



Article

Proteomic Characterisation of Virulence Factors and Related Proteins in *Enterococcus* Strains from Dairy and Fermented Food Products

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1. Supplemental Data 1

Table S1. Peptides corresponding to bacterial resistance to antibiotics and other toxic substances, identified in the *Enterococcus* strains analyzed.

Function	Protein	Sequence	Strain
Antibiotic resistance	TetR family transcriptional regulator	IETTSEMINQK	F1
	TetR family transcriptional regulator	EEVM*DAVIM*RVVEK	F15
	TetR family transcriptional regulator	DVLEVIYAVLNAETIK	F2
	N-acetyltransferase domain-containing protein	SLGYARQTVAKLTADLLAEGK	F7
	PadR domain-containing protein	DLMDGFYKGDE	F3
	GNAT family acetyltransferase	GLGRKM*LGDGMTK	F1
	GNAT family N-acetyltransferase	KAKEMNVSQIDLHVFAHNK	F3
	GNAT family acetyltransferase	QEVHDHEDVYKVYNQFAKENH GALQR	F13
	Cass2 domain-containing protein	TYKSDVEHYRK	F15
	MarR family transcriptional regulator	M*NEHDIGMLIKQLYDAKEK	F16
	MarR family transcriptional regulator	M*ENQM*NEQFMK	F5
	Penicillin-binding protein2B	M*NNAYELNTVFIK	F10
	Penicillin-binding protein t	EITENALGTITSAPGSVVK	F9
	Penicillin-binding protein	VDKDDSTYSFSYK	F3
	Daunorubicin resistance protein DrrC	DVSTRIPQGVMTVISGPAGSGK	F7
	OmpR/PhoB-type domain-containing protein	EVTKILSM*IDQKDHLIR	F7

	PASTA domain-containing protein	KETTPKQTAPEPASVNVSK	F9
	vanY D-Ala-D-Ala carboxypeptidase	LDKRVVGEYQK	F3
	vanY D-Ala-D-Ala carboxypeptidase	NGVSEEDAIAEVK	F1
	vanY D-Ala-D-Ala carboxypeptidase	IDNDFSVVTPK	F1
	vanY D-Ala-D-Ala carboxypeptidase	SVAAQQEVFSTNVNSLMSSEGLSEADAIK TK	F9
Additional resistances and tolerances	Cold shock-like protein CspD	GFGFITTEGGEDIFVHFSAIQGDGFK	F2
	Cold-shock protein (CspA)	TLEEGQSVSFDVEDSDRGPQAVNVEKN	F1
	General stress protein	LVNSDDVTSGINTEVGK	F1
	CsbD-like protein	EGFEDLKDKFSK	F15
	YitT family protein	MAPVLMVAVTGR	F2
	Tellurite resistance protein TelA	TQDDLIETIQETLR	F13
	MerR family transcriptional regulator	KLQFYTAKITAQQDSFGWTFEEAER	F5
	MerR family transcriptional regulator	IVQLQKALNPK	F15
	SugE protein	DKQSFVLLM*LTFGSSFLFLFLAM*K	F3
	Chaperone protein DnaK	AAVEANDIELMKEKR	F5
	Chaperone protein DnaK	DAEANAADKLR	F3

M* methionine oxidation; C* carbamidomethylation of Cys.

Table S2. Peptides corresponding to antibacterial compounds and proteins involved in antibacterial production, identified in the *Enterococcus* strains analyzed.

Function	Protein	Sequence	Strain
Antimicrobial compounds	Lantibiotic biosynthesis protein	VEDADVEDDC*LC*HGNYGNK	F13
	Type 2 lantipeptide synthetase LanM	FLSILDYPYYLMDQNHVELILEKNLSKK	F11
	LanM family lanthionine synthetase	YINDLKNQNSNK	F5
	Thiopeptide-type bacteriocin biosynthesis domain protein	DSTIKNLESIM*RSLLSNVEYTGYSR	F13
	Bacteriocin Protein	M*VEAAAQRGYIYKK	F2
	Radical SAM additional 4Fe4S-binding SPASM domain-containing protein	KVVFTGGEIGLTHDSLK	F1

M* methionine oxidation; C* carbamidomethylation of Cys.

Table S3. Peptides corresponding to bacterial toxicity, identified in the *Enterococcus* strains analyzed.

