

Women's health is a team effort: probiogenomics supports the development of a multi-species vaginal probiotic

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Online Resource 2. Genes included in the custom database and NCBI accessions.

Vaginal adaption genes

Group	NCBI accession number	Annotation	Organism	Reference
Adhesion and Colonization	pdb 7BVX A	SpaCBA	<i>Lacticaseibacillus rhamnosus</i>	(F. Zhang et al., 2021)
Adhesion and Colonization	pdb 6M48 B	MSCRAMM family adhesin SdrC	<i>Lacticaseibacillus rhamnosus</i>	(F. Zhang et al., 2021)
Adhesion and Colonization	SPS13880.1	Collagen adhesin can	<i>Lactobacillus helveticus</i>	(F. Zhang et al., 2021)
Adhesion and Colonization	AAY41912.1	S-layer protein SlpA	<i>Lactobacillus crispatus</i>	(Sanozky-Dawes & Barrangou, 2022)
Adhesion and Colonization	AAY41916.1	S-layer protein SlpB	<i>Lactobacillus crispatus</i>	(Sanozky-Dawes & Barrangou, 2022)
Adhesion and Colonization	KAA8781809.1	S-layer protein SlpX	<i>Lactobacillus crispatus</i>	(Sanozky-Dawes & Barrangou, 2022)
Adhesion and Colonization	WP_270223762.1	Beta-N-acetylglucosaminidase AcnB S-layer	<i>Lactobacillus acidophilus</i>	(Sanozky-Dawes & Barrangou, 2022)
Adhesion and Colonization	AGT42024.1	Lectin-like protein 1	<i>Lacticaseibacillus rhamnosus</i>	(Petrova et al., 2016)
Adhesion and Colonization	WP_014569179.1	Lectin-like protein 2	<i>Lacticaseibacillus rhamnosus</i>	(Petrova et al., 2016)
Adhesion and Colonization	WP_239665380.1	Adhesin	<i>Lactobacillus</i>	(Dertli et al., 2016; Lebeer et al., 2008)
Antimicrobial Production and Microbial Interactions	WP_225907783.1	Lantibiotic dehydratase	<i>Lactobacillus crispatus</i>	(Darvishi et al., 2021)
Antimicrobial Production and Microbial Interactions	AAA88606.1	Nisin	<i>Lactococcus lactis</i>	(Darvishi et al., 2021)
Antimicrobial Production and	CAA87640.1	Mersacidin	<i>Bacillus sp.</i>	(Darvishi et al., 2021)

Microbial Interactions				
Antimicrobial Production and Microbial Interactions	QHM5128 9.1	Lysostaphin	<i>Lactiplantibacillus plantarum</i>	(Darvishi et al., 2021)
Antimicrobial Production and Microbial Interactions	WP_11232 4691.1	Pesticin	<i>Enterobacteriaceae</i>	(Darvishi et al., 2021)
Antimicrobial Production and Microbial Interactions	WP_22026 9064.1	Colicin	<i>Lactobacillus</i>	(Darvishi et al., 2021)
Antimicrobial Production and Microbial Interactions	WP_01089 0686.1	Lantibiotic lacticin	<i>Bacilli</i>	(Darvishi et al., 2021)
Antimicrobial Production and Microbial Interactions	WP_01100 5836.1	Lactocin 705 family bacteriocin	<i>Latilactobacillus</i>	(Darvishi et al., 2021)
Antimicrobial Production and Microbial Interactions	WP_19818 3798.1	Helveticin J family class III bacteriocin	<i>Lactobacillus</i>	(Darvishi et al., 2021)
Antimicrobial Production and Microbial Interactions	WP_27822 9227.1	lanthionine synthetase LanC family protein	<i>Lactococcus lactis</i>	(Perez et al., 2022)
Antimicrobial Production and Microbial Interactions	VTU64604 .1	Pediocin PapC-like protein	<i>Lacticaseibacillus rhamnosus</i>	(Perez et al., 2022)
Antimicrobial Production and Microbial Interactions	WP_08914 4005.1	enterocin L50 family leaderless bacteriocin	<i>Bacilli</i>	(Perez et al., 2022)
Antimicrobial Production and Microbial Interactions	ALJ02606.1	Plantaricin	<i>Lactiplantibacillus plantarum</i>	(Perez et al., 2022)
Antimicrobial Production and Microbial Interactions	pdb 1OHN A	Sakacin chain A	<i>Latilactobacillus sakei</i>	(Perez et al., 2022)
Carbohydrate metabolism in the vaginal environment	CAX67156 .1	inulosucrase InuJ	<i>Lactobacillus johnsonii</i>	(J. Zhang et al., 2022)

