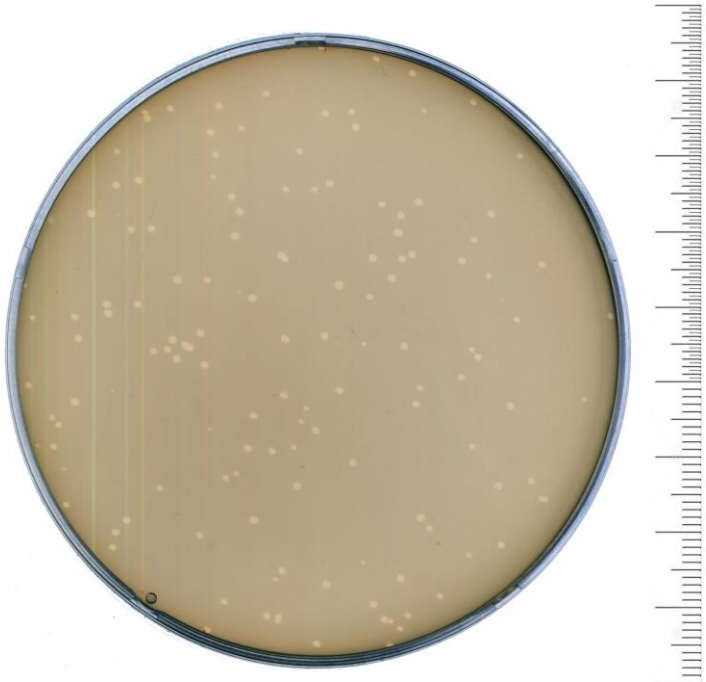
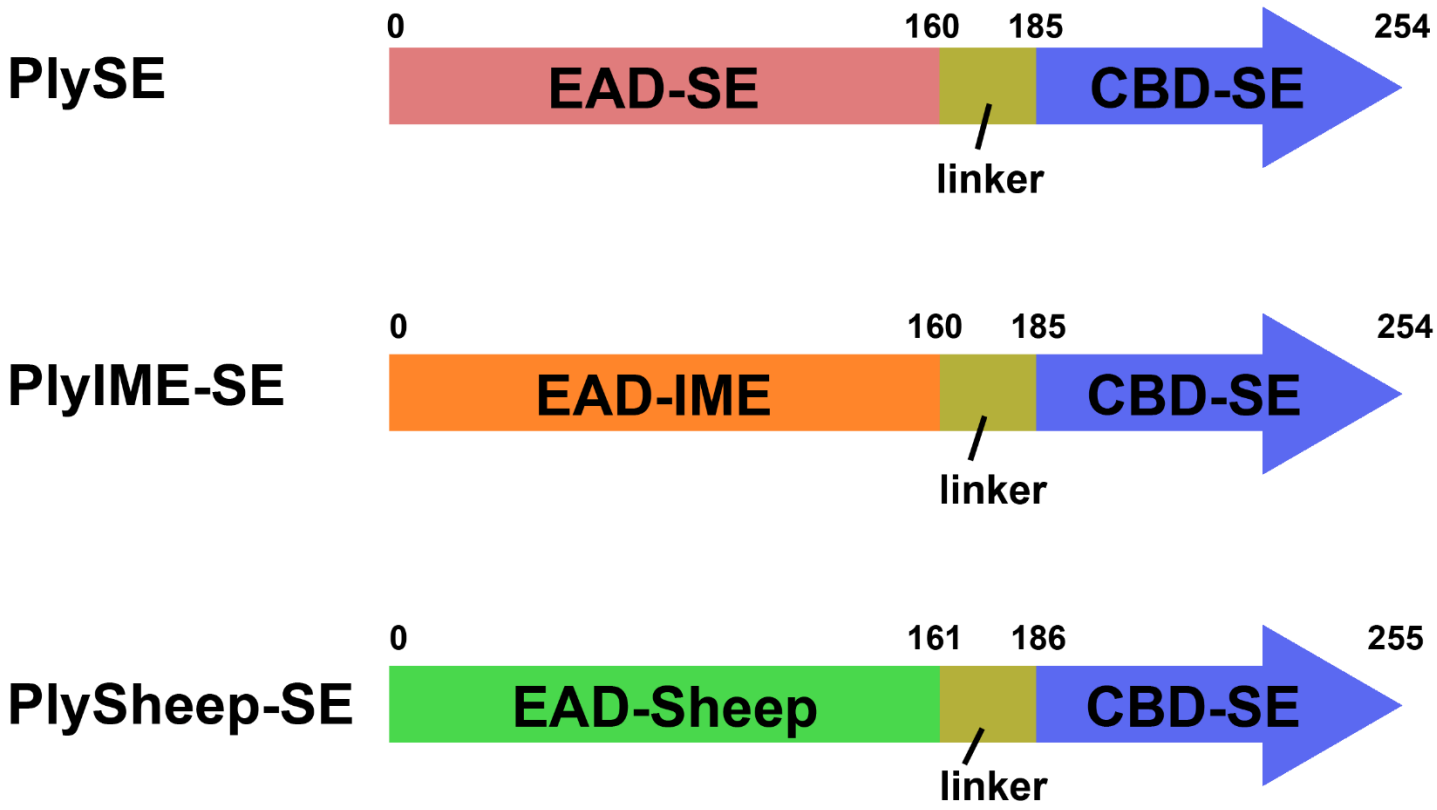
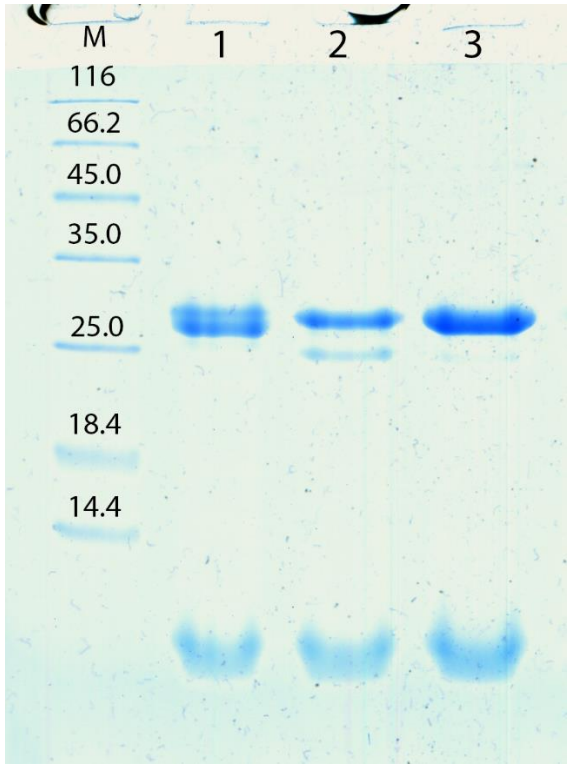
# Supplementary Information:



