDKKQLKF RKYVI (SEQ ID NO: 645)	346	phage integrase family protein [Staphylococcus aureus subsp.aureus USA300_TCH1516]	ZP_02761075.1	0,0 (338/341)	integrase	phiLC3 phage and phage-related integrases	cd01189	1e-34
					integrase [Staphylococcus aureus phage phiNM3]	YP_908790.1	0,0 (335/341)				
28	26416	25661	LNGGESVSENKGEMM THNIEKRINKLKTSGNP KFKKLDSDIHYLLKRFE GEKNHKGFYPKFKQGE IVFVDFGINVNKEFSNS HFAIVMNKNDSNTEDIV NVIPLSSKENKKYLKMN FDLKWEYYLRLFLNLIS AQNNSAILKEVFDKKYQ KNNTEFITKDYFSEFISD SLEIENKLNKIDRNINNI VSAIDKVKKLKGNSYAC INSFQPISKFRIRKVLPQ KIKNPVIDSSDIMLLINRI NNNILQIPDIR (SEQ ID NO: 646)	251	hypothetical protein SaurJH9_2059 [Staphylococcus aureus subsp. aureus JH9]	YP_001247418.1	1e-134 (244/245)	No putative conserved domains have been detected			
					77ORF017 [Staphylococcus phage 77]	NP_958624.1	1e-129 (236/237)				

FIG. 17M

29	26634	26452	MKITNCKIKKETIVYEVL TSGNQPFTYELPKDLS SHNARKYLEFISQKIDG DKLTKEDSL (SEQ ID NO: 647)	60	hypothetical protein phi12p03 [Staphylococcus phage phi 12]	NP_803309.1	3e-27 (60/60)		**No putative conserved domains have been detected**		
30	26890	26705	MSTYKEIEHLHINTGGK ELTQEQIEEAKAFIDSQ EFKDMIREAKESHQRV MESKITDRTKL (SEQ ID NO: 648)	61	hypothetical protein SaurJH9_2057 [Staphylococcus aureus subsp. aureus JH9]	YP_00124741 6.1	4e-27 (61/61)		**No putative conserved domains have been detected**		
					hypothetical protein phiPV83p04 [Staphylococcus prophage phiPV83]	NP_061594.1	1e-25 (58/61)				
31	27033	26887	MDFKEVDINIEEWEMV EIPFYTEEELTYRLNNG LPITKSELEEQESKK (SEQ ID NO: 649)	48	hypothetical protein SaurJH9_2056 [Staphylococcus aureus subsp. aureus JH9]	YP_00124741 5.1	9e-19 (48/48)		**No putative conserved domains have been detected**		
					hypothetical protein phiETA_05 [Staphylococcus phage phiETA]	NP_510899.1	1e-17 (46/48)				
32	27961	27107	MKPRKQDEKILSDQYS YFEPIISDSCDIKFDENK RRMGSIFISHEEICFIRK EEDYIFKISLSEVIDYNT VVTIWKNQAFLTLNDN RKLTVYFVTNSPLTGFI SILKTYMQLSKNKETIIS NDCLPINDDEQTKVEIF DVVGLNYEGRRKELKK LIKKMKNNDDFFFLYSD LKGNELKEELLYEDKVY EISDYEVIPGVFLQKEP DNPYDENAIKVMISNEY SEFHVGYVPREYASRL VNHMDNIVSCNAYING GKYKTLDYLEEKIVTKE	284	HIRAN [Staphylococcus aureus subsp. aureus JH9]	YP_00124741 4.1	3e-162 (284/284)	DNA binidng protein, putative helicase	HIRAN domain	pfam087 97	6e-11
					phage protein [Streptococcus phage 10750.3]	YP_602821.1	0,005 (45/151)				
					SNF2 family helicase, putative [Aspergillus fumigatus A1163]	EDP51408.1	0,0004 (22/46)				

FIG. 17N

		SDYGLRVHLEYKV (SEQ ID NO: 650)										
33	28689	27973	MNSFKDRLKQIMSERKI SQSELSRRTGIGRNSIS DYLNGKYEAKQDKVFE LAKALNVNEAWLMGFD ISKNRKIENNDITSIYSK LTPPRQSNVLKYATNQ LEEQNNDSDNLVDFNS YIQEKSEVDIYGCASAG IGERLYNEPISKEFVRG YVPAHDIALKVNGDSM EPLFKNGQIIFIEKSHTIK DGQIGVFIINGDAYVKK VYVEDNRLTLVSLNKKY KDLYFYDNESVRLVGK VIL (SEQ ID NO: 651)	238	putative phage repressor [Staphylococcus aureus subsp. aureus JH9]	YP_001247413.1	8e-135 (238/238)	cI-like repressor	Peptidase S24 LexA-like proteins	cd06529	1e-16
				similar to phage phi PVL repressor [Staphylococcus phage phiETA]	NP_510900.1	1e-108 (189/238)		Helix-turn-helix XRE-family like proteins	cd00093	9e-10
34	28853	29095	MIYNFDYSLLYERMAEY RYSQSSLANAIPISRTSI NHKLQGKNLFTQIWEIK RICELLEIPPTKVGRYFF EQNVQKPVQMS (SEQ ID NO: 652)	80	hypothetical protein SaurJH9_2053 [Staphylococcus aureus subsp. aureus JH9]	YP_001247415.2.1	1e-40 (80/80)	cro-like repressor	Helix-turn-helix XRE-family like proteins	cd00093	0,006
					putative cro-like repressor [Staphylococcus phage phiPVL108]	YP_918897.1	3e-39 (78/80)				
35a	29108	29236	MEQITLTKEELKEIIAKE VREAINGKKPISSGSNF QQSKNQP (SEQ ID NO: 653)	42	77ORF023 [Staphylococcus phage 77]	NP_958630.1	2e-10 (34/39)			**No putative conserved domains have been detected**		
35b	29178	29555	MARNQSVQVLIFNKVRI SHNDFDEINKKFAYTER LRGADNLGLGHPLSLK KYQHGIGCYENYKAYA SEIHDHIRKLTLSAFGVT LNSDLKESEYDEASRM YDMLKNFYLYRYQKRIE TLSIEDFE (SEQ ID NO:	125	77ORF023 [Staphylococcus phage 77]	NP_958630.1	1e-28 (64/115)			**No putative conserved domains have been detected**		

FIG. 17O

			654)									
36	29570	29710	MLQKFRIAKEKNKLKLK LLKHASYCLERNNNPE LLRAVAELLKKVS (SEQ ID NO: 655)	46	77ORF117 [Staphylococcus phage 77]	NP_958631.1	1e-16 (46/46)		No putative conserved domains have been detected			
37	29912	29703	MKLLVTLKDGSKKHVS DLKKIVFPGYEGIETVT KEEIETFFLDPTKTYVF VGSQTLSVEAGQILTVE FS (SEQ ID NO: 656)	69	77ORF066 [Staphylococcus phage 77]	NP_958632.1	9e-31 (69/69)		No putative conserved domains have been detected			
38	29969	30718	MQALQTKSNIGEMFNI QEKENGEIAISARELYK ALEVKKRFSAWAEINLK HFKENRDFTSVLTSTVV NNGAVRQLEDYALTLD VAKHVAMMSGTEKGF DFREYFIQVEKAWNSP EMIMQRALKIANNTINQ LETKIERDKPKIVFADAV ATTKTSILVGELAKIIKQ NGVNIGQRRLFEWLRQ NGFLIKRKGVDYNMPT QYSMERELFEIKETSIT HSDGHTSISKTPKVTGK GQQYFVNKFLGEKQTS (SEQ ID NO: 657)	249	ORF017 [Staphylococcus phage 71]	YP_240419.1	1e-143 (247/249)	antirepressor	Phage antirepressor protein KilAC domain	pfam03374	6e-36
39a	30731	30991	MEQITLTKEECVEQCIN KDLKLLDYRVQQILEGV LSESTTYGDARNKLETL KIIAESHFKTEHASVIYK LALKKLDKKINATPIKE (SEQ ID NO: 658)	86	transcriptional regulator [Staphylococcus phage phiPVL108]	YP_918899.1	3e-32 (68/68)	transcriptional regulator	No putative conserved domains have been detected			

FIG. 17P

39b	31011	31148	MFKILNDIKTSLKNHPW GWKEHLPYLLMLTLSL VALIFGVLSAIL (SEQ ID NO: 659)	45	transcriptional regulator [Staphylococcus phage phiPVL108]	YP_918899.1	2e-17 (44/45)		**No putative conserved domains have been detected**		
40	31215	31544	MIEMPHVLNVTVPIPET HVLITKDEYEELIAYSLD PVWNMSDLKKKLKIAS DETIKDRLLFHPRFEKE LRAQGIVHYPDENFNR WRFNARKMNKFVDEH FNEIYKERIK (SEQ ID NO: 660)	109	ORF045 [Staphylococcus phage 69]	YP_239609.1	7e-55 (104/106		Domain of unknown function (DUF771)	pfam055 95	1e-32
41	31541	31702	MSKTYKSYLLAVLCFTV LAIVLMPFLYFTTAWSIA GFASIATFIFYKEYFYEE (SEQ ID NO: 661)	53	similar to phage phi PVL ORF38 [Staphylococcus phage phiETA]	NP_510908.1	2e-21 (53/53)		Protein of unknown function (DUF1270)	pfam069 00	2e-10
42	31797	32057	MYYKIGDVCQKVINVD GFDFKLAVKKQDYSILV NVLDLEDRFIDSINITDE NDLYTALDILNQSIYEWI EENTDERDRLINLVMR W (SEQ ID NO: 662)	86	phi PVL orf 39-like protein [Staphylococcus phage phi13]	NP_803365.1	8e-41 (85/86)		Protein of unknown function (DUF1108)	pfam065 31	1e-33
43	32066	32329	MVGISMRDTERNILNIF KTLFDEYTLSNQRALLE IERNHHGYLSINFLHYH DSYKTNNKLVQIHEINP DSHERIKNLIIEVLRGHR KIKKGA (SEQ ID NO: 663)	92	hypothetical protein NM3_gp18 [Staphylococcus aureus phage phiNM3]	YP_908807.1	3e-46 (92/92)		**No putative conserved domains have been detected**		

FIG. 17Q

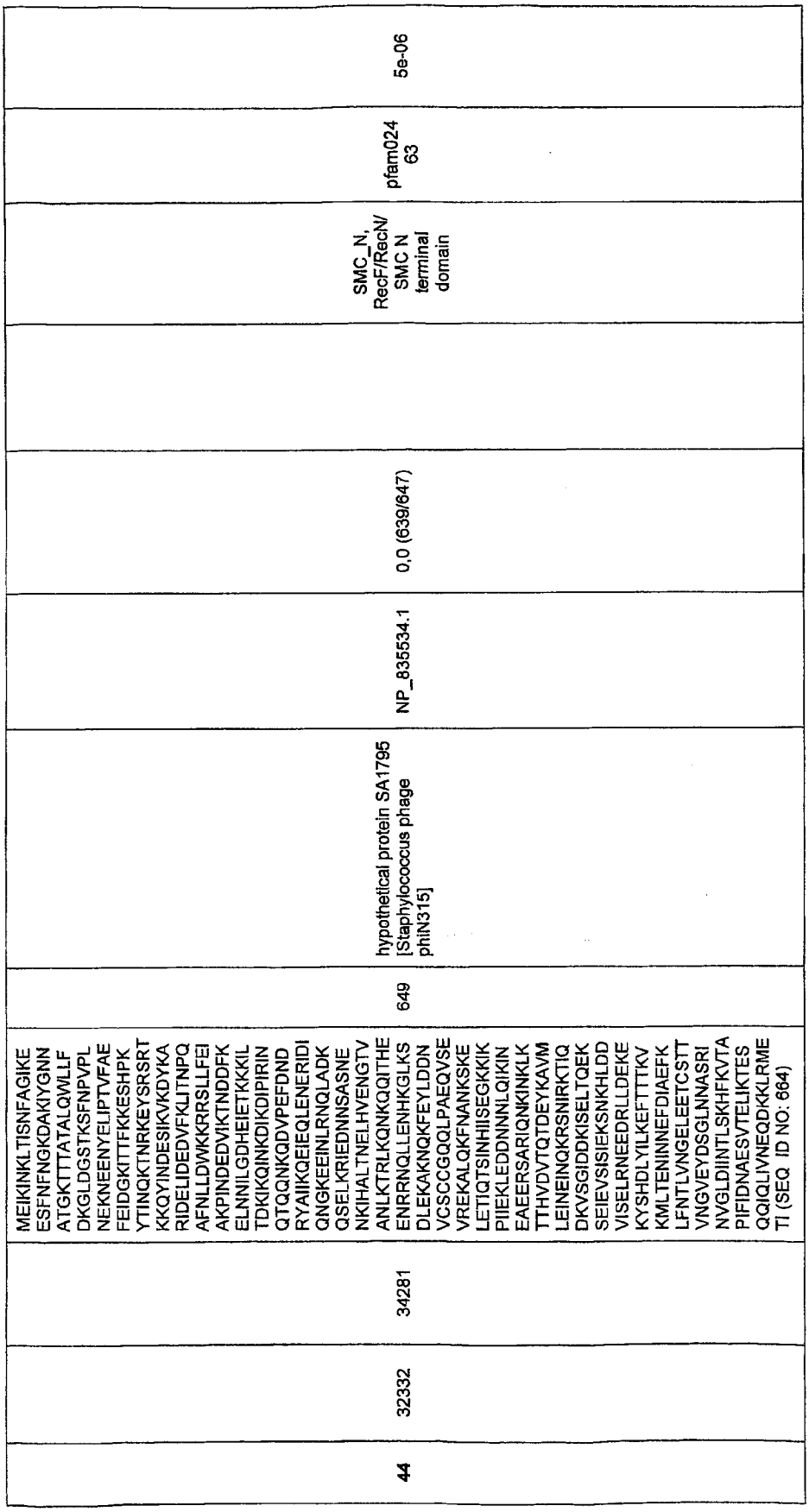

44
32332
34281
MEIKINKLTISNFAGIKE
ESFNFNGKDAKIYGNN
ATGKTTTATALQWLLF
DKGLDGSTKSFNPVPL
NEKNEENYELIPTVFAE
FEIDGKITTFKKESHPK
YTINQKTNRKEYSRSRT
KKQYINDESIKVKDYKA
RIDELIDEDVFKLITNPQ
AFNLLDVKKRRSLLFEI
AKPINDEDVIKTNDDFK
ELNNILGDHEIETKKKIL
TDKIKQINKDIKDIPIRIN
QTQQNKQDVPEFDND
RYAIIKQEIEQLENERIDI
QNGKEEINLRNQLADK
QSELKRIEDNNSASNE
NKIHALTNELHVENGTV
ANLKTRLKQNKQQITHE
ENRRNQLLENHKGLKS
DLEKAKNQKFEYLDDN
VCSCCGQQLPAEQVSE
VREKALQKFNANKSKE
LETIQTSINHIISEGKKIK
PIIEKLEDDNNNLQIKIN
EAEERSARIQNKINKLK
TTHVDVTQTDEYKAVM
LEINEINQKRSNIRKTIQ
DKVSGIDDKISELTQEK
SEIEVSISIEKSNKHLDD
VISELRNEEDRLLDEKE
KYSHDLYILKEFTTTKV
KMLTENINNEFDIAEFK
LFNTLVNGELEETCSTT
VNGVEYDSGLNNASRI
NVGLDIINTLSKHFKVTA
PIFIDNAESVTELIKTES
QQIQLIVNEQDKKLRME
TI (SEQ ID NO: 664)
649
hypothetical protein SA1795 [Staphylococcus phage phiN315]
NP_835534.1
0,0 (639/647)
SMC_N, RecF/RecN/ SMC N terminal domain
pfam02463
5e-06