Carbohydrate metabolism in the vaginal environment	RXF55115.1	Levansucrase (InuCA e InRA)	<i>Lactobacillus crispatus</i>	(J. Zhang et al., 2022)
Carbohydrate metabolism in the vaginal environment	KAA9244007.1	Sialidase	<i>Lactobacillus mulieris</i>	(Ferreira et al., 2022)
Carbohydrate metabolism in the vaginal environment	GMB71175.1	Amylopullulanase	<i>Lacticaseibacillus rhamnosus</i>	(Hertzberger et al., 2022)
Carbohydrate metabolism in the vaginal environment	WP_052542819.1	Type I pullulanase pulA	<i>Lactobacillus</i>	(Hertzberger et al., 2022)
Carbohydrate metabolism in the vaginal environment	BBD47863.1	Alpha-amylase	<i>Lactobacillus paragasseri</i>	(Nunn et al., 2020)
Carbohydrate metabolism in the vaginal environment	KRK35887.1	Glucan 1,6-alpha-glucosidase	<i>Lactobacillus crispatus</i>	(Nunn et al., 2020)
Carbohydrate metabolism in the vaginal environment	GBA94374.1	Oligo-1,6-glucosidase	<i>Lactobacillus gasseri</i>	(Nunn et al., 2020)
Carbohydrate metabolism in the vaginal environment	EEU19064.1	Intracellular maltogenic amylase	<i>Lactobacillus crispatus</i>	(Nunn et al., 2020)
Carbohydrate metabolism in the vaginal environment	CAA0276191.1	Trehalose synthase/amylase TreS	<i>Klebsiella oxytoca</i>	(Nunn et al., 2020)
Carbohydrate metabolism in the vaginal environment	CAH9055892.1	Glycogen operon protein GlgX	<i>Pseudoalteromonas haloplanktis</i>	(Nunn et al., 2020)
Carbohydrate metabolism in the vaginal environment	KWU04919.1	Pullulanase	<i>Lactobacillus crispatus</i>	(Nunn et al., 2020)
Carbohydrate metabolism in the vaginal environment	KRK32829.1	Neopullulanase	<i>Lactobacillus crispatus</i>	(Nunn et al., 2020)
Carbohydrate metabolism in	WP_013439216.1	UTP--glucose-1-phosphate	<i>Lactobacillus</i>	(F. Zhang et al., 2021)