**Supplementary figure S1.** The morphology of negative colonies of vB_EfS_SE-phage *Enterococcus hirae* VKPM B-12152 lawn.




**Supplementary Figure S2.** The scheme of chimeric endolysins.




**Supplementary Figure S3.** SDS-PAGE assay of purified endolysins fractions PlySE (track 1, 28.4 kDa); PlyIME-SE (track 2 ,28.4 kDa); and PlySheep-SE (track 3, 28.7 kDa).

**Supplementary Table S1.** Annotation of Enterococcus phage vB_EfS_SE genome

| ORF# | Start codon | Stop codon | Strand | Blast results | | Conserved domains, Blast | | Hhpred results | Annotation |
|---|---|---|---|---|---|---|---|---|---|
| | | | | Name | E-val | Name, (region) | E-val | (Prob./E-val) | |
| 1 | 1 | 597 | + | terminase small subunit [Enterococcus phage VD13] | 2e-137 | Terminase_2 - Terminase small subunit; (34-150) | 1.84e-11 | Terminase small subunit; DNA-binding protein, DNA pakaging, Bacillus phage SF6 / 2.2e-15 | Terminase small subunit |
| 2 | 612 | 989 | + | hypothetical protein X878_0012 [Enterococcus phage VD13] | 9e-52 | - | - | DUF 2951; Protein of unknown function / 0.51 | hp |
| 3 | 1008 | 1256 | + | holin [Enterococcus phage VD13] | 2e-41 | - | - | Phage_holin_5_1; Bacteriophage A118-like holin, Hol118 / 8.7e-19 | Holin |
| 4 | 1319 | 2122 | + | terminase large subunit [Enterococcus phage BC611] | 0.0 | Terminase_3, Phage terminase large subunit; (29-226) | 1.65e-67 | Large subunit terminase; large terminase, VIRAL PROTEIN; 2.2A Deep-sea thermophilic phage D6E / 4.7e-28 | Terminase large subunit |
| 5 | 2253 | 2855 | + | homing endonuclease [Enterococcus phage VD13] | 2e-126 | grpIintron_endo group I intron endonuclease, (3-190) | 4.48e-25 | SegE_GIY-YIG; Putative endonuclease segE, GIY-YIG domain / 3.2e-12 | Homing endonuclease |
| 6 | 2836 | 2943 | + | - | - | - | - | DUF2996; Protein of unknown function / 43 | hp |
| 7 | 3140 | 3529 | + | Terminase large subunit [Enterococcus phage VD13] | 6e-88 | Terminase_3C, Terminase RNAseH like domain, (8-110) | 6.81e-18 | Terminase_3C; Terminase RNAseH like domain / 1.5e-14 | Terminase_3C or Terminase large subunit |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 8 | 3588 | 5123 | + | portal protein [Streptococcus phage SP-QS1] | 0.0 | Phage_prot_Gp6, Phage portal protein, SPP1 Gp6-like, (40-456) | 2.07e-81 | Portal protein; Bacteriophage, SPP1, Portal Protein, Head completion proteins, Connector Complex, DNA Channel, VIRAL PRO / 1.1e-37 | Portal protein |
| 9 | 5135 | 5890 | + | head morphogenesis [Enterococcus phage BC611] | 3e-163 | - | - | COG2369; Uncharacterized conserved protein, contains phage Mu gpF-like domain [Function unknown] / 1.5e-18 | hp |
| 10 | 6001 | 6669 | + | head scaffolding protein [Enterococcus phage vB_EfaS_IME198] | 9e-152 | DUF4355, Domain of unknown function, (60-171) | 3.34e-06 | Scaffold protein; major capsid protein, HK97-like fold, scaffolding protein, procapsid, VIRUS; 3.72A [Staphylococcus phage] / 4.4e-16 | head scaffolding protein |
| 11 | 6718 | 7524 | + | major head protein [Enterococcus phage vB_EfaS_IME198] | 0.0 | major capsid protein, N4-gp56 family, (6-132) | 9.34e-15 | major capsid protein; acne, bacteriophage, HK97-like, VIRUS; 3.7A {Propionibacterium phage PA6} / 8.4e-25 | major head protein |
| 12 | 7679 | 8116 | + | major tail protein [Streptococcus phage SP-QS1] | 3e-92 | Uncharacterized conserved protein YjdB, contains Ig-like domain, (61-144) | 6.75e-08 | b.1.2.1 (A:8-124) Rim binding protein 2 {Human (Homo sapiens) [TaxId: 9606]} \| CLASS: All beta proteins, FOLD: Immunoglo / 20.93 | hp |