FIG. 17R

45	34283	35203	MTENNKLQTIEQQLVQ EKNVSDNVLNKVRVLE SQGNLELPNDYSPSNA MKQAWLQISQDNKLMS CNDTSKANALLDMVTQ GLNPAKNQCYFIPYGN KMQLQRSYHGNVMML KRDAGAQDVVAQVIYK GDTFKQEMGETGRIKAI KHEQDFFNIDKENIIGA YCTIVFNDGRDNYIEVM TIEQIKQAWMQSSMIKD EKALQNSKTHNNFKEE MAKKTVINRAAKRYINT STDSNLFKYAQESEQR QRKEVLDAEVEENANQ EQLDFEQPVLEEAQYT ELENDKPIDVSDFEEIK EPATEKESEEEPF (SEQ ID NO: 665)	306	hypothetical protein PVL_43 [Staphylococcus phage PVL]	NP_058482.1	1e-179 (306/306)	recombinase	RecT family	pfam03837	8e-45
46	35548	35901	VAFLLQSTLGYKVLYVT DTKYLKYKFNGITHMML EVNYIYEQMQENIKNG SVHSTLANRIMESHFSL EHAIGMLKANDLTRLEE IHLIHLSSQNSNAKYIKS EIQKVTGAPVYFGGL (SEQ ID NO: 666)	117	phiPVL ORF044-like protein [Staphylococcus aureus subsp. aureus USA300]	YP_494610.1	4e-62 (117/117)	partial metallo-beta-lactamase domain	PhnP, Metal-dependent hydrolases of the beta-lactamase superfamily I	COG1235	1e-05
					hypothetical protein NM3_gp21 [Staphylococcus aureus phage phiNM3]	YP_908810.1	3e-61 (116/117)				
47	35902	36372	MLNRTILVGRLTRDPEL RTTQSGVNVASFTLAV NRTFTNAQGEREADFI NIIVFKKQAENVNKYLS KGSLAGVDGRLQTRNY ENKEGQRVYVTEVIAD SIQFLEPKNSNDTQQDL YQQQVQQTRGQSQYS NNKPVKDNPFANANGP IELNDDDLPF (SEQ ID NO: 667)	156	single-strand DNA-binding protein [Staphylococcus aureus subsp. aureus Mu50]	NP_372507.1	3e-85 (156/156)	ssDNA-binding protein	Single-strand DNA-binding protein	PRK06751	5e-41
					single-strand DNA-binding protein [Staphylococcus phage phiN315]	NP_835537.1	8e-84 (153/156)				

FIG. 17S

48	36402	37295	MTGWISIDRSIQNHWLF KEKRTFSKFEAWIYLLM EANHSEAKVPIGNQIVT VERGQRLTSILTLSDLF NWSRFKVKTFLDLLES DGMLEVKTTSKYTLITIV NYDFYQSEQGRNQHQ NDIKPTSKQHQSNINPT SKQHQTNTNNNDNKD NNEKNVNNEKKKVTAF DFFQDNGFGITPYNLD DLNYYLDSFENDSDEIV TASLKIAKDRNKVTWG YAKSILNTWLNANLKSI EQVRAFEKQQLESKKKQ NYKPFVKQSKEKTPKW LTDSTRETKTPEVDENL EKDREAFIKRLNSKWE (SEQ ID NO: 668)	297	hypothetical protein PVL_46 [Staphylococcus phage PVL]	NP_058485.1	8e-171 (295/297)	primosome component	DnaD, putative primosome component and related proteins	COG3935	1e-41			
49	37302	37520	MDAFDKYYLFDHDGNK MFSVTPHFKDGRHLVV GLKHTKFNGRRWYLDD YELKTLIDNEQMELGH QTSLFEYI (SEQ ID NO: 669)	72	hypothetical protein PVL_47 [Staphylococcus phage PVL]	NP_058486.1	3e-35 (72/72)		No putative conserved domains have been detected					
50	37623	37931	MPTKYTEHKKYLQNQM PKLNLENALKIELEFYFT PPKSWSKKKKTQAIGQ LKVTKPDIDNLMKTVLD ACNNYLWKDDNQIAEIT SSKRYGIEPKIIIRIEEI (SEQ ID NO: 670)	102	putative endodeoxyribonuclease RusA [Staphylococcus aureus phage phiNM3]	YP_908814.1	5e-53 (102/102)	endodeoxy-ribonuclease	Endodeoxy-ribonuclease RusA	pfam05866	2e-15	
51	37944	38312	MARKARIVTINDKPYRF TKSEMELIESHGITAGM VSKRVKDGWELHEAM DAPEGTRLSEYREKKTI ERLEQARLERKLERKR	122	phiPVL ORF050-like protein [Staphylococcus aureus subsp. aureus USA300]	YP_494605.1	4e-65 (122/122)		PVL ORF-50-like family	pfam07768	9e-30		

FIG. 17T

			KKEAELRRKKPHLFNV PQKHPRGRYACYLME NDIFVKVKK (SEQ ID NO: 671)		hypothetical protein PVL_49 [Staphylococcus phage PVL]	NP_058488.1	1e-61 (117/122)				
52	38316	38568	MTDNARKEYLNQFFGS KRYLYQDNERVAHIHV ANGNYYFHGHIVPGWQ GVKKTFDTAEELEIYIK QHGLEYEKQKQLTLF (SEQ ID NO: 672)	80	ORF062 [Staphylococcus phage 69]	YP_239629.1	1e-38 (76/80)		Phage conserved open reading frame 51	pfam061 94	2e-32
53	38701	38802	MQDALKEDIGLDEAVGI MTGQVVYKYEEAQENE (SEQ ID NO: 673)	33	hypothetical protein phi2958PVL_gp24 [Staphylococcus phage phi2958PVL]	YP_00226799 4.1	2e-09 (32/33)		Protein of unknown function (DUF1024)	pfam062 60	2e-04
54	38795	39331	MNNTLTIDQLQELLQIQ KEFDDRIPTLNLRDSKI AYVVEFFEWFNTLETF KNWKKKPGKPLDVQLD ELADMLAFGLSIANQVG VSSEEIKEAIESSFKDTE FHKMFNFKDKEFAQDA VVSTPQIIFKEFYPDQQ AIVIVIDIAYNLYSIDQLID AYKKKMKRNHERQDG TADAGKGYV (SEQ ID NO: 674)	178	hypothetical protein SAPPV1_gp31 [Staphylococcus phage phiNM]	YP_873980.1	9e-99 (177/178)	dUTPase	dUTPase_2	pfam087 61	1e-12
55	39368	39613	VSDMLEIFLIGFGVYLFY RIAIIFLKSKKTIHTNIYE MLMLATIFMISTFAYKH QKTHILIAFLVMFFMSKL KQVQGSYEE (SEQ ID NO: 675)	81	ORF063 [Staphylococcus phage 52A]	YP_240665.1	1e-37 (80/81)		**No putative conserved domains have been detected**		
56	39610	39816	MTQYLVTTFKDSTGRK HTHITKAKSNQRFTVVE AESKEEAKEKYEKQVK RDAVIKVGQLFENIREC GK (SEQ ID NO: 676)	68	similar to phage phi PVL ORF55 [Staphylococcus phage phiETA]	NP_910929.1	1e-31 (68/68)		Protein of unknown function (DUF1381)	pfam071 29	4e-08

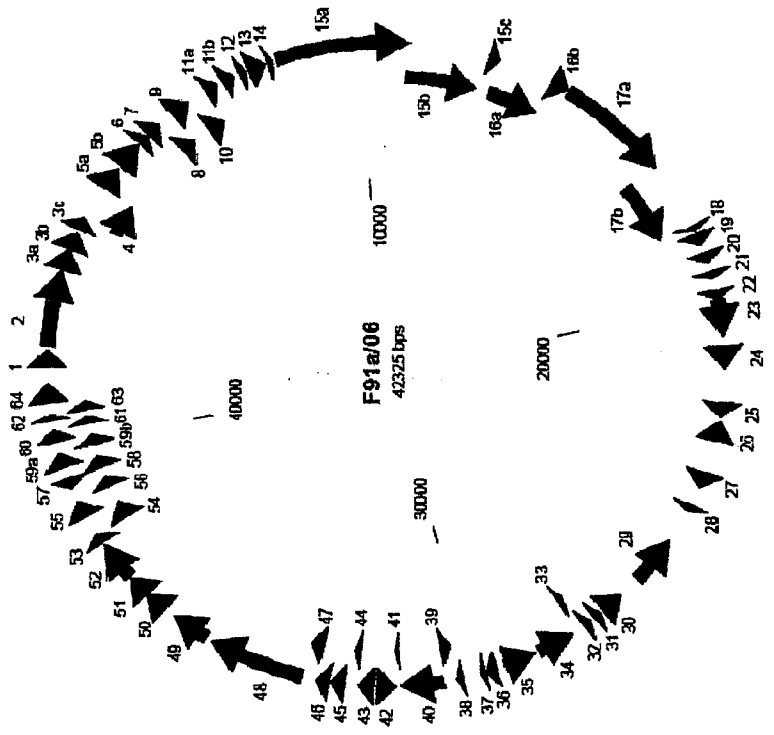
FIG. 17U

57	39813	40199	MIKKLKNMDGFDIFIVGI LSLFGITALLLVVALPIYT VASYQNKEVHQGTITD KYNKRQDKEDKFYIVLD DKQVIENSDLFFKGKFD SADIQARLKVGDKVKV KTIGYRIHFLNLYPVLYE VKKVDKK (SEQ ID NO: 677)	128	hypothetical protein phiETA_36 [Staphylococcus phage phiETA]	NP_510930.1	6e-66 (128/128)		Protein of unknown function (DUF1523)	pfam075 09	2e-05
58	40196	40345	MIKQILRLLFLLAMYELG KYVTEQVYIMMTANDD VEAPSDYVFRAEVSE (SEQ ID NO: 678)	49	hypothetical protein SAS062 [Staphylococcus phage phiN315]	NP_835548.1	4e-20 (49/49)	transcriptiona l activator	Transcription al activator RinB	pfam061 16	2e-15
59	40345	40545	MWITMTIVFAILLLVCISI NSDRAREIQALRYMND YLLDEVVKTKGYNGLK EYRIELKRMNNDIKK (SEQ ID NO: 679)	66	phi PVL ORF 60 homologue [Staphylococcus prophage phiPV83]	NP_06623.1	3e-30 (66/66)		Protein of unknown function (DUF1514)	pfam074 38	4e-22
60	40573	40989	MIKIEKHDIKKLEEYIQHI DNYRRELKMREYELLE SHEPDNAGAGKSNLPG NPIERCAIKKFSDNRYN TLRNIVNGVDRLIDESD EDTLELLRFRYWDCPIG CYEWEDIAHYFGTSKT SILRRRNALIDKLAKYIG YV (SEQ ID NO: 680)	138	hypothetical protein SA1780 [Staphylococcus phage phiN315]	NP_835550.1	2e-75 (138/138)	transcriptiona l regulator	**No putative conserved domains have been detected**		
					putative regulator RinA [Staphylococcus phage CNPH82	YP_950663.1	5e-58 (106/138)				
61	41221	41520	MMTKDERIRFYKSKEW QTTRKRVLERDNYECQ QCKRDGKLTTYDKSKR KSLDVDHILSLEHHPEF AHDLNNLETLCIKCHNK KEKRFIKKENKWKDEK W (SEQ ID NO: 681)	99	hypothetical protein NM3_gp37 [Staphylococcus aureus phage phiNM3]	YP_908826.1	1e-50 (99/99)	endonucleas e	McrA, restriction endonucleas e [defense mechanisms]	COG140 3	7e-05

FIG. 17V

Phage	Titer (pfu/ml)	Phage sensitivity (%) of STA strains (n=100)					Total of infected strains (%)
		++++	+++	++	+	-	
F87s/06	$7,4x10^{10}$	0	47	33	15	5	95
	$7,4x10^{9}$	0	17	20	18	45	55
	$7,4x10^{7}$	0	4	3	2	91	9
	$7,4x10^{5}$	0	1	1	2	96	4
	$7,4x10^{3}$	0	0	0	1	99	1

FIG. 18



orf	Putative function
2	terminase large subunit
3a-3-c	portal protein
4	Clp protease
5a-5b	capsid protein
8	head-tail adapter
11a-11b	major tail protein
15a-15c	tail tape measure protein
16a-16b	tail protein
17a-17b	minor structural protein
22	holin
23	CHAP endolysin
24	staphylokinase
25	cell wall hydrolase remnant
26	chemotaxis-inhibiting protein
27	staphylococcal complement inhibitor

orf	Putative function
29	integrase
34	DNA binding protein, putative helicase
35	cI-like repressor
36	cro-like repressor
40	antirepressor
49	recombinase
50	partial metallo-beta-lactamase domain
51	ssDNA binding protein
52	primosome component
54	endodeoxyribonuclease
59a-59b	dUTPase
62	transcriptional activator
64	transcriptional regulator