Function	Protein	Sequence	Strain
Toxin	Type II toxin-antitoxin system PemK/MazF family toxin	VNVPKQGDILLNNAAPR	F1
	Type II toxin-antitoxin system RelE/ParE family toxin	KDGTSEFEEFLNSIPEK	F3
	Addiction module toxin RelE O	ETEVNGM*LVAQRLK	F5

	Toxin-antitoxin system, antitoxin component, AbrB family	SRLQGNSVVVTLPADHGK	F13
	Toxin PIN	KVEKENFLDR	F14
	Exfoliative toxin A/B	KHFLKIPIPIC*GM*ILGLASLGNLFK	F15
	Prevent-host-death family antitoxin (Phd antitoxin)	STEATTEELKC*GNDHSDYR	F15
	LXG domain-containing protein	ISSGGKLTGDGLK	F5
	LXG domain-containing protein	SLESVSDDLDSVK	F13

M* methionine oxidation; C* carbamidomethylation of Cys.

Table S4. Peptides corresponding to proteins involved in host colonization and immune evasion, identified in the *Enterococcus* strains analyzed.

Function	Protein	Sequence	Strain
Colonization and immune evasion factors	Internalin	EVVEAKEEVDEPTTGVEGSKAEVK	F5
	Sortase	TVDDVTQSIHIQNDK	F5
	LPXTG cell wall anchor domain-containing protein	DAQNQLSNGAK	F3
	LPXTG cell wall anchor domain-containing protein	AEVGFYAPTNGESDKNDTVSNEGTISPNTNTQ GK	F3
	LPXTG cell wall anchor domain-containing protein	MVGM*LMLVLMIPTVC*HAQETETQTIR	F3
	LPXTG cell wall anchor domain-containing protein	LTSAYPAQRNARNVIK	F5
	LPXTG cell wall anchor domain-containing protein	TGETANIALSVLGSLMVLGSGIIFKK	F13
	LPXTG cell wall anchor domain-containing protein	IVTM*PIILTIPK	F14
	LPXTG cell wall anchor domain-containing protein	FTLPDKVTIGLEEKDAVYLIVETK	F15
	LPXTG cell wall anchor domain-containing protein	MHTEEIETANWAEIK	F1
	LPXTG cell wall anchor domain-containing protein	ENLLLD SKM*R	F2
	LPXTG cell wall anchor domain-containing protein	DPDENLAAGQTITIPKGNETLYAVWKK	F2
	LPXTG cell wall anchor domain-containing protein	NTNSKQSSDSKASFNHPSTFFNNNK	F13
	LPXTG cell wall anchor domain-containing protein	VELYTYDAQTK	F14

LPXTG cell wall anchor domain-containing protein	ETMEFLFEFLVDGC*KLAGKGLSFSEWLQAK	F16
Adhesin BspA	EM*FKEM*SNLTSLDVSSFDTSK	F3
Adhesin BspA	GASETLSATVSPVDATDK	F2
Adhesin BspA	TIPISMNGVVTPGTSSGK	F5
Adhesin BspA	ADYC*TAC*GALKEYAPNFVENGITNKEC*K	F9
Fibronectin/fibrinogen-binding protein	EKVFEILSM*TSEINGK	F15
Collagen-binding protein	GFKITLIGTYQSNM*TK	F16
Ig domain-containing protein	MNKTIATLTVGATETLSATVSPETATDKSVK	F2
DUF4097 domain-containing protein	GDLLIQQM*DAAM*LEITGTNNEIELRK	F1
Cell surface protein	LAASSEDNLNIEIAM*PK	F1
Flagellar hook-associated protein 2	NFDQVASLLGGEDGLAAK	F5
Fn3_like domain-containing protein	NDGEIAGKESVLVFRLLGGAVIQR	F15
Fimbrial isopeptide formation D2 domain-containing protein	NITATFNVKIGR	F3
Fimbrial isopeptide formation D2 domain-containing protein	KLADIPSIGDRSLIR	F5
Fimbrial isopeptide formation D2 domain-containing protein	VHVYPKNELPTNDVKFIK	F9
Fimbrial isopeptide formation D2 domain-containing protein	GFKNEANVDNGHTVVK	F1
SpaA domain-containing protein	TAGGDEDKAK	F16
Endopeptidase NlpC/P60 family protein	ALIDTLGSLPASQDPAPPEAR	F13
Endopeptidase NlpC/P60 family protein	ADLNRQKAEAEAEQAR	F1
M20/M25/M40 family peptidase	SLEDGKM*HAC*GHDAHTAM*LLTAAR	F11
M20 peptidase	VGESGLSVTIGKAGK	F15
Peptidase_M78	IIFGAGDSIKVLK	F2
Peptidase M28	LVTEVVARLDNEALAEIK	F2
Peptidase T	TIVEIIKENAKFQK	F2
DD-transpeptidase	IAGSALHNITNRGGLQGGLTQQLIK	F3
Peptidase	GISMNKQSSTPLGGLGRGSDK	F12
Dipeptidase PepV	GSSDDKGPTMAAAYYGLK	F13
Dipeptidase PepV	GSSDDKGPTM*AAYYGLK	F16
C-terminal processing peptidase	IQNENNLPATGALDDK	F5
Endopeptidase La	MDFKGVYVM*SVEK	F5
Peptidase_S8	M*SDSLNQYYFAFGM*GMVLYVLSHFVKKSR	F5
Dipeptidyl aminopeptidase	ILGGGMSPEDFLK	F5
Peptidase U32	SIHYVSTVSNVYKAAVDSYM*EDPENYVC*K	F15
Peptidase S74	QAGEQAQAAAEQASSDAQAAK	F13