the vaginal environment				
Carbohydrate metabolism in the vaginal environment	CBJ19544.1	Glucosyltransferase gtf	<i>Lentilactobacillus hilgardii</i>	(Dertli et al., 2016; Lebeer et al., 2008)
Degradation of biogenic amines	EEL71807.1	Putrescine aminotransferase	<i>Bacillus mycoides</i>	(Guarcello et al., 2016; Puebla-Barragan et al., 2021)
Host Interaction and Immunomodulation	WP_198194524.1	SLAP domain-containing protein	<i>Lactobacillus</i>	(Sanozky-Dawes & Barrangou, 2022)
Host Interaction and Immunomodulation	WP_198182809.1	UDP-GlcNAc/MurNAc family	<i>Lactobacillus</i>	(Chee et al., 2020)
Host Interaction and Immunomodulation	WP_089147280.1	LTA synthase family protein	<i>Lactobacillus</i>	(Chee et al., 2020)
Host Interaction and Immunomodulation	UQD53807.1	Biosurfactants production protein	<i>Bacillus methanolicus</i>	(Chee et al., 2020)
Host Interaction and Immunomodulation	WP_005687638.1	Peptidoglycan hydrolase Msp1	<i>Lactocaseibacillus rhamnosus</i>	(Chee et al., 2020)
Host Interaction and Immunomodulation	CUS16278.1	S-ribosylhomocysteine lyase / quorum-sensing autoinducer 2 (AI-2) synthesis protein LuxS	<i>Lactobacillus delbrueckii subsp. Bulgaricus</i>	(Dertli et al., 2016; Lebeer et al., 2008)
Production of biogenic amines	WP_002319546.1	Tyrosine decarboxylase	<i>Enterococcus</i>	(Guarcello et al., 2016)
Production of biogenic amines	CBX24604.1	Histidine decarboxylase	<i>Streptococcus thermophilus</i>	(Guarcello et al., 2016)
Production of biogenic amines	WP_001292415.1	Ornithine decarboxylase	<i>Escherichia</i>	(Guarcello et al., 2016)
Production of biogenic amines	WP_001295383.1	Lysine decarboxylase	<i>Enterobacteriaceae</i>	(Guarcello et al., 2016)
Production of biogenic amines	WP_009911777.1	Agmatine deiminase	<i>Listeria monocytogenes</i>	(Guarcello et al., 2016)
Production of biogenic amines	WP_001381593.1	Arginine decarboxylase	<i>Enterobacteriaceae</i>	(Guarcello et al., 2016)
Production of biogenic amines	BAM13386.1	Arginine racemase	<i>Pseudomonas taetrolens</i>	(Guarcello et al., 2016)

Production of biogenic amines	BBG56304.1	Lysine racemase	<i>Leuconostoc mesenteroides</i>	(Guarcello et al., 2016; Puebla-Barragan et al., 2021)
Stress Response and Survival	WP_001189647.1	Multicopper oxidase	<i>Enterobacteriaceae</i>	(Guarcello et al., 2016; Puebla-Barragan et al., 2021)
Stress Response and Survival	ABM21381.1	Eps transcriptional regulator	<i>Lactobacillus johnsonii</i>	(Dertli et al., 2016; Lebeer et al., 2008)
Stress Response and Survival	WP_394857538.1	MMPL transporter FarE	<i>Staphylococcus aureus</i>	(Zhu et al. 2024)
Stress Response and Survival	gi 489752033 ref WP_003656035.1	MMPL family transporter	<i>Lactobacillus sp.</i>	(Zhu et al. 2024)
Stress Response and Survival	SNX31820.1	oleate hydratase	<i>Limosilactobacillus fermentum</i>	(Zhu et al. 2024)

Probiotic factor genes

Functional group	NCBI accession number	Annotation	Reference
Mechanisms of active response to stress related to GIT passage	AAD01782.1	ClpE [<i>Lactococcus cremoris</i> subsp. <i>cremoris</i> MG1363]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAG44707.1	EpsC [<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAG44708.1	EpsD [<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAG44709.1	phospho-glucosyltransferase EpsE [<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAG44712.1	beta(1,3)galactosyltransferase EpsH [<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAK64290.2	ClpL [<i>Lacticaseibacillus rhamnosus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAS08038.1	conjugated bile salt hydrolase [<i>Lactobacillus johnsonii</i> NCC 533]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAS08969.1	conjugated bile salt hydrolase [<i>Lactobacillus johnsonii</i> NCC 533]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAS09179.1	ABC transporter ATPase component [<i>Lactobacillus johnsonii</i> NCC 533]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAS09244.1	hypothetical protein LJ_1476 [<i>Lactobacillus johnsonii</i> NCC 533]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAV42845.1	amino acid permease [<i>Lactobacillus acidophilus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAV43253.1	hypothetical protein LBA1428 [<i>Lactobacillus acidophilus</i> NCFM]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAV43254.1	putative transporter-membrane protein [<i>Lactobacillus acidophilus</i> NCFM]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAV43256.1	two-component response regulator [<i>Lactobacillus acidophilus</i> NCFM]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAV43257.1	hypothetical protein LBA1432 [<i>Lactobacillus acidophilus</i> NCFM]	Leeber et al., 2008