FIG. 19

orf	Start position	Stop position	Aminoacidic sequence	Size (aa)	Homologous/similar proteins				Conserved Domains		
					Organism/Name	Acc No	E value and identity	Predicted function	Name	Acc No	E value
1	3	383	PPSYNHFKAGDEMEIIVDENL VLKEKERLQVLYKDIPSNKLK VVDGLIIQAARLRVMLDYMW EDIKEKGDYDLFTQSEKAPPY ERERPVAKLFNARDAAYQKII KQLSDLLPEEKEDTETPSDD YL (SEQ ID NO: 682)	126	hypothetical protein SaurJH9_2024 [Staphylococcus aureus subsp. aureus JH9]	YP-001247384.1	2e-66 (126/126)		No putative conserved domains have been detected		
					hypothetical protein SA1778 [Staphylococcus phage phiN315]	NP_835552.1	4e-58 (114/114)				
2	456	2042	LISLIIYKQHIYSRDDVYFDEQ KIEDCIKFIEKWYFPTLPFQRF IIANIFLIDKNTDEAFFTEFAIF MGRGGGKNGLISAISDFLSTP LHGVKEYHISIVANSEDQAKT SFDEIRTVLMDNKRNKTGKT PKAPYEVSKTEIINRATKSVIR YNTSNTKTKDGGREGCVIFD EIHYFFGPEMVNVKRGGLGK KKNRRTFYISTDGFVREGYID AMKHKIASVLSGKVKNSRLFA FYCKLDDPKEVDDRQTWEK ANPMLHKPLSEYAKTLLSTIE EEYNDLPFNRSNKPEFMTKR MNLPEVDLEKVIAPWKEILAT NREIPNLDNQMCIGGLDFANI RDFASVGLLFRKNDDYIWLG HSFVRQGFLDDVKLEPPIKE WEKMGLLTIVDDDVIEIEYIVD WFLKAREKYGLEKVIADNYR TDIVRRAFEDAGIKLEVLRNP KAIHGLLAPRIDTMFAKHNVIY GDNPLMRWFTNNVAVKIKPD GNKEYIKKDEVRRKTDGFMA FVHALYRADDIVDKDMSKAL	528	phage terminase [Staphylococcus aureus subsp. aureus JH9]	YP_001247383.1	0,0 (523/528)	terminase large subunit	Phage terminase-like protein, large subunit	COG4626	3e-132
					77ORF003 [Staphylococcus phage 77]	NP_958603.1	0,0 (517/521)				

FIG. 20A

			DALMSIDF (SEQ ID NO: 683)								
3a	2058	2516	MSILEKIFKTRKDISYMLDLDM IEDLSQQAYVKRLAIDSCIEFV ARAVAQSHFKVLEGNRIQKN DVYYKLNIKPNTDLSSDSFW QQVIYKLIYDNEVLIVVSDSKE LLIADSFYREEYALYDDIFKDV TVKDYTYQRTFTMQEVILFKV QQQ (SEQ ID NO: 684)	152	HK97 family phage portal protein [Staphylococcus aureus subsp. aureus JH9]	YP_001247382.1	3e-79 (146/148)	portal protein	Phage portal protein	pfam04860	1e-13
					hypothetical protein SA1776 [Staphylococcus phage phiN315]	NP_835554.1	7e-79 (145/148)				
3b	2518	2904	VTHFVESLFEDYGKIFGRMIG AQLKNYQIRGILKSASSAYDE KNIEKLQAFTNKLFNTFNKNQ LAIAPLIEGFDYEELSNGGKN SNMPFSELSELMRDAIKNVAL MIGIPPGLIYGETADLEKKHA CI& (SEQ ID NO: 685)	128	hypothetical protein SA1776 [Staphylococcus phage phiN315]	NP_835554.1	3e-66 (123/123)				1e-09
3c	2975	3223	MYLKDTRIEIVGVNKKDPLQY AEAIDKLVSSGSFTRNEVRIM LGEEPSDNPELDEYLVTKNY EKANENGSTLKGGDEDESG D (SEQ ID NO: 686)	82	HK97 family phage portal protein [Staphylococcus aureus subsp. aureus JH9]	YP_001247382.1	1e-40 (82/82)				4e-05
4	3207	3944	MKVEIKGVIVSNEDKWVYEM LGMDSTCPKDVLTQLEFSDE DVDIIINSNGGNLVAGSEIYTH LRAHKGKVNVRITAIAASAAS LIAMAGDHIEMSPVARMMIHN PSSIAQGEAKDLNHAAETLEH VGQIMAEAYAVRAGKNKQEL IEMMAKETWLNADEAIEQGF ADSKMFENDNMQIVASDTQV LSKDVLNRVTALVSKTPEVNI DIDAIANKVIEKINMKEKESEI DVADSKLSANGFSRFLF (SEQ ID NO: 687)	245	peptidase S14, ClpP [Staphylococcus aureus subsp. aureus JH9]	YP_001247381.1	1e-139 (245/245)	Clp protease	Clp protease	pfam00574	2e-34
					77ORF015 [Staphylococcus phage 77]	NP_958605.1	1e-138 (243/245)				

FIG. 20B

5a	3967	4473	MTINLSETFANAKNEFINAVN NGEPQERQNELYGDMINQLF EETKLQAKAEAERVSSLPKS AQTLSANQRNFFMDINKSVG YKEEKLLPEETIDRIFEDLTTN HPLLADLGIKNAGLRLKFLKS ETSGVAVWGKIYGEIKGQLD AAFSEETAIQNKLTAFVVLTK RFK (SEQ ID NO: 688)	168	phi77 ORF006-like protein, putative capsid protein [Staphylococcus aureus subsp. aureus JH1]	YP_001317173.1	5e-90 (164/165)	capsid protein	**No putative conserved domains have been detected**
					hypothetical protein SA1774 [Staphylococcus phage phiN315]	NP_835556.1	1e-87 (160/165)		
5b	4532	5113	VALETAFLKGTGKDQPIGLNR QVQKGVSVTEGAYPEKEEQ GTLTFANPRATVNELTQVFK YHSTNEKGKSVAVKGNVTMV VNPSDAFEVQAQYTHLNANG VYVTALPFNLNVIESTVQEAG KVLTYVKGLYDGYLAGGINV QKFKETLALDDMDLYTAKQF AYGKAKDNKVAAVWKLDLKG HKPALEGTEETL (SEQ ID NO: 689)	193	phi77 ORF006-like protein, putative capsid protein [Staphylococcus aureus subsp. aureus USA300]	YP_494589.1	5e-108 (193/193)		
					hypothetical protein SA1774 [Staphylococcus phage phiN315]	NP_835556.1	5e-108 (193/193)		
6	5133	5360	MVKFKVVRAFKDIEHNQHKY KVGELYPAEGYNNPRVELLT NQIKNKYDKVYIVPLDKLTKQ ELLELCESLQKKDV (SEQ ID NO: 690)	75	hypothetical protein SA1773 [Staphylococcus phage phiN315]	NP_835557.1	5e-35 (73/73)		**No putative conserved domains have been detected**
7	5396	5692	MVKTMTIDDLLVKFKSLEKID HNSEDEYLKQLLKMSYERIK NQCGVFELENLIGQELILIRAR YAYQDLLEHFNDNYRPEIIDF SLSLMEVSEDEESV (SEQ ID NO: 691)	98	hypothetical protein NWMN_1894 [Staphylococcus aureus subsp. aureus str. Newman]	YP_001332928.1	3e-49 (98/98)		**No putative conserved domains have been detected**
					hypothetical protein SA1772 [Staphylococcus phage phiN315]	NP_835558.1	1e-46 (94/94)		

FIG. 20C

8	5676	6038	MKKVFKKPRITTKRLNTRVHF YKYTENNGPEAGEKEEKLLY SCWASIDGVWLRELEQAISN GTQNDIKLYIRDPQGDYLPSE EHYLEIESRYFKNRLNIKQVS PDLDNKDFIMIRGGYSS (SEQ ID NO: 692)	120	hypothetical protein SA1771 [Staphylococcus phage phiN315]	NP_835559.1	2e-65 (120/120)	head-tail adapter	**No putative conserved domains have been detected**
					phage head-tail adaptor, putative [Staphylococcus aureus subsp. aureus JH9]	YP_001247377.1	2e-65 (120/120)		
9	6035	6439	MSVKVIGDKALERELEKRFGI KEMVKVQDKALIAGAKVIVEE VKKQLKPSKDTGALINEVSFS KPEWINGKRTITVHWRGSKD RYKIVHLIEYGHVQKGTGKFI KPKAMGGVNRAIRQGQNKY FETLKRELKKL (SEQ ID NO: 693)	134	hypothetical protein SA1770 [Staphylococcus phage phiN315]	NP_835560.1	7e-71 (134/134)		**No putative conserved domains have been detected**
10	6436	6843	VIDILYKVHEVISQDRIIREHVN INNIKFNKYPNVKDTDVPFIVI DDIDDPIPTTYTDGDECAYSY IVQIDVFVKYNDEYNARIIRNK ISNRIQKLLWSELKMGNVSN GKPEYIEEFKTYRSSRVYEGI FYKEEN (SEQ ID NO: 694)	135	hypothetical protein SA1769 [Staphylococcus phage phiN315]	NP_835561.1	6e-71 (134/135)		**No putative conserved domains have been detected**
11a	6844	7113	MAIKHASAPKAYFNITGLGFA KLTKEGAELKYSDITKTRGLQ KIGVETGGELKTAYADGGPIE SGNTDGEGKISLQMHAFPKEI RKIVF (SEQ ID NO: 695)	89	phi13 family phage major tail protein [Staphylococcus aureus subsp. aureus JH9]	YP_001247374.1	2e-44 (89/89)	major tail protein	**No putative conserved domains have been detected**
					77ORF020 [Staphylococcus phage 77]	NP_958612.1	1e-43 (87/89)		
					hypothetical protein NM3_gp48 [Staphylococcus aureus phage phiNM3]	YP_908837.1	4e-43 (86/89)		

FIG. 20D

11b	7237	7488	MFTNPKIDGETAEKDWDFSS EEVEGEALFPLVDNKKSVRK YIFDSANMTNHDGDGEKGEE AFLKKILGEEYTGNVTEGNEE TL (SEQ ID NO: 696)	83	hypothetical protein NM3_gp48 [Staphylococcus aureus phage phiNM3]	YP_908837.1	7e-41 (83/83)			No putative conserved domains have been detected
12	7614	7754	LKYTTDQTNIVSINSDGQVTA EAQGIATVKATVGNMSDTITI NVEA (SEQ ID NO: 697)	46	hypothetical protein SAR2053 [Staphylococcus aureus subsp. aureus MRSA252]	YP_041424.1	3e-17 (46/46)			No putative conserved domains have been detected
					hypothetical protein NM3_gp49 [Staphylococcus aureus phage phiNM3]	YP_908838.1	1e-16 (45/46)			
13	7804	8154	MAKLKRNIIQLVEDPKANEIKL QTYLTPHFISFEIVYEAMDLID DIEDENSTMKPREIADRLMD MVVKIYDNQFTVKDLKERMH APDGMNALREQVIFITQGQQ TEETRNFIQNMK (SEQ ID NO: 698)	116	hypothetical protein SA1767 [Staphylococcus phage phiN315]	NP_835563.1	2e-61 (116/116)			No putative conserved domains have been detected
14	8193	8309	MLKNMDTLMMDLIENGKDAN EVLKMPFHYYLSIYQNKNNDI S (SEQ ID NO: 699)	42	77ORF100 [Staphylococcus phage 77]	NP_958614.1	5e-16 (42/42)			No putative conserved domains have been detected
15a	8400	11051	MGERIKGLSIGLDLDAANLNR SFAEIKRNFKTLNSDLKLTGN NFKYTEKSTHSYKQRIKELDG TITGYKKNVDDLAKQYGKVS QEQGENSAEAQKLRQEYNK QANELNFLEKELEKTTTEFEE FKKAQVEAQRMAESGWGKT SKVFESMGPKLTKMGDGLKS IGKGLMIGVTAPVLGIAAASG KAFAEVDKGLDTVTQATGAT GGELKKLQNSFKDVYGNFPE DAETVGGVLGEVNTRLGFTG KELESATESFLKFSHITGSDG	883	TP901 family phage tail tape measure protein [Staphylococcus aureus subsp. aureus JH9]	YP_001247370.1	0,0 (871/872)	tail tape measure protein	Phage-related minor tail protein	COG5280	3e-120
					hypothetical protein SA1766 [Staphylococcus phage phiN315]	NP_835564.1	0,0 (854/870)			

FIG. 20E

15b	11036	12613	VQAVQLITRAMGDAGIEADE YQSVLDMVAKAAQASGISVD TLADSITKYGAPMRAMGFEM KESIALFSQWEKSGVNTEIAF SGLKKAISNWGKAGKDPREE FKKTLAEIERTPDIASATSLAI EAFGAKAGPDLADAIKGGRF SYQEFLKTIEDSQGTVNQTFK DSESGSERFKVAMNKLKLVG ADVWASIESAFAPVMEELIKK LSVAVDWFSSLSDGSKRSIVI FGGIAAAIGPVVFGLGAFISTV GNAVTVLAPLLASIAKADGLIS FLSTKVPILGTVFTALTGPIGI VLGVLAGLAVAFTIAYKKSET FRNFVNGAINSVKQTFSNFIQ FIQPFIDSVKNVFKQAVSAIVD FAKDIWSQINGFFNENGISIV QALQNICNFIKAIFEFILNFVIK PIMFAIWQVMQFIWPAVKALI VSTWENIKGVIQGALNIILGFI IKGIFTKSLSAIWNATKSIFGF LYNSVKSIFTNMKNWLSSTW NNIKSNTVGKAHSLFTGVRS KFTSLWNATKDIFTKLRNWM SNIWNSIKDNTVGIAGRLWIK YVISSETCVTV (SEQ ID NO: 700)	MRDGLKSIIGKIKDHIGGMVD AIKKGLNKLIEGLNWVGGKLG MDEIPRLHTGTEHTHTTTRLV KNGKIARDTFATVGDKGRGN ALNGFRNEMIEFPNGIRVITP NTDTTAYLPKGSKVYNGAQT	526	TP901 family phage tail tape measure protein [Staphylococcus aureus subsp. aureus JH9]	YP_001247370.1	0,0 (521/524)		Phage-related protein	COG5412	7e-62