Peptidase, M24 family	KVGLIGWKMFTAK	F13
Proline dipeptidase	FEALNGFLPGTDFSLDITPVIQK	F5
Oligoendopeptidase PepF/M3 family protein	LSTYKLHGITDFLQKPLEYNRLQK	F16
Peptidase C51	EGIAAILGNYSVESGINPK	F16
Peptidase_S9 domain-containing protein	ILGGGMSPEDFIK	F5
ImmA/IrrE family metallo-endopeptidase	LKSLM*AYPINALSERK	F15
ImmA/IrrE family metallo-endopeptidase	TEIVLELLRSNK	F13
Isoaspartyl dipeptidase	ETLDIDTVIAKGEIM*VQEK	F2
Isoaspartyl dipeptidase	GGTIDFTASEDPDFWEK	F3
Signal peptidase I	YIGYFISFMK	F7
Signal peptidase I	NVLLAILALFSLWFLFNIR	F5
Signal peptidase I	DSNDSLPEIQWIEK	F1
Immune inhibitor A	LDNPATGTPAATGPVK	F2
ClpA protease	TEVTVQLSKALGIELLR	F11
ClpC protease	M*GVNETSNASQGTGSRR	F5
Zinc protease	DPEINEANLNLLK	F15
Capsular polysaccharide biosynthesis protein CpsC	KRWLLILATTLAGFALAAGVTFFLITPK	F13
Capsular polysaccharide biosynthesis protein CpsC	MEEMVSLGEMFILLKKR	F16
N-acetylmuramoyl-L-alanine amidase	AFGDQKKVNLETK	F2
LysM domain protein	ILKVLAIGITVGGM*ALAIHTEK	F9
LysM domain protein	KKILVGALVALFFMPTAVLAAK	F13
Hemolysin III family channel protein	SKKFTHVIWHLFVILGALLM*FFAVYLY	F16
Autolysin modifier protein	M*NIGSGASVVANNNGTAR	F1
Mga domain-containing protein	YDGKIWLLNDNNKR	F5
Mga domain-containing protein	LLQM*NERLIFQYC*MLLRVIFIK	F9
Mga domain-containing protein	KYDLIITNVSKPNAYRSVK	F4
Mga domain-containing protein	AYPENEREIIISGILLSSQRAR	F9
Mga domain-containing protein	QVIDWSWELHYC*EKTVIQK	F1
Mga domain-containing protein	SEFSKEVNQLYSPLIQELR	F1
Mga domain-containing protein	MNFFSILDKNTQTQLTILENIYISK	F1
Mga domain-containing protein	KAVYPLENGIALATVSPK	F16
Mga domain-containing protein	FNIIIAFIDHLK	F13
Mga domain-containing protein	DIHPEHESIMLRAGKINLENISATLDEYR	F7
Mga domain-containing protein	QLIFPKTNSSFVEQLKQLR	F13
Toxin secretion/phage lysis holin	KVM*ILFVVAVSVK	F4