| 13 | 8177 | 8581 | + | hypothetical protein EnPhBC-611_gp49 [Enterococcus phage BC611] | 3e-95 | - | - | Head completion protein gp15; Bacteriophage, SPP1, Portal Protein, Head completion proteins, Connector Complex, DNA Chan / 9e-15 | hp |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 14 | 8597 | 9874 | + | hypothetical protein EnPhBC-611_gp48 [Enterococcus phage BC611] | 4e-80 | - | - | b.1.2.1 (R:2-100) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens) [TaxId: 9606]} \| CLASS: All beta proteins, FO / 270 | hp |
| 15 | 8959 | 9339 | + | hypothetical protein BN19_012 [Streptococcus phage SP-QS1] | 8e-75 | - | - | COG5005; Mu-like prophage protein gpG [Mobilome: prophages, transposons]. / 4.6e-15 | hp |
| 16 | 9352 | 9786 | + | tail terminator [Streptococcus phage SP-QS1] | 4e-102 | DUF3168 Protein of unknown function, (30-106) | 1.87e-05 | Tail terminator protein Rcc01690; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus} / 1.8e-17 | Tail terminator protein |
| 17 | 9807 | 10499 | + | major tail protein [Enterococcus phage IMEEF1] | 5e-166 | Phage_tail_2, Phage tail tube protein, (9-135)// Big_2, Bacterial Ig-like domain (group 2), (154-215) | 6.07e-26 //4.11e-08 | Tail tube protein; Tail tube, siphoviridae, helical, VIRAL PROTEIN; 5.4A {Escherichia phage lambda} / 7e-15 | Tail tube protein |
| 18 | 10639 | 11079 | + | hypothetical protein AVT94_gp38 [Enterococcus phage vB_EfaS_IME198] | 3e-100 | - | - | DUF5055; Domain of unknown function / 5.7e-14 | hp |
| 19 | 11018 | 11314 | + | hypothetical protein BN19_016 [Streptococcus phage SP-QS1] | 2e-45 | - | - | Phage_TAC_6; Phage tail assembly chaperone protein, TAC / 49.02 | hp |
| 20 | 11327 | 14212 | + | tail length tape measure protein [Enterococcus phage BC611] | 0.0 | tape_meas_TP901, phage tail tape measure protein, | 4.56e-58 | Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; | tail length tape measure protein |

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|---|---|---|---|---|---|---|---|---|---|
| | | | | | | TP901 family, core region; (97-432) | | 3.7A {Staphylococcus virus 80alph} / 3.3e-15 | |
| 21 | 14226 | 18218 | + | tail protein [Enterococcus phage IMEEF1] | 0.0 | - | - | Tail component; bacteriophage infection, Lactobacillus casei / 3.9e-23 | Putative tail protein |
| 22 | 18231 | 20681 | + | virion structural protein [Enterococcus phage IMEEF1] | 0.0 | put_anti_recept, phage minor structural protein, N-terminal region; (31-359) | 6.24e-13 | PblB; Phage-related protein [Mobilome: prophages, transposons] / 2.1e-23 | virion structural protein |
| 23 | 20629 | 20982 | + | hypothetical protein X878_0032 [Enterococcus phage VD13] | 1e-61 | - | - | DUF2977; Protein of unknown function / 0.0051 | hp |
| 24 | 21031 | 21744 | + | endolysin [Enterococcus phage VD13] | 2e-158 | CHAP domain, (20-110) | 2.61e-06 | Lysin; Lysin, HYDROLASE; 1.75A {Enterococcus phage IMEEF1}/1.2e-28 | endolysin |
| 25 | 22194 | 21793 | - | hypothetical protein AVT94_gp45 [Enterococcus phage vB_EfaS_IME198] | 5e-20 | - | - | a.24.30.1 (A:504-592) CRISPR-Cas type III-B interference complex protein Cmr2, D2 {Pyrococcus furiosus [TaxId: 2261]} \|/ 30.33 | hp |
| 26 | 22655 | 22227 | - | hypothetical protein AVT94_gp46 [Enterococcus phage vB_EfaS_IME198] | 3e-93 | - | - | 60 kDa polyprotein; VIRAL PROTEIN; 1.9286A {African swine fever virus / 29.33 | hp |
| 27 | 22881 | 22657 | - | NUMOD4 domain-containing protein [Clostridium perfringens] | 1e-06 | IENR1, Intron encoded nuclease repeat motif, (32-66) | 1.87e-03 | HNH homing endonuclease; HNH catalytic motif, Helix-turn-helix DNA binding domain, protein-DNA complex, DNA binding protein / 0.012 | HNH homing endonuclease |