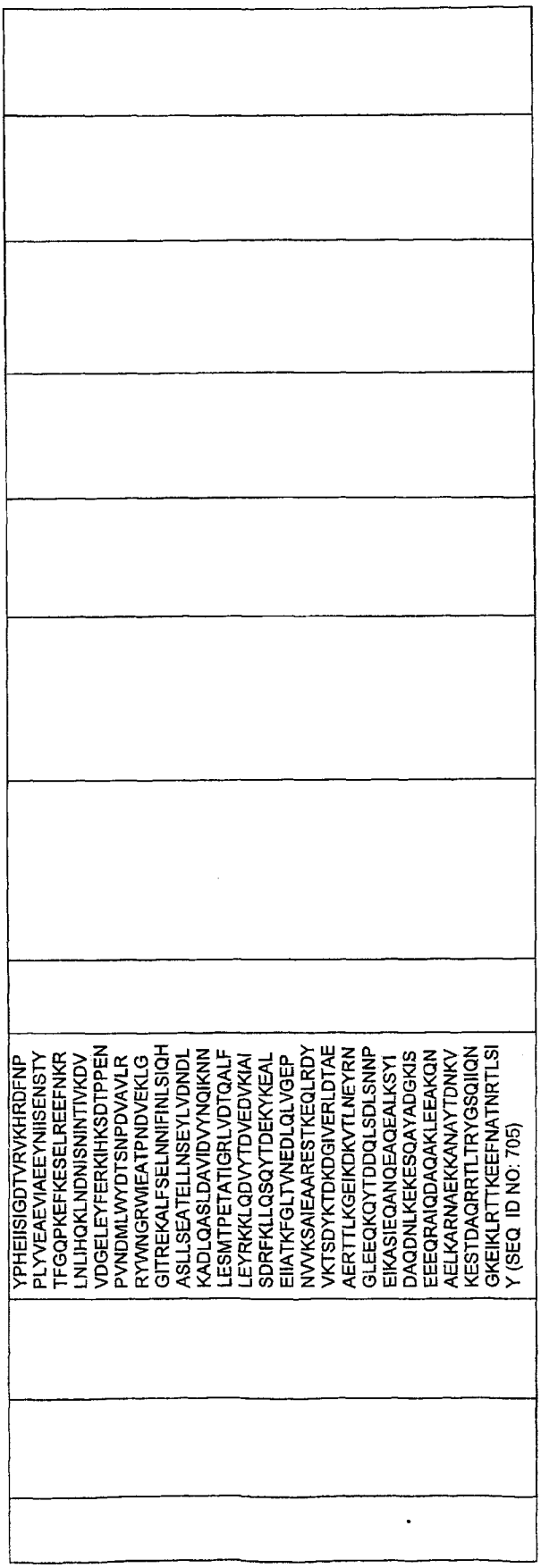
FIG. 20F

		YSMLNGTLPRFHFGTTIMVK DIKSSASSAFNWTKDQIGKG TKVILGDIKVGDVLDFMENPG KLLNYILEAFGIDFNSLTKGM GIAGDITKAAWSKIKKSATDW IKENLEAMGGGDLVGGILDP DKINYHYGRTAAYTAATGRP FHEGVDFPFVYQEVRTPMG GRLTRMPFMSGGYGNYVKIT SGVIDMLFAHLKNFSKSPPS GTMVKPGDVVGLTGNTGFST GPHLHFEMRRNGRHFDPEP YLRNAKKKGRLSIGGGGATS GSGATYASRVIRQAQSILGG RYKGKWIHDQMMRVAKRES NYQSNAVNNWDINAQRGDP SRGLFQIIGSTFRANAKRGYT NYNNPVHQGISAMQYIVRRY GWGGFKRAGDYAYATGGKV FDGWYNLGEDGHPEMIIPTD PARKK (SEQ ID NO: 701)	phage tail tape measure protein [Staphylococcus aureus phage phiNM3]	ABF73212.1	0,0 (510/524)			LT_GEWL, lytic transglycosyl ase (LT) and goose egg whitelysozym e (GEWL) domain	cd00254	1e-06
15c	12688	LSNVNGFDDPSLLLKMIEQQ QQQIALLLKIAQSNDVIADKD YQPIIDEYAFDKKVNASIEKRE RQESTKVKFRKGGIAIQ (SEQ ID NO: 702)	80	TP901 family phage tail tape measure protein [Staphylococcus aureus subsp. aureus JH9]	YP_001247370.1	5e-39 (80/80)	No putative conserved domains have been detected			
				hypothetical protein SA1766 [Staphylococcus phage phiN315]	NP_835564.1	2e-38 (79/80)				
16a	12927	MIDTIKVNNKTIPWLYVERGF EIPSFNYVLKTENVDGRSGSI YKGRRLESYSFDIPLVVRNDY LSHNGIKTHDDVLNELVKFFN YEEQVKLQFKSKDWYWNAY FEGPIKLHKEFAIPVKFTIKVV LTDPYKYSVTGNKNTAISDQV SVVNSGTADTPLIVEARAIKP SSYFMITKNDEDYFMVGDDE	382	hypothetical protein SA1765 [Staphylococcus phage phiN315]	NP_835565.1	0,0 (357/359)	tail fiber protein			
				phage tail fiber protein [Staphylococcus aureus subsp.	YP_001332921.1	0,0 (355/359)				

FIG. 20G

			VTKEVKDYMPPVYHSEFRDF KGWTKMITEDIPSNDLGGKV GGDFVISNLGEGYKATNFPD AKGWVGAGTKRGLPKAMTD FQITYKCIVEQKGKGAGRTA QHIYDSDGKLLASIGYENKYH DRKIGHIVVTLYNQKGDPKKI YDYQNKPIMYNLDRIVVYMRL RRVGNKFLLKLGNLITLKTQID VNLLIWMRKSG (SEQ ID NO: 703)		aureus str. Newman]				
					hypothetical protein PVL_18 [Staphylococcus phage PVL]	NP_058457.1	9e-137 (239/242)			
16b	14054	14410	MDEKEWIDGGKFYQRPASIIA IYSAKYNGYKWMEMNGLGS FNTEILPKPKGARDVIIQKGDL VKIDMQAKSVVINEEPMLSEK SFGSNYFNVDSGYSELIIQPE NVFDTTVKWQDRYL (SEQ ID NO: 704)	118	hypothetical protein PVL_18 [Staphylococcus phage PVL]	NP_058457.1	2e-63 (118/118)		**No putative conserved domains have been detected**	
					phage tail fiber protein [Staphylococcus aureus subsp. aureus str. Newman]	YP_001332921.1	2e-63 (118/118)			
17a	14426	16798	VIHVLDFNDKIIDFLSTDDPSL VRAIHKRNVNDNSEMLELLIS SERAEKFRERHRVIIRDSNKQ WREFIINWVQDTMDGYTEIE CIASYLADITTAKPYAPGKFE KKTTSEALKDVLSDTGWEVS EQTEYDGLRTTSWTSYQTRY EVLKQLCTTYKMVLDFYIELS SNTVKGRYVVLKKKNSLFKG KEIEYGKDLVGLTRKIDMSEIK TALIAVGPENDKGKRLELVVT DDEAQSQFNLPMRYIWGIYE PQSDDQNMNETRLSSLAKTE LNKRKSAVMSYEITSTDLEVT	790	phage minor structural protein [Staphylococcus aureus subsp. aureus JH9]	YP_001247368.1	0,0 (787/788)	minor structural protein	TolA protein	pfam06519	4e-04
					77ORF002 [Staphylococcus phage 77]	NP_958617.1	0,0 (784/788)			
					structural protein [Staphylococcus phage phi13]	NP_803398.1	0,0 (747/752)			

FIG. 20H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Y (SEQ ID NO: 705)

FIG. 20I

17b	16767	18209	MQPIVHFQYIKRDCPNVTDG TTIRYDDNGVAQALNVGPRGI RLNADKIDINGNREINLLIQNM RDKVDKTDIVNSLNLSREGLD INVNRIGIKGGNNNRYVQIQN DSIELGGIVQRTWKGKRSTD DIFTRLKDGHLRFRNNTAGG SLYMSHFGISTYIDGEGEDG GSSGTIQWWDKTYSDSGMN GITINSYGGVVALTSDNNRVV LESYASSNIKSKQAPVYLYPN TDKVPGLNRFAFTLSNADNA YSSDGYIMFGSDENYDYGAG IRFSKERNKGLVQIVNGRYAT GGDTTIEAGYGKFNMLKRRD GNRYIHIQSTDLLSVGSDDAG DRIASNSIYRRTYSAAANLHIT SAGTIGRSTSARKYKLSIENQ YNDRDEQLEHSKAILNLPIRT WFDKAESEILARELREDRKLS EDTYKLDRYVGLIAEEVENLG LKEFVTYDDKGEIEGIAYDRL WIHLIPVIKEQQLRIKKLEESK NAG (SEQ ID NO: 706)	480	structural protein [Staphylococcus phage phi13]	NP_803398.1	0.0 (465/467)		No putative conserved domains have been detected
18	18199	18351	MQDNKQGLQANPEYTIHYLS QEIMRLTQENAMLKAYIQENK ENQQCAEEE (SEQ ID NO: 707)	50	hypothetical protein phiPV83p56 [Staphylococcus prophage phiPV83]	NP_061644.1	2e-20 (50/50)		No putative conserved domains have been detected
19	18398	18619	MAKEIINNTERFILVQIDKEGT ERVVYQDFTGSFTTSEMVNH AQDFKSEENAKKIAETLNLLY QLTNKKQRVK (SEQ ID NO: 708)	73	hypothetical protein PVL_21 [Staphylococcus phage PVL]	NP_058460.1	4e-35 (73/73)		No putative conserved domains have been detected
20	18608	19038	MLSTLNEIKLGQKTQEQVNIK LDKTLDAIQKEREIDEKNKKE NDKNIRDMKMWVLGLVGTIF GSLIIALLRMLMGI (SEQ ID NO: 709)	76	phi PVL orf 17-like protein [Staphylococcus phage phi13]	NP_803400.1	3e-34 (76/76)		No putative conserved domains have been detected

FIG. 20J

21	19230	19364	MVALLKSLERRRLMITISTML QFGLFLIALIGLVIKLIELSNKK (SEQ ID NO: 710)	44	hypothetical protein SAR2042 [Staphylococcus aureus subsp. aureus MRSA252]	YP_041413.1	8e-15 (44/44)		No putative conserved domains have been detected		
					ORF087 [Staphylococcus phage 42E]	YP_239882.1	4e-14 (43/44)				
22	19629	19832	LSAIFLFAQNIAKAIGYDIQVY TEQLTDGLNAILGFLVLTGVIQ DPTTKGIGDSHQALEYEEPR RKY (SEQ ID NO: 711)	67	holin [Staphylococcus aureus subsp. aureus str. JKD6008]	ZP_03564466.1	9e-32 (67/67)	holin	Phage_holin_1	pfam04531	1e-22
					holin [Staphylococcus prophage phiPV83]	NP_061647.1	5e-31 (66/67)				
23	19844	20599	MKTYSEARARLRWYQGRYID FDGWYGYQCADLAVDYIYWL LEIRMWGNAKDAINNDFKNM ATVYENTPSFVPQIGDVAVFT KGIYKQYGHIGLVFNGGNTN QFLILEQNYDGNANTPAKLR WDNYYGCTHFIRPKYKSEGL MNKITNKVKPPAQKAVGKSA SKITVGSKAPYNLKWSKGAY FNAKIDGLGATSATRYGDNR TNYRFDVGQAVYAPGTLIYVF EIIDGWCRIYWNNHNEWIWH ERLIVKEVF (SEQ ID NO: 712)	251	amidase [Staphylococcus phage phi13]	NP_803402.1	2e-146 (251/251)	CHAP endolysin	CHAP domain	pfam05257	1e-17

FIG. 20K

24	20790	21281	MLKRGLLFLTVLLLLFSFSSIT NEVSASSSFDKGKYKKGDDA SYFEPTGPYLMVNVTGVDGK GNELLSPHYVEFPIKPGTTLT KEKIEYYVEWALDATAYKEFR VVELDPSAKIEVTYYDKNKKK EETKSFPITEKGFVVPDLSEHI KNPGFNLITKVIIEKK (SEQ ID NO: 713)	163	staphylokinase precursor [Staphylococcus aureus phage phiNM3]	YP_908850.1	5e-88 (163/163)	staphylokina se precursor	Staphylokina se / Streptokinase family	pfam02821	8e-18
25	21970	22266	VPAGYTLDKNNVPYKKETGY YTVANVKGNNVRDGYSTNS RITGVLPNNATIKYDGAYCIN GYRWITYIANSGQRRYIATGE VDKAGNRISSFGKFSAV (SEQ ID NO: 714)	98	peptidoglycan hydrolase [Staphylococcus phage phi 12]	NP_803355.1	3e-49 (96/98)	cell wall hydrolase remnant	Bacterial SH3 domain	pfam08460	1e-05
26	22810	22361	MKKKLATTVLALSFLTAGIST HHHSAKAFTEPFPTNEEIES NKKMLEKEKAYKESFKNSGL PTTLGKLDERLRNYLKKGTK NSAQFEKMVILTENKGYYTV YLNTPLAEDRKNVELLGKMY KTYFFKKGESKSSYVINGPG KTNEYAY (SEQ ID NO: 715)	149	chemotaxis-inhibiting protein CHIPS [Staphylococcus aureus phage phiNM3]	YP_908852.1	8e-80 (149/149)	chemotaxis-inhibiting protein	Chemotaxis-inhibiting protein CHIPS	PRK13032	1e-64
27	23495	23845	MKIRKSILAGTLAIVLASPLVT NLDKNEAQASTSLPTSNEYQ NEKLANELKSLLDELNVNELA TGSLNTYYKRTIKISGQKAMY ALKSKDFKKMSEAKYQLQKIY NEIDEALKSKY (SEQ ID NO: 716)	116	Staphylococcal complement inhibitor [Staphylococcus aureus phage phiNM3]	ABF73224.1	1e-58 (116/116)	staphylococcal complement inhibitor	No putative conserved domains have been detected		
28	24234	24389	LVNKINKFNQYVARFIPYIATK IPIKKNIAPMIKQKSDAELLKN EVFRVRK (SEQ ID NO: 717)	51	hypothetical protein NM3_gp65 [Staphylococcus aureus phage phiNM3]	YP_908854.1	6e-20 (50/51)		No putative conserved domains have been detected		

FIG. 20L

29	26143	25106	MKTRCYDGKKWQYEFKYEG KRYRKKGFRTKREANSAGLD KLNELRSGFNIDNYITLEEYFE NWIKTYKQPVVKENTYRHYR NALQHIQKHKIGKMELSKINR QVYQKFINDYSKEHAKETIRK TNGAIRSALDDALYDGLIFKN PAYKVNYKAGKPTKSEQEKFI SVTEYEILKDHVRKKRTRSSL ALFIMICTGCRVSGARNIKIEH INQVKNTIFIDERKTDTSPRYI SIAKSDMKHIMDVISTFAISYD GYIFKEAGSIINLQAINNALKS ACRVNNIPIITSHALRHTHCSY LLAKGVSIHYISKRLGHKNIAI TTSVYSHLLEEKFNEEDKKTT KILESM (SEQ ID NO: 718)	345	phage integrase family protein [Staphylococcus aureus subsp. aureus JH9]	YP_001247419.1	0,0 (345/345)	integrase	phiLC3 phage and phage-related integrases	cd01189	1e-34
					Integrase [Staphylococcus phage phiN315]	NP_835517.1	0,0 (343/345)					
30	27088	26615	LNGGESVSENKGEMMTHNIE KRINKLKTSGNPKFKKLDSDI HYLLKRFEGEKNHKGFYPKF KQGEIVFVDFGINVNKEFSNS HFAIVMNKNDSNTEDIVNVIP LSSKENKKYLKMNFDLKWEY YLRLFLNLISAQNNSAILKEVS IKNTKKQHRIHH (SEQ ID NO: 719)	157	hypothetical protein SaurJH9_2059 [Staphylococcus aureus subsp.aureus JH9]	YP_001247418.1	2e-73 (137/138)		Uncharacterized protein conserved in bacteria (DUF2234)	pfam09993	0,005
					77ORF017 [Staphylococcus phage 77]	NP_958824.1	3e-69 (130/130)					
31	27309	27151	MKITNCKIKRETIVYEVLTSGN QPFTYELPKDLSSHNARKYL EFISQKIRWR (SEQ ID NO: 720)	52	hypothetical protein SaurJH9_2058 [Staphylococcus aureus subsp. aureus JH9]	YP_001247417.1	3e-21 (49/49)		No putative conserved domains have been detected			
					hypothetical protein phi12p03 [Staphylococcus phage phi 12]	NP_803309.1	8e-21 (48/49)					