	Type VII secretion protein EssC	QIENSFDDVNKALRANIPAGMTGTR	F5
	Type VII secretion effector	IAQAVFLASSNLQSVAK	F11
	Type VII secretion protein EssC	DQVLNSLYQILK	F13
	LysR family transcriptional regulator	IAIGGGETQAFSFLAARLNELQQK	F15
	LytR_cpsA_psr domain-containing protein	LIIVFLVLLMGIVSAGTAYAIR	F3
	LytR_cpsA_psr domain-containing protein	IDFTLDGIHVAKGKQTLDEK	F13
	LytTR family transcriptional regulator	YQISRFAETQMAGINIIM*KNGLTDYVSR	F3
	HTH-type transcriptional regulator KdgR	FLNGRYGNM*SQETK	F1
	ArpU family transcriptional regulator	MLLFPKIDRK	F2
	Competence protein ComEA helix-hairpin-helix repeat region	LIEEQGKLTEELAKSIQK	F3
	Control of competence regulator ComK, YlbF/YmcA	ALQEAYSNVKANEEAHALFK	F5
	Regulatory protein YlbF	M*IAVIVNEELFQLEDQC*LRVAEM*IKK	F9
	Spore coat protein	MENVLC*C*DQIKC*LVGETVKVNL	F2
	Sporulation protein YjcZ	MGLGGNGGGEAGQAGK	F7
	Restriction endonuclease type IV, Mrr	NKSLYFERMQM*IDM*IR	F13
	SfiI restriction endonuclease	IVMGEVYVIPVYEYDDQAM*INNQVKFKSR	F12
	Type-2 restriction enzyme	VYANVEAM*KIELNINLSLIGSQNVEK	F9
	O-antigen ligase	MLVWQAIYLLVVFQIGK	F7
	Methyl-accepting chemotaxis protein (MCP) signalling domain	STESKLKSMAELPAM*K	F14
	N-acetylglucosamine-6-phosphate deacetylase	M*GATTPADILGEKKIGK	F1
	Glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC	FVQVVEAGEHTVQNM*LK	F9

M* methionine oxidation; C* carbamidomethylation of Cys.

Table S5. Peptides corresponding to transporters associated to virulence factors, identified in the *Enterococcus* strains analyzed.

Function	Protein	Sequence	Strain
ABC transporters	Copper ABC transporter permease	YANNNTLLMDGFTGIKYNISK	F2
	Copper ABC transporter permease	APTPM*QYLVIILLVSGEAIINTR	F11
	Ferrichrome transport ATP-binding protein PhuC	DTGEIYLDHNEVKAWKSNEKAK	F13

	Cobalt ABC transporter permease	TKISEWIAALK	F1
	Lantibiotic protection ABC transporter ATP-binding subunit	ERLGIGLALVGNPK	F13
	Multidrug ABC transporter ATP-binding protein	AGEITTANLRR	F3
	Multidrug ABC transporter ATP-binding protein	SNMQWIWR	F2
	Multidrug ABC transporter ATP-binding protein	DADKILYM*QDGDIK	F3
	Spermidine/putrescine ABC transporter-binding protein	EVMGLSLNSLGYSLSKNNQELR	F5
	Glycine betaine ABC transporter	EMQDELLELQAKVKK	F1
	Glycine betaine/L-proline ABC transporter ATP-binding protein	RPLIDFLDENVMVIGK	F5
	Peptide ABC transporter substrate-binding protein	AMRMADSQEDAK	F1
	Peptide ABC transporter peptide-binding protein	LDEVKTNVVK	F2
	Peptide ABC transporter substrate-binding protein	WKTLLQKADQLVAEEAPLVPLYQLTEAR	F5
	Peptide ABC transporter substrate-binding protein	TDGLSIGYLSFNVK	F7
	Peptide ABC transporter ATP-binding protein	M*KKVLLNVQGLK	F13
	His/Glu/Gln/Arg/opine family amino ABC transporter, permease, 3-TM region	IPDLIMNLKNNK	F1
	Amino acid ABC transporter amino acid-binding/permease	IM*VPSFVNQFVITLK	F1
	Amino acid ABC transporter amino acid-binding/permease	DTTIISAIGVVELLQTGK	F1
	Branched-chain amino acid ABC transporter substrate-binding protein	FTAGDKDYQAM*LTKVK	F2
	Amino acid ABC transporter ATP-binding protein	ALAMKPDVMLFDEPTSALDPEMVGEVLGVMQR	F5
	Amino acid ABC transporter ATP-binding protein	ASYTEKAVALAK	F15
	Amino acid ABC transporter substrate-binding protein	VGTSAEFAPFEFHTLIDGKDK	F16
	Excinuclease ABC subunit A	LALDNGAKHNPK	F2