Mechanisms of active response to stress related to GIT passage	AAV43343 .1	two-component sensor histidine kinase [<i>Lactobacillus acidophilus</i> NCFM]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAV43545 .1	phospho-glucosyltransferase [<i>Lactobacillus acidophilus</i> NCFM]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAV43548 .1	exopolysaccharide biosynthesis protein [<i>Lactobacillus acidophilus</i> NCFM]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AAV41912 .1	SlpA [<i>Lactobacillus crispatus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ABB59702 .1	EpsE [<i>Lactobacillus helveticus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ABC59818 .1	LuxS [<i>Lactocaseibacillus rhamnosus</i> GG]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ABD96538 .1	epsJ [<i>Streptococcus thermophilus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ABO43774 .1	ClpE [<i>Limosilactobacillus reuteri</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ABQ95536 .1	LuxS [<i>Limosilactobacillus reuteri</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ABS84230. 1	multidrug resistance (MDR) ABC transporter ATP-binding and permease protein, partial [<i>Limosilactobacillus reuteri</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ABX27751 .1	LuxS [<i>Lactobacillus helveticus</i> DPC 4571]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ACB28477 .1	LuxS [<i>Streptococcus suis</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AEA56341 .1	S-ribosylhomocysteinase [<i>Lactocaseibacillus paracasei</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AGK94888 .1	Tyrosine-protein kinase EpsD [<i>Lactobacillus acidophilus</i> La-14]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AGT21521 .1	S-ribosylhomocysteinase luxS [<i>Lactiplantibacillus plantarum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AHI39593. 1	ATP-dependent Clp protease, ATP-binding subunit ClpL [<i>Enterococcus faecalis</i> DENG1]	Leeber et al., 2008

Mechanisms of active response to stress related to GIT passage	AHN70215 .1	DNA starvation/stationary phase protection protein Dps [<i>Lactiplantibacillus plantarum</i> DOMLa]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AJP46403. 1	ornithine decarboxylase [<i>Lactobacillus acidophilus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AJP46761. 1	histidine kinase [<i>Lactobacillus acidophilus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AJP47033. 1	glycosyltransferase [<i>Lactobacillus acidophilus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AKH34865 .1	ClpE [<i>Streptococcus thermophilus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AKM5175 8.1	epsH [<i>Limosilactobacillus fermentum</i> 3872]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AOR73929 .1	DNA starvation/stationary phase protection protein Dps [<i>Limosilactobacillus fermentum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ARB50240 .1	bile salt hydrolase [<i>Lactobacillus gasseri</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AUO27119 .1	low molecular weight protein-tyrosine-phosphatase Wzb [<i>Limosilactobacillus fermentum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AWD6141 9.1	Clp ATPase [<i>Limosilactobacillus reuteri</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	AYN50070 .1	Putative glycosyltransferase EpsE [<i>Lactobacillus johnsonii</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	BBA82415 .1	copper-transporting ATPase [<i>Lactiplantibacillus plantarum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CAI97829. 1	Putative fibronectin-binding protein [<i>Lactobacillus delbrueckii subsp. bulgaricus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CAQ67279 .1	ClpL [<i>Lactocaseibacillus paracasei</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CAR88394 .1	ClpL [<i>Lactocaseibacillus paracasei</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CAX67044 .1	epsA [<i>Lactobacillus johnsonii</i> FI9785]	Leeber et al., 2008