FIG. 20M

32	27565	27380	MSTYKEIEHLHINTGGKELTQ EQIEEAKAFIDSQEFKDMIRE AKESHQRVMESKITDRTKL (SEQ ID NO: 721)	61	hypothetical protein SaurJH9_2057 [Staphylococcus aureus subsp. aureus JH9]	YP_001247416.1	4e-27 (61/61)		**No putative conserved domains have been detected**		
					hypothetical protein phiPV83p04 [Staphylococcus prophage phiPV83]	NP_061594.1	1e-25 (58/61)				
33	27708	27562	MDFKEVDINIEEWEMVEIPFY TEEELTYRLNNGLPITKSELE EQESKK (SEQ ID NO: 722)	48	hypothetical protein SaurJH9_2056 [Staphylococcus aureus subsp. aureus JH9]	YP_001247415.1	9e-19 (48/48)		**No putative conserved domains have been detected**		
					hypothetical protein phiETA_05 [Staphylococcus phage phiETA]	NP_510899.1	1e-17 (46/48)				
34	28635	27856	MKPRKQDEKILSDQYSYFEPI ISDSCDIKFDENKRRMGSIFIS HEEICFIRKEEDYIFKISLSEVI DYNTVVTIWKNQAFLTLNDN RKLTVYFVTNSPLTGFISILKT YMQLSKNKETIISNDCLPIND DEQTKVEIFDVVGLNYEGRR KELKKLIKKMKNNDDFFFLYS DLKGNELKEELLYEDKVYEIS DYEVIPGVFLQKEPDNPYDE NAIKVMISNEYSEFHVGYVPR EYASRLVNHMDNIVSCNAYIN GGKYKT (SEQ ID NO: 723)	259	HIRAN [Staphylococcus aureus subsp. aureus JH9]	YP_001247414.1	7e-148 (259/259)	DNA binidng protein, putative helicase	HIRAN domain	pfam08797	7e-11
					SNF2 family helicase, putative [Aspergillus fumigatus A1163]	EDP51408.1	3e-4 (22/46)				
35	29361	28687	MNSFKDRLKQIMSERKISQS ELSRRTGIGRNSISDYLNGKY EAKQDKVFELAKALNVNEAW LMGFDISKNRKIENNDITSIYS KLTPPRQSNVLKYATNQLEE	224	putative phage repressor [Staphylococcus aureus subsp. aureus JH9]	YP_001247413.1	4e-125 (221/221)	cI-like repressor	Peptidase S24 LexA-like proteins	cd06529	1e-15

FIG. 20N

		QNNDSDNLVDFNSYIQEKSE VDIYGCASAGIGERLYNEPIS KEFVRGYVPAHDIALKVNGD SMEPLFKNGQIIFIEKSHTIKD GQIGVFIINGDAYVKKVYVED NRLTLVSLNKKYKDYIL (SEQ ID NO: 724)		similar to phage phi PVL repressor [Staphylococcus phage phiETA]	NP_510900.1	1e-99 (174/221)					
36	29526	MIYNFDYSLLYERMAEYRYS QSSLANAIPISRTSINHKLQGK NLFTQWEIKRICELLEIPPTKV GRYFFEQNVQKPVQMS (SEQ ID NO: 725)	80	hypothetical protein SaurJH9_2053 [Staphylococcus aureus subsp. aureus JH9]	YP_001247412.1	1e-40 (80/80)	cro-like repressor	Helix-turn-helix XRE-family like proteins	cd00093	0.006	
				putative cro-like repressor [Staphylococcus phage phiPVL108]	YP_918897.1	3e-39 (78/80)					
37	29781	MEQITLTKEELKEIIAKEVRNA IKGEKPISSGAISVK (SEQ ID NO: 726)	37	hypothetical protein phiPV83p07 [Staphylococcus prophage phiPV83]	NP_061597.1	2e-10 (35/37)		No putative conserved domains have been detected			
38	30241	MLQKFRIAKEKNKLKLKLLKH ASYCLERNNNPELLRAVAELL KKVS (SEQ ID NO: 727)	46	hypothetical protein phiPV83p08 [Staphylococcus prophage phiPV83]	NP_061598.1	1e-16 (46/46)		No putative conserved domains have been detected			
39	30583	MKLLVTLKDGSKKHVSDLKKI VFPGYEGIETVTKEEIETFFLD PTKTYVFVGSQTLSVEAGQIL TVEFS (SEQ ID NO: 728)	69	77ORF066 [Staphylococcus phage 77]	NP_958632.1	9e-31 (69/69)		No putative conserved domains have been detected			
40	30840	MQALKTKSNIGEMFNIQEKE NGEIAISARELYKALEVKKRF SAVAEINLKHFKENRDFTSVL TSTVVNNGAVRQLEDYALTL DVAKHVAMMSGTEKGFDFR EYFIQVEKAWNSPEMIMQRA LKIANNTINQLETKIERDKPKI VFADAVATTKTSILVGELAKII KQNGINIGQRRLFEWLRQNG FLIKRKGVDYNMPTQYSMER	286	phage anti-repressor [Staphylococcus aureus subsp. aureus MW2]	NP_646749.1	4e-142 (245/245)	antirepressor	ANT, phage antirepressor protein KilAC domain	pfam03374	4e-36	
				anti-repressor [Staphylococcus phage phiSauS-	YP_002332482.1	9e-142 (244/245)					

FIG. 20O

			ELFEIKETSITHSDGHTSISKT PKVTGKGQQYFVNKFLGENK QLNRRNEQCKLKTKKSSITT MTKKVIDDPLIFNTTMATT (SEQ ID NO: 729)		IPLA88]						
41	31500	31601	MIDQRFIEMTLERHPHLKNNF YGLIDGKEFKLD (SEQ ID NO: 730)	33	hypothetical protein PVL_35 [Staphylococcus phage PVL]	NP_058474.1	2e-11 (33/33)		**No putative conserved domains have been detected**		
42	31968	31588	MKLDHDCVRHLLLEIETNKKI GEPLTEYNFKDNVVFGKYDF ETVMYALLKLEEAKYVSVKF GWEDGHIYGYTINDITWSGH EFLDNIRDNHTWKEVKKVAN KTTSMSVTLLSKLAFNYLTQK FNLT (SEQ ID NO: 731)	126	hypothetical protein PVL_36 [Staphylococcus phage PVL]	NP_058475.1	6e-68 (126/126)		Hypothetic al protein (DUF2513)	pfam10711	2e-28
43	32023	32346	MPHILNVTVPIPETHVLITKDE YEELIAYSLDPVWNMSDLKK KLKIASDETIKDRLLFHPRLEK ELRAQGIVHYPDENFNRWRF NARRMHKFVDEHFNEIYKGG HNK (SEQ ID NO: 732)	107	hypothetical protein SA1799 [Staphylococcus phage phiN315]	NP_835529.1	8e-57 (107/107)		Uncharacte rized protein conserved in bacteria [Function unknown]	COG4707	3e-37
44	32343	32504	MSKTYKSYLVAVLCFTVLAIV LMPFLYFTTAWSIAGFASIAT FIFYKEYFYEE (SEQ ID NO: 733)	53	hypothetical protein SAS063 [Staphylococcus phage phiN315]	NP_835530.1	2e-21 (53/53)		Protein of unknown function (DUF1270)	pfam06900	1e-10
45	32599	32901	MTKNYKDMTQEEIKDLLSEK TAELYELAKEIKGESKFDILLF SSIGVIDGDYLAGSSSVIGHT FDLAYLLDSTKSYKDIVNVLQ MCKSQKILGIDDDKED (SEQ ID NO: 734)	100	hypothetical protein SA1798 [Staphylococcus phage phiN315]	NP_83553.1	7e-49 (100/100)		Hypothetic al protein of unknown function (DUF2482)	pfam10655	3e-39

FIG. 20P

46	32906	33166	MYYKTGDVCRKIFNVDGFDF QLRVKKRAYSVEIVVLDHEG NSIDGLLVSDENDLYTALDILK QSIYEWIENNTDEQDRLINLV MKW (SEQ ID NO: 735)	86	hypothetical protein SA1797 [Staphylococcus phage phiN315]	NP_835532.1	8e-43 (86/86)		Protein of unknown function (DUF1108)	pfam06531	7e-35
47	33160	33438	MVGISMRDTERNILNIFKTLF DEYTLSNQRALLEIERNHHG YLSINFLHYHDSYKTNNKLVQ IHEINPDSHERIKNLIIEVLRGH RKIKKGA (SEQ ID NO: 736)	92	hypothetical protein NM3_gp18 [Staphylococcus aureus phage phiNM3]	YP_908807.1	3e-46 (92/92)		**No putative conserved domains have been detected**		
48	33447	35390	MKINKLTISNFAGIKEEKFNFD GKDAKIYGNNATGKTTTATAL QWLLFDKGLDGSTKSFNPVP LNEKNEENYELIPTVFAEFEID GKITTFKKESHPKYTINQKTN RKEYSRSRTKKQYINDESIKV KDYKARIDELIDEDVFKLITNP QAFNLLDWKKRRSLLFEIAKP INDEDVIKTNDDFKELNNILGD HEIETKKKILTDKIKQINKDIKD IPIRINQTQQNKQDVPEFDND RHTIIKQEIEQLENERIDIQNG AEEINLRNQLADKQSELKRIE ANNSASNENKIHALTNELHVE NGTVANLKTRLKQNKQQITH EENRRNQLLENHKGLKSDLE KAKNQKFEYLDDNVCSCCG QQLPAEQVSEVREKALQKFN ANKSKELETIQTSINHIISEGK KIKPIIEKLEDDNNNLQIKINEA EERSARIQNKINKLKITHVDVT QTDEYKAVMLEINEINQKRSN IRKTIQDKVSGIDDKISELTQE KSEIEVSISIEKSNKHLDDVIS ELRNEEDRLLDEKEKYSHDL YILKEFTTTKVKMLTENINNEF DIAEFKLFNTLVNGELEETCS TTVNGVEYDSGLNNASRINV GLDIINTLSKHFKVTAPIFIDNA ESVTELIKTESQQIQLIVNEQD	647	hypothetical protein SA1795 [Staphylococcus phage phiN315]	NP_835534.1	0,0 (647/647)		SMC_N, RecF/RecN /SMC N terminal domain	pfam02463	7e-06

FIG. 20Q

			KKLRMETI (SEQ ID NO: 737)								
49	35513	36313	MKSAMLQLQELKGSKKDGY KPALEFATSTSIANALMDMVV QGLNPAKNQGYFIMYGDKVQ FQRSYHGTMAVTKRVAGAE EINAEVIFEGDEVKYKTKNGKI VELEHTQSFGNRNTQNIIGAY ATVVFKDESRNYTEIMTFEEI EEAWKQSQMVYNGVFKEDG THRRFPQEMAKKTVINRACK KILNSTDDASLLSNQIKESEQ RQRKEVLDAEVEENANQEQL DFEPPVFEEAQYTELENEKPI DVSDFEEIKEPATEKESEEEP F (SEQ ID NO: 738)	266	hypothetical protein SA1794 [Staphylococcus phage phiN315]	NP_835535.1	2e-154 (266/266)	recombinase	RecT, recombinational DNA repair protein (RecE pathway)	COG3723	6e-65
50	36526	37011	MTAGTQRAMDFESHRLCTIK AKQELRIGTWSILPFDIEHDA NEPVAFLLQSTLGYKVLYVTD TKYLKYKFNGITHMMLEVNYI YEQMQENIKNGSVHSALANR IMESHFSLEHAIGMLKANDLT RLEEIHLIHLSSQNSNAKYIKS EIQKVTGAPVYVGGL (SEQ ID NO: 739)	161	hypothetical protein SA1793 [Staphylococcus phage phiN315]	NP_93553.1	2e-91 (161/161)	partial metallo-beta-lactamase domain	PhnP, Metal-dependent hydrolases of the beta-lactamase superfamily I	COG1235	1e-14
51	37012	37482	MLNRTILVGRLTRDPELRTTQ SGVNVASFTLAVNRTFTNAQ GEREADFINIIVFKKQAENVN KYLSKGSLAGVDGRLQTRNY ENKEGQRVYVTEVIADSIQFL EPKNSNDTQQDLYQQQVQQ TRGQSQYSNNKPVKDNPFA NANGPIEIDDNDLPF (SEQ ID NO: 740)	156	single-strand DNA-binding protein [Staphylococcus phage phiN315]	NP_835537.1	3e-85 (156/156)	ssDNA binding protein	single-strand DNA-binding protein	PRK06751	1e-40

FIG. 20R

52	37512	38348	MTGWISIDRSIQNHWLFKEK RTFSKFEAWIYLLMEANHSK AKVPIGNQIVTVERGQRLTSIL TLSDLFNWSRFKVKTFLDLLE SDGMLEVKTTSKYTLITIVNY DFYQSEQGRNQHQNDIKPTS KQHQSNINPTSKQHQTNTNN NDNKDNNEKNVNNEKKKTTA FDFFQDNGFGFITSYNLDDLN YYLDSFENDSDEIVTASLKIAK DRNKVTWGYAKSILNTWLNA NLKSIEQVRAFEKQQLESKK QNYKPFVKQSKEKTTQMAH RQHERNENAGSR (SEQ ID NO: 741)	278	hypothetical protein SA1791 [Staphylococcus phage phiN315]	NP_835538.1	5e-150 (261/263)	primosome component	DnaD, putative primosome component and related proteins	COG3935	6e-37
53	38413	38631	MDAFDKYYLFDHDGNKMFS VTPHFKDGRHLVVGIKETKFN GRRWYLDDYELNTLIDNEQM ELGHQTSLFEYI (SEQ ID NO: 742)	72	hypothetical protein SA1790 [Staphylococcus phage phiN315]	NP_835539.1	2e-35 (72/72)		**No putative conserved domains have been detected**		
54	*38628*	*39044*	MRDYMEIEIKFNEVFNAPMG SPRPRFRNTGRFVQTYMPTS YTKHKAYIQGQMPKLNLERA LKIELDFYFPLLKSWSKKKKS EMVGQYKVTKPDIDNLIKTVL DACNGHVWKDDNQITEITSS KRYGIEPKIIIRIEEI (SEQ ID NO: 743)	138	hypothetical protein SA1789 [Staphylococcus phage phiN315]	NP_835540.1	5e-74 (134/134)	endodeoxy-ribonuclease	Endodeoxy - ribonucleas e RusA	pfam05866	4e-22
55	39057	39428	MARKARIVTINDKPYRFSKFE MELIESHGITAGMVSKRVKD GWELHEAMDAPEGTRLSEY REKKTIERLEQARLERKLERK RKREAELRRKKPHLFNVPQK HSRDPYWFDNTYNQMFKKW SEA (SEQ ID NO: 744)	123	hypothetical protein SA1788 [Staphylococcus phage phiN315]	NP_835541.1	3e-66 (123/123)		PVL ORF-50-like family	pfam07768	3e-34