Sulfate ABC transporter ATP-binding protein	LPTGNFIPNTDYQAM*YDDATREVKISGILR	F2
C4-dicarboxylate ABC transporter	DMETYFGQDENK	F4
Multiple sugar ABC transporter substrate-binding protein	AITVPLKSTGQAQMANFVVSNTSK	F5
Sugar ABC transporter permease	NTALFAFTVVPISLFLSLGIAWVIFEKVK	F7
Sugar ABC transporter	ALGDNMGVAAAYPTIDFGSGAKQMKAFLGVK	F9
Carbohydrate ABC transporter substrate-binding protein	DGGKTETITFINHKTDWETNGK	F14
Sugar ABC transporter permease	STIIIM*LIM*KVGSILTTGFDQIYLM*TNQLNR	F15
Sugar ABC transporter permease	VGYASAASMVLFFILLLLGLAQMKLGGGKND V	F16
ABC transporter domain-containing protein	M*RIEVD AISYAYDKNK	F1
ABC transporter-like protein	GRTTLVIAHRLSTIVDADK	F2
ABC transporter permease	RSALTM*FGIVIGIAAVIAILSIGRAFER	F2
ABC transporter permease	GKVATVISGVAVLALIAAATLGAGQSSAK	F2
ABC transporter domain-containing protein	M*GMFQRMSANDWQK	F2
ABC transporter domain-containing protein	NLSGGQRQRVALAR	F2
ABC transporter ATP-binding protein	IM*ALNSSISYM*LMR	F4
Basic membrane protein (BMP) family ABC transporter substrate-binding protein	GVGTAVQDIANR	F2
ABC transporter ATP-binding protein	KYVIDDLNLAIK	F2
ABC transporter domain-containing protein	FGKQEV LKGIDLDVGK	F1
ABC transporter substrate-binding protein	DM*AEALGIDPESIKEPA	F1
ABC transporter, ATP-binding protein	NNFLKDNYSLLEGNYPEK	F3
ABC transporter permease	TFPETFM*EYWPSLIIGLK	F3
ABC transporter, ATP-binding protein	EKAVNLNNINMEYTLKK	F3
ABC transporter ATP-binding protein	ALATEPSLLLLDEPFSALDVVTAK	F5
ABC transporter permease	NMSFKSFYFFTLIGMAILYGTM*WGGR	F5
ABC transporter domain-containing protein	MIIENINKDMDQRRVVLK	F5
ABC transporter permease	WDSFSTPEFVGIQNFSR	F5

	ABC transporter domain-containing protein	GNAEKFALSMTLAR	F5
	ABC transporter permease	TEENGQLEILKSLGIGAR	F5
	ABC transporter substrate-binding protein	EYNVDGQVTAVNRGEADFAANDFGM*SEERS K	F7
	ABC transporter ATP-binding/permease	SNM*QWIWGYIK	F7
	ABC transporter domain-containing protein	DLAIMIGQEIVK	F9
	ABC transporter permease	M*LFYENMLMGLLSLVIGIVIGSLLSKGFLK	F9
	ABC transporter domain-containing protein	ILMLAEGRTVAYDTPENLK	F9
	ABC transporter ATP-binding protein	GEIVLTGTVAELK	F10
	ABC transporter permease	NRLPNYRVSFDFTPAK	F11
	ABC transporter domain-containing protein	VVTVVFFENFTAELETAIK	F13
	ABC transporter substrate-binding protein	VVALLALSTLVGLGAC*GGNSAKSKTEDTK	F13
	Heme ABC transporter ATP-binding protein	KAATPKEVVLSIK	F10
	Thiol reductant ABC exporter subunit CydC	EM*IEKLDPDGLQTM*VDEAGLR	F14
	ABC transporter domain-containing protein	M*GM*FQRMSANDWQK	F14
	ABC transporter	IGLGATLLLALGGC*GTANSSSAKSDDSK	F14
	ABC transporter ATP-binding protein	SQQLTAFMVTHDMEDAIRYGNRLIM*LHQGK	F14
	ABC transporter permease	KM*VWLM*LLASLIM*PFM*AFLLFNYR	F15
	ABC transporter domain-containing protein	IQEVLLQIVSLTNTGKK	F15
	ABC transporter ATPase	GLRYALYGFIADVVLIMAITLPSGAPLR	F16
	ABC transporter domain-containing protein	MVSMVMAQVVGIDTGSNEPMLK	F16
Other transporters	Major facilitator superfamily (MFS) transporter	LILGIFLFILGFLIGC*LLK	F2
	Major facilitator superfamily (MFS) transporter	SKKSDSNNSLVK	F7
	Major facilitator superfamily (MFS) transporter	KVM*NESQDAIALKEITQ	F15
	Multidrug resistance MFS transporter	ENLGLAGSLNSFAR	F2

	Cation diffusion facilitator family transporter	KTKGSTAVIAALFANLLVAVSK	F4
	EamA/RhaT family transporter	FIIAFVVLYGILKLAEEKK	F5
	Copper-exporting P-type ATPase	IEKNYGVRGMTTC*ASC*SQTVEK	F2
	Copper-transporting ATPase CopB	KVDVIM*M*DK	F2

M* methionine oxidation; C* carbamidomethylation of Cys.