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|---|---|---|---|---|---|---|---|---|---|
| 28 | 23101 | 22973 | - | - | - | - | - | COG3803; Uncharacterized conserved protein, DUF924 family [Function unknown]. / 22.15 | hp |
| 29 | 23450 | 23325 | - | - | - | - | - | DUF1764; Eukaryotic protein of unknown function (DUF1764) / 18 | hp |
| 30 | 23380 | 24204 | + | hypothetical protein AVT94_gp47 [Enterococcus phage vB_EfaS_IME198] | 0.0 | - | - | gp32 single stranded DNA binding protein; Zn2+ binding subdomain, 5-stranded beta-sheet, OB fold / 0.0000011 | hp |
| 31 | 24694 | 25080 | + | hypothetical protein AVT94_gp49 [Enterococcus phage vB_EfaS_IME198] | 7e-90 | - | - | Minimized B-domain of Protein A Z34C; IgG1 fc, protein A, fc complex, b-domain, IMMUNE SYSTEM; HET: BMA, MAN, GAL, FUL,/ 33 | hp |
| 32 | 25080 | 25280 | + | hypothetical protein AVT94_gp50 [Enterococcus phage vB_EfaS_IME198] | 3e-40 | - | - | b.34.20.1 (A:7-71) Uncharacterized protein YorP {Bacillus subtilis [TaxId: 1423]} \| CLASS: All beta proteins, FOLD: SH3- / 1.4 | hp |
| 33 | 25678 | 25562 | - | - | - | - | - | Ly49 ; Ly49-like protein, N-terminal region / 7.7 | hp |
| 34 | 25779 | 25904 | + | hypothetical protein BN19_031 [Streptococcus phage SP-QS1] | 3e-17 | - | - | Transmembrane protein, putative; Electron transport chain, supercomplex, membrane protein, Tetrahymena thermophila, ELEC / 17 | hp |
| 35 | 26183 | 26016 | - | - | - | - | - | Eco57I; Eco57I restriction-modification methylase / 73 | hp |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 36 | 26388 | 26287 | - | - | - | - | - | DUF3565; Protein of unknown function (DUF3565) /17 | hp |
| 37 | 26486 | 26659 | + | - | - | - | - | Interleukin-6; CYTOKINE, INTERLEUKIN, SIGNALING, GP-130, TRANSCRIPTION; NMR {Mus musculus} SCOP: a.26.1.0/ 34 | hp |
| 38 | 26729 | 26929 | + | - | - | - | - | Beta-lactamase; colibactin peptidase, S12 peptidase, HYDROLASE, HYDROLASE-INHIBITOR complex; HET: 2PE, Z9A, Z9G, 97N, AV / 10 | hp |
| 39 | 26942 | 27088 | + | host RecBCD nuclease inhibitor [Enterococcus phage IMEEF1] | 2e-23 | PHA00442, host recBCD nuclease inhibitor (13-47) | 9.85e-04 | DUF6388; Family of unknown function / 11 | hp |
| 40 | 27069 | 27233 | + | hypothetical protein FDH83_gp78 [Enterococcus phage IMEEF1] | 7e-19 | - | - | PrgA; Protease domain, CAP domain, CELL ADHESION; HET: EPE; 1.5A {Enterococcus faecalis} / 0.48 | hp |
| 41 | 27328 | 27465 | + | hypothetical protein AVT94_gp53 [Enterococcus phage vB_EfaS_IME198] | 8e-22 | - | - | hypothetical protein yoaG; Alpha/Beta protein, homodimer, OCSP, NESG, PROTEIN STRUCTURE INITIATIVE, structural genomics, / 0.14 | hp |
| 42 | 27465 | 27719 | + | hypothetical protein FDH83_gp77 [Enterococcus phage IMEEF1] | 9e-55 | - | - | APC1_3rd; APC1 beta sandwich domain / 95 | hp |
| 43 | 27716 | 27874 | + | hypothetical protein X878_0045 [Enterococcus phage VD13] | 4e-24 | - | - | DUF6489; Family of unknown function / 4.1 | hp |
| 44 | 27874 | 28062 | + | hypothetical protein AVT94_gp55 [Enterococcus phage vB_EfaS_IME198] | 8e-37 | - | - | DUF4926; Domain of unknown function / 42 | hp |