FIG. 20S

56	39428	39685	MSVISNRKVDMNEIQDNVKQ PAHYTYGDIEIIDFIEQVTAQY PPQLAFAIGNAIKYLSRAPLK NGHEDLAKAKFYVQRAFDLW EQ (SEQ ID NO: 745)	85	hypothetical protein SA1787 [Staphylococcus phage phiN315]	NP_835542.1	1e-43 (85/85)		**No putative conserved domains have been detected**		
57	39935	39685	VPGWQSVKKTFDTAEELEIYI KQHGLEYEEQKQLTLF (SEQ ID NO: 746)	38	hypothetical protein SA1786 [Staphylococcus phage phiN315]	NP_835543.1	2e-13 (37/37)		Phage conserved open reading frame 51	pfam06194	2e-10
58	39935	40189	MEMMNNREQIEQSVISASAY NGNDTEGLLKEIEDVYKKAR AFDEILDGMTNAIQHSVKEGI ELDEAVGIMAGQVIYKYEEEQ GK (SEQ ID NO: 747)	84	hypothetical protein SA1785 [Staphylococcus phage phiN315]	NP_835544.1	2e-39 (82/82)		Protein of unknown function (DUF1024)	pfam06260	6e-26
59a	40186	40491	MTNTLTIDQLQELLQIQKKFD DRIPTRNLNDTVASMIIEFAE WVNTLEFFKNWKKQPGKPL DTQLDEIADYLAFSLQLTLTIV DEEDLEETTEVMVDLIRK (SEQ ID NO: 748)	101	hypothetical protein phiPV83p30 [Staphylococcus prophage phiPV83]	NP_061619.1	6e-50 (99/99)	dUTPase	dUTPase_ 2	pfam08761	4e-06
59b	40488	40724	MKLLYLNYIQFIFVHVMHTLT EQFVKGIDNSIVQVLIMPFLYA NTYYTIDQLIDAYKKKMKRNH ERQDGTADAGKGYV (SEQ ID NO: 749)	78	hypothetical protein phiPV83p30 [Staphylococcus prophage phiPV83]	NP_061619.1	2e-32 (66/66)		**No putative conserved domains have been detected**		
60	40761	41006	VSDMLEIFLIGFGVYLFYRIAII FLKSKKTIHTNIYEMLMLATIF MISTIAYKHQKTHILIAFLVMF FMSKLKQVQGSYEE (SEQ ID NO: 750)	81	hypothetical protein SauraJK_03538 [Staphylococcus aureus subsp. aureus str. JKD6008]	ZP_03562520.1	1e-37 (80/81)		**No putative conserved domains have been detected**		
					ORF063 [Staphylococcus phage 52A]	YP_240665.1	5e-37 (79/81)				

FIG. 20T

61	41003	41209	MTQYLVTTFKDSTGQPHEHF TTARDNQTFTVVEAESKEEA ERKYEAQVKRGAVIKLGQLF ENIRECGK (SEQ ID NO: 751)	68	hypothetical protein SA1782 [Staphylococcus phage phiN315]	NP_835547.1	1e-32 (68/68)		Protein of unknown function (DUF1381)	pfam07129	1e-11
62	41206	41355	MIKQILRLLFLLAMYELGKYVT EQVYIMMTANDDVEAPSDYV FRAEVSE (SEQ ID NO: 752)	49	hypothetical protein SAS062 [Staphylococcus phage phiN315]	NP_835548.1	5e-20 (49/49)	transcriptional activator	Transcripti onal activator RinB	pfam06116	2e-15
63	41355	41555	MWITMTIVFAILLLVCISINSDH AREIQALRYMNDYLLDEVVKT KGYNGLEEYRIELKRINNDIK K (SEQ ID NO: 753)	66	hypothetical protein SA1781 [Staphylococcus phage phiN315]	NP_835549.1	2e-30 (66/66)		Protein of unknown function (DUF1514)	pfam07438	8e-22
64	41583	41999	MIKIEKHDIKKLEEYIQHIDNY RRELKMREYELLESHEPDNA GAGKSNLPGNPIERCAIKKFS DNRYNTLRNIVNGVDRLIDES DEDTLELLRFRYWDCPIGCY EWEDIAHYFGTSKTSILRRRN ALIDKLAKYIGYV (SEQ ID NO: 754)	138	hypothetical protein SA1780 [Staphylococcus phage phiN315]	NP_835550.1	2e-75 (138/138)	transcriptional regulator	**No putative conserved domains have been detected**		
					RinA family phage transcriptional regulator [Staphylococcus aureus subsp. aureus JH9]	YP_001247386.1	2e-75 (138/138)				

FIG. 20U

Phage	Titer (pfu/ml)	Phage sensitivity (%) of STA strains (n=100)					Total of infected strains (%)
		++++	+++	++	+	-	
F91a/06	$5x10^8$	0	42	29	14	15	85
	$5x10^7$	0	12	17	16	55	45
	$5x10^5$	0	2	0	0	98	2
	$5x10^3$	0	0	1	1	98	2

FIG. 21

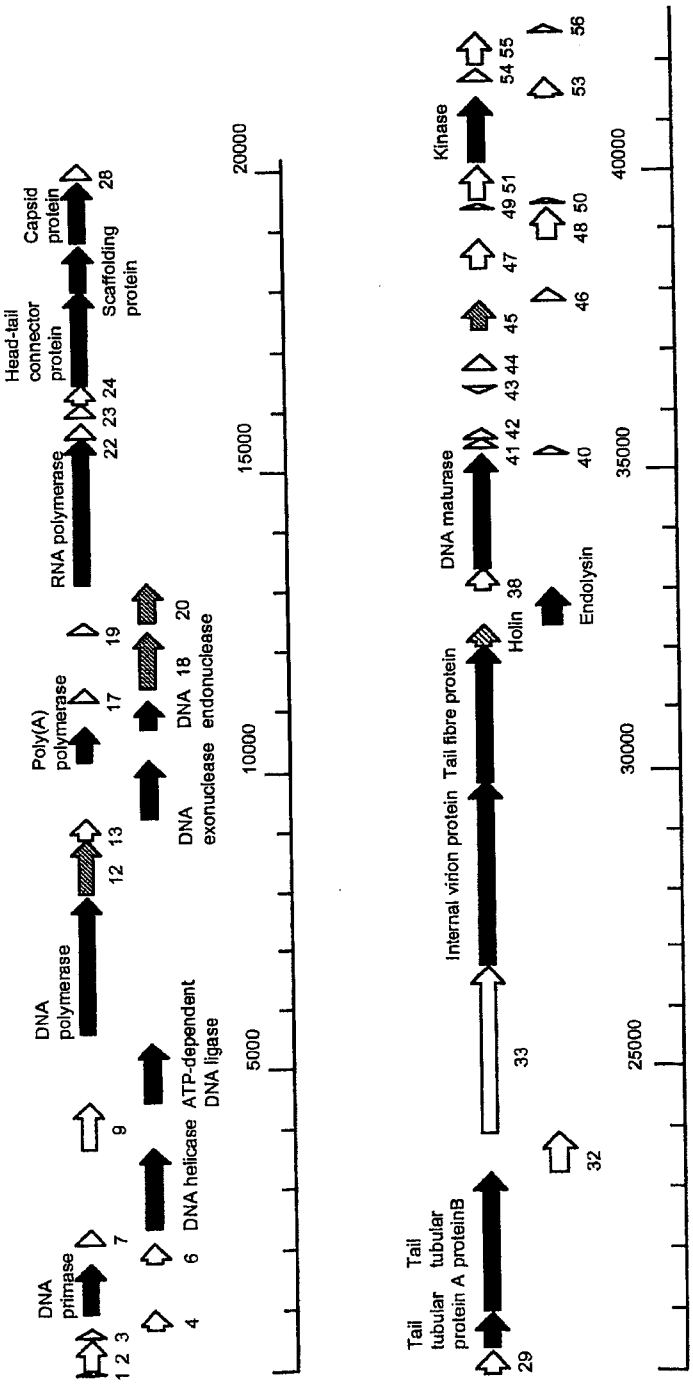

DNA primase
DNA helicase
ATP-dependent DNA ligase
DNA polymerase
DNA exonuclease
DNA endonuclease
Poly(A) polymerase
RNA polymerase
Head-tail connector protein
Scaffolding protein
Capsid protein
Tail tubular protein A
Tail tubular proteinB
Internal virion protein
Tail fibre protein
Hollin
Endolysin
DNA maturase
Kinase
5000
10000
15000
20000
25000
30000
35000
40000

FIG. 22

orf	Start position	Stop position	Aminoacidic sequence	Size (aa)	Homologous/similar proteins				Conserved Domains		
					Name[organism]	Acc No	E value and identity	Predicted function	Name	Acc No	E value
1	<1	85	GFDVTIEPIAQDKYFLVDSKQ IREYRG (SEQ ID NO: 761)	27	**No significant similarity found**						
2	87	584	MFLKLFIAIYTEQHLNAAKNE LERLGYKCTSDFHSALDQPV THITTYPNGTYTIWTLDLDMC RRLARANTTVRVINLRQLRG VHRRLRTSFSQDNHSKLEIV PVRSVNIFPELEKLSPLETEA MQAAIKWSSPKVPTPNVFFK LWYNTAISWTKAIVNRLVRH FK (SEQ ID NO: 762)	165	**No significant similarity found**				**No putative conserved domains have been detected**		
3	594	767	VSKIKMNEYRGKPPYSMDDL AEDPQLERRYIQRERRNHVK ERDLDRRNKRQAKRNGY (SEQ ID NO: 763)	57	**No significant similarity found**				**No putative conserved domains have been detected**		
4	724	1035	LIDVTNAKPSETGIRIPVRIKIK SVKHYCKVVQCLKDYGVQV PAELADELNLRRNKEYCKRA WWWGTNDVAWVFGSYKIV KFAKVMTRKEYVTWRQSTA LNG (SEQ ID NO: 764)	103	**No significant similarity found**						
5	1005	1823	VATIHSSEWLDQAKKVPVGQ KRRVYHGAEMTPAMDVWN NEDSWSCYCHRCHAGGKV YKQFLQRVNPEQPVYRKYL NTKDLITIDELYSTDKLKYKRL MKLLHDKGMSMITIAALKPM YNKVDDRLVFRFKGVDIGRD CTGLHGAKWLVYHSDNPSG YVYLQGKNPYCTREPVILCE DLFSAQKVRYYTGWSSLFL MGTNFKDETAHFLMSRLPVI ATDGDAAGWAARKVIRTRC	272	putative DNA primase [Pseudomonas phage LKA1]	YP_001522861 .1	4e-21 (80/264)	DNA primase	TOPRIM_primas es	cd0102 9	6e-04

FIG. 23A

			EMFNIPVQSVDVPVGLDPKD M (SEQ ID NO: 765)								
6	1816	2130	MGSKYNRIKFRVSRRSEWLL GIQHAENNGFPVGPDHEWKI ERYRGGKALINVRLDYNDTG LNPESWYSTPIGTALWVDTL GDFKHAVNCFCHDGYLDVD NLKVV (SEQ ID NO: 766)	104	**No significant similarity found**				**No putative conserved domains have been detected**		
7	2132	2383	MAIIRIPIRTEAEANQFISIVKS QGLALPDLDVVHRLGLATAR VGSDACVWTGIEQYIGTRHD FPHSDETVTVNQLYKRLQER (SEQ ID NO: 767)	83	**No significant similarity found**				**No putative conserved domains have been detected**		
8	2383	3690	MSDLNLLRVMMERKQFTGS FKSIPMDLYDPHTVTMLGWF KLYYKSYEDHERIDVDTLGS LIKLKTKPHEDKAKRDAQTAL MNEMLRNLKQPLPLDIRATT LNALEERRLSAEAAMICRKY DEGEEIDVIFELNKLAIATKQ RVELQTHAAWCDTDVWELI QADADDAGYVFDFLPEEFYT NIKGVNEGNNIGVAAPTDKG KTSFLVRVAVSFAKQRFKRM QNDDSMKFRPVLYLVNEGT AEVITPRVYQTALEIN (SEQ ID NO: 768)	435	putative DNA helicase [Pseudomonas phage LKA1]	YP_001522864 .1	4e-62 (132/408)	DNA helicase	DnaB helicase C terminal domain	cd0098 4	0.003

FIG. 23B

9	3687	4469	MKFKRGDIVKAVMTGGCYSI TSGQMYEVLDVRAGGNINIK PSRGPCNWSKSHRFELVRS KEDTVGVQPTMNIKLYDTVV RTTISHHLKIGEKYTVTTLYP QSNHIAVEGFPNMRFSAADF IVVPDLEDRPKSLGFDKVCA ALKDGTPLQYFFNEKWVDV VRPDSISIGMINKSIWRYAINT IDYYGQEIPAPIKQYPSTGLV YGISLTKHEVYKCNVNKRLG QLHYKTAEDAHAVLTTILAPF GITPKALDFSLT (SEQ ID NO: 769)	260	**No significant similarity found**				**No putative conserved domains have been detected**		
10	4466	5458	MSLREQVRKYLDVTKSPVQL VKHMDEVLEKNIKYPLIAQHK YDGVYVLVAVTDGIPTLYSR TGKECFEGLYNTDFVMSLN GITDGIYIGELCNSKFSLEVF NGLVSTNRKKSWEDSESQD TIQLLEEHTFIMFHDYIFHNCL LEGHCKLPYWARYDLLRKRL RVAELLDYLVVSDEVKSRED ADAYAQLIIDVGGEGAVFKH PAEEWVAGHKGYRTMKIVR DLVLDLLCVGVEYGKGKREG QIAKLKFSYKGSVF (SEQ ID NO: 770)	330	ATP-dependent DNA ligase-like protein [Erwinia amylovora phage Era103]	YP_001039660 .1	1e-42 (120/320)	ATP-dependent DNA ligase	ATP dependent DNA ligase domain	pfam01 068	7e-05
11	5632	7956	MSQINWLVLDFEVQNHDHY GSLASPHHPDNYLVATGWS EDGNSVQAEYHHSKDEQYC KRFADALSRAKNLVAHNLTF ELHWLMKVYPNDLQAFINRG GRFFCTQYAEYILSNQIEMY PNLEDTARKYGGSPKVDAV KLLWEQGVLTADIDQALLMT YLAADGKNEWSNPEDPSFQ GDVANTRRACFAQVAELRK RGMMGMFKERMDSLLFNA WATYNGLYVDLPTAQRNQA EQEKQIAQIKSDILGMLPNDL	774	putative DNA polymerase [Pseudomonas phage LKA1]	YP_001522870 .1	0,0 (383/809)	DNA polymerase	DNA polymerase family A	pfam00 476	3e-21