Table S6. Peptides corresponding to other virulence factors, identified in the *Enterococcus* strains analyzed.

Function	Protein	Sequence	Strain
Alternative virulence factors	Transposase	EMDSLALANAQLNLDK	F5
	Transposase	EM*DSLALANAQLNLDK	F15
	Transposase	LVEMSTPLDIAIPFKK	F5
	Tnp_DDE superfamily	M*TIINATQYLKQLLSSELNRIGK	F15
	Tnp_DDE superfamily	MTIINATQYLKQLLSSELNRIGK	F16
	Tnp_DDE superfamily	M*FLLIFLLK	F2
	IS4 family transposase	RAFSLDKLIM*DAGYK	F5
	Transposase InsI for insertion sequence element IS30C	SRFLLAGRILK	F2
	IS30 family transposase	KDGLPKEM*DFNQVDQSFVYAVASLR	F14
	IS4 family transposase	QTIERIFSDEK	F13
	IS6 family transposase	LIRVYGQPRSIVTDK	F13
	Conjugative transposon protein	KVPM*IKVGTHK	F5
	Conjugal transfer protein TraG	M*AINNEDVTDFKAQRNK	F1
	Mutator family transposase	QTVSKEAIYIAI	F3
	Mutator family transposase	WIQVFDELK	F15
	Mutator family transposase	EEAM*DQISFMIDK	F2
	Integrase core domain protein	IESYYHQNIKIVK	F5
	Integrase core domain protein	GYPYHNASLESWHGHLK	F9
	Tyrosine-type recombinase/integrase	AWKFFQAYLGINPETGKSVK	F9
	Recombinase family protein	EGRPKKFNQQQINLAM*NLLEDHSYK	F9
	Tyrosine-type recombinase/integrase	C*PFTNEPPC*LSC*NNGNPC*K	F7
	<i>Enterococcus faecalis</i> plasmid pPD1 bacI	ETQKIADQLNSSGSQHNAGSYEFYDMAAMLK	F14
	Putative plasmid replication protein	TVLWSGVLHLADK	F2
	PrgI family protein	M*AVEVKVPKDIK	F1
	Pheromone response system RNA-binding regulator PrgU	M*EAVVEREAKGM*K	F3

	Regulatory protein RecX	GFSGDITNLVLANLELEIDEDLEKEALKK	F13
	Regulatory protein RecX	TNVRLSDKGPK	F2
	CRISPR-associated endonuclease Cas9	QSVSINQKLLKEK	F3
	CRISPR-associated endonuclease Cas10	KYRAFFGDNSVNGYAGYIEGHATQEDFYK	F9
	CRISPR-associated endonuclease Cas2	MSYRYMRM*ILM*FDM*PTETAEEER	F16
	YqaJ domain-containing protein	KKGIGGSDVGILGLNK	F1
	Luciferase family oxidoreductase, group 1	EAFPEDHLYSK	F1
Phage proteins	HK97 family phage major capsid protein (<i>Enterococcus</i> sp. 8G7_MSG3316)	AAAGTLTFAKNTIVSELAGVM*KK	F3
	Phage capsid protein (<i>Enterococcus casseliflavus</i>)	EAEERENEAAAR	F1
	Phage head protein gp7 (<i>Enterococcus</i> phage phiFL2A and <i>Enterococcus faecalis</i>)	M*DEIMAYVDK	F3
	Minor head protein (<i>Enterococcus casseliflavus</i>)	MNKEKIM*TDSFLGFDYR	F5
	Capsid protein (<i>Enterococcus villorum</i>)	EKDLEIAIEEAKTEEEQQVVEDEVNK	F5
	Long-tail fiber protein gp35 (<i>Enterococcus saccharolyticus</i>)	M*LLNISEKLM*AK	F13
	Phage tail protein (<i>Enterococcus faecium</i>)	LFMDDISQAMGEGADINLEF	F5
	Phage tail protein (<i>Enterococcus faecium</i>)	EMGITITNGRIEQNMDMFSESTRK	F7
	Phage tail tape measure protein (<i>Enterococcus avium</i>)	M*SSIGSTLTM*SVTAPIAAGFGAATK	F2
	Phage tail tape measure protein TP901 (<i>Enterococcus durans</i>)	GLAIASAIFGSM*SLLTGGLVVALGALIGALVVAY TK	F2
	Phage tail tape measure protein, TP901 family, core region (<i>Enterococcus faecalis</i>)	WGTDVGKATDGALTK	F3
	Phage tail tape measure protein (<i>Enterococcus avium</i> and <i>Enterococcus devriesei</i>)	GVQYM*NEYQDGVNTNAEK	F3
	Phage tail sheath (<i>Enterococcus</i> phage 163 , <i>Enterococcus</i> phage vB_OCPT_Ben, <i>Enterococcus</i> phage	IVQDVTTYNDK	F3