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|---|---|---|---|---|---|---|---|---|---|
| 45 | 28074 | 29018 | + | DNA primase [Enterococcus phage BC611] | 0.0 | TOPRIM_primases, nucleotidyl transferase/hydrolase domain (204-287) | 1.99e-11 | DnaG; DNA primase (bacterial type) / 6e-32 | DNA primase |
| 46 | 29093 | 29446 | + | transcriptional regulator [Enterococcus phage IMEEF1] | 2e-77 | - | - | Putative uncharacterized protein; DNA BINDING PROTEIN; NMR {Hyperthermus butylicus} / 3.6e-8 | hp |
| 47 | 29495 | 30271 | + | DnaC-like helicase loader [Enterococcus phage BC611] | 0.0 | DnaC, DNA replication protein DnaC, (97-256) | 1.09e-09 | Primosomal protein DnaI; primase, helicase loader, DnaB, DnaG, DnaI, DNA replication, REPLICATION; HET: MSE; 6.1A / 2.8e-20 | DnaC-like helicase loader |
| 48 | 30858 | 32201 | + | Replicative DNA helicase [Enterococcus phage IMEEF1] | 0.0 | DnaB, Replicative DNA helicase | 3.52e-10 | DnaB-like replicative helicase; phage, complex, helicase, REPLICATION-DNA-RNA complex; HET: AGS;{Escherichia phage T4} / 3.6e-39 | Replicative DNA helicase |
| 49 | 32214 | 32966 | + | DNA methyltransferase [Streptococcus phage SP-QS1] | 0.0 | Cyt_C5_DNA_methylase, Cytosine-C5 specific DNA methylases, (59-149) | 1.65e-05 | C-5 cytosine-specific DNA methylase [Transcription] / 2.6e-18 | DNA methyltransferase |
| 50 | 32932 | 33156 | + | hypothetical protein EnPhBC-611_gp73 [Enterococcus phage BC611] | 5e-44 | - | - | VPS38; Vacuolar protein sorting 38 / 26 | hp |

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|---|---|---|---|---|---|---|---|---|---|
| 51 | 33229 | 33669 | + | HNH endonuclease [Streptococcus phage SP-QS1] | 1e-102 | HNH endonuclease (60-103) | 8.46e-07 | HNH homing endonuclease; HNH catalytic motif, Helix-turn-helix DNA binding domain / 3.2e-20 | HNH homing endonuclease |
| 52 | 33662 | 34690 | + | CRISPR/Cas system associated [Enterococcus phage vB_EfaS_IME198] | 0.0 | - | - | Uncharacterized protein; Cas4, CRISPR, MCSG, Exonuclease, PSI-Biology, STRUCTURAL GENOMICS, UNKNOWN FUNCTION / 8.1e-13 | Putative CRISPR/Cas system associated |
| 53 | 34690 | 35019 | + | hypothetical protein X878_0053 [Enterococcus phage VD13] | 8e-70 | - | - | TRANSCRIPTION INITIATION FACTOR IIE SUBUNIT ALPHA, TFA1; TRANSCRIPTION, PRE-INITIATION COMPLEX, RNA POLYMERASE / 7 | hp |
| 54 | 35142 | 35005 | - | - | - | - | - | WWamide peptide / 24 | hp |
| 55 | 35285 | 35590 | + | crossover junction endodeoxyribonuclease RuvC [Enterococcus phage IMEEF1] | 2e-64 | Crossover junction endodeoxyribonuclease RuvC, (11-66) | 2.94e-11 | RuvC; Holliday junction resolvasome RuvABC endonuclease subunit / 2.6e-9 | RuvC-like Holliday junction resolvase |
| 56 | 35587 | 36156 | + | AAA domain protein [Enterococcus phage VD13] | 1e-98 | AAA_18, AAA domain, (7-141) | 1.46e-03 | Phosphomevalonate kinase; parallel beta-sheet with the strand order 23145, Walker A motif / 1.3e-15 | monophosphate kinase |
| 57 | 36149 | 36781 | + | hypothetical protein EnPhBC-611_gp20 [Enterococcus phage BC611] | 8e-104 | - | - | RNA polymerase sigma-H factor; Sigma factor, / 1.5e-16 | hp |
| 58 | 36879 | 37442 | + | glycosyltransferase | 8e-108 | - | - | Transcriptional regulatory protein RcsB; Response | hp |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | regulator Transcriptional factor / 0.23 | |
| 59 | 37442 | 37552 | + | - | - | - | - | Vpu protein / 3.3 | hp |
| 60 | 37568 | 37747 | + | hypothetical protein FDH83_gp59 [Enterococcus phage IMEEF1] | 9e-16 | - | - | fvmX3; FtsH ternary system domain X3 / 21 | hp |
| 61 | 37749 | 38018 | + | hypothetical protein BN19_054 [Streptococcus phage SP-QS1] | 0.001 | - | - | Putative salt-induced outer membrane protein YdiY / 12 | hp |
| 62 | 38032 | 38253 | + | hypothetical protein X878_0058 [Enterococcus phage VD13] | 4e-42 | - | - | TFA2 Winged helix domain 2 / 1.3 | hp |
| 63 | 38253 | 38462 | + | hypothetical protein AVT94_gp73 [Enterococcus phage vB_EfaS_IME198] | 6e-37 | - | - | Protein Cue2 hypothetical protein YKL090W / 48 | hp |
| 64 | 38465 | 38677 | + | hypothetical protein AVT94_gp74 [Enterococcus phage vB_EfaS_IME198] | 4e-39 | - | - | d.58.18.6 (A:105-187) Acetolactate synthase small subunit, IlvH / 0.4 | hp |
| 65 | 38678 | 39055 | + | hypothetical protein X878_0060 [Enterococcus phage VD13] | 2e-38 | - | - | Protein ymcA; ymcA, regulate community development, Structural Genomics, PSI-2, / 0.57 | hp |
| 66 | 39059 | 39244 | + | hypothetical protein EnPhBC-611_gp67 [Enterococcus phage BC611] | 5e-35 | - | - | DUF5495; Family of unknown function / 3.3 | hp |
| 67 | 39323 | 41854 | + | DNA polymerase [Enterococcus phage vB_EfaS_IME198] | 0.0 | PolA, DNA polymerase I - 3'-5' exonuclease and polymerase domains, (107-774) | 1.24e-86 | PolA; DNA polymerase I - 3'-5' exonuclease and polymerase domains / 4.4e-80 | DNA polymerase |
| 68 | 41930 | 42334 | + | hypothetical protein BN19_061 [Streptococcus phage SP-QS1] | 1e-19 | - | - | c.1.18.0 (A:) automated matches {Thermococcus kodakarensis [TaxId: 69014]} \| CLASS: | hp |