FIG. 23C

			PDD (SEQ ID NO: 771)								
12	8010	8912	MTFNALELVQGIDTSTLADM TDTTTGGGSKRGLLPAGFAF AVFSSYIEYGKQPQMFDGKK KDPALEFRLGFHIVGGVGTN LAGEDEDYVQDGFLPTISTW DTAQSRNEKSKAVKYFNAINI VPKGTHFIQKLGTMYLVEVK VTKNKKTGKDQNEFDFTSLQ QARDQATRKAYTSYTNAAGI EVAMGELKPEDYKVFLWNR PTNVTIEQYQAMWDSIEIKG ETEIKDAAGNVTGKRSKNFL QEKCQRALDFEGSSL (SEQ ID NO: 772)	300	hypothetical protein PPLKA1_gp31 [Pseudomonas phage LKA1]	YP_001522872 .1	2e-27 (91/251)		hypothetical protein	PHA020 30	4e-30
13	8915	9262	MEDTNRATGRTTRMILKAVE YLIKHPKKTVRIVCYNNYGCV WMADYIKSIVSDRLWQRIEL ATYQHWQCSGIGKRDDYFF DHHCFYHEVYNLNNRLKEVK AQLERAEKDYRKYDA (SEQ ID NO: 773)	115	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 23D

14	9252	10223	MMPNLSHFGLDAQTLSDQS TFKPSKGDSNILLYDGDGGC YQSAAGAAKQETAMRRFER DILENMFLAGCTKARVHLTP SGCFKNGRHLLLGAKKYQD NRSNKNKPQHLEYLRSPASV EYFKDHEDIEIILNYRVEADD ALMMDHYRYHNGILVSPDKD LNISPFKSYKAELGKHLVLPE GDRYGWIDREFWLTPSQKP SSKMIGKGTKFFLAQLLMGD TADNVKGILKLNGKLCGESA AFDALNPITDEHEAVNF (SEQ ID NO: 774)	323	putative DNA exonuclease [Pseudomonas phage LKA1]	YP_001522873 .1	8e-56 (136/319)	DNA exonuclea se	5'-3' exonuclease	cd0000 8	4e-04
15	10213	10782	MNYNETLKRAEFAVQILNAA GYDAHIVGGALRVQALGGTT NDIDIAVITTFKEGELLNKDVN ILLDRLGFNFKLQHQNSDYT DDSDLFIADWCSGDINLIAYN RSVTPTVRDLVNTFDLSINM FYKENGVLKNDVWLQGVCA VVLNPNRLGHNPKLNERIAR FKQEYDHLDWSPVDKQLAIE EHMNAIL (SEQ ID NO: 775)	189	poly(A) polymerase [Pseudomonas aeruginosa PAO1]	NP_253415.1	0,001 (28/81)	Poly(A) polymeras e	tRNA nucleotidyltransfe rase/poly(A) polymerase	COG06 17	8e-05
16	10769	11218	MPSSRPLQRISRQQLKGIMIA LYQRQGNKCAICGKPIDFSIT GHKANYAVDHNHETGEIRGT LHKSCNSAEGKVTNAAGRW GCKSTDYNDVIPWLESLINYL KTAHRNGTGMMYPDHKTPE QQKDAANLKRRKQYAAKKA AERMNASRK (SEQ ID NO: 776)	149	putative DNA endonuclease [Pseudomonas phage LKA1]	YP_001522874 .1	2e-32 (64/110)	DNA endo-nuclease	Endonuclease_7	pfam02 945	2e-10
17	11202	11420	MQVGSKVVCVYAGDSTLIET HGTYEVLGFSSYDGPNSHV EIGLDGRLLGSYSPKRFMTV EEVTKQTQENLND (SEQ ID NO: 777)	72	**No significant similarity found**						

FIG. 23E

18	11413	12342	MTKKHHALKGIKLDIMKLWW DGKSYQQIAEVVCKPYDTVY GIVQRYRDQQPPVQHTRKP TIFVIGDTQCKQGIDLAYLHY VGNYILEKRPDIIVHIGDHYD MASLSTYDKGQLSAEGRRV AEDIKAGDKGIEIIENYIARAK DYNPRKVVTLGNHEERIDRF VNHNPEFEGLIGTDKLAFAN YGWEVYPFLTPANICGINFV HFVQNGMTGKPLGGTVMTR LKNVGESFVMGHQQVLDHC LRYLPLSGKAQIGVI (SEQ ID NO: 778)	309	hypothetical protein PPLUZ24_gp44 [Pseudomonas phage LUZ24]	YP_001671917 .1	6e-43 (96/245)			**No putative conserved domains have been detected**		
19	12339	12515	MIIDGTKLRCINDKGQRIVKE GSLYTAWVRDGIGIDGRIFIK EHKRFALLITRFEVVE (SEQ ID NO: 779)	58	**No significant similarity found**					**No putative conserved domains have been detected**		
20	12512	13165	MKIGLIGLAGAGKDTSAVILQ RVLAEQGLKFEIDRYAAPLK NAAKEVFGANFDERNVKEV DVFVDQDTMIEASFRCLRQL GFTDDEDEKASELFFEHIGFL EYLSPRLYQQLLGTEVVRAV RPSAWVDRIRRLNRNIIIPDA RFENEVSDCNLLITRFQNIDK PKHPSEHLAWDLQFTGKVLP VDTININNEQGTTLELLEERIR SVVSLINFNEVV (SEQ ID NO: 780)	217	hypothetical protein Bpse38_32660 [Burkholderia thailandensis MSMB43]	ZP_02468156. 1	2e-06 (64/203)			**No putative conserved domains have been detected**		
21	13170	15599	MSLYQRQLELEEKYSTMSLV AGQQQILDAFKQGRASDVG SGRILLAKAFAASLEDVKALL DKKITGIGGKYKKLLTLASPD VLVMAVLREVVNGCASPEPV TMQQFLRSVGRIIESESMLA CMDKVSPEYTSRTVQYLDS AGTKSIQHRYRTFLKGAENIN LHWDQWSSEERTGTAKLILG VIYESTGLFKWKTNPHSASD SMYYLVPSEELEKHFGEVQA	809	putative RNA polymerase [Pseudomonas phage LKA1]	YP_001522878 .1	1e-102 (271/835)	RNA polymeras e	T3/T7-like RNA polymerase	PHA004 52	3e-142

FIG. 23F

			AARAVVKYPPMLIPPMDWQ GYNEGGYITDWFRMH (SEQ ID NO: 781)								
22	15609	15872	MLLLIITILVVVLAVVIYKSEKE TVRECFGILVEGVTLAKAKS DILKVAKVWFYTLKLTGELIL VPFLTIALILFIIAGATYRAIIK (SEQ ID NO: 782)	87	**No significant similarity found**				**No putative conserved domains have been detected**		
23	15979	16173	MSVDKIPNFTEDQIYWLDSIF PENTQLTTNPNEVYVKLGQR QVIQRIKQDTARKRNAYNRA NGG (SEQ ID NO: 783)	64	**No significant similarity found**				**No putative conserved domains have been detected**		
24	16175	16483	MGLGSFLKKSIKNSFRGGSL YKLSDKGDNMLRDVFGLNA FKDLAAGQDAQIRAMAEQN KLNTANEIQNVVQFEDDVNT GGSSDQRRRKNSAGAYARA LNLNV (SEQ ID NO: 784)	102	**No significant similarity found**				**No putative conserved domains have been detected**		
25	16494	18059	MAGVPELHYSLSSLFHQYRD DGLLDRIETYALWTIPSVFPR DEHTFYNANKNRTIEYDYQSI GALLVNRLASKLARSLFPAN TSFFRIDSDDPRLQQIFKARK LDSVIEYENAACARLFYNAS YAQLVQALRLLIITGECLLYR VNDSMRVYSLKDYVVKRNN VGEVLDIVICEHKFMEELDPA MKVKVGVVPADTTVKLYTRV QRQLINGITSWKVTQEINGR DVGTNMVYRDKLCPYIPVV WNFVNGDSYGRG (SEQ ID NO: 785)	521	putative head-tail connector protein [Pseudomonas phage LKA1]	YP_001522882 .1	4e-81 (179/480)	head-tail connector protein	**No putative conserved domains have been detected**		

FIG. 23G

26	18072	18815	MSVENLPEGHPAREAAQPT PSVTPAVTPAPTTQPEPQVV YQNIPTYDTDSITDTAVNVFA TSAGIEASRFDAALVNALNY GDEKLIDYTALTQGLKPDQA AQAKALAASVFKDRVAREQA HIQASTQKVYAVAGSAEAWK EASDAFNVSAPDHLKAIVRQ MLDNGDVENAAKFVIETARG TGMVNNGTPPIQGGTGAVQ QGLTQEQYYAELAKLERSAG NRSFESGQVGAEFQRLRNA RILGRKQGL (SEQ ID NO: 786)	247	putative scaffolding protein [Pseudomonas phage LKD16]	YP_001522823 .1	4e-05 (51/178)	scaffolding protein	scaffolding protein	PHA019 29	3e-08
27	18857	19879	MAQGTIYQPNTTRDHWGGA NSDVDQHLEDYTGIVDSRFQ YTQIFGALSAQRSVADRSNT VRVDRFNTSKVKGRKAGEAI ESQRVTSDKLNVIVECMMYI RNPIDWMDDWTAPDRLVEM SRNNGTEFAIAYDEAHIIRLQ KARSWVAPDHLKPAFSDGM FVPATLKLTTAGVADLEANA SALVVAHGKIVEALIKRRVPL TDMVTLVTPTVFTELVNHPK LINKDYVESNGDFADRRVVR VNGINVVECTTFPTAP (SEQ ID NO: 787)	340	capsid protein [Pseudomonas phage LKA1]	YP_001522884 .1	4e-53 (123/324)	capsid protein	capsid protein	PHA020 04	2e-62
28	19930	20178	MPQLCEAIISPALTGQALEVG DRAFEQGNTPAANDRVATL EGQVQALLALLQGQQAAGA PVAPVEVVAEEVKAPAKKAT AEK (SEQ ID NO: 788)	82	**No significant similarity found**						
29	20180	20545	MQLDPIDYKDFYRNAGLTEL EETITDLINTLDLKVHSTEAIV HDTTVNTDCNVLVNGRHVV YTDGTGNAPPTAGLYLLEQT YITTEVDQEAIAQTATRYSTG LFYTRIRRSGVWTSWNKVG	121	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 23H

30	20646	21203	MKLLDAVNAALSYMGEHKIT RVEGSNHPTVDSIVSAINRQ RAALLSTGWWFNELHLTIPV ETDGRIQTPARSLAIYGKSTR VSMEGEHLFNLDTGSVYFTE PVDVRIVRDIDFEDLPEYAAQ YSLYVATAEVYSAELGVDNV VSVLDGLAKDAIANLRQENL RNRRYNPRRNAVRQSRYTW FRNR (SEQ ID NO: 789)	185	tail tubular protein A [Pseudomonas phage LUZ19]	YP_001671978 .1	1e-13 (50/148)	tail tubular protein A	tail tubular protein A	PHA004 28	1e-19
31	21212	23506	MAVREGTYKSLIQGVSQQIP QERSDGQLGSQWNMLSDP VTGLRRRAGVKLHARLTNLS SSSYIRMVDILGVYYFMCIDT STGTMKIYTYDGVLKKTYTS EYLKAVSKASIRSTVSRSSC YVVNTDKVPQKVVGATSSTF NPAHGGYFSIRAGAFSKQYT ITVKWGTVTKEFSIMSDGGS ADQVTPAALAQRLWALVGT DPQVTAVFDVVNDGPTVALK AKAGQNPAQLSIETGDSSTYI MVSNASRVASRNDLLG (SEQ ID NO: 790)	764	putative tail tubular protein B [Pseudomonas phage LKA1]	YP_001522886 .1	7e-87 (238/792)	tail tubular protein B	**No putative conserved domains have been detected**		
32	23506	24186	MAGNFTAGVNTGMQGAQL GANFGPQGAVIGGIAGFALG FQTPDYEKIAREKYNSEVLK NFAKSLFDTRKVQNIENMRT AQALAAYQDNLRVQGSSYN AQYGAADMIGSSTTALKQAM DFQTQEAKRGVLINWETQV DNMNTSIDAMANQSMAGLR RTKGDTRQMDYAGLVKTGL DLYGQYRNTFNNPNTSTTQL GINKIPDNMSDFGSYGKSGS MGGFGGSGSLFG (SEQ ID NO: 791)	226	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 23I

33	24201	27068	MPTMVQSPDLITPTISREQAI DRPVEQDGLSTFLQDVLPKV KEGYDQYQKENQDHYIALG MNDELNQITRDVSWLDSRN YEQGKEFQKVSSTQEAQKK AFTDTVTRMAREGKNADEIF DAGREYLTAYTNSVYNSQLS PDLKNALYEAGIKENTIYQKLI TKTMSAVAEEREQFDAQTR VAGLYQTVSTGLDDQEINDA LEAHVRKAYAAKIAVGVDPK EAMNAAQNEISATFKFWNG QIDPSSPNASEQVNNLR (SEQ ID NO: 792)	955	**No significant similarity found**				**No putative conserved domains have been detected**		
34	27084	30212	MASKYGVGKDIRTLEAVQPD IPENIGTGKGKKLIGTLAADS YKPLGRANTADLLVPEQQLQ DAKAREEASLLETVTAAVAP TARDWGNAIYESYKFTPDVF YRPDADAQEFFNEYQITNQD EVAYINAANSYEDMEFRKRR ILDRRDDQQKIADNPITGIVA SMFDIDAAAMLVPAVGEVAG AAKFGRIAQRTANASIGAGG AYAINSALEDKSTRTQTERD LDSLTFGLVGFMSPIKYKPKE LDAAITKEMADV (SEQ ID NO: 793)	1042	putative internal virion protein [Pseudomonas phage LKA1]	YP_001522889 .1	1e-16 (125/511)	internal virion protein	gp37 virion protein	PHA020 06	3e-17
35	30214	32505	MAINQKQSYSEYDVSTPQG DFAIGFEDYNEGEKDRINVT VDGDDAASKGYTVLRKNALT IAMTPFVPSGIVRLTRETNID TTFYKFTAGAIFDAANVDANF TQVLHSQQEVRDRQSYVEG RVLPLVTGLEDALAKADEAS KAAQEAAEAAAEAAQQTRS ADKVIDASGLTQQDINNRLAI TYPTAVGLVGKPNLKDADVV YVQSYSNIFDGGDGYYRVSA DTTTVADGAYVIRINPNLIAT MLNTTGSVDVARFG (SEQ	763	putative tail fiber protein [Pseudomonas phage PT5]	YP_002117764 .1	0,066 (36/122)	tail fiber protein	**No putative conserved domains have been detected**		