EfsSzw-1 , <i>Enterococcus</i> phage EFP01, <i>Enterococcus</i> phage EFDG1, <i>Enterococcus</i> phage PEF771, <i>Enterococcus</i> phage EfV12-phi1, <i>Enterococcus</i> phage 156)		
Phage tail tape measure protein (<i>Enterococcus faecium</i> , <i>Enterococcus hirae</i>)	IDMNNLMEASDVLSDIGDKLTELGK	F1
Phage tail tape measure protein, TP901 family, core region (<i>Enterococcus hermanniensis</i>)	EQTSEM*ITALGNLSEK	F1
Phage tail tape measure protein, TP901 family (<i>Enterococcus faecalis</i>)	KTPTSPFSDPK	F5
Phage tail tape measure protein (<i>Enterococcus hirae</i>)	VM*IEGIRSEQGQEQM*NHVMMDLQR	F5
Tail length tape-measure protein (<i>Enterococcus</i> phage PBEF129, <i>Enterococcus</i> phage EFLK1, <i>Enterococcus</i> phage phiEF17H , <i>Enterococcus</i> phage phiEF24C, <i>Enterococcus</i> phage vB_EfaM_Ef2.3, <i>Enterococcus</i> phage vB_EfaH_EF1TV, <i>Enterococcus</i> phage ECP3, <i>Enterococcus</i> phage 156, <i>Enterococcus</i> phage phiM1EF22)	TRAENNAEESANLSIYSK	F5
HK97 gp10 family phage protein (<i>Enterococcus faecalis</i>)	RSETPSIKDDGMTGEVEAMADYSAYVEYGTR	F1
Phage portal protein, HK97 family (<i>Enterococcus faecalis</i>)	EDGKDIKGAK	F5
Putative phage portal protein, SPP1 family (<i>Enterococcus faecalis</i>)	DLFLGNVSAKIKAPK	F3
Phage portal protein <i>Enterococcus gallinarum</i>	ITAHVWKFAMAVNTILC*GNSYSR	F3
Phage portal protein (<i>Enterococcus plantarum</i>)	AGSQLHIM*KGITPEITDEGIK	F5
Phage/plasmid primase, P4 family domain protein <i>Enterococcus faecium</i>	DM*IVTSEVLAKELEIK	F16
PBSX family phage terminase, large subunit (<i>Enterococcus faecalis</i>)	VNKSPM*KITYK	F15
Phage terminase large subunit	QFNTAYIEIAKKQGK	F3

(<i>Enterococcus cecorum</i> , <i>Enterococcus faecium</i>)		
Phage integrase (<i>Lactococcus garvieae</i>)	RTISRESLMLYR	F2
Phage_integrase domain-containing protein (<i>Enterococcus malodoratus</i>)	IANGAVEAM*VGK	F3
Site-specific recombinase, phage integrase family (<i>Enterococcus faecalis</i>)	AGEMIALTWSDIDFYNQTVR	F3
Phage integrase family protein (<i>Enterococcus faecium</i>)	VHQLTRVEIEAYLSELNMM*GIKPSTITGR	F5
Cro/CI family transcriptional regulator (<i>Enterococcus faecium</i>)	NLNIGNNIKNIR	F13
HTH cro/C1-type domain-containing protein (<i>Enterococcus</i> sp.)	M*LDSNVNMSYGGENLTEDEK	F14
HTH cro/C1-type domain-containing protein (<i>Enterococcus rotai</i>)	DYKALFLHC*AQNM*HDENK	F15
HTH cro/C1-type domain-containing protein (<i>Enterococcus saccharolyticus</i> subsp. <i>saccharolyticus</i>)	FIVSEDEKDFENTVISGHYQLKK	F16
HTH cro/C1-type domain-containing protein (<i>Enterococcus moraviensis</i>)	KKEYEEC*LYYLK	F1
Cro/CI family transcriptional regulator (<i>Enterococcus rotai</i> , <i>Enterococcus haemoperoxidus</i> , <i>Enterococcus caccae</i>)	ETSINVADFQNK	F13
XRE family transcriptional regulator (<i>Enterococcus thailandicus</i>)	EGTKMSLGDKLK	F10
XRE family transcriptional regulator (<i>Enterococcus termitis</i>)	DNIKQFLVDAK	F2
XRE family transcriptional regulator (<i>Enterococcus faecalis</i>)	MSQDLAIEVRAALIRAGK	F16
BppU family phage baseplate upper protein (<i>Enterococcus faecium</i>)	LGDLKPVEGLTDVWSLTITPTK	F2