Mechanisms of active response to stress related to GIT passage	CCE46032.1	mannose specific adhesin, partial [<i>Limosilactobacillus fermentum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CDF66781.1	Copper-transporting ATPase [<i>Lactobacillus acidophilus</i> DSM 20079 = JCM 1132 = NBRC 13951 = CIP 76.13]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CDF67676.1	Bile salt hydrolase [<i>Lactobacillus acidophilus</i> DSM 20079 = JCM 1132 = NBRC 13951 = CIP 76.13]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CDI59344.1	Bile salt hydrolase [<i>Lactobacillus helveticus</i> CIRM-BIA 951]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CDR84439.1	DNA starvation/stationary phase protection protein Dps [<i>Lactobacillus delbrueckii subsp. lactis</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CUR37483.1	Tyrosine-protein kinase EpsD [<i>Limosilactobacillus reuteri</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	CYV39199.1	putative ATP-dependent protease ATP-binding subunit ClpL [<i>Streptococcus suis</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	EEU19018.1	ATP-dependent Clp protease ATP-binding subunit ClpE [<i>Lactobacillus crispatus</i> 125-2-CHN]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	EEW52510.1	fibronectin-binding protein (FnBP) A domain protein [<i>Lactobacillus iners</i> DSM 13335]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	EEW69041.1	fibronectin-binding protein (FnBP) A domain protein [<i>Lactobacillus helveticus</i> DSM 20075 = CGMCC 1.1877]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	EFQ44947.1	fibronectin-binding protein (FnBP) A domain protein [<i>Lactobacillus crispatus</i> CTV-05]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	EFQ46198.1	fibronectin-binding protein (FnBP) A domain protein [<i>Lactobacillus gasseri</i> MV-22]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	EGD27294.1	DNA starvation/stationary phase protection protein Dps [<i>Lactobacillus delbrueckii subsp. lactis</i> DSM 20072]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	EGF35484.1	copper-transporting atpase [<i>Lactobacillus helveticus</i> MTCC 5463]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	EHM3365 9.1	ClpE [<i>Enterococcus faecium</i> E4453]	Leeber et al., 2008

Mechanisms of active response to stress related to GIT passage	EHS83684.1	ATP-dependent Clp protease, ATP-binding subunit ClpE [<i>Lactiplantibacillus plantarum</i> subsp. <i>plantarum</i> NC8]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ELA79786.1	ATP-dependent Clp protease ATP-binding subunit ClpL [<i>Enterococcus faecium</i> EnGen0004]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ERL65647.1	ClpC [<i>Schleiferilactobacillus shenzhenensis</i> LY-73]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	ERL66139.1	ClpE [<i>Schleiferilactobacillus shenzhenensis</i> LY-73]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	GAN41145.1	copper-transporting ATPase [<i>Lacticaseibacillus paracasei</i> NRIC 1981]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	GDZ84074.1	S-ribosylhomocysteine lyase luxS [<i>Leuconostoc citreum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	GEL33985.1	ATP-dependent Clp protease ATP-binding subunit ClpC [<i>Lactiplantibacillus plantarum</i> subsp. <i>plantarum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	GFP01202.1	cell division protein [<i>Lactobacillus helveticus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	GFP15270.1	ATP-dependent Clp protease ATP-binding subunit ClpC [<i>Lactobacillus helveticus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	GHN19320.1	ATP-dependent Clp protease ATP-binding subunit [<i>Lactobacillus delbrueckii</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	KPH21867.1	copper-transporting ATPase [<i>Limosilactobacillus fermentum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	KRK29711.1	mucus binding protein [<i>Lactobacillus acidophilus</i> DSM 20079 = JCM 1132 = NBRC 13951 = CIP 76.13]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	KRK44693.1	copper-transporting ATPase [<i>Lactobacillus amylovorus</i> DSM 20531]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	KRK59947.1	DNA starvation stationary phase protection protein Dps [<i>Limosilactobacillus antri</i> DSM 16041]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	KRK74393.1	DNA starvation stationary phase protection protein Dps [<i>Lacticaseibacillus nasuensis</i> JCM 17158]	Leeber et al., 2008