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|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Alpha and beta proteins (a/b) / 120 | |
| 69 | 42324 | 42554 | + | hypothetical protein FDH85_gp21 [Enterococcus phage SAP6] | 2e-11 | - | - | RNA polymerase II mediator complex subunit 20; beta barrel, channel / 47 | hp |
| 70 | 42547 | 43143 | + | ATP-dependent protease [Enterococcus phage vB_EfaS_IME198] | 2e-14 | - | - | AtpI2; FoF1-type ATP synthase assembly protein I / 7 | hp |
| 71 | 43199 | 43840 | + | Putative cytidine deaminase [Streptococcus phage SP-QS1] | 4e-118 | - | - | YorP protein / 0.059 | hp |
| 72 | 43852 | 44058 | + | hypothetical protein BN19_066 [Streptococcus phage SP-QS1] | 2e-36 | - | - | c.37.1.0 (A:316-647) automated matches {Escherichia coli [TaxId: 562]} \| CLASS: Alpha and beta proteins / 9.8 | hp |
| 73 | 44072 | 44485 | + | hypothetical protein BN19_067 [Streptococcus phage SP-QS1] | 5e-52 | - | - | mRNA interferase toxin HicA; toxin-antitoxin, TA, protein complex, DNA-binding / 26 | hp |
| 74 | 44563 | 44751 | + | hypothetical protein BN19_068 [Streptococcus phage SP-QS1] | 2e-31 | - | - | YtcA family / 11 | hp |
| 75 | 44751 | 45008 | + | hypothetical protein BN19_070 [Streptococcus phage SP-QS1] | 1e-51 | - | - | DNA-binding transcriptional regulator, XRE-family HTH domain / 1.8 | hp |
| 76 | 45008 | 45223 | + | hypothetical protein BN19_071 [Streptococcus phage SP-QS1] | 3e-39 | - | - | AAR2 C-terminal repeat region / 170 | hp |
| 77 | 45213 | 45404 | + | hypothetical protein X878_0073 [Enterococcus phage VD13] | 2e-36 | - | - | Cdh1_DBD_1; Chromodomain helicase DNA-binding domain 1 / 14 | hp |
| 78 | 45467 | 45715 | + | hypothetical protein FDH83_gp34 [Enterococcus phage IMEEF1] | 6e-49 | - | - | Bypass of Forespore C, N terminal /9.9 | hp |