	BppU_N domain-containing protein (<i>Enterococcus faecalis</i>)	DEIPDLSGGIITFESEPAGGK	F11
	phage infection protein YhgE/Pip domain-containing protein (<i>Enterococcus asini</i>)	RIAKSPVAVFLIVALM*ILPSLYAWFNIK	F13
	Uncharacterized protein (<i>Enterococcus</i> phage vB_EfaM_Ef2.3, <i>Enterococcus</i> phage phiEF24C, <i>Enterococcus</i> phage EFLK1, <i>Enterococcus</i> phage vB_EfaM_Ef2.1, <i>Enterococcus</i> phage 156)	YAQSMWKLANTIQQSGISR	F16
	Uncharacterized protein (<i>Enterococcus</i> phage LY0323, <i>Enterococcus</i> phage IME-EF4, <i>Enterococcus</i> phage vB_EfaS_AL2, <i>Enterococcus</i> phage Ec-ZZ2)	GNSKSFDPM*RAGQHDDVVVIESTEK	F15
	Uncharacterized protein (<i>Enterococcus hirae</i>)	KTM*TAILAEMTKK	F5
	Phage protein (<i>Enterococcus</i> phage 156)	KTNEEYLK	F3
	Uncharacterized protein gp54 (<i>Enterococcus</i> phage phiFL3A, <i>Enterococcus casseliflavus</i>)	LDEGIM*GLFVK	F2
	Membrane protein (<i>Enterococcus</i> phage heks)	DQHAANM*M*LDAM*IK	F3
	Phage-associated protein, HI1409 family (<i>Enterococcus faecalis</i>)	NDFM*LGNGK	F1

M* methionine oxidation; C* carbamidomethylation of Cys.

Table S7. Peptides corresponding to bacteriophage proteins, identified in the *Enterococcus* strains analyzed, that were determined as homologues to proteins found in different *Enterococcus* bacteriophages.

Bacteriophage protein	Bacteriophage	Peptide sequence	Strain
Phage head protein gp7	<i>Enterococcus</i> phage phiFL2A and <i>Enterococcus faecalis</i>	M*DEIMAYVDK	F3
Phage tail sheath	<i>Enterococcus</i> phage 163, <i>Enterococcus</i> phage vB_OCPT_Ben, <i>Enterococcus</i> phage EfsSzw-1, <i>Enterococcus</i> phage EFP01, <i>Enterococcus</i> phage EFDG1, <i>Enterococcus</i> phage	IVQDVTTYNDK	F3

	PEf771, <i>Enterococcus</i> phage EfV12-phi1, <i>Enterococcus</i> phage 156		
Tail length tape-measure protein	<i>Enterococcus</i> phage PBEF129, <i>Enterococcus</i> phage EFLK1, <i>Enterococcus</i> phage phiEF17H, <i>Enterococcus</i> phage phiEF24C, <i>Enterococcus</i> phage vB_EfaM_Ef2.3, <i>Enterococcus</i> phage vB_EfaH_EF1TV, <i>Enterococcus</i> phage ECP3, <i>Enterococcus</i> phage 156, <i>Enterococcus</i> phage phiM1EF22	TRAENNAEESANLSIYSK	F5
Uncharacterized protein	<i>Enterococcus</i> phage vB_EfaM_Ef2.3, <i>Enterococcus</i> phage phiEF24C, <i>Enterococcus</i> phage EFLK1, <i>Enterococcus</i> phage vB_EfaM_Ef2.1, <i>Enterococcus</i> phage 156	YAQSMWKLANTIQQSGISR	F16
Uncharacterized protein	<i>Enterococcus</i> phage LY0323, <i>Enterococcus</i> phage IME-EF4, <i>Enterococcus</i> phage vB_EfaS_AL2, <i>Enterococcus</i> phage Ec-ZZ2	GNSKSFDPM*RAGQHDTVVIESTEK	F15
Phage protein	Phage protein	KTNEEYLK	F3
Uncharacterized protein gp54	<i>Enterococcus</i> phage phiFL3A, <i>Enterococcus casseliflavus</i>	LDEGIM*GLFVK	F2
Membrane protein	<i>Enterococcus</i> phage heks	DQHAANM*M*LDAM*IK	F3

M* methionine oxidation; C* carbamidomethylation of Cys.