Mechanisms of active response to stress related to GIT passage	KRM8463 2.1	DNA starvation stationary phase protection protein Dps [<i>Lactobacillus hominis</i> DSM 23910 = CRBIP 24.179]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	PMC47034 .1	DNA starvation/stationary phase protection protein Dps [<i>Lactobacillus iners</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	QAS50172 .1	ATP-dependent Clp protease ATP-binding subunit ClpC [<i>Latilactobacillus curvatus</i> JCM 1096 = DSM 20019]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	QHM3891 9.1	putative sugar transferase EpsL (plasmid) [<i>Lactiplantibacillus plantarum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	QPP16258. 1	glutamate:gamma-aminobutyrate (Glu/GABA) antiporter [<i>Lactobacillus crispatus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	RNE38687 .1	putative sugar transferase EpsL [<i>Lactocaseibacillus paracasei</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	SPS15181. 1	putative sugar transferase EpsL [<i>Lactobacillus helveticus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	SPX68388. 1	ATP-dependent Clp protease ATP-binding subunit ClpL [<i>Lactiplantibacillus plantarum</i> subsp. <i>plantarum</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	UHX60220 .1	bile salt hydrolase [<i>Lactobacillus johnsonii</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	UUZ04888 .1	BSHa [<i>Lactobacillus johnsonii</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	UZZ85054. 1	S-layer protein [<i>Lactobacillus crispatus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_01925 2340.1	D-alanyl-lipoteichoic acid biosynthesis protein DltD [<i>Limosilactobacillus reuteri</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_01989 8995.1	peptide-methionine (R)-S-oxide reductase MsrB [<i>Lactocaseibacillus paracasei</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_04858 8304.1	D-alanine--poly(phosphoribitol) ligase subunit DltA [<i>Lactobacillus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_10414 2777.1	peptide-methionine (R)-S-oxide reductase MsrB [<i>Lactococcus lactis</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_10483 2728.1	peptide-methionine (R)-S-oxide reductase MsrB [<i>Enterococcus faecium</i>]	Leeber et al., 2008

Mechanisms of active response to stress related to GIT passage	WP_109241568.1	peptide-methionine (R)-S-oxide reductase MsrB [<i>Ligilactobacillus salivarius</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_109918411.1	peptide-methionine (R)-S-oxide reductase MsrB [<i>Lactobacillus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_118980074.1	peptide-methionine (R)-S-oxide reductase MsrB [<i>Lactobacillus delbrueckii</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_153232390.1	peptide-methionine (R)-S-oxide reductase MsrB [<i>Lactobacillus gasseri</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_195212129.1	adhesin [<i>Lactobacillus</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_220437225.1	peptide-methionine (R)-S-oxide reductase MsrB [<i>Lactococcus raffinolactis</i>]	Leeber et al., 2008
Mechanisms of active response to stress related to GIT passage	WP_229036516.1	adhesin [<i>Lactobacillus</i>]	Leeber et al., 2008
Shikimate and folate biosynthesis pathway (CHORISMATE)	QJU49979.1	3-deoxy-7-phosphoheptulonate synthase [<i>Lactiplantibacillus paraplantarum</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (CHORISMATE)	SFE47508.1	3-dehydroquinate synthase [<i>Lactobacillus rogosa</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (CHORISMATE)	EIW13109.1	3-dehydroquinate dehydratase I [<i>Lactiplantibacillus pentosus</i> KCA1]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (CHORISMATE)	WP_172985744.1	Shikimate dehydrogenase [<i>Lactobacillus</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (CHORISMATE)	WP_072544160.1	Shikimate kinase [<i>Lactobacillus</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (CHORISMATE)	CUS17452.1	3-phosphoshikimate 1-carboxyvinyltransferase [<i>Lactobacillus delbrueckii subsp. bulgaricus</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (CHORISMATE)	WP_231128327.1	Chorismate synthase [<i>Lactobacillus</i>]	D'Aimmo et al., 2023