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|---|---|---|---|---|---|---|---|---|---|
| 79 | 45708 | 45974 | + | hypothetical protein EnPhBC-611_gp11 [Enterococcus phage BC611] | 6e-58 | - | - | DarA_C ; Defence against restriction A C-terminal / 0.23 | hp |
| 80 | 45976 | 46281 | + | DNA binding protein [Enterococcus phage IMEEF1] | 4e-66 | NTP-PPase_u3, Nucleoside Triphosphate Pyrophosphohydrolase, (5-79) | 7.42e-28 | Hypothetical protein ypjD; Pyrophosphatase, YPJD / 1.8e-10 | Putative Pyrophosphatase |
| 81 | 46378 | 46875 | + | HNH endonuclease [Enterococcus phage vB_EfaS_IME198] | 4e-32 | HNH_3, HNH endonuclease, (57-99) | 5.28e-08 | HNH homing endonuclease; HNH catalytic motif, Helix-turn-helix DNA binding domain, protein-DNA complex / 5.8e-28 | HNH endonuclease |
| 82 | 47066 | 46932 | - | - | - | - | - | Csm1_B; Csm1 subunit domain B / 72 | hp |
| 83 | 47125 | 47262 | + | - | - | - | - | Sec61 protein translocation complex, beta subunit / 1.6 | hp |
| 84 | 47411 | 47527 | + | - | - | - | - | Domain of unknown function (DUF4795) / 6.7 | hp |
| 85 | 47631 | 47951 | + | hypothetical protein EnPhBC-611_gp09 [Enterococcus phage BC611] | 4e-67 | - | - | LydB; LydA-holin antagonis / 14 | hp |
| 86 | 47944 | 48048 | + | hypothetical protein EnPhBC-611_gp60 [Enterococcus phage BC611] | 4e-13 | - | - | Ins_allergen_rp ; Insect allergen related repeat, nitrile-specifier detoxification / 25 | hp |
| 87 | 48051 | 48437 | + | hypothetical protein FDH83_gp29 [Enterococcus phage IMEEF1] | 5e-87 | - | - | Designed dimeric coiled coil peptide with two terpyridine side chains; designed peptide, synthetic / 0.12 | hp |
| 88 | 48430 | 48801 | + | hypothetical protein FDH83_gp28 [Enterococcus phage IMEEF1] | 6e-77 | - | - | Rossmann 2x3 fold protein; Structural Genomics / 31 | hp |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 89 | 48879 | 49013 | + | hypothetical protein FDH83_gp27 [Enterococcus phage IMEEF1] | 9e-22 | - | - | COG5346; Uncharacterized membrane protein [Function unknown] / 14 | hp |
| 90 | 49042 | 49140 | + | - | - | - | - | LegK7; translocated effector, Ser/Thr protein kinase / 7.8 | hp |
| 91 | 49157 | 49309 | + | hypothetical protein BN19_083 [Streptococcus phage SP-QS1] | 3e-22 | - | - | Beta propeller; bladed beta propeller, unknown function / 3.6 | hp |
| 92 | 49445 | 49879 | + | hypothetical protein X878_0084 [Enterococcus phage VD13] | 3e-77 | - | - | Family of unknown function (DUF6120) / 140 | hp |
| 93 | 49866 | 50075 | + | hypothetical protein BN19_085 [Streptococcus phage SP-QS1] | 5e-41 | - | - | ACRIIC5Nch; Anti-CRISPR, CRISPR-Cas, Cas9, inhibition / 0.94 | hp |
| 94 | 50113 | 50235 | + | - | - | - | - | NqrC; Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrC / 13 | hp |
| 95 | 50331 | 50633 | + | hypothetical protein AVT94_gp11 [Enterococcus phage vB_EfaS_IME198] | 2e-58 | - | - | Cell division protein FtsB; bacterial cell division, peptidoglycan synthesis, membrane protein complex, MEMBRANE PROTEIN /3.5 | hp |
| 96 | 50898 | 50990 | + | - | - | - | - | DUF3660; Receptor serine/threonine kinase / 17 | hp |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 97 | 51115 | 50987 | - | hypothetical protein FDG77_gp88 [Enterococcus phage VD13] | 2e-09 | - | - | G0-G1_switch_2 ; G0/G1 switch protein 2 / 40 | hp |
| 98 | 51279 | 51112 | - | - | - | - | - | ND3; Complex-I, ELECTRON TRANSPORT; HET: PTY, CDL, PC7, 8Q1; 2.97A {Polytomella sp. Pringsheim 198.80} / 120 | hp |
| 99 | 51615 | 51394 | - | hypothetical protein FDH85_gp11 [Enterococcus phage SAP6] | 2e-09 | - | - | HTH-type transcriptional repressor phnF; PhnF, GntR, HutC, transcription, regulator, UTRA, DNA-bindin / 96 | hp |
| 100 | 51928 | 51749 | - | hypothetical protein X878_0087 [Enterococcus phage VD13] | 1e-32 | - | - | LsbB; Bacteriocin, antimicrobial peptide, receptor binding domain / 120 | hp |
| 101 | 52567 | 52076 | - | NUMOD4 motif family protein [Enterococcus phage VD13] | 2e-49 | HNH_3, HNH endonuclease, (54-98) | 2.85e-06 | HNH homing endonuclease; HNH catalytic motif, Helix-turn-helix DNA binding domain / 40e-30 | hp |
| 102 | 52852 | 52640 | - | hypothetical protein X878_0088 [Enterococcus phage VD13] | 4e-37 | - | - | Protein of unknown function (DUF3087) / 17 | hp |
| 103 | 53030 | 52854 | - | - | - | - | - | Putative Rab5-interacting protein / 4 | hp |
| 104 | 53898 | 53077 | - | hypothetical protein X878_0090 [Enterococcus phage VD13] | 3e-159 | Smc, Chromosome segregation ATPase, (4-167) | 3.75e-06 | Predicted coiled-coil protein [Function unknown] / 0.27 | hp |

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|---|---|---|---|---|---|---|---|---|---|
| 105 | 54731 | 53973 | - | HNH endonuclease [Bacillus mojavensis] | 6e-21 | HNH endonuclease, (137-180) | 2.07e-04 | HNH homing endonuclease n=1 Tax=Enterococcus phage EF-P29 TaxID=1932891 RepID=A0A1L7DQ76_9CAUD / 3/2e-142 | HNH homing endonuclease |
| 106 | 55008 | 55136 | + | - | - | - | - | Uncharacterized protein n=2 Tax=unclassified Saphexavirus / 4.6e-34 | hp |
| 107 | 55487 | 55182 | - | - | - | - | - | Uncharacterized protein n=1 Tax=Enterococcus phage vB_EfaS_Ef2.2 / 7.5e-64 | hp |
| 108 | 55855 | 55484 | - | ABC transporter [Enterococcus phage VD13] | 1e-18 | - | - | Uncharacterized protein n=1 Tax=Enterococcus phage vB_EfaS_IME198 / 3.4e-45 | Hp |
| 109 | 56115 | 55855 | - | thioredoxin domain [Enterococcus phage VD13] | 1e-53 | NrdH-redoxin (NrdH) family; (3-79) | 2.37e-17 | GLUTAREDOXIN-LIKE PROTEIN NRDH; ELECTRON TRANSPORT, NRDH, THIOREDOXIN / 2.7e-10 | thioredoxin domain |
| 110 | 56277 | 56128 | - | hypothetical protein X878_0006 [Enterococcus phage VD13] | 4e-21 | - | - | HalOD2; Halobacterial output domain 2 / 0.43 | hp |
| 111 | 56661 | 56281 | - | methyltransferase [Enterococcus phage SAP6] | 3e-49 | - | - | 6Z26_A Spindle assembly abnormal protein 6 homolog; centriole, centrosome, cartwheel, coiled coil, complex, alpha helical, / 0.0000011 4ZXQ_B Tail needle protein gp26; Viral protein, P22, Tail Needle, Membrane penetration; 2.75A {Enterobacteria phage P22} / 0.0000042 | hp |

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|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 6GAP_C Outer capsid protein sigma-1; cell attachment protein, reovirus sigma1, coiled coil, beta-spiral repeat, VIRAL PROTEIN / 98.65 | |
| 112 | 57053 | 56658 | - | hypothetical protein AVT94_gp21 [Enterococcus phage vB_EfaS_IME198] | 7e-58 | - | - | Protein of unknown function (DUF1642) / 2e-09 | hp |
| 113 | 57310 | 57053 | - | hypothetical protein X878_0009 [Enterococcus phage VD13] | 1e-48 | - | - | Putative ESAT-6-like protein 7; Structural Genomics / 4.4 | hp |
| 114 | 57624 | 57310 | - | hypothetical protein BN19_105 [Streptococcus phage SP-QS1] | 3e-62 | - | - | LXG domain of WXG superfamily / 3.5 | hp |
| 115 | 57664 | 57762 | + | - | - | - | - | Protein of unknown function (DUF565) / 25 | hp |

Supplementary table S2. Oligonucleotide primers used for cloning the PlySE, PlyIME-SE and PlySheep-SE endolysin genes.

| gene | vector | Oligonucleotide primer name | Oligonucleotide primer sequence (5'-3') |
|---|---|---|---|
| *plySE* | pBAD18 | Fd plySE | GCTCGGTACCCGGGGATCCTAAGGAGATATACATATGAATCACAAAGTGCATCATCATCA TCATCATATCGAAGGTAGGGGTACCATGGTTAAAGTAAACGATGTAG |
| | | Rv plySE | CTCATCCGCCAAAACAGCCATTATAACTTAACTTGTGGGTAAG |
| *plyIME-EF1-CHAP_lysSE-CBD* | pBAD18-PlySE | Fd plyIME-EF1 | CATATCGAAGGTAGGGGTACCATGGTTAAATTAAATGATGTACTAAGCTACGTGAATGGT |
| | | Rv plyIME-EF1_EAD | GCAAGTGGTTTAGGCGTTGATGCGGCTTCGTACGGTGG |
| | | Fd linker_CBD_plySE | TCAACGCCTAAACCACTT |
| *plyShip-CHAP_lysSE-CBD* | pBAD18-PlySE | Fd plyShip | CATATCGAAGGTAGGGGTACCATGGTCAAAAAGTCAGATGTTG |
| | | Rv plyShip_EAD | GCAAGTGGTTTAGGCGTTGACTCGAGCGCCTCATAATT |