FIG. 23J

			ID NO: 794)								
36	32515	32880	MNIVDQIYFGLVYVWSSLDK LIMGAAATAFVVALLRTRKR DGKASWIEATLCGIFATIALV GFSFIAPILVGILAGMGITINLP VDPSAGIAGIVAGFIGWYGT ERTIEFVEDNLGGDKNG (SEQ ID NO: 795)	121	**No significant similarity found**				holin*	**No putative conserved domains have been detected**
37	32873	33460	MGKFITLDEITSKAKEYGIET AALRAVMDVECKGHGFNSD GAPVILFERHKFYYGLQAIN WITKSKEWYKLYPDICNPSW GGYGKESQQHERLRRASAL NRDVALESASWGLGQVLGE NWKDLGYKSLQDFINAMYK DEVSQLDAMCRFIKHNGLIK HIQSKSWAKFARAYNGPKYA DNKYDTKLAAAYKKFGGI (SEQ ID NO: 796)	195	hypothetical protein RPRSA1_gp14 [Ralstonia phage phiRSA1]	YP_001165263.1	4e-38 (85/189)	endolysin	**No putative conserved domains have been detected**
					Putative phage-related protein (hydrolase) [Ralstonia solanacearum GMI 1000]	NP_520052.1	2e-37 (85/189)		**No putative conserved domains have been detected**
38	33460	33816	MAKRNSASVSLMNELHAAIA SYMLARLKASIPDPNAPVEY DEETGEEIPAFFIPLAASELQ VMVTFLNNNKITATPDVEHM AALANEFKGDLEAARKERAE SITKVNENDAFMASLLS (SEQ ID NO: 797)	118	**No significant similarity found**					**No putative conserved domains have been detected**

FIG. 23K

39	33825	35777	MGRVSRITEQTKRRLAMLLE RCNRYKDNPVAIPAEEREEL SMMFAATFKGFAEFAELGM KYLGFDLSEIQDDIAEYMQY GPAKKMVQAQRGQAKSTLA ALYCIWRLIQNPTARILIVSGG ERQASDVALLIRIIMQWGILC WMRPDTSKGDRTSASAFDI HYSLKGIDKSASVSCVGITAN LQGMRADFILADDIETQRNS MTQTEREKLLLLTKEFAAICIT GEIMYLGTPQTKDSVYRSLP ARGYDVRVWCG (SEQ ID NO: 798)	650	putative DNA maturase B [Pseudomonas phage LKA1]	YP_001522892 .1	7e-140 (270/623)	DNA maturase B	**No putative conserved domains have been detected**
40	35774	35872	MSPEEIRRRLDTITERIANAV MIVNLIKEKSK (SEQ ID NO: 799)	32	**No significant similarity found**				
41	35869	36027	MSTKREVVVQAVDNAVSVA KAVNANAEYKHKDKVTKGLE LAGNVLQLLKLFK (SEQ ID NO: 800)	52	**No significant similarity found**				
42	36038	36193	MDGFESTVKVGVKHTQYEE LRDLKQRGETFDDVIRRLLD AHKSLKSIGLLD (SEQ ID NO: 801)	51	**No significant similarity found**				**No putative conserved domains have been detected**
43	36916	36788	LYSSLSSIYSITLIVISIYIYIVIS YCSLFMFFILYSYTCSIQ (SEQ ID NO: 802)		**No significant similarity found**				
44	37209	37427	MKTLTHHIAVQCTCGATGQT GDFLVDIEHFKLTGELIALDG MVFRSLTALYAYANTYGLPT KRLNTPIVYQS (SEQ ID NO: 803)	72	**No significant similarity found**				**No putative conserved domains have been detected**

FIG. 23L

45	37868	38386	MKLLLNVQEINKAIESIANRG KKLDHDIHVAGVSVLKHVAE HGDTTLLDKLVNAMPKGARK GAFCEWALAFGNVRMLDRS NEADKLAIEQGRLFAKDKTK EYNEVEAMAKAWYDFKPEP DLLTTFDAAQAVKSLLKKYKT ALDNGAEIKGGDVAMQQLK SFMQTLNTMDEQV (SEQ ID NO: 804)	172	hypothetical protein PPLKD16_gp03 [Pseudomonas phage LKD16]	YP_001522792 .1	8e-17 (55/144)	PHA01782 hypothetical protein	PHA0 1782	8e-25
46	38383	38586	MKVKVRNKFAAATSINYKGH YVVRNGNGTLTLGAEHITEE QAAVLNLQEFSKVREWLGP SYSVEIIV (SEQ ID NO: 805)	67	**No significant similarity found**			**No putative conserved domains have been detected**		
47	38912	39406	MVTDMTDTKDQGYDLGDEN LLSVAKLAMRRGEYLLSAWD QFAAMDIVDGLNRIPSADGLI VYLKHGLCTNIRFEISPMANH RLRGSQALDSLLELAYPQW DGYSGNSTYPVDGYYEYEG YTEDGEHDAGMYHEPNLFR NPKRKELLTWLVTSFLPEYIK HWSAE (SEQ ID NO: 806)	164	**No significant similarity found**			**No putative conserved domains have been detected**		
48	39406	39915	MLIVPKVNPNVTVTLNIGLGE SIAWGKYKKENAEHGPVQSL VDILDTPHRVARILERIQGMA YNPNQHHHGPHVAHNSYGI DYGHHVLPNVNWRTVQVGN EMTLVVKFEAVARDIIGQVFY LAEELKQDCIAVWIHNDTNG GIGQLIGRYNYVWSGGYFNP EYFVHLEV (SEQ ID NO: 807)	169	**No significant similarity found**			**No putative conserved domains have been detected**		
49	39917	40021	MFKEYNYCGQCRVNYINCH CPTHYPERNKDDHHL (SEQ ID NO: 809)	34	**No significant similarity found**					
50	40018	40101	MKKLGLIVVYTAAYAAISLVQ WLQDDK (SEQ ID NO: 810)	27	**No significant similarity found**			**No putative conserved domains have been detected**		

FIG. 23M

51	40101	40670	MFVLKSTHQKALDEIKSLRA QLDAAAKTKRELQERIDSVR KVRDTVIKYNACLTALCQYLP EGVYRIDYGAERRSCSTLRK TSVVSYSTSVTVDHKAAKMT NRNYTIQHEPLARTCKQAEL TARLVALEVQYNIINRDIVVLD QTIKLAQALYDVPTVCHSVT KRSVLSKQRKRIKHELDLVK VELNNL (SEQ ID NO: 811)	189	**No significant similarity found**				**No putative conserved domains have been detected**		
52	40720	41838	MKYYDNSHPELQGYKQFIPE NPNQWFDLMSANRAVFIRE DKRVDADVWDMIVQHLTGV SYKPHRYGEGKRHYTEFQLL QGHRKLGEGYCSRVYTHPT NPERVVKFFERYHEDVCCY EYLRMCVQGKLPVFDWLPE VHSLACIKVLIREDDKVRIITY GVAVFPRYDPIESDYEKQNR FVQDGINAEFKKYVHPYLPH ARIDLHWGNIMWDRRLNQY VATDPVINSAPVETHVQTID WFPKEISAKYSGATACSRP (SEQ ID NO: 812)	372	*protein kinase* [Enterobacteria phage T7]	YP_041959.1	0,16 (47/174)	kinase	protein kinase	PHA0 0451	0,002
53	41822	42127	MVVYGNVIFERDLAQTMYKR MSSRLADGVRRCCMVDEHT LYFESEVSDRLSRKKFNNILT GQRIAPYSEIKYPKVGEHTL MSDQAIAEAKAILSSETRTRS (SEQ ID NO: 813)	101	**No significant similarity found**				**No putative conserved domains have been detected**		
54	42105	42308	VKHVHVVEVIMWILIMSIVVG SYRGVSATTQEFTSKERCM VAAQMALDKKMGGGDNSN RLTAICVPK (SEQ ID NO: 814)	67	**No significant similarity found**				**No putative conserved domains have been detected**		

FIG. 23N

55	42382	42912	MSLAKQFNAAGIRGSKPKSD KGWTFKAQKAYVRNRFENV ERVIAPVYNHKVEQVARAIIV ETPLASLNVVAQGSSLHYDY SPDTLVRIGKLTRKGATFSA DSNSALAILGLNGAAVLYWL GGLRINIDEQQYEVITNDGEY IYATVGIILQLARDCVFNRDA VLANFQGAKRVRAK (SEQ ID NO: 815)	176	No significant similarity found		No putative conserved domains have been detected
56	42896	43015	VSAPNNIFHKGMRVIVTKAD RDDVRLGLHGDTIATVVGVH (SEQ ID NO: 816)	39	No significant similarity found		

FIG. 23O

Spot test	Phage	Titer (pfu/ml)	633/05	638/05	644/05	645/05	649/05	648/05	650/05	651/05	664/05	665/05	930/05	1194/05	1195/05	1270/05	1305/05	1327/05	1357/05	1362/05	1387/05
	F1245/05	$1,4x10^{10}$	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	++++	+++	+++	+++	+++	+++
		$1,4x10^{8}$	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++
		$1,4x10^{6}$	+++	+++	++	++	+++	++	+++	++	++	++	+++	++	+++	+++	+++	++	+++	+++	+++
		$1,4x10^{4}$	+	+	+	+	+	+	+	+	++	+	+	+	+	++	+	+	-	+	+

FIG. 24A

1433/05	1614/05	1515/05	1517/06	1632/06	2023/05	2025/05	2083/05	2197/05	2159/05	2160/05	130/06	149/06	441/06	858/06	681/06	887/06	986/06	398/05	609/05	611/05	852/05
+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	-	+++	+++	+++	+++	-	-	-	-	-
+++	+++	+++	+++	+++	+++	+++	+++	+++*	+++	+++	+++	-	+++	+++	+++	+++	-	-	-	-	-
+++	++	+++	+++	+++	+++	+++	-	-	++	+++	+++	-	+++	+++	+++	+++	-	-	-	-	-
+	-	+	+	++	+	+	-	-	-	+	-	-	+	++	+	+	-	-	-	-	-

FIG. 24B

ACB strains (n=100)

653/05	1079/05	2041/05	77/06	78/06	129/06	211/06	212/06	309/06	318/06	319/06	382/06	415/06	416/06	454/06	492/06	493/06	620/06	659/06	682/06	683/06	725/06	728/06
-	-	-	+++	+++	+++	+	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	-	+++	+++	+++	+++	+++
-	-	-	+++	+++	+++	-	+++	+++	++	+++	+++	+++	+++	+++	+++	+++	-	+++	+++	+++	+++	+++
-	-	-	++	+++	+++	-	+++	+++	+	+++	+++	+++	+++	++	+++	+++	-	+++	+++	+++	+++	+++
-	-	-	-	++	++	-	+	+	-	-	+	+	+	-	+	+++	-	++	-	+	+	+

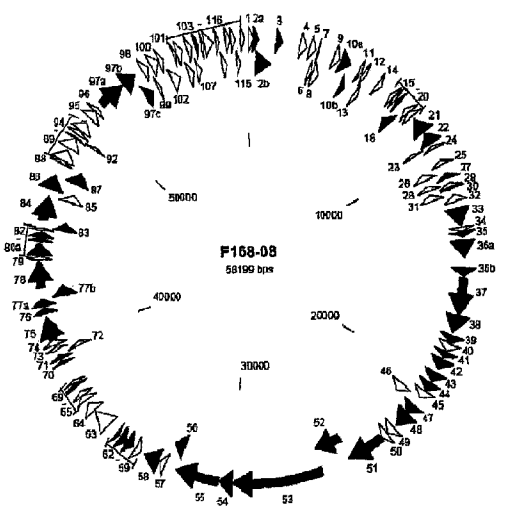
FIG. 24C

770/06	806/08	831/06	854/06	855/06	874/06	875/06	909/08	910/06	916/06	950/06	976/06	1016/06	1046/06	1056/06	1210/06	1190/05	1193/05	1268/05	1512/05	1701/05	2084/05	1371/05
+++	-	+++	++++	+++	+++	+++	-	+++	-	-	+++	++++	-	+++	+++	+++	+++	+++	+++	+++	-	-
+++	-	+++	+++	+++	+++	+++	-	+++	-	-	+++	++++	-	+++	+++	+++	+++	+++	+++	+++	-	-
++	-	+++	+++	+++	+++	+++	-	+++	-	-	+++	+++	-	+++	+++	+	++	+++	+++	++	-	-
-	-	++	++	+	+	+	-	+	-	-	+	++	-	+	+			++	+	+	-	-

FIG. 24D

1083/06	1127/05	892/08	538/05	1367/05	471/06	893/06	702/08	924/06	925/06	1006/06	1008/08	1215/06	Infected strains (%)
+++	+++	-	-	-	+++	+++	-	-	+++	+++	-	+++	77
+++	+++	-	-	-	++	+++	-	-	-	+++	-	+++	75
+++	+++	-	-	-	-	+++	-	-	-	+++	-	++	72
+	+	-	-	-	-	+	-	-	-	+	-	-	59

FIG. 24E



orf	Putative function
2a-2b	RNA ligase
3	regulation of murein tase-2 export
18	endodeoxyribonuclease
22	endonuclease
27	ribonucleoside-diphosphate reductase class Ib glutaredoxin subunit
33	terminase small subunit
35	holin
36a-36b	terminase large subunit
37	portal protein
38	virion morphogenesis
39	ribonuclease phage related protein
41	major head protein
42	major capsid protein
43	major tail protein
48	major tail protein
51	tail length tape measure protein
52	minor capsid protein

orf	Putative function
53	tail component
54	phage minor structural protein
55	minor structural protein
56	host interaction protein
58	CHAP endolysin
61	endonuclease
67	tRNA-Trp
68	tRNA-Ser
75	DNA primase
76	DNA binding protein
77a-77b	DNA replication
78	DNA helicase
80a-80b	C5 methylase
83	endonuclease
86	crossover junction endodeoxyribonuclease
87	nucleoside/nucleotide kinase
97a-97c	DNA polymerase I