Shikimate and folate biosynthesis pathway (para-aminobenzoic acid, PABA)	QJU49551.1	Aminodeoxychorismate synthase [<i>Lactiplantibacillus paraplantarum</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (para-aminobenzoic acid, PABA)	GBA87487.1	Aminodeoxychorismate lyase [<i>Lactobacillus paragasseri</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (6-hydroxymethyl-7,8-dihydropterin pyrophosphate, DHPPP)	QAA29097.1	Dihydroneopterin triphosphate diphosphatase [<i>Lactiplantibacillus plantarum</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (6-hydroxymethyl-7,8-dihydropterin pyrophosphate, DHPPP)	WP_261937608.1	Dihydroneopterin aldolase [<i>Lactobacillus</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (6-hydroxymethyl-7,8-dihydropterin pyrophosphate, DHPPP)	KRL59967.1	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase [<i>Lactobacillus</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (tetrahydrofolate, THF)	WP_172985600.1	Dihydropteroate synthase [<i>Lactobacillus</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (tetrahydrofolate, THF)	QJU51066.1	Dihydrofolate synthase [<i>Lactiplantibacillus paraplantarum</i>]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (tetrahydrofolate, THF)	KRK54541.1	Tetrahydrofolate synthase [<i>Lactobacillus johnsonii</i> ATCC 33200]	D'Aimmo et al., 2023
Shikimate and folate biosynthesis pathway (tetrahydrofolate, THF)	WP_172985207.1	Dihydrofolate reductase [<i>Lactobacillus</i>]	D'Aimmo et al., 2023
Tryptophan pathway	ASW11534.1	Aromatic amino acid aminotransferase [<i>Lactobacillus delbrueckii subsp. lactis</i>]	Pan et al., 2023
Tryptophan pathway	ALT48283.1	Lactate dehydrogenase [<i>Lactobacillus delbrueckii subsp. lactis</i>]	Pan et al., 2023
Tryptophan pathway	sp J7SHB8.1	Indolelactate dehydrogenase [<i>Clostridium sporogenes</i>]	Pan et al., 2023
Tryptophan pathway	VDG20848.1	Cinnamoyl-coa--phenyllactate coa-transferase [<i>Lactiplantibacillus mudanjiangensis</i>]	Pan et al., 2023
Tryptophan pathway	sp Q93AM0.1	Phenyllactate dehydratase activator [<i>Clostridium sporogenes</i>]	Pan et al., 2023

Tryptophan pathway	GEK41904.1	Indolepyruvate decarboxylase [<i>Ligilactobacillus aviarius</i>]	Pan et al., 2023
Tryptophan pathway	AEO49255.1	Phenylpyruvate decarboxylase [<i>Rhodospirillum rubrum</i>]	Pan et al., 2023
Tryptophan pathway	GHN33536.1	Aldehyde dehydrogenase [<i>Lactobacillus delbrueckii</i>]	Pan et al., 2023
Tryptophan pathway	POD81577.1	Tryptophan 2-monooxygenase [<i>Lactiplantibacillus paraplantarum</i>]	Pan et al., 2023
Tryptophan pathway	GEB91345.1	Amidase [<i>Lactobacillus delbrueckii subsp. lactis</i>]	Pan et al., 2023
Tryptophan pathway	WPX87954.1	Tryptophan decarboxylase [<i>Pseudomonas asiatica</i>]	Pan et al., 2023
Tryptophan pathway	BEC98836.1	Diamine oxidase [<i>Escherichia coli</i>]	Pan et al., 2023
Tryptophan pathway	sp J7TF92.1	3-(aryl)acrylate reductase [<i>Clostridium sporogenes</i>]	Pan et al., 2023
Tryptophan pathway	KAA9236053.1	Copper amine oxidase [<i>Lactobacillus jensenii</i>]	Pan et al., 2023
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_102732122.1	Glycosyl hydrolase family 2 (GH2) [<i>A. muciniphila</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_102727023.1	Glycosyl hydrolase family 2 (GH2) [<i>Akkermansia</i> sp. CAG: 344]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	CDA71244.1	Glycosyl hydrolase family 2 (GH2) [<i>B. coprocola</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_130053801.1	Glycosyl hydrolase family 2 (GH2) [<i>B. dorei</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_005822521.1	Glycosyl hydrolase family 2 (GH2) [<i>B. fragilis</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_055167711.1	Glycosyl hydrolase family 2 (GH2) [<i>Bacteroides</i> spp.]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_025866948.1	Glycosyl hydrolase family 2 (GH2) [<i>B. nordii</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	EDO11197.1	Glycosyl hydrolase family 2 (GH2) [<i>B. ovatus</i>]	(Ervin et al., 2019)

Host Interaction and Immunomodulation (estrogen deconjugation)	WP_00429 8526.1	Glycosyl hydrolase family 2 (GH2) [<i>B. ovatus</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_11758 8613.1	Glycosyl hydrolase family 2 (GH2) [<i>Bacteroides</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_12237 5735.1	Glycosyl hydrolase family 2 (GH2) [<i>Parabacteroides</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_01627 2112.1	Glycosyl hydrolase family 2 (GH2) [<i>Bacteroides</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_02250 2167.1	beta-glucuronidase (GUS) [<i>Lachnospira</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_06671 4276.1	beta-glucuronidase (GUS) [<i>Clostridium</i> sp. Marseille-P299]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_00155 1153.1	beta-glucuronidase (GUS) [<i>Enterobacteriaceae</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	CDA40053 .1	Glycosyl hydrolase family 2 (GH2) [<i>Eubacterium eligens</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	HCG85850 .1	Glycosyl hydrolase family 2 (GH2) [<i>Faecalibacterium</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	SCH31850. 1	beta-glucuronidase (GUS) [uncultured <i>Faecalibacterium</i> sp.]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_09777 4993. 1	beta-glucuronidase (GUS) [<i>F. prausnitzii</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_06915 2983.1	Glycosyl hydrolase family 2 (GH2) [<i>Eisenbergiella tayi</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	CBK98066 .1	beta-glucuronidase (GUS) [<i>F. prausnitzii</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	CBJ55484. 1	beta-glucuronidase (GUS) [uncultured bacterium]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	HAN02355 .1	beta-glucuronidase (GUS) [<i>Lactobacillus</i> sp.]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	HBH98519 .1	beta-glucuronidase (GUS) [<i>L. rhamnosus</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_12220 5889.1	Glycosyl hydrolase family 2 (GH2) [<i>Parabacteroides</i>]	(Ervin et al., 2019)

Host Interaction and Immunomodulation (estrogen deconjugation)	WP_010800018.1	Glycosyl hydrolase family 2 (GH2) [<i>Prevotella</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_118445354.1	beta-glucuronidase (GUS) [<i>Ruminococcus gnavus</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_118587093	Glycosyl hydrolase family 2 (GH2) [<i>Roseburia inulinivorans</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_118581144.1	Glycosyl hydrolase family 2 (GH2) [<i>Roseburia inulinivorans</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_118096903.1	Glycosyl hydrolase family 2 (GH2) [<i>R. hominis</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	WP_055167711.1	Glycosyl hydrolase family 2 (GH2) [<i>Clostridia</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	CDE36900.1	Glycosyl hydrolase family 2 (GH2) [<i>Eubacterium</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (estrogen deconjugation)	CDE18721.1	beta-glucuronidase (GUS) [<i>Acidiphilium sp.</i>]	(Ervin et al., 2019)
Host Interaction and Immunomodulation (Steroid hormones degradation)	pdb 1HXX A	Chain A, 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE [<i>Comamonas testosteroni</i>]	(Li et al., 2021)
Host Interaction and Immunomodulation (Steroid hormones degradation)	pdb 1HXX B	Chain B, 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE [<i>Comamonas testosteroni</i>]	(Li et al., 2021)
Host Interaction and Immunomodulation (Steroid hormones degradation)	pdb 1HXX C	Chain C, 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE [<i>Comamonas testosteroni</i>]	(Li et al., 2021)
Host Interaction and Immunomodulation (Steroid hormones degradation)	pdb 1HXX D	Chain D, 3BETA/17BETA-HYDROXYSTEROID DEHYDROGENASE [<i>Comamonas testosteroni</i>]	(Li et al., 